XVI ANNUAL CONVENTION

OF INDIAN SOCIETY OF ANIMAL GENETICS AND BREEDING

and National Conference on
Innovations in Animal Genetics &
Breeding for sustainable productivity of
livestock and poultry

2nd & 3rd December 2022

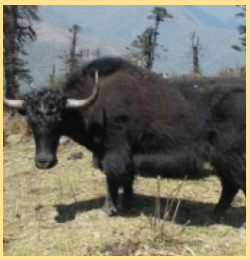
ISAGBCON2022

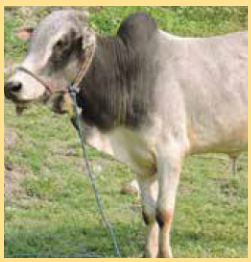




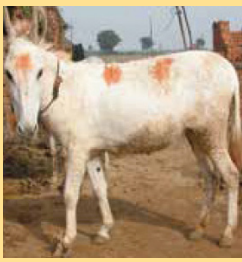












Organized by

Indian Society of Animal Genetics and Breeding

&

ICAR-Directorate of Poultry Research

Rajendranagar, Hyderabad, Telangana-500030, India

Supported by NABARD

ISAGBCON 2022, ICAR-DPR

HYDERABAD

XVI Annual Convention of Indian Society of Animal Genetics and Breeding

and

National Conference on

Innovations in Animal Genetics & Breeding for sustainable productivity of livestock and Poultry

Organized by

ICAR Directorate of Poultry Research, Hyderabad

In Collaboration with

Indian society of Animal Genetics and Breeding

ICAR-DPR, Hyderabad | December 2-3, 2022

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परशोत्तम रूपाला
PARSHOTTAM RUPALA

सत्यमेव जयते

आज़ादी का अमृत महोत्सव

मंत्री
मत्स्यपालन, पशुपालन एवं डेयरी
भारत सरकार
MINISTER
FISHERIES, ANIMAL HUSBANDRY & DAIRYING
GOVERNMENT OF INDIA

D.O. No. 1485 MIN(FAH&D)/2022-23

09 NOV 2022

MESSAGE

I am glad to know that ICAR-Directorate of Poultry Research (ICAR-DPR), Hyderabad is organizing the XVI Annual Convention of Indian Society of Animal Genetics & Breeding (ISAGB) and a National Conference on "Innovations in Animal Genetics & Breeding for Sustainable Productivity of Livestock and Poultry" during the 2nd & 3rd December 2022.

The current world population is expected to reach 9.8 billion by 2050 and providing balanced nutritional security for all the people is going to be a major challenge. The agriculture productivity and total production needs to be greatly improved by using advanced research methodologies. I strongly believe that the deliberations during the Conference will help the Agriculture Sector to meet the challenges of the farming community and address the needs of the farmers to enable India to become a Global Leader in Agriculture.

I congratulate ICAR-DPR and wish the Conference a grand success.

(Parshottam Rupala)

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MESSAGE

I am extremely delighted to know that the XVI Annual Convention of ISAGB and a National Conference on "Innovations in Animal Genetics & Breeding for sustainable productivity of livestock and poultry" is being organized at ICAR-DPR, Hyderabad during 2nd & 3rd December 2022.

India is the world's 8th most biodiverse region with 1, 02,718 species of fauna and 23.39% of the nation's geographical area under forest and tree cover. These hotspots have numerous endemic species. India as an agriculture-based country needs the immense contribution of our well-recognized breeds/population of livestock and poultry to maintain and augment the livelihood of rural and peri-urban farmers/animal keepers, who are mostly landless and marginal. But, production levels of these breeds are not up to the mark to mitigate the ever-increasing demands of human beings. However, to make these breeds more productive and economical, systematic innovative breeding and genetic strategies are to be pursued with utmost commitment and dedication. It is, therefore, highly appropriate to discuss, deliberate, and come up with suitable strategies for improving livestock production, productivity, and conservation of genetic resources.

This conference would allow scientists, policymakers, and research administrators to exchange ideas and explore the possible avenues to meet the challenges in amalgamating conventional and novel technologies in the context of globalization and the open market. Therefore, viewed from this perspective, the deliberations of this conference, I am sure, would give a definite direction to the researchers and policymakers to bring about positive changes in the livestock sector in such a way that it provides nutritional and financial security to the teeming millions of the country in the coming years.

(PROF. V. RAVINDER REDDY)

Indian Society of Animal Genetics and Breeding
Animal Science Division, Room No. 409, ICAR, Krishi Bhavan, Dr. Rajendra Prasad Road, New Delhi-110001

MESSAGE

F. No: ISAGB/2022-23/
Dated: 25.11.2022

I strongly believe that the XVI Annual Convention of Indian Society of Animal Genetics and Breeding (ISAGBCON 2022) and "National Conference on Innovations in Animal Genetics & Breeding for sustainable productivity of livestock and poultry" will be an excellent opportunity for the delegates to interact with eminent speakers and peers in the field. I am sure that the national conference will address the various contemporary research needs and ensure thought provoking dialogue between researchers, academicians, policy makers, industry and all other stakeholders regarding the appropriate strategies that need to be devised and implemented for sustainable utilization and improvement of livestock and poultry.

I congratulate the organizing committee for their sincere efforts in scrupulously designing the technical sessions of the conference keeping in view the latest trends and future scope of innovative breeding technologies as well about the genomics, phenotype variability and trait expression in animals. Wishing the National conference all the best and the delegates a fruitful learning experience.

I wish the ISAGBCON-2022 a grand success!

(B P Mishra)
President, ISAGB

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भाकृअनुप - कुककुट अनुसंधान तनदेशालय

ICAR-DIRECTORATE OF POULTRY RESEARCH

(Receipent of Sardar Patel Best Outstanding Institute Award for the year 2013)

भारतीयकृषिअनुसंधानपरिषद, कृषि अनुसंधान एवं शिक्षा विभाग

Indian Council of Agricultural Research, Department of Agricultural Research & Education

कृषि एवं किसान कल्याण मंत्रालय, भारत सरकार

MINISTRY OF AGRICULTURE& FARMERS WELFARE, GOVERNMENT OF INDIA

राजेंद्रनगर, हैदराबाद 500 030 तेलंगाना, भारत

Rajendranagar, Hyderabad 500 030 Telangana, India

Dr. R.N. Chatterjee

Director

MESSAGE

It is a matter of pride that Indian Society of Animal Genetics and Breeding has chosen ICAR-Directorate of Poultry Research, Rajendranagar, Hyderabad as the host institute for organizing the national conference on "Innovations in Animal Genetics and Breeding for sustainable productivity of livestock and poultry" and XVI Annual Convention of the Indian Society of Animal Genetics and Breeding during 2nd and 3rd December 2022. This institute is mandated to carry out basic and applied research to enhance productivity of poultry, develop new germplasm for rural poultry husbandry and capacity building. The conference will provide a platform to review achievements vis-a-vis challenges in the field of animal genetics and breeding, facilitate dialogue and exchange of ideas among researchers, academicians, policy makers, industry leaders and all other stakeholders regarding identification of strategies needed for sustainable management and improvement of animal genetic resources of the country. I would like to take this opportunity to thank the organizing committee for their sincere efforts in meticulously designing the technical sessions of the conference in tune with the latest advancement in the field. I warmly welcome all the delegates and life members of the society from different parts of the country to this conference and wish the conference a grand success

(R.N. Chatterjee

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ISO Certified 9001:2015
ICAR-DIRECTORATE OF POULTRY RESEARCH
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Indian Council of Agricultural Research, Department of Agricultural Research & Education
कृषि एवं किसान कल्याण मंत्रालय, भारत सरकार
MINISTRY OF AGRICULTURE& FARMERS WELFARE, GOVERNMENT OF INDIA
राजेंद्रनगर, हैदराबाद 500 030 तेलंगाना, भारत
Rajendranagar, Hyderabad 500 030 Telangana, India

MESSAGE

It's a great honour and privilege to organize the XVI Annual Convention of Indian Society of Animal Genetics and Breeding (ISAGBCON2022) and National Conference on Innovations in Animal Genetics & Breeding for sustainable productivity of livestock and poultry during 2nd & 3rd December 2022. India as an agriculture-based country needs immense contribution of the well-recognized breeds/population of livestock and poultry to maintain and augment livelihood of farmers who are mostly landless and marginal. But, production levels of these breeds are not up to the mark to mitigate the ever-increasing demands of human beings. However, to make these breeds more productive and economical, systematic innovative breeding and genetic strategies are to be pursued with utmost commitment and dedication. Integration of the latest innovative technologies with the conventional approaches is very much essential for rapid and sustainable genetic gains in our indigenous breeds. The technical sessions of this National conference have been meticulously designed to put forth the current trends and future scope of innovative breeding technologies to exploit variability and genetic gains in animals. The recent trends in computational genetics and artificial intelligence in understanding genome complexity will also be discussed in this national conference in detail in the form of various lead papers by eminent scientists. Moreover, a session for students and young researchers to present their work and share their views in the present scenario will also be conducted. The session on scientist Industry Interface on “Agripreneurship in Animal Breeding & Genetics” will benefit the researchers and industry sector to focus upon the needs of the farmers in the present scenario. We gratefully acknowledge the financial support we received from Research and Development Fund of National Bank for Agriculture and Rural Development (NABARD) towards printing of the proceedings of the conference is greatefully acknowledged. We also thank all the firms for taking out time in understanding our purpose and being able to decide to sponsor us for smooth conduct of this mega event. We have received an overwhelming response from the speakers and participants of this National conference and would like to thank everyone for displaying such great enthusiasm and participating in large number. We are thankful to the scientists of ICAR-DPR and all the committees for their cooperation in making all the necessary arrangements for successfully organizing the conference. We express our sincere thankfulness to ISAGB for entrusting us with the responsibility to organize this important event. We believe that the discussion and deliberations that will be made during the two-day program will enable us to chalk out well drawn recommendations for sustainable productivity of livestock and poultry.

(T.K Bhattacharya) & (U. Rajkumar)

Indian Society of Animal Genetics and Breeding (ISAGB)

The Indian Society of Animal Genetics and Breeding (ISAGB) is one of the oldest Societies of Animal Sciences that was registered under Societies Registration Act XXI of 1860 on 17th April 1984 with main aims and objectives of (i) Advancement of science and art of Animal Genetics and Breeding in all aspects by dissemination and application of knowledge gained from experiments and experience, (ii) Provision of opportunities for exchange of knowledge and ideas through discussions and other means and for collaboration between persons interested in different fields of Animal Genetics and Breeding, (iii) Organization of conference, symposia, seminars etc., and other periodicals meetings. (iv) Initiation and promotion of research in all fields of Animal Genetics and Breeding, (v) Publication of scientific and technical journals, policy papers, memoirs, monographs, bulletin, pamphlets etc., on subjects related to Animal Genetics and Breeding, (vi) Providing financial and other assistance for education and research or development activities in the field of Animal Genetics and Breeding. Society is publishing a research journal "Indian Journal of Animal Genetics and Breeding" and also organizing National symposium/ conference on annual basis. All income of the society is utilized towards the protection of aims and objectives of the society. The membership of the society is open to academician, scientists, research scholars and students studying in different institutes/universities/colleges. The membership and other details are on the society website (http://www.isagb.org).

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XVI Annual Convention of ISAGB (ISAGBCON-2022) and National Conference on "Innovations in Animal Genetics & Breeding for sustainable productivity of livestock and poultry"

2nd & 3rd December 2022

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Principal Scientist, ICAR-DPR, Hyderabad

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ICAR-Directorate of Poultry Research, Hyderabad

The ICAR-Directorate of Poultry Research (formerly Project Directorate on Poultry) was established on 1st March 1988 at Hyderabad, Andhra Pradesh under the aegis of Indian Council of Agricultural Research. The Institute originated from All India Coordinated Research Project (AICRP) on Poultry Breeding, an all India Net Work project launched by the Indian Council of Agricultural Research during IV five-year plan with the objective of augmenting commercial poultry production and achieving self-sufficiency in the country.

In the beginning, the coordinating unit of AICRP was located at the Poultry Research Division, Indian Veterinary Research Institute, Izatnagar till 1979, which later shifted to Central Avian Research Institute, Izatnagar till its elevation to the Directorate status in 1988 with its headquarters at Hyderabad. The institute was elevated from Project Directorate to Directorate on 18th September 2013. Further elevation to “Indian Institute of Poultry Research” (as recommended by QRT) is under active consideration at the Council. The Regional Station, Bhubaneswar was transferred from CARI to DPR during July 2020. Accordingly, the total scientific strength of DPR has increased to 33.

The primary research focus at the Institute has been towards the application of quantitative genetic principles to enhance productivity of various chicken germplasm with special emphasis to meet the needs of rural and tribal people of the country. To support the core research programme, research on nutrition, health, physiology and molecular genetics has been made an integral component. In addition, several externally funded projects were also carried out at the Directorate to achieve the Institute’s primary goals and objectives. The AICRP on Poultry Breeding was started during IV plan and has made significant contribution in the development of poultry sector in India over the years. Seven promising varieties of chicken were released for commercial exploitation for the benefit of the intensive poultry farming. Rural component of the project was added during XI plan with two centres and further strengthened in XII plan period by adding 4 more centres to carryout research in rural poultry farming.

The AICRP on poultry breeding was completely re-oriented towards the rural poultry from 2014- 15 with all the 12 centres to cater to the needs of the rural/tribal farmers across the country. The primary objective of the AICRP centre is to develop location specific rural chicken varieties utilizing the local native germplasm. The constant efforts of the scientists led to the development of 5 location specific varieties, viz. *Pratapdhan* (MPUAT, Udaipur), *Kamrupa* (AAU, Guwahati), *Jharsim* (BAU, Ranchi), *Narmadanidhi* (MPUAT, Jabalpur) and *Himsamridhi* (CSKHPKVV, Palampur).

During XI plan, the activities of the Directorate were further expanded by introduction of the Poultry Seed Project with six centres located in different states to increase the availability of rural chicken germplasm for rearing in remote areas of the nation. The Poultry Seed Project was further strengthened by addition of five new centres from 2014-15 and 3 centres from 2017-18. However, 2 centres were discontinued from 2017-18 onwards, thus making 12 centres at present.

The Directorate, besides coordinating the ICAR network projects, is carrying out research in core areas of Poultry Science and supplying rural chicken germplasm to meet the demand in rural and tribal areas. At this Directorate, three promising chicken varieties for rural poultry farming were evolved i.e., *Vanaraja,* a dual-purpose bird, *Gramapriya*, predominantly a layer, and *Srinidhi*, a dual purpose bird meant for free-range and backyard farming. Recently, a new dual purpose variety *Janapriya* was developed for rural poultry farming, which will be released shortly by the ICAR-NBAGR, the nodal agency. *Vanashree* (PD- 4) an improved native chicken has been developed from Aseel and is being

popularised. These chicken varieties have become extremely popular and are being reared in every part of the country. Several user agencies in the country are involved in dissemination of the varieties covering the southern, northern, eastern and north-eastern states including Jammu and Kashmir, Lakshadweep, and Andaman and Nicobar Islands.

The Directorate also developed two crosses viz. *Krishibro*, a multi-coloured broiler and *Krishilayer*, a high yielding egg producing bird for commercial purposes. Further research in this direction is underway for developing new crosses that could be tailor-made for better adaptability under diversified regions in rural and tribal backyard conditions.

Active research is being pursued to prepare package of practices for providing optimum nutrition, management and health coverage to the pure lines as well as crosses developed by the Directorate for intensive and backyard systems of rearing. Research in nutrition at this Directorate resulted in development of technologies that have been adopted by the commercial and rural farmers to reduce cost of production. Besides nutritional knowhow, the Directorate is also familiar among poultry farming community for its services in disease diagnosis, seromonitoring and health care. The nutritional and health care solutions are being offered to the stake holders of poultry farming including network programmes and contract research programmes being operated by the Directorate.

The studies on advanced molecular genetic tools like RNAi (gene silencing), gene editing (CRISPR cas9), SNP typing, microsatellite analysis, DNA marker based selection, etc. have also been undertaken in evaluating and augmenting the productivity of various chicken germplasm maintained at this Directorate. The Directorate thus is actively engaged in augmenting the productivity of chicken by undertaking research in different aspects of Poultry Science to cater to the needs of the country.

Regional Station, Bhubaneswar

Realizing the slow development of poultry production in Eastern and North-Eastern parts of India, the Regional Center of Central Avian Research Institute (presently under ICAR-Directorate of Poultry Research, (DPR) from 23 July, 2020) was established by the ICAR to initiate research on various aspects of poultry, particularly duck production, which are of direct relevance to this region. The regional Centre has Avian Genetics and Breeding, Avian Production Management, Avian Nutrition and physiology, Extension, Avian Medicine sections.

In addition, the Centre has Hatchery, Experimental farms and Feed Technology unit, marketing section etc. Duck is the priority area of research. Supply of duckling and eggs are the prime revenue generating commodity for the centre. This centre transferred from administrative control of CARI to DPR as per the ICAR order dated 23rd July 2020.

Regional Centre had taken birth on 26th July, 1992 at Choudwar of Cuttack district of Orissa. Here, the activities of the centre started initially in a rented house. Extension works on popularization of backyard poultry was initiated from there when the rural farmers of Orissa were quite ignorant of the production practices and the benefits of it. In October, 1998 the centre was shifted to Bhubaneswar and had started functioning in a rented house at Baramunda. Research activities to certain extent were carried out by keeping few experimental birds in one of the deserted-shed of Central Poultry Development Organization, Bhubaneswar.

The foundation stone for the present office- cum- laboratory building was laid by Hon'ble Chief Minister of Orissa, Sri. Naveen Pattanaik on 21st June, 2000 in the presence of Hon'ble Dr. Debendra

Pradhan, Minister of State for Agriculture, Govt. of India and Dr. R. S. Paroda, Secretary DARE & DG ICAR. The Centre's office was finally shifted to its own new campus on 6th October, 2003, which was inaugurated by Dr. Mangala Rai, Secretary DARE & DG, ICAR. Subsequently, the brooder shed, duck shed, experimental hatchery and feed plant came up.

The present campus is situated on a land of 62 acres (31 acres for each) shared by both the ICAR institutes i.e. Directorate of Research for Women in Agriculture (DRWA) and Regional Centre, CARI The original land was a part of O.U.A.T. and was subsequently transferred to ICAR for establishment of these two institutes. This is a place, which is well connected by road, rail and air to all parts of the country.

Vision

To enhance productivity of chicken for household nutritional security, income and employment generation.

Mission

To develop and propagate improved varieties of chicken for sustainable production under intensive and extensive systems.

Mandate

1. Basic and applied research to enhance productivity of poultry
2. Development of new germplasm for rural poultry husbandry
3. Capacity building

AICRP on Poultry Breeding (12 centres)

- AAU, Anand
- KVAFSU, Bengaluru
- AAU, Assam
- GADVASU, Ludhiana
- BAU, Ranchi
- MPUAT, Udaipur
- CSHPKVV, Palampur
- NDVSU, Jabalpur
- KVASU, Mannuthy
- ICAR-CARI, Izatnagar
- OUAT, Bhubaneswar
- ICAR Res. Complex for NEH Region, Agartala

Poultry Seed Project (12 centres)

- WBUAFS, Kolkata
- ICAR Res. Complex for NEH Region, Sikkim
- ICAR Res. Complex for NEH Region, Nagaland
- ICAR Res. Complex for NEH Region, Manipur
- ICAR Res. Complex for NEH Region, Barapani, Meghalaya
- BASU, Patna
- TANUVAS, Hosur
- ICAR-CCARI, Goa
- ICAR-CIARI, Port Blair
- SVVU, Tirupati
- PVNRTVU, Warangal
- SKUAST, Srinagar

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LP-1

A MISSION TOWARDS ZERO NON-DESCRIPT ANIMAL GENETIC RESOURCES OF INDIA: CHALLENGES AND OPPORTUNITIES

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Animal genetic resources (AnGR) for food and agriculture have a long history of about 10 to 12 thousand years. Over the years, a number of mammalian and avian species have been domesticated of which only cattle, sheep, goat, pig, and chicken - known as 'Big Five' - are widely distributed and densely populated species, across the globe. The AnGR is not only the great source of food but also provides agricultural and transport power, manure as bio-fertilizer and energy, fuel etc. including many byproducts. Contribution of the AnGR towards food is quite high in many parts of the world and account for one-fifth of the world's food. About 12 percent of the global population is solely dependent on animal food.

Our country is bestowed with a large AnGR diversity in form of various animal species and their distinct populationsand breeds. With 14 livestock and five poultry species, the country possesses 536.8 million livestock and 851 million poultry population (20th Livestock Census, DAHD, GoI). The farm animals produced 209.96 million tonnes of milk, 8.8 million tonnes of meat, and 122billion egg production during year 2020-21. Growth of AnGR based product is also significant, ranging from 4 to 10 percent annual in recent years. This progress has also largely contributed in improving food and nutritional security in the country.

AnGR diversity preservation: Global efforts

Farm animal diversity is essential to meet our ever increasing food demand. The role of indigenous breeds, as a valuable gene pool, becomes more pertinent to various future challenges including climate change. Since native breeds are evolved in specific climatic conditions, therefore, these breeds become well-synchronized to the native production system with sustained production and resilience. Identifying such synchronous and well-adapted breeds, nationwide, always remain an utmost priority to complete our national inventory.

Sincere efforts for preserving the AnGR diversity and their sustainable utilization may be tracked back to the commencement of the Convention on Biological Diversity (CBD) in 1992. Under the aegis of CBD, the Commission on Genetic Resources for Food and Agriculture (CGRFA) in 1999, worldwide initiated the process to identify the national priorities for the management of AnGR for its sustainable use and preserving biodiversity. United Nation's Food and Agriculture Organization (FAO) initiated its sincere efforts for AnGR biodiversity preservation through the Global Plan of Action (GPA) for Animal Genetic Resources in 2007. Also known as 'Interlaken declaration', it is the first internationally accepted framework for the management of AnGR. After its adoption, the countries have realized the necessity of inventory of native germplasm and most of the countries hasten the process to inventories such populations. As per Global data bank on Animal Genetic Resources of FAO, total 8774 breeds of 38 species were reported, worldwide (data from 182 countries) in 2014. Importance of the native breed preservation has also been emphasized by United Nations (UN), through their Sustainable Development Goals (SDGs) set in 2015, wherein it appealed for management of all genetic resources globally specifically to promote sustainable agriculture and achieving food security. SDG Goal 2 (Zero Hunger), Target 2.5 (Indicator 2.5.1: Number of plant and animal genetic resources for food and agriculture secured in either medium or long-term conservation facilities, and Indicator

2.5.2: Proportion of local breeds classified as being at risk of extinction) are well related to the farm animal biodiversity.Giving due importance to the AnGR diversity, the Government of India has also included as a National Indicator for achieving the Sustainable Development Goal of the UN.

AnGR diversity and breed status

At present, the country possesses 536.82 million livestock and 851.81 million poultry, with the count in 20th Livestock Census, 2019 (Table 1). The species wise proportion of total livestock is 36.04% cattle, 20.47% buffalo, 27.74% goat, 13.83% sheep, 1.69% pig and rest 0.23% represented by Mithun, yak, horses and ponies, mule, donkey and camel.As compared to the year 1956, the population of cattle, buffalo, sheep, goat, pig, mule, yak and poultry has increased and horses & ponies, camel and donkey have declined, may be due to faster adoption of mechanization in agriculture.

Table 1: Livestock and poultry population (in million) over the years in India

Species	1956	1961	1972	1982	1992	2003	2012	2019
Cattle	158.70	175.60	178.30	192.45	204.58	185.18	190.90	193.46
Buffaloes	44.90	51.20	57.40	69.78	84.21	97.92	108.70	109.85
Sheep	39.30	40.20	40.00	48.76	50.78	61.47	65.07	74.26
Goats	55.40	60.90	67.50	95.25	115.28	124.36	135.171	148.88
Horses	1.50	1.30	0.90	0.90	0.82	0.75	0.63	0.34
Camels	0.80	0.90	1.10	1.08	1.03	0.63	0.40	0.25
Pigs	4.90	5.20	6.90	10.07	12.79	13.52	10.29	9.00
Mules	0.04	0.05	0.08	0.13	0.19	0.18	0.20	0.08
Donkeys	1.10	1.10	1.00	1.02	0.97	0.65	0.32	0.12
Yaks	NC	0.02	0.04	0.13	0.06	0.06	0.08	0.06
Total livestock	306.60	335.40	353.60	419.59	470.85	485.00	512.06	535.82
Poultry	94.80	114.20	138.50	207.74	307.07	489.01	729.21	851.81

In India, there are 209 registered indigenous AnGR breeds, which includes 53 of cattle, 20 of buffalo, 37 of goat, 44 of sheep, 7 of horses and ponies, 9 of camel, 13 of pig, 3 of donkey and one of yak in livestock and 19 of chicken, one of geese and two of duck in poultry. Three breeds of dog have also been registered recently during 2020, the first time in the country. The proportion of animal breeds in India is very less in comparison to number of breeds in the world. As per Global data bank on Animal Genetic Resources of FAO, total 8774 breeds of 38 species were reported, worldwide (data from 182 countries) in 2014. Among these, 7718 are local breeds (in one country) and 510 are regional transboundary breeds (in one region) and 546 are international transboundary breeds (in more than one region).

Table 2: Number of AnGR breeds in India vis-à-vis Asia and world

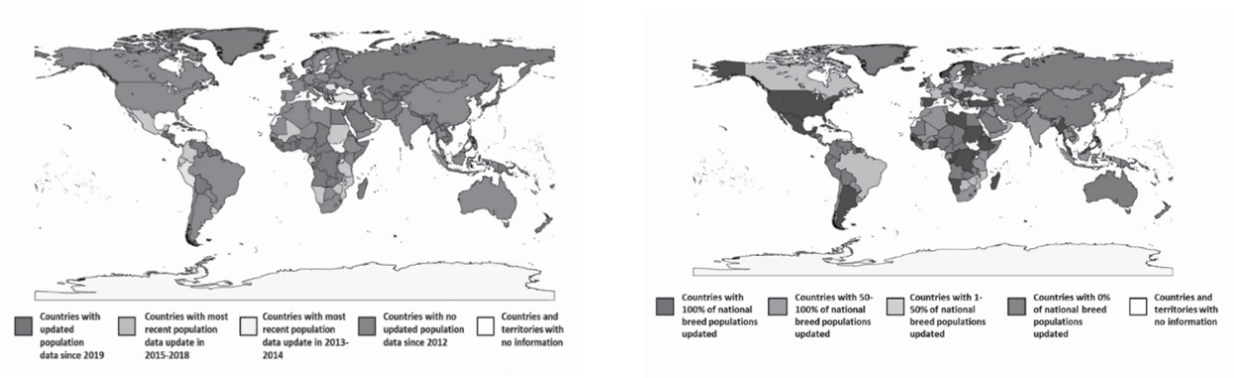
Species	India			Asia	World
	Extant breeds	New breeds	Total		
Asses	0	3	3	42	170
Bactrian camel	0	0	0	9	14
Buffalo	10	10	20	107	128
Cattle	30	23	53	261	1224
Dromedarian camel	8	1	9	14	89
Goat	21	16	37	195	662
Horse	6	1	7	148	818
Pig	0	13	13	216	602
Sheep	39	5	44	276	1382
Yak	0	1	1	25	28
Others	0	3	3	33	457
Total mammals	114	76	190	1318	5584
Chicken	15	4	19	308	1669
Duck	0	2	2	94	279
Geese	0	1	1	46	205
Other avian	0			77	390
Total avian	15	7	22	525	2543
Total breeds	129	83	212	1853	8127

FAO DAD-IS: Ombudsman of SDG 2.5

The Domestic Animal Diversity -Information System (DAD-IS) possesses the global information about the domestic populations for each of the country, which is further extrapolated, region-wise and/or country-wise for metadata for various purposes including SDG indicators. The DAD-IS comprises the information about the breeds/wild populations/variety etc. with three major sections about the breed 1) Phenotypic and performance 2) Population dynamics 3) Cryopreserved germplasm. New entry can be made as per the breed inventory as well as new information about the existing breed by the NBAGR on behalf of the National Coordinator.

NBAGR has been chosen the nodal agency to provide information for NIF 2.5.1 Component: b) Animal Genetic Resources for Food & Agriculture, and NIF 2.5.2 by the NSO. The bureau is providing all necessary information related to the NIF 2.5.1 whenever required, through SMD/ICAR to the NSO.
Present status of India in DAD-IS

There are total 353 breeds/populations entries in the DAD-IS, as on 31.10.2022. The entries include all 202 animal breeds registered by the NBAGR. The populations, other than registered breeds, are 151, which are mostly wild, exotic, variety or others. These populations have been entered during initial phase (2001 to 2006), before the registration system started in year 2008, based on the information about the well-known or lesser known breeds/populations available in the country. Information about the cryopreservation of semen, somatic cells and DNA of native breeds available at National Gene Bank of ICAR-NBAGR has been included in the DAD-IS. This information is important for SDG indicator 2.5.1 (NIF 2.5.1).



DAD-IS: Current status of AnGR population (left) and cryomaterial (right) updates in world

Status of non-descript AnGR

India possesses nearly 10 percent of the global livestock population; however, the breed proportion is only about 4 percent of the total number of breedsof the globe. There is one breed per 3 million livestock population in India, which is much lower than the world average (one breed per 0.9 million animals), about 4 to 6.5 million for cattle, buffalo and goat, the three most populous species in India. Around 54% percent of population of different species falls under the non-descript category.As per livestock Census (2019) species-wise non-descript population included 51.8 per cent of cattle, 45.4 per cent of buffaloes, 50.6 per cent of sheep, 63.5 per cent of goat and 70.9 per cent of pigs.The descript and non-descript populations of different livestock also widely varyacross the states. There is also possibility to have large number of mixed populations in different states.

Table 3: Total population (in thousands) and proportion of non-descript population of major livestock species in Indian states (20th Livestock Census, 2019)

States	Cattle		Buffalo		Sheep		Goat		Pig		Total Livestock	
	Total population	% Non-descript	Total population	% Non-descript	Total population	% Non-descript	Total population	% Non-descript	Total population	% Non-descript	Total population	% Non-descript
Andhra Pradesh	4600	41.7	6219	36.0	17626	48.2	5522	91.7	91	90.1	34067	52.2
Arunachal Pradesh	339	97.9	6	100.0	7	100.0	159	100.0	271	95.2	1161	98.1
Assam	10909	30.2	421	89.8	332	97.9	4315	88.2	2099	60.9	18092	50.3
Bihar	15397	60.9	7719	69.3	213	80.8	12821	55.3	343	92.4	36540	61.2
Chhattisgarh	9983	71.5	1174	78.0	180	99.4	4005	95.6	526	98.1	15872	79.2
Goa	60	51.7	27	96.3			9	100.0	35	91.4	132	74.2
Gujarat	9633	27.4	10543	30.2	1787	19.9	4867	60.9			26893	34.0
Haryana	1928	10.4	4368	11.9	288	57.3	334	56.3	108	39.8	7046	16.0
Himachal Pradesh	1828	40.8	646	39.8	791	28.1	1108	60.6	2	100.0	4412	43.3
Jammu & Kashmir	2539	42.9	690	72.2	3247	40.2	1730	77.9	1	100.0	8325	52.0
Jharkhand	11223	57.6	1350	47.9	641	47.6	9121	23.6	1276	79.6	23614	44.8
Karnataka	8469	23.4	2984	57.1	11050	42.7	6169	80.2	323	78.0	29013	46.9
Kerala	1341	4.7	101	68.3	1	100.0	1359	21.0	103	2.9	2908	14.5
Madhya Pradesh	18750	76.7	10307	67.5	324	98.8	11064	88.2	164	97.0	40637	77.8
Maharashtra	13992	57.3	5603	58.6	2680	78.5	10604	78.0	161	91.3	33079	66.1
Manipur	224	92.4	36	97.2	6	100.0	38	94.7	235	88.5	550	91.1
Meghalaya	903	96.3	15	100.0	15	100.0	397	100.0	706	57.8	2039	83.7
Mizoram	45	53.3	2	100.0	0.4	0.0	14	100.0	292	100.0	359	20.6
Nagaland	78	76.9	15	100.0	0.3	0.0	31	96.8	404	47.8	553	58.0
Odisha	9903	79.5	458	89.7	1279	87.6	6393	63.1	135	99.3	18170	74.7
Punjab	2531	7.5	4015	3.6	85	61.2	347	19.6	52	17.3	7050	6.7
Rajasthan	13937	56.6	13693	42.6	7903	48.1	20840	63.4	154	96.8	56800	54.6
Sikkim	148	18.2	1	100.0	2	50.0	90	100.0	27	55.6	274	50.7
Tamil Nadu	9518	15.9	518	76.1	4500	43.1	9888	76.3	66	75.8	24500	46.7
Telangana	4232	77.4	4226	60.1	19063	53.7	4934	92.3	177	96.0	32640	63.7
Tripura	739	82.5	7	100.0	5	100.0	360	25.8	206	48.5	1318	61.8
Uttar Pradesh	19019	47.9	33016	41.3	984	82.6	14480	64.0	408	88.5	68012	48.9
Uttarakhand	1852	9.5	866	42.6	284	32.7	1371	78.4	17	58.8	4427	39.1
West Bengal	19077	55.8	630	61.1	952	82.6	16279	21.1	540	72.6	37483	41.7
INDIA	193462	51.8	109851	45.4	74260	50.6	148884	63.5	9055	70.9	536761	53.9

Efforts to document non-descript AnGR

In the year, 2008, ICAR-National Bureau of Animal Genetic Resources (NBAGR), Karnal was given the temporary authority for the registration of germplasm related to livestock and poultry in the country. First time in the year 2008, all 129 extant breeds of livestock and poultry were registered by the NBAGR. Further 83 breeds were newly added and by 2022, the number reached 212.Further, to provide legal safeguards for germplasm protection, notification of indigenous breeds has started in the year 2019 through publishing Official Gazette by the Government of India. The Government of India has notified all registered breeds of livestock and poultry for keeping and rearing for the purposes of animal husbandry, production, breeding, conservation, utilization, consumption, and trade through five Gazette Notifications.Breeds of specie like pig, donkey, yak, dog and geese were first time registered in the country in the last decade.

Several new breeds have also been reported from the remote regions of the country. Importantly, many of breeds were registered from remote areas like NEH and also for the minor species; which are although less in population but contributes significantly to the society.Many of the new breeds have been added in breed inventory by the states like Gujarat, Odisha and Tamil Nadu, mainly because of active participation of local agencies and NGOs in these states.Registration of new breeds during last decade has put more than 25 million livestock and poultry into the descript category in the country.

Table 4: State-wise number of animal breeds

State	Total breeds			New breeds registered			State	Total breeds			New breeds registered		
	Pr.	Sec.	Total	Pr.	Sec.	Total		Pr.	Sec.	Total	Pr.	Sec.	Total
Rajasthan	28	5	33	6	1	7	West Bengal	4	1	5	1	0	1
Gujarat	23	4	27	8	1	9	Andaman & Nicobar	3	-	3	2	0	2
Tamil Nadu	21	0	21	8	0	8	Chhattisgarh	3	0	3	2	0	2
Maharashtra	15	2	17	5	0	5	Haryana	3	3	6	1	0	1
Jammu & Kashmir	11	0	11	3	0	3	Nagaland	3	0	3	3	0	3
Karnataka	12	3	15	5	0	5	Sikkim	3	0	3	0	0	0
Odisha	12	1	13	9	0	9	Uttarakhand	3	1	4	3	0	3
Uttar Pradesh	11	3	14	3	1	4	Arunachal Pradesh	2	1	3	1	0	1
Andhra Pradesh	7	2	9	0	1	1	Goa	2	1	3	2	1	3
Assam	7	0	7	5	0	5	Manipur	3	1	4	2	1	3
Himachal Pradesh	7	1	8	2	1	3	Meghalaya	4	1	5	3	1	4
Punjab	6	0	6	2	0	2	Jharkhand	2	1	3	1	1	2
Bihar	5	1	6	3	1	4	Mizoram	1	0	1	1	0	1
Kerala	4	0	4	0	0	0	Telangana	1	0	1	1	0	1
Madhya Pradesh	4	4	8	0	0	0	Tripura	1	1	2	1	0	1

Pr. - Primary home tract; Sec.- Secondary home tract (Red Sindhi cattle is available in Organized farms only)

Need for a different approach

Considering country's vast geographic and ecological regions, contrasting climatic conditions along with diverse necessity of the farmers, it is obvious that there is still a sizable undefined population. FAO also predicted a greater number of livestock breeds in the country.Recognition of new breeds, in recent time, could be able to induct only 5% of the native livestock population, in the descript category. The non-descript population of different species definitely have large number of unique/ homogenous population of different species and also large number of mixed populations those neither falls in registered breeds nor a unique population. The country still possesses a sizeable proportion of livestock and poultry undocumented, which includes several homogenous/unique populations those may have potential to be breeds. Further, there are large proportion of mixed populations that do not conform to any of the breed due to non-homogeneity in population, and/or cross breeding and other demographic factors. Admixture analysis including population and diversity studies of such admixed population vis-à-vis established breeds can aide in drawing a diversity representation of the native breeds of major livestock species adapted to their geographical and ecological niche.Besides, it can further facilitate in cataloguing, characterization and documentation of the native populations. In recent times, the genome wide analysis has been advocated to provide better resolution of population structure as well as admixture status. Such kind of efforts may provide important information not only from historical or geographical perspective but would also unfold the recent admixture and divergence status amongst the populations. Such gigantic tasks can only be completed in the mission mode with immense cooperation, coordination and support of all of the involved agencies.

Mission towards Zero Non-descript AnGR

ICAR-NBAGR has undertaken the characterization and documentation of entire native livestock and poultry in the country in Mission mode in the next coming years. "Mission towards Zero Non-Descript AnGR of India' was launched by Dr. T Mohapatra, Secretary, DARE & Director General, ICAR in a National Workshop organized on 11th August, 2021 virtually by NBAGR. The Mission is aimed to lowering down of proportion of non-descript livestock and poultry, significantly, along with identification of potential breeds in the country as well as to understand the architecture of mixed populations of livestock species. Since its launch, the Mission received a great momentum across the country, and has been prioritized by the ICAR. For sensitization of the stakeholders the institute is also organizing State Interface Meets and after the launch of the mission, interface meets with 13 state/UT have been completed. The efforts would also yield the identification of unique populations and registering as native breeds. It is expected that the strategy would yield more than 100 distinct breeds of different livestock and poultry in coming years, which would be registered and notified further.

Approach and strategy for mission

The task is highly demanding, surely it needed a larger collaboration with various central and state agencies including AHD of all States, SAU/SVUs, other ICAR institutes, NGOs etc.

Documentation of native AnGR and identification of potential breeds: Unique/homogenous population of different livestock and poultry species may be identified in whole countryby initial surveys. Survey may be conducted in "All Blocks- All Districts- All States" of the country. Survey and documentation would include only indigenous stock of livestock and poultry species in collaboration with AHD of the state. Crowd sourcing facility may be created at NBAGR to get photos and brief description of any population of livestock and poultry, online from the public, which would be compiled and verified

and further considered for characterization and documentation. All the data including photographs, performance and production system would be analysed for identification, using Image Analyser (Photogrammetry).

Characterization of homogenous population: Survey for characterization of homogenous population may be conducted at farmer's herds/flocks. Stratified two stage sampling design would be adopted for the survey. The survey may be conducted in three districts in breeding tract. Each district may be divided in four strata and from each stratum, 5 villages may be randomly selected. Data on physical and morphometric traits, production and reproduction performances may be recorded for different species.All the unique/homogenous populations of different species may be documented in the shape of breed monographs and breed descriptors. All the eligible unique/homogenous populations of different species may be registered as distinct breed.

Grading of admixed populations: Genetic characterization of all homogenous populations and admixture analysis may be carried out as per FAO recommended markers identify the grades of registered breeds and mixed populations. Admixture mapping capitalizes on the long-range linkage disequilibrium that exists in admixed populations.

Bureau's scientists have made the visits in various states after launch of the Mission towards Zero Non-descript AnGR. About 25 new populations of native livestock and poultry have been identified after launch of Mission, which are being characterized in their respective breeding tracts falling in various states.

Conclusion

Documentation of Non-descript AnGR in all states across the country in mission mode is certainly need of the hour, therefore the mission is extremely vital for the management of native AnGR of the country. It is important to identify potential breeds as well as define grades of mixed population, non-conforming to any breeds. Such data on native AnGR is highly required for more accurate breed-wise data and livestock census. Describing all AnGR in the country would also help in policy formulation for development programs for native breeds as well as their conservation. Further, policy may also be formed for mixed population based on their genetic architect and their compatibility with improver breeds. Such information would have a foundation for genetic improvement of native AnGR for increasing productivity with sustenance in longer run.

LP-2

RATE OF LAY AS SELECTION CRITERION TO IMPROVE THE EGG PRODUCTION.

T.Kotaiah
Indbro Research & Breeding Farms Pvt. Ltd., Hyderabad, India

Indbro Research & Breeding Farms Pvt.Ltd. is a poultry breeding farm with R&D facilities since the year 2000. The company is promoted by a self employed poultry geneticist, Dr.T.Kotaiah, M.V.Sc (poultry science). The company is presently involved in developing high yeilding coloured birds suitable for rural poultry. The company planned to develop a strain of brown layers to produce large brown eggs.

INTRODUCTION

Number of eggs up to 40weeks is being used as the selection criterion to improve the annual egg production of the layer birds, with the assumption that part record selection will improve the annual egg production also and the generation interval can be kept low. Reduction in age at maturity is considered to be favourable as the early egg weight is not an issue in the markets, where the eggs are sold by numbers, not by weight. The number of eggs to 40weeks can go up by lengthening the laying record, which happens by reduction in age at maturity. The bird maturing 10 days in advance has 10 days more to lay compared to the bird, which starts 10 days later. The other factor which decides the number of eggs laid is the rate at which the bird is laying in other words “percent production” calculated as “Number of eggs*100/number of days at the disposal of the bird to lay (280 – age at maturity)”.

When the number of eggs are increased by reducing the age at maturity, the physiological effects on the bird are different. The early maturing bird is of low body weight and naturally lays smaller eggs. There is physiological stress on the small and younger bird, which may lead to more breaks in egg laying or smaller clutch cycles of egg laying during the early days of laying. The stress also can lead to prolapse of oviduct and compromise on the immunocompetance of the bird. Early maturity and small early egg size has been noticed in many of the selection programs run at AICRP, where birds were being selected basing on osborne’s index for number of eggs to 40weeks of production.

MATERIAL

The company took up a long term selection program in a brown layer flock synthesized in the year 2011. The aim of selection was to improve the production of good quality eggs termed in this article as “hatching eggs”. Eggs not small,(below 50gms), not double yolked, not broken, Not white coloured nor misshapen. Eight generations are completed by 2022. The response from generation to generation was phenominal and the length of recording was raised every year from 40weeks to 65weeks in the current generation.

METHOD

Population size is about 3300 females and 450 males pedigreed, housed in single cages on an isolated farm on “all in all out” basis.
All birds were weighed on completion of 18 weeks and abnormally under eight birds were not housed. The birds were weighed again on the day of first egg and the weight at maturity was recorded. The birds alive on 40th week and above were weighed and the adult weight recorded.

Age at Sexual maturity - The birds were housed in single cages by 16 weeks. The egg production

was recorded from day one all days. The date on which the 1st egg was produced was recorded and the days to first egg from the hatch date was calculated.
The first 5 eggs were weighed to get the initial egg weight. 4 weeks data blocks 20-1 to 24 weeks, 24.1 to 28weeks, 28.1 to 32weeks 32-1 to 36weeks and 36.1 to 40weeks and so on were used for data collection. The eggs laid in one week during each period were weighed. The average egg eight was calculated by averaging egg weights of all the periods separately and pooled for the final average. After two generations, it was decided to extend the recording period beyond 40weeks to 50, 60 and 65 weeks.

Egg production was marked on every day in a calender type sheet when laid. Each egg was examined. If the egg is below 50gms, it is marked as S (small), B for Broken, M for miss happen, D for double yolk egg, W for light or white egg were recorded. Total eggs (T.E), and hatching eggs (H.E), average egg weight for each period were recorded. Selected stock for pedigree breeding - 500 females (17%) in females. Males were selected on family average breeding values calculated on females. Inbreeding avoided by looking at parents and the grand parents in each mating.

There was no genetic control population to compare the genetic progress. Selection was based on Hatching eggs percent production. Osborne index considering sire deviation from Mean, dam deviation from sire average and individual deviation from dam family average, termed as breeding value of the individual. The data was tabulated family wise and culling levels were used for family mortality, abnormal body weights and total eggs produced. About 10 to 15% birds were rejected out of the birds selected from the breeding value on the judgement of the breeder.
Genetic parameters were calculated.

RESULTS
The Heritability of total eggs (TE) and hatching eggs (HE) was low (0.2 and below). Heritability of age at maturity and egg weight were little higher (0.3 to 0.4). The heritability of body weight was higher.

The genetic correlations of age at maturity was negative with 18weeks weight. Higher weight birds mature early. Positive with average egg weight. Negative with Egg production. Rate of lay was calculated as Percent production (total eggs laid*100/ number of days in lay). The number of days in lay was the days between the date of last collection recorded less the age at maturity. PP was less related to Age at first egg and egg weight copared to TE. Hence we decided to follow PP rather than TE. HE was found to be a better parameter to maintain the average egg weight and good quality eggs. HEPP (Hatching eggs percent production) was found to be the best to improve the egg production without premature laying of birds and without losing the egg size.
To reduce the volume of presentation the data of 1st, 3rd, 5th and 8th generation data are presented. The progress has been linear.

1st generation - We closed the records at 50weeks (350days) the averages and heritabiities were as follows. We could select 17% of the best birds whose averages are also given. The selection was effective. The average of egg weight appears low because the egg weights up to 40weeks only were included.

The selection results

Trait	Flock mean3300	Selected mean500	Heritability	c.v%
Age at maturity	144	146	0.12	8.84
Weight Maturity	1766	1596	0.45	8.92
Wt40wks	1800	1874	0.36	8.7
TE	124	177	0.20	9.86
HE	120	172	0.20	32.22
HEPP	60.7	83.9	0.17	29.6
EGG WEIGHT	50.8	54	0.38	5.64

We continued selection. The hen day percentages improved and peak periods were all above 90%. We closed the records at 370 days. Selected same number of birds birds for next generation. The flock mean selected mean and heritabilites were as follows.

Generation 3

Trait	Flock mean	Selected mean	Heritability	c.v%
Age at maturity	144	143	0.26	5.16
Weight at 18weeks	1370	1409	0.35	9.44
Weight at maturity	1712	1751	0.34	8.12
Weight at 40weeks	1719	1807	0.26	10.66
TE	215	251	0.07	23.84
HE	180	232	0.12	30.1
HEPP	79.8	93	0.07	23.77
EGG WEIGHT	52.3	53.7	0.39	5.32

The selection results of the 5th generation were as follows. Records closed at 400 days (57weeks)
Generation -5

Trait	Flock mean	Selected mean	Heritability	c.v%
Age at maturity	142	142	0.32	8.03
Weight at 18weeks	1352	1360	0.30	10.74
Weight at maturity	1632	1629	0.35	8.69
Weight at 40weeks	1964	1949	0.25	8.58
TE	257	270	0.05	9.58
HE	230	250	0.02	14.08
HEPP	82.6	90.9	0.07	13.89
Egg Weight	54.9	55.4	0.40	5.19

The selection results of the latest (8th generation closed in 2022) were as follows. Records closed at 450 days (65weeks)

Generation -8

Trait	Flock mean	Selected mean	Heritability	c.v%
Age at maturity	146	144	0.38	6.80
Weight at 18weeks	1370	1381	0.33	11.29
Weight at maturity	1726	1719	0.43	8.51
Weight at 40weeks	1990	1987	0.35	9.80
TE	271	298	0.07	11.1
HE	257	289	0.05	20.0
HEPP	84.9	94.9	0.06	20.05
Egg Weight	59.3	59.4	0.46	5.35

The egg weight increments of his flock is interesting. The weights remain constant as the age advances. This helps in maintaining the shell quality

Period	1sr period	2nd period	3rd period	4th period	5th period	6th period	7th period	8th period	9th period	10th period
Av.eggwt	46.1	54.1	58.9	59.1	59.2	60.6	58.7	58.3	58.9	59.5
increment		8.0	4.8	0.2	0.1	1.4	-1.9	-0.4	0.6	0.6
Eggs/ period	19	27	26	26	26	26	26	25	25	25
% 28days	68	96.4	92.8	92.8	92.8	92.8	92.8	89.2	89.2	89.2
H.E	13	25	25	24	24	25	24	24	24	24

The egg weights increased rapidly and not more than 2 eggs would be below 50gms. The marginal drop in egg eights in period 7 and 8 was because of summer.

Summary of all generations

GENERATION	01	03	05	08
WEEKS DATA	40	50	58	63
Age at maturity	144	144	142	146
Weight at 18weeks		1370	1352	1370
Weight at maturity	1766	1712	1632	1726
Weight at 40weeks	1800	1719	1964	1990
TE	124	215	257	271
HE	120	180	230	257
HEPP	60.7	79.8	82.6	84.9
Egg Weight	50.8	52.3	54.9	59.3
Egg weight at Peak	59.9	54.0	59.8	60.6
Expected eggs to72weeks. (H.D)	291	297	318	324

Conclusions

17% selection has progressively improved the performance of over the generations.

Selection for Rate of lay did not reduce the age at maturity. The egg size is well maintained over 8 generations. There has been a consistent improvement in biosecurity and vaccination programs. No medication was used. Besides the breeding value, subjective selection was done basing on family mortality, abnormal body weights, abnormal egg weights etc. All selected birds were tested for Avian Leucosis Virus shredding. The flocks were maintained Salmanella free. All the physical progress seen may not be genetic. This is a commercial selection program. No genetic control population was maintained.

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LP-3

RECENT ADVANCES OF BREEDING STRATEGIES FOR PIG

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Animal husbandry is an important sub-sector of agriculture in India and among various animals; piggery is the sector that directly influences the socio-economic status of the rural poor, more particularly the tribal population of the country as it acts as an insurance coverage for the downtrodden and socially weaker section of the society. Pig production in India has enormous potential to upscale the economics of rural masses of the country due to its high fecundity, good feed conversion efficiency, shorter generation interval and relatively smaller space requirement.

Pig farming has the potential to provide employment opportunities to seasonally employed rural farmers notably in the rain-fed areas and supplementary income generation to womenfolk in their households for improving living standards. For realizing the potential, this sector requires a thorough understanding, appreciation of the present scenario, meticulous planning, mobilization of resources and training of manpower on a larger scale. Suitable circumspective measures are the need of the hour to popularize the piggery husbandry with adequate technical interventions to modernize this sector and improve the productivity of smaller sized rural pig farms.

1. Pig population statistics

According to the 20th livestock census of India's pig population is about 9.06 million in comparison to the world population of 967.39 million (FAOSTAT, 2017 data (http://faostat.fao.org) which constitutes 0.94% of world pig population. Pig constitutes a mere of 1.69 percent of total livestock population (535.75 million) of the country; still needs much attention for its improvement. A gradual decrease in population may be essentially due to diminishing population size of native pigs and higher interest of farmers towards faster growing crossbred pigs like Hampshire crosses in north and north-eastern part, Large White Yorkshire crosses in southern and central part and Tamworth crosses in central and eastern part of India along with heavy mortality and low fertility due to introduction of different diseases like ASF, CSF and PRRS.

2. Pig genetic resources:

Pigs are widely distributed in all the eco-regions of the country and are an important occupation of the rural society especially the tribal masses. People of certain ethnic groups prefer to keep more pigs, especially black ones, for festivals and ceremonial purposes. Broadly Indian pig population consists of three types; indigenous, exotic and crossbred.

2.1 Indigenous pig germplasm:

Out of total pig population, 79.03% are indigenous and non-descript. Most of these breeds/varieties are yet to be characterized with proper scientific intervention. These pigs are of smaller size and almost no efforts have been made for any conservation and selection experiment to improve its economic traits, such as litter size, birth weight, weaning weight, average daily gain, feed conversion efficiency and carcass traits. These animals are well adapted to hot and humid environment and supposed to have better disease tolerance. The indigenous pigs of India identified as a distinct group as a result of gradual domestication of wild pigs to their surroundings. These pigs differ in their characteristics and colour from region to region within the country depending the topography and climatic conditions. Following (Table 1) are the native/indigenous pig germplasm available in different parts of the country:

Table 1: Registered pig breeds of India

Sl.	Name of the breed	Distribution (state)	Accession No.
	Ghungroo	West Bengal	INDIA_PIG_2100_GHOONGROO_09001
	Niang Megha	Meghalaya	INDIA_PIG_1300_NIANGMEGHA_09002
	Agonda Goan	Goa	INDIA_PIG_3500_ AGONDAGOAN _09003
	Tanyi-Vo	Nagaland	INDIA_PIG_1400_ TENYIVO _09004
	Nicobari	A&N Island	INDIA_PIG_3300_ NICOBARI _09005
	Doom	Assam	INDIA_PIG_0200_ DOOM _09006
	Zovawk	Mizoram	INDIA_PIG_2700_ ZOVAWK _09007
	Gurrah	Uttar Pradesh	INDIA_PIG_2000_GHURRAH_09008
	Mali	Tripura	INDIA_PIG_1900_MALI_09009
	Purnea	Bihar, Jharkhand	INDIA_PIG_0325_ PURNEA_09010
	Banda	Jharkhand	INDIA_PIG_2500_BANDA_09011
	Manipuri Black	Manipur	INDIA_PIG_1200_MANIPURIBLACK_09012
	Wak Chambil	Meghalaya	INDIA_PIG_1300_WAKCHAMBIL_09013

Some other prominent variants of pigs like Andaman Wild, Andaman Local, Ankamali, Burudi, Dome, Golla, Lepchamoun, and Pondi/Jhinga are yet to be characterized for registration.

2.2 Exotic pig germplasm:

Due to poor performance of indigenous pig germplasm and for further upscaling the performance of piggery sector in India, exotic pigs have been imported by different Government and non-Government organizations during past as per recommendation of National Commission on Agriculture (NCA). These breed were extensively used for subsequent crossbreeding programme. Berkshire, Charmukha, Duroc, Hampshire, Landrace, Large Black, Large White Yorkshire, Middle White Yorkshire, Tamworth and Wessex Saddleback are the major known exotic breeds imported in India for piggery developmental programme. These breeds have well studied in different All India Coordinated Research Project on Pig (AICRP), State Government and privet sector farms.

2.3 Crossbred pig germplasm:

Piggery developmental programme undertaken by central and state departments namely DADHF of Government of India, Veterinary and Animal Husbandry Department and Animal Resource Development Departments of different states and research organization viz. ICAR, CAU, SAUs has resulted in noticeable progress over the time. During the initial period of development, focus was on genetic improvement of indigenous pig through selective breeding. Subsequently exotic breeds were imported to India and efforts were made for stabilize their performance in Indian agro-climatic condition. Consequent to slow progress of indigenous pigs and based on demand, crossbreeding of native pigs with exotic boars gained momentum in different parts of the country. Several crossbred pig germplasm has been reported till today by different organizations.

The crossbred germplasm of India includes high-producing varieties viz. Rani, Asha, HD K-75, Lumsniang, Jharsuk, Mannuthy White, TANUVAS KPM Gold, SVVU T-17 and Landlly suitable for different agro-climatic condition of the country.

3. Conventional pig breeding:

Genetic improvement in pigs began several centuries ago leading to a clear transformation from the wild pig to the domestic pig. The genetic improvement at that time was based on empirical methods or due to 'unconscious selection', as termed by Darwin (1859). The methods became more scientific after the discovery of Mendel's principles and the development of genetics as a scientific discipline.

In Scientific breeding programme, pig breeding operate in a three-tier pyramidal structure (Fig. 1). At the peak of the pyramid is the nucleus breeding *farms* that actually generate the genetic changes, followed by the next tier of *multiplier farms* that carry out specific mating or crossbreeding for the production of large numbers of females. These females are then sold to *commercial producers* for *piglet production* and *finishing* to produce market pigs that are sent to slaughterhouses to produce the pork.

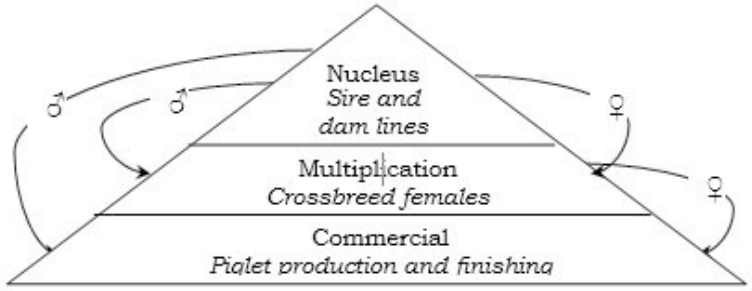


Fig. 1. Pig breeding pyramid (Source: Dekkers et al., 2011)

The nucleus farm actually conducts breeding and selection for the genetic improvement of specific breeds or lines. They target their selection programmes to the needs of their customers, the pork producers and processors. However, there is a time delay between the genetic improvement in the nucleus farms and the transfer of genetic gains to commercial producers through multipliers. This delay is typically 3–5 years and is called *genetic lag*. It is, therefore, very important for the nucleus breeders to evaluate the future needs of producers ahead of time and decide their breeding goals accordingly.

The conventional genetic improvement programmes are driven by measuring phenotypes for traits of interest on selection candidates in the nucleus or on close relatives of the selection candidates. These phenotypes are then used to estimate the breeding values of selection candidates for traits and incorporate these in a multi-trait selection index to identify individuals that best meet the breeding objective. Although this has led to impressive increases in performance for several traits, the phenotype-based approach to genetic improvement suffers from several important limitations.

- Several traits have low heritability, e.g. reproduction, disease resistance and survival traits. This limits the accuracy and efficiency of selection and, therefore, genetic improvement for these traits.
- Several traits can only be measured later in an animal's life, e.g. sow lifetime productivity. This either increases generation intervals if the choice is made to wait until the phenotype can be observed on the selection candidates, or reduces accuracy of selection if the choice is made to make selection decisions before the phenotype is observed.
- Several traits cannot be measured directly on selection candidates. For example, many meat quality traits require slaughter of the animal. Thus, for these traits, genetic evaluation is based on phenotypes of relatives that are slaughtered, limiting the accuracy of selection as well as the selection intensity, as individuals that may be potential selection candidates are slaughtered.
- Some traits are expensive to measure (e.g. disease resistance). Phenotype-based programmes

require routine collection of large numbers of phenotypes on the selection candidates themselves or their close relatives, resulting in costs that may not outweigh the benefits.

- The increased emphasis that is placed on relatives in many of the above situations also leads to greater rates of inbreeding within the selection lines. The higher rates of inbreeding result from family members having very similar estimates of breeding values (EBV) if these EBVs are heavily based on phenotypes of parents, full sibs and half sibs rather than on own performance or progeny performance. Thus, selection tends to be of families rather than individuals within a family, resulting in selected individuals being more closely related and higher rates of inbreeding.
- Whereas the main focus in pig breeding programmes has been on the genetic improvement of additive genetics through selection on EBV, most traits of interest exhibit non-additive effects, e.g. through heterosis when crossing breeds. Traditional quantitative genetics, however, offers limited opportunities to select for non-additive effects.

With the implementation of molecular genetics in the 1980s and 1990s, in particular the discovery of new classes of DNA polymorphisms, prospects to overcome these limitations of phenotype-based selection emerged with the potential to directly select on an individual's genotype for genes or genetic markers that are associated with the trait.

4. Advanced pig breeding:

4.1 Open Nucleus Breeding Scheme (ONBS):

Open Nucleus Breeding Scheme (ONBS) is a three tier system of pig production comprising of nucleus herd, multiplication herd and commercial herd. The nucleus herd actually conducts breeding and selection for the genetic improvement of specific breeds or lines. They target their selection programmes based on the needs of customers, the pork producers and processors. However, there is a time delay between the genetic improvement in the nucleus farms and the transfer of genetic gains to commercial producers through multipliers. This delay is typically 3 to 5 years and is called genetic lag. It is, therefore, very important for the nucleus breeders to evaluate the future needs of producers ahead of time and decide their breeding goals accordingly. Open nucleus breeding schemes (ONBS) should be followed as a model for pig industry in developing countries. The reasons for following ONBS are that the breeding stock is concentrated in a few herds from where the quality animals are disseminated to other units and moreover good record keeping and data management at reasonable cost, will ease the functional operation.

In order to have a successful ONBS at a large scale, use of artificial insemination (AI) with frozen semen is essential. AI using frozen or liquid semen is a prerequisite for large scale development of any animal husbandry sector. AI in pig using frozen semen still remains as a formidable challenge in India with limited success only on experimental basis.

4.2 The Quantitative Trait Loci (QTL) explosion and deception:

Since the late 80's and 90's, the availability of neutral molecular markers, such as the microsatellites, encouraged the development of a plethora of experimental studies to locate genomic regions and Quantitative Trait Loci (QTL) associated with traits of economic interest.

Initially, two basic designs were used. The first uses the linkage disequilibrium between markers and QTL generated by crosses. Typically, animals are generated by crossing breeds that are highly divergent for the traits of interest (for example European wild boar and domestic Large White). The second design uses mainly the within-family linkage disequilibrium. This design is especially well suited analysis of large half-sib families within a breed. This activity has been very successful. By

January 2014, in the data base http://www.animalgenome. org/QTLdb/, a total of 9862 QTL for 653 different traits have been identified for pigs.

After detecting a QTL, the next task is to locate the gene responsible (causal mutation). In QTL detection studies, we can locate one QTL in a chromosome as a region of about 20-40 cM (probably harbouring 200-400 genes) which made it difficult to identify the underlying gene responsible. To refine the position several actions can be taken: to increase the number of individuals, to carry out fine mapping or to try the 'candidate gene approach'. All these approaches are difficult, expensive in terms of time and money and success is not guaranteed, thereby making the location of the responsible gene a formidable task. The difficulties for finding the causal mutations can be exemplified by more than 9000 QTLs reported in pigs, of which less than a dozen of causative mutations have been firmly established. Interestingly, the first QTL reported in livestock was FAT1 QTL located in swine chromosome 4 (Andersson et al., 1994); however, its causal mutation is still unknown.

4.3 Marker-Assisted Selection (MAS):

Various candidate gene and quantitative trait loci (QTL) analyses have recognized substantial chromosomal regions and individual genes linked with traits of economic interest in pig. These comprise QTL for meat quality traits, back fat, growth and reproduction. Some commercially used traits for Marker Assisted Selection (MAS) in pig industry are given below.

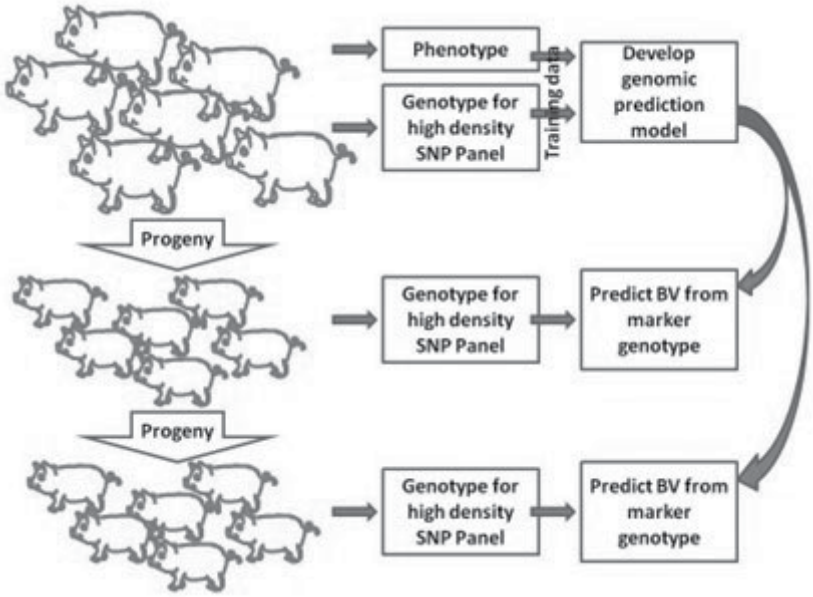
Table 2: Commercially used traits in Marker Assisted Selection (MAS) in swine industry

Trait	Marker	Name	Chromosome
Litter size	Oestrogen receptor	ESR	1
	Osteopontin	OPN	8
	Prolactin receptor	PRLR	16
Lean growth	Marker for fat	SO112	1
	Insulin like growth factor	IGF2	2
	Myogenic factor 3	MYF3	2
	Marker for fat	SO107	4
	Leptin receptor	LEPR	6
	Marker for fat	SO102	7
	Myostatin	GDF8	15
Meat quality	Skeletal muscle calpain	CAPN	1
	Calpastatin	CAST	2
	Halothane gene	RYR1	6
	Rendement Napole	RN	15
Intramuscular fat	Heart fatty acid binding protein	H-FABP	6
Immunity	Tumour necrosis factor	TNFB	7
	Histocompatibility	SLA-1	7
Coat color	Dominant white	KIT	8

4.4 Genomic selection:

Recent developments in technology have removed some of the limitations of previous applications of QTL-mapping results for MAS, which, as already mentioned, have limited the use of markers in commercial breeding. These developments include genome sequencing, the identification of large numbers of genetic markers across the genome in the form of SNPs, and the cost-effective high-throughput genotyping of tens of thousands of such SNPs on individual animals. Combined with the further development of statistical methods for analysis of molecular data, this has led to a paradigm shift in the strategy of using genetic markers for the prediction of breeding values in the form of what has been termed 'genomic selection' (Meuwissen et al., 2001). Genomic selection (GS) is an enhanced version of MAS that involves the selection of animals for breeding on the basis of their genotype for tens of thousands of 'random' SNPs that cover the genome. In GS, the association of each SNP with phenotype is estimated using sophisticated statistical and quantitative genetics models without pre-screening markers based on significance.

The first step in GS is to collect phenotypes and DNA from a large group of individuals that have been phenotyped for the trait, or that have progeny with those phenotypes, and to genotype each animal using the SNPChip. The resulting 'training data' are used to 'train' a statistical model that estimates the effect of each of the SNPs on the SNPChip with the trait phenotype. In principle, the estimate for a given SNP is based on the comparison of the average phenotypes of individuals that have alternative genotypes at that SNP, as described above, but with GS this is done simultaneously for all markers on the SNPChip. The resulting estimates can then be used to predict the 'Genomic' EBV (G-EBV) of new individuals based on their genotypes for the SNPChip.



(Reproduced from: Dekkers et al., 2011)

(SNP: single nuclear polymorphism; BV: breeding variation)

Fig. 2. Steps in genomic selection.

In the pig breeding industry GS had raised great interest. The accuracy of the breeding values for the target traits, generally low compared to dairy cattle, can be significantly increased, preserving the generation interval and control of inbreeding. The effectiveness of GS depends largely on the level of linkage-disequilibrium (LD) that can be captured by markers within the target population. The higher the level of LD, the fewer markers are needed to capture the genomic regions contributing to the phenotype. In a survey of several swine lines, Deeb et al. (2010) found that a few thousand equally-spaced SNP achieved average LD of 0.2 or higher in most pure lines and crosses evaluated. Moreover, of the 62k markers on the commercially available PorcineSNP60 BeadChip, over 50k SNP had allele frequencies of 5% or higher in most pure-lines and crosses, indicating that the commercial chip provided enough markers to be effectively used for genomic selection of all line groups. The improvement of genetic gain on the nucleus has an important impact on the large commercial populations and can make GS economically feasible, given the large influence of elite individuals. Pig breeding schemes currently have developed a very efficient data recording scheme which easily could include genomic information. However, in spite of these advantages, GS in pig has only recently be implemented and it is still not so common as in dairy cattle. First, the rather recent availability of the SNP chip technology for pigs has delayed its introduction. Second, the peculiarities of pig breeding schemes (e.g. small nucleus size, diversity of breeding goals, pyramid system) made genomic evaluation strategies not straight forward to implement. In the last years, many efforts have been done to evaluate new methods and strategies to allow efficient implementation of GS on pigs.

5. Assisted Reproductive Technologies (ART) in pig breeding:

Global needs for foods and animals require the development of strategies beyond traditional breeding ensuring offspring of value characteristics, of high productivity but maintaining genetic diversity. In any livestock venture, reproductive performance is often the number one contributor to profitability. Improved reproductive performance requires an understanding and utilization of innovative approaches to the synchronization of breeding and farrowing, while maintaining adequate litter size and maximizing the contribution of elite genetics to future progeny. Below are some of the reproductive technologies that are currently being applied in swine industry.

5.1 Oestrus synchronization

Synchronization of oestrus in swine herds is essential to maintaining large farrowing groups and has permitted efficiencies in production, management and marketing. The most common method of oestrus synchronization in sows is weaning litters at the same time. Generally, most of the sows will begin oestrus within 4-7 days following weaning. This method is widely used throughout the swine industry and is consistently reliable in sows. Gilts, in contrast, represent a significant proportion of the breeding inventories for most swine herds, and synchronizing gilt oestrus can be more challenging.

In pigs, PMSG is exclusively used to induce superovulation (SO). Superovulation is stimulated in prepuberal gilts by application of 1000-1500 IU PMSG followed by an injection of 500 IU hCG 72 h after PMSG. In cycling gilts SO is induced after estrus synchronisation (feeding of Regumate® for 15 days) by administration of 1500 IU PMSG and of 500 IU hCG 78 h later. Multiparous sows are injected with 1000-1250 IU PMSG 24 h after weaning and 500 IU hCG 58 h after PMSG. The use of GnRH is an alternative to hCG in triggering ovulation. Gilts and sows are fixed-time inseminated 24 h and 38 h after hCG injection.

5.2 Artificial Insemination (AI)

AI has dramatically advanced the genetic improvement of pigs and is the standard operating procedure on major swine farms. The downside of AI in pigs is that the long uterine horns of females

require a volume and sperm count that limits the boar to producing an average of 20-30 AI doses per ejaculate. To overcome this, investigators have been developing approaches to insemination that can reduce both the volume and sperm numbers required per dose. These approaches require the delivery of the semen past the cervix (i.e. post-cervical or intrauterine insemination) or further into the uterine horns (deep intrauterine insemination, also referred to as low-dose insemination). Strategies capable of maintaining average litter size while significantly reducing sperm numbers are required to advance the utilization of sex-sorted sperm and frozen-thawed semen to widespread commercial application.

Currently, swine producers typically utilize two doses of semen, each about 24 h apart, and beginning at the onset of oestrus. The reason that two doses are used is because the length of behavioural oestrus is highly variable between females (24-72 h), and, given that the timing of ovulation relative to the duration of oestrus is quite variable, it is difficult to establish appropriate insemination timing for a single dose.

5.3 Semen and embryo cryopreservation

Cryopreservation of semen and embryos from pigs has presented more of a challenge than in many other species. Although boar semen has been frozen and used for AI for 35 years, the success rates are still low. Boar semen is sensitive to changes in osmotic balance, oxidative stress, low temperatures and the toxic effects of exposure to cryoprotectants. As sperm survivability after cryopreservation can be low, deep uterine insemination is the preferred method of AI.

Similar to sperm, pig embryos are especially sensitive to a decrease in temperature. Interestingly, removal of the numerous lipid droplets appears to alleviate this sensitivity. However, the lipid removal techniques generally compromise the zona pellucida, thus creating the possibility of pathogen entry. Other strategies, such as destabilizing the cytoskeleton, altering the vitrification conditions or using a solid surface for cryopreservation, have been successfully employed. Additional research is needed to develop these technologies for widespread commercial application.

5.4 Embryo transfer (ET)

Utilization of ET in the swine industry is much less advanced than the significant progress in the beef industry. The greatest advantage of any ET programme is that it permits an increase of the genetic contributions of select females to the herd. Perhaps one of the most limiting aspects of ET in pigs is that non-surgical collection and transfer of embryos is not nearly as successful as surgically removing and transferring embryos. While investigators have been capable of producing piglets following non-surgical ET, the efficiency still lags significantly behind surgical methodologies.

More recently, pig ET has become somewhat commercialized in an effort to flush embryos encapsulated in their zona pellucida from diseased herds, appropriately wash/sanitize them and transfer them to recipient pigs that have a specific pathogen-free status. While this strategy is not economically viable for many swine herds, it is being utilized as a method for salvaging elite and/or valuable genetic stock from herds before depopulation.

6. National guideline for formulation of state pig breeding policies:

The National Guidelines for formulation of State Pig Breeding Policy of Department of Animal Husbandry, Dairying & Fisheries, Government of India developed in collaboration with ICAR-National

Research Center on pig focused on outline of pig-breeding needs of the country, leaving flexibility to States to work upon as per their requirement within the frame-work with the following objectives:

1. Genetic improvement of local pigs through selective breeding
2. Conserve/maintain nucleus hard of well-developed indigenous pig germplasm.
3. Genetic improvement of local/non-descript animals by crossbreeding and gradually replacing the non-descript animals with crossbred germplasm of desired level of exotic inheritance.
4. Maintenance of well-developed planned crossbred animals at farmers' field.
5. Expansion and strengthening of breeding infrastructure and support mechanism to propagate elite germplasm through Artificial Insemination (AI).
6. Holistic development of piggery sector *w.r.t.* breeding, feeding, management, housing, value addition and marketing. The target is to improve the integration and position of local farmers and entrepreneurs into a pig-production and marketing value chain.

As per the national guideline, pig breeding operate in a three-tier pyramidal structure (fig.3). At the peak of the pyramid is the nucleus breeding *farms* that actually generate the genetic changes, followed by the next tier of *multiplier farms* that carry out specific mating or crossbreeding for the production of large numbers of females. These females are then sold to *commercial producers* for *piglet production* and *finishing* to produce market pigs that are sent to slaughterhouses to produce the pork. The functionalities of different tire is delineated in figure 4 for development of high producing crossbred pig varieties.

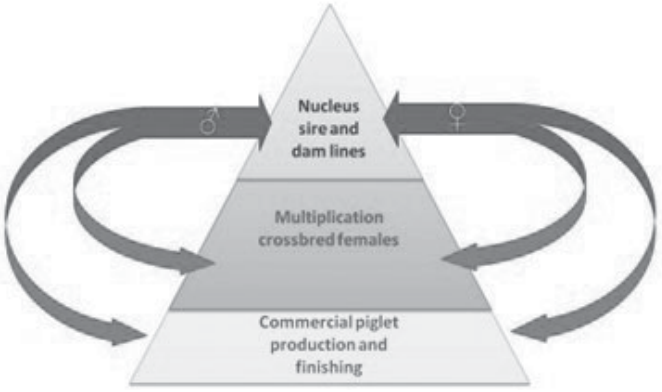


Fig.3. Breeding Pyramid

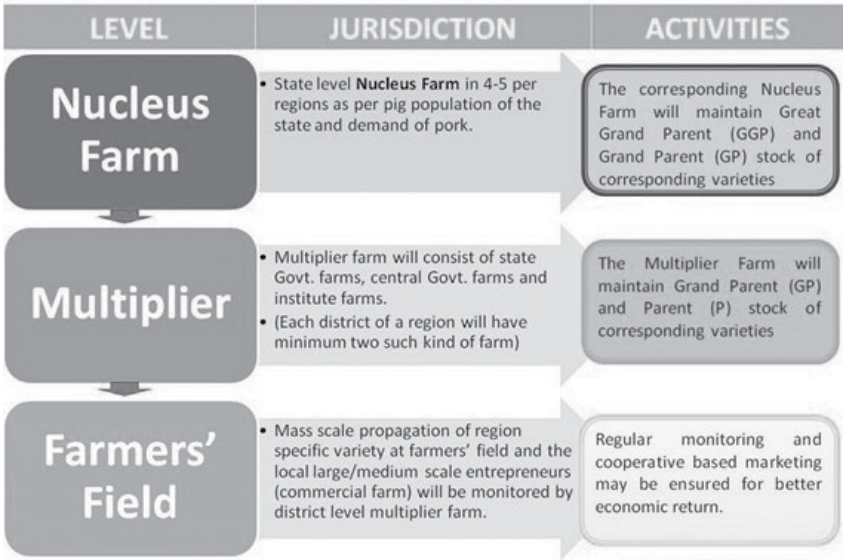


Fig. 4. Schematic diagram for pig breeding programme at different tire

The policy also delineated issues on culling, Traceability and disease control, Capacity building, subsidy and financial support and Infrastructure development in the states.

7. Implementation of National Guideline and formulation of state specific pig breeding policies:

In line with National guideline for formulation of pig breeding policies, different states have already formulated and notified state pig breeding policies with main objective of conservation of indigenous breed as well as development of high-producing crossbred varieties. The state pig breeding policies follows the pyramid structure for pig breeding as given in figure 3. Following (Table 3) are the states with choice of exotic breeds:

Table 3: States with Pig breeding policies

Sl. No.	Name of the state	Choice of exotic breed as per state pig breeding policy
	Assam	Hampshire, Large Black, Large White Yorkshire and Landrace
	Arunachal Pradesh	Hampshire, Large White Yorkshire and Large Black
	Nagaland	Hampshire or Large Black
	Tripura	Large White Yorkshire, Landrace and Hampshire
	Manipur	Large White Yorkshire and Hampshire
	Mizoram	Large White Yorkshire, Hampshire and Landrace
	Meghalaya	Hampshire and Large White Yorkshire
	Sikkim	Hampshire, Large White Yorkshire and Tamworth
	Punjab	Large White Yorkshire and Landrace

A total of 262 exotic pig of Large White Yorkshire and Hampshire bred was imported to India in the month of February, 2020 from the United Kingdom. This imported germplasm will be maintained at the nucleus farm by selective breeding. Further, the potential of exotic germplasm will be exploited for planned crossbreeding programme with local breeds. This will also help in developing the new replacement stock of existing high-producing crossbred varieties. The imported animals will be kept at nucleus farm following necessary recommended bio-security measures.

Conclusion

The pig breeding programmes have been very successful in effecting genetic improvement of economically important traits, especially daily gain, back fat thickness, and feed efficiency. However, this is not enough for the future protein requirement. In commercial pig breeding programmes selection limits have not been reached yet. The steps taken by different state Government bodies including the central Government for piggery developmental activities will not only target socio-economically weak communities including women folk in terms of their sustainable livelihood security but also address the issues of pig production system under changing climatic scenario by improved production and productivity. It is also expected to mitigate the current demand supply gap and open avenues for development of entrepreneurship and export of pork and pork products.

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LP-4

STEM CELLS: AN EFFECTIVE TISSUE ENGINEERING AND EX-SITU CONSERVATION APPROACH IN ANIMALS

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Stem cell biology has attracted tremendous interest recently. It is hoped that it will play a major role in the treatment of a number of incurable diseases via transplantation therapy. Several verities of stem cells have been isolated and identified *in vivo* and *in vitro*. Very broadly they comprise of two major classes: embryonic/fetal stem cells and adult stem cells.

Stem cells from adult tissues are attractive materials for cell therapy, gene therapy, and tissue engineering. These cells generally have restricted lineage potential when compared to embryonic stem cells, and this may be advantageous in certain therapeutic applications. Till and McCulloch in 1961 describes the presence of hematopoietic progenitor cells in bone marrow. After this, the concept of MSCs is brought to light by Friedenstein and co-workers who demonstrated the osteogenic potential of BM cells by heterotrophic transplantation. Friedenstein and Owen called this cell an osteogenic stem cell or a BM stromal stem cell. Although the pioneering work of Friedenstein and Owen is firmly established, the concept of non-hematopoietic stem cell came into light only after the publication of similar work by Pittenger *et al*. in 1999. The term mesenchymal stem cells (MSCs) are first coined by Caplan (1991) as an alternative to “stromal” or “osteogenic” stem cell.

Stem cells are defined by the following three criteria. First, stem cells undergo self-renewing cell divisions; that is, they can give rise to at least one daughter cell that is identical to the initial cell. A characteristic required to maintain the stem cell pool. Second, stem cells undergo lineage commitment and differentiation, giving rise to more differentiated progenitors, precursor cells, and ultimately terminally differentiated cells. Third, stem cells repopulate in a robust fashion, a given tissue where they differentiate in response to specific cause to differentiate into cell types of that tissue that can take over the function of that tissue. The best example of a stem cell is the bone marrow derived mesenchymal stem cell (BM-MSC) that is unspecialized and able to specialize into bone, cartilage, liver, or blood cells under different signals /environment with new special function.

Mesenchymal stem cells (MSCs) are multipotent stem cells and ability to self-renewal and can differentiate into several mesodermal cell types including osteoblasts, chondrocytes, adipocytes, myocytes, tenocytes, beta-pancreatic islets cells and neuronal cells. Minimal criteria for defining MSC according to International Society of Cell Therapy (ISCT) are (1) they must be plastic-adherent when maintained in a standard culture conditions, (2) MSC must express some surface antigen such as CD105, CD73, CD90, CD44 and must not express CD34, CD45, CD 14, CD19, and HLA-DR, and (3) MSC must differentiate *in vitro* into osteoblast, adipocytes and chondrocytes under specific differentiating condition.

Although traditionally MSC is isolated from bone marrow, more recent reports have detailed the isolation of cells with MSC characteristics from a variety of tissues including umbilical cord blood, chorionic villi of the placenta, Wharton’s jelly, peripheral blood, fetal liver and lung, adipose tissue, skeletal muscle, periosteum, deciduous teeth, amniotic fluid, synovium and the circulatory system. As MSCs comprise a mere 0.01□0.0001% of total bone marrow nucleated cells, *in vitro*

cell culture expansion is essential in order to get sufficient numbers for clinical applications. Isolation technique is based on the adherent properties of the MSC.

The main characteristics of MSC are: Immunomodulation, Trophic support, Differentiation, Homing, Revascularization, Anti-Apoptosis, Neuroprotection and Neuroregeneration.

Mesenchymal stem cells are characterized morphologically by a small cell body with a few cell processes that are long and thin. The cell body contains a large, round nucleus with a prominent nucleolus which is surrounded by finely dispersed chromatin particles, giving the nucleus a clear appearance. The remainder of the cell body contains a small amount of Golgi apparatus, rough endoplasmic reticulum, mitochondria, and polyribosome. The cells, which are long and thin, are widely dispersed and the adjacent extracellular matrix is populated by a few reticular fibrils but is devoid of the other types of collagen fibrils (MSC Wikipedia).

Mesenchymal stem cells have generated a great amount of enthusiasm as a novel therapeutic tool for a variety of incurable degenerative and inflammatory disease**.** MSCs are advantageous over other stem cells like ES for many reasons. First, they avoid the ethical controversy and teratoma formation that surround embryonic stem cell research. Second, many studies confirm that MSCs are immune-privileged, and therefore, represent an advantageous cell type for allogenic transplantation, reducing the risks of rejection and complications of cell transplantation therapy.

Mesenchymal stem cells uses in clinical regenerative medicine owing to their unique immunomodulatory and engraftment promoting properties. The mechanisms through which MSC exert their therapeutic potential rely on some very important biological properties of these cells: the ability to secrete some soluble molecules capable of stimulating survival and recovery of injured cells (trophic support); the ability to home to sites of inflammation following tissue injury when injected parenteral (homing); the ability to differentiate into various cell types (differentiation) and lack of immunogenicity and the ability to perform immunomodulatory function. One of the attractive advantage of BM-MSCs as a source of cell transplantation is their low immunogenicity. Recently, several studies have reported that BM-MSCs may be immune-privileged cells that do not elicit immune response due to an absence of their immunologically relevant cell surface markers. BM-MSCs also are known to inhibit proliferation of T lymphocytes, B lymphocytes, dendritic cells and natural killer cells.

Some striking examples of the therapeutic uses of MSCs have been reported recently in applications such as coronary artery disease, cardio-vascular repair, spinal cord injury, Parkinson's disease, liver regeneration, diabetes and leukemia. In orthopedics, stem cell therapy is now routinely uses in bone, cartilage and tendon repair and in the treatment of osteoarthritis.

These cells have been successfully employed in graft versus host disease treatment, heart regeneration after infarct, cartilage and bone repair, skin wounds healing, neuronal regeneration and many others. The list of reports indicating that MSCs contribute to tissue repair *in vivo* enlarges. There are examples of MSC utilization in the repair of kidney, muscle and lung. The cells are also found to promote angiogenesis. Of special importance is their use in the treatment of osteogenesis imperfecta, which appeared to be the only reasonable therapeutic strategy. MSCs seem to represent a future powerful tool in regenerative medicine.

The mechanisms of bone formation entail an orchestration of cellular, humoral and mechanical factors resulting in formation of skeletal bony tissues capable of controlled growth, structural response to stress, and repair of injury, uniquely without scar. The MSC is the basic cellular unit of

bone formation. Secondary bone healing mimics bone formation with proliferation of MSC then their differentiation into components of fracture callus. Bone regeneration, mimics bone healing can be achieved with MSC combined with strategies of osteogenesis, osteoinduction, osteoconduction, and osteopromotion. MSC based strategies first employed with isolated and culture expanded stem cells in an osteoconductive carrier to successfully regenerate new bone in an critical bone defect in animal models. This bone regeneration is as effective as autologous cancellous bone. Because MSC appear to be immunologically privileged, a study using mismatched allogenic stem cell demonstrate that these cells would regenerate bone without inciting an immunologic response, documenting the possibility of banked allogenic MSC for bone regeneration.

We have used mesenchymal stem cells-seeded bio-ceramic construct for bone regeneration in large critical-size bone defect in rabbit model. The objective of the study is to determine whether the addition of recombinant human bone morphogenetic protein (rhBMP-2) and insulin-like growth factor (IGF-1) to a silica-coated calcium hydroxyapatite (HASi) - rabbit bone marrow derived mesenchymal stem cell (rBMSC) construct promoted bone healing in a large segmental bone defect beyond standard critical -size radial defects (15mm) in rabbits. An extensively large 30mm long radial ostectomy is performed unilaterally in thirty rabbits divided equally in five groups. Defects are filled with a HASi scaffold only; HASi scaffold seeded with rBMSC; HASi scaffold seeded with rBMSC along with rhBMP-2 and IGF-1 in another two groups. An empty defect serves as the control group. Radiographically, bone healing is evaluated at 7, 15, 30, 45, 60 and 90 days post implantation. Histological qualitative analysis with microCT (μ-CT), haematoxylin and eosin and Masson's trichrome staining are performed 90 days after implantation. All rhBMP-2-added constructs induce the formation of well-differentiated mineralized woven bone surrounding the HASi scaffolds and bridging bone-implant interfaces as early as eight weeks after surgery. Bone regeneration appears to develop earlier with the rhBMP-2 constructs than with the IGF-1 added construct. Constructs without any rhBMP-2 or IGF-1 shows osteoconductive properties limited to the bone junctions without bone ingrowths within the implantation site. In conclusion, the addition of rhBMP-2 to a HASi scaffold could promote bone generation in a large critical-size-defect.

Bone marrow derived mesenchymal stem cells (MSCs) have the potential to inhibit the death of hepatocytes. It is found to stimulate liver regeneration via a paracrine mechanism, or it directly differentiates into hepatocytes and repopulates the injured liver. MSCs can differentiate into hepatocytes-like cells both *in vitro* and *in vivo* and can secrete trophic factors, including growth factors, cytokines and chemokines, which promote the regeneration of the impaired liver. We have evaluated mesenchymal stem cells for regeneration of liver tissue after partial hepatectomy in rats and concluded that rat bone marrow derived stem cells in combination with epidermal growth factor and conditioned media accelerated regeneration in liver after partial hepatectomy in rats.

It is reported that mesenchymal stem cells have tremendous role in skin wound healing. Bone marrow derived mesenchymal stem cells could promote wound healing *in vivo*, and fibroblasts originated from bone marrow are found in the repaired tissue. Allogenic mesenchymal stem cell seeded with Chitosan shows better healing potentiality than Chitosan alone in the repair of full thickness skin wound in rat model. Acellular fish swim bladder matrix seeded with bone marrow derived mesenchymal stem cells is found to be novel bioengineered biomaterials in full thickness skin repair. Excellent full thickness skin burn wound healing is observed using gene embedded porcine acellular matrix with transfected mesenchymal stem cells in rat model.

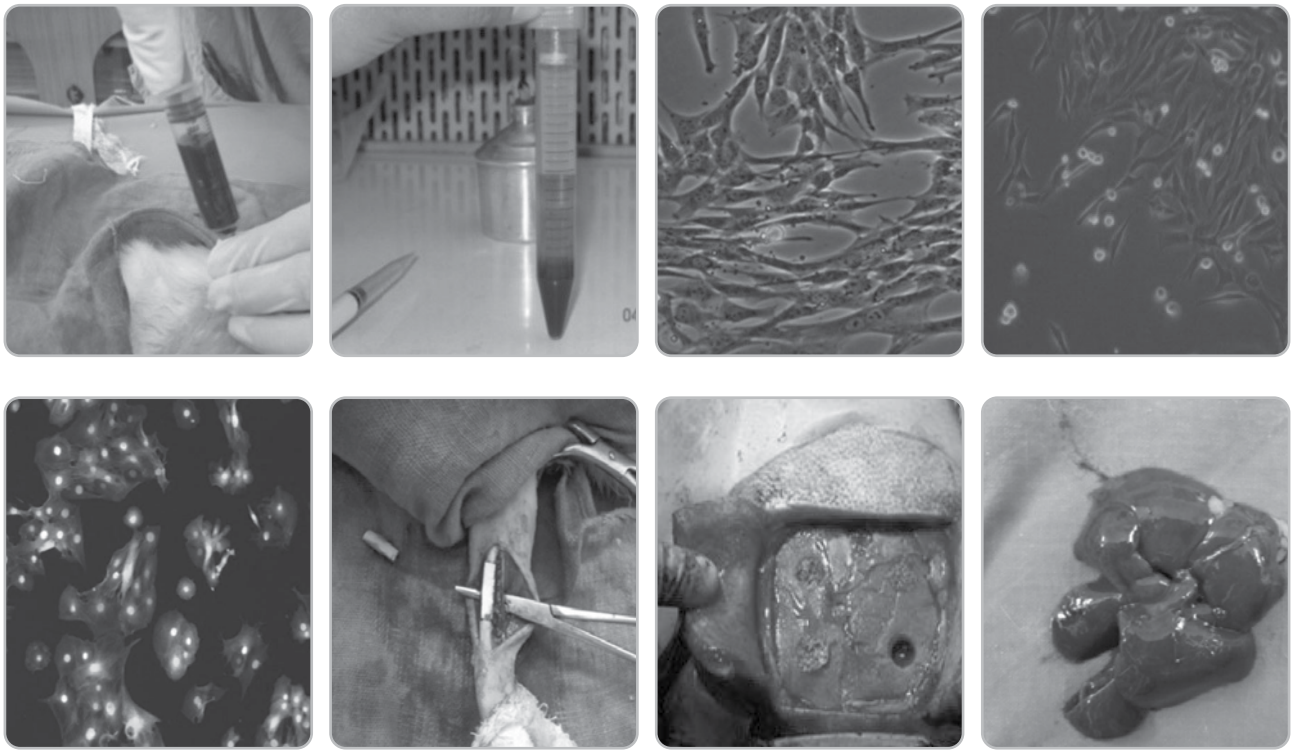
Corneal ulceration is one of the most common ophthalmic disorders in veterinary medicine. Rabbit bone marrow derived mesenchymal stem cells seeded decellularized porcine small intestinal sub-

mucosa and porcine corneas have been evaluated for their healing potential in lamellar keratectomy wound in rabbit model. It is observed that decellularized porcine cornea seeded with mesenchymal stem cells is found to have better healing potential for the repair of corneal defect and MSCs prove as immune privileged.

Chronic liver diseases like liver cirrhosis are commonly occurring potentially life-threatening conditions affecting both humans and animals. During hepatic injury, the liver regeneration processes fails due to replacement by abundant extracellular matrix (ECM) including fibrillar collagen in hepatocytes. In addition, repeated damage to hepatic cells leads to fibrosis in the liver. The end-stage of progressive fibrosis is “cirrhosis” which can be distinguished by the development of scar rings as well as a septum that encompasses the hepatocyte nodules. Liver fibrosis is usually subtle and most of the associated morbidity and mortality happens after the development of cirrhosis. In our study, we have evaluate the hepatoprotective effect of rat adipose tissue-derived stem cells (AD-MSC) with platelet-rich plasma (PRP) and rat hepatocyte growth factor HGF) individually and in combination on liver cirrhosis models in rats and revealed the synergistic ameliorative and regeneration ability of AD-MSC, PRP and HGF on chlolestasis-induced liver fibrosis/cirrhosis and they have potential to be put into clinical practice.

In this conference, I will be discussed about the procedures for collection of bone marrow from different species of animals, their isolation, culture, expansion or proliferation, cell morphology, characterization and their differentiation procedures by CD-markers, flow cytometry, staining and by using different primers.

I will also discuss and evaluate the role of tissue engineered mesenchymal stem cells impregnated with different bioscaffold and growth proteins and ex-situ conservation and therapeutic approach in animals in the field of healing of full thickness skin wound, burn wound, critical sized- bone defect, larger bone defect, corneal wound repair, liver regeneration and in cirrhosis in different species of animals.



LP-5

IMPROVEMENT OF EFFICIENCY AND PROFITABILITY FROM PACK ANIMALS

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Status of Equine and Camel Genetic Resources: World

There are 60 m horses in the world, which are found in nearly 134 countries. Most horses are found in the United States, followed by Mexico, China, Brazil, Mongolia, Argentina etc. India has 0.34 m horses and is ranked at 28th position in the world. There are 52.96 m donkeys in the world, which are found in around 104 countries. Most asses are found in Ethiopia, Sudan, Pakistan, Chad, Mexico, China etc. India has 0.25 m donkeys and is 25th in the world in terms of holding the population of the donkeys, while there are 7.91 m mules in the world, which are found in about 65 countries. Most mules are found in Mexico, followed by China, Brazil, Ethiopia and Morocco. India has 0.08 m mules and is 12th in the world from the perspective of mule population. There are 38.65 m camels in the world, which are found in nearly 46 countries. Most camels are found in Chad, Somalia, Sudan, Kenya, Niger, Ethiopia etc. India has 0.22 m camels and is ranked at 21st place in the world in terms of holding the camel population. (FAOSTAT data 2020).

Table 1. Population of equines and camels in the world (FAO 1985-2020)

Year	Camels	Mules & Hinnies	Horses & Ponies	Asses
1985	19.01	13.96	60.02	40.86
1990	19.79	14.83	61.00	43.76
1995	20.20	14.48	59.78	42.75
2000	21.84	12.88	57.73	41.50
2005	24.85	11.93	59.42	42.20
2010	29.67	9.55	58.17	40.12
2015	32.98	8.87	57.18	50.40
2020	38.65	7.91	60.00	52.96

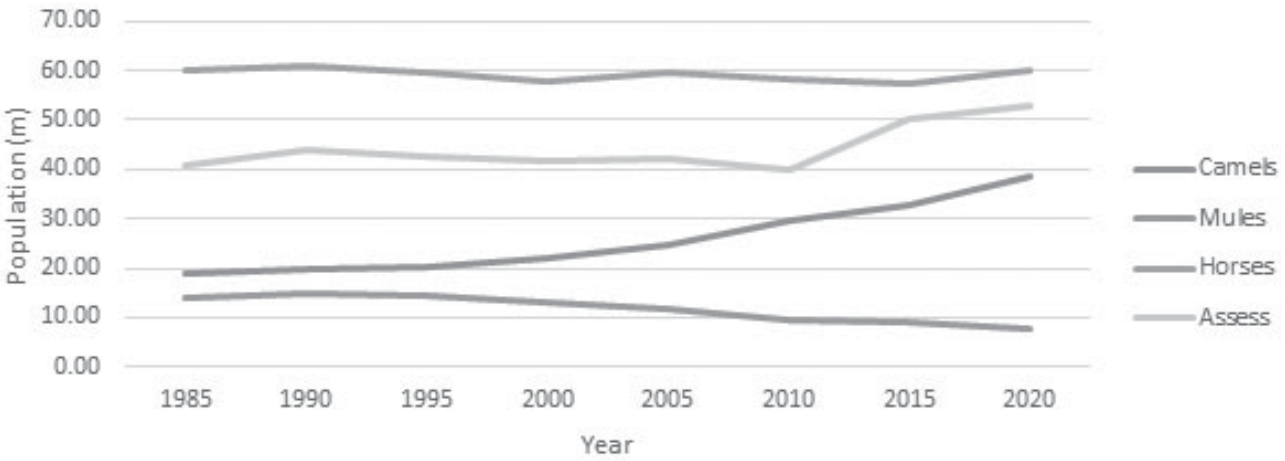

Fig. 1. Population Trend of Pack Animals in the World (FAO 1985-2020)

It is clear from above figures that the population of camels and donkeys (asses) is increasing in the world, whereas that of horses is static and mules is decreasing. The distribution of horse population is very wide as it extends over 134 countries, which indicates its stability in the world over time. Though the donkeys do have wide distribution (104 countries) but the population of donkeys in the world is increasing mainly because it is increasing in Africa, which has 62.59% of world population. In rest of the continents the population of donkeys is decreasing. The distribution of camel in the world is relatively narrow (46 countries) and around 87% of them are found in Africa and 12.82% in Asia. The population of camels is increasing in both the continents.

Table 2. Distribution of donkeys: Continents

Regions	Population	Share	Trend
World	52961925	-	Increasing
Africa	33148206	62.59%	Increasing
Americas	6665687	12.59%	Decreasing
Asia	13028473	24.60%	Decreasing
Europe	110665	0.21%	Decreasing
Oceania	8894	0.02%	Decreasing

The country-wise distribution of donkey population shows that the Ethiopia, Sudan and Pakistan have 20.4%, 14.4 % and 10.4% of the world's donkey population. Hence the trend in donkey population is largely defined by these three countries.

Status of Equine and Camel Genetic Resources: India

The population of equines and camels in the country is dwindling at a very fast rate. The 19th and 20th Livestock Census (2012-2019) data reveals that the population of horses, donkeys, mules and camels in the country is 0.34 m, 0.12 m, 0.08 m and 0.25 m, respectively and they have gone down by 45.58%, 61.23%, 57.09% and 37.10% respectively. Collectively, the equines have reduced by 52.71% during this period. (Table 3, Fig. 2).

Table 3: Population of Equines and Camels in the Country (in thousands)

Year	Horses & Ponies	Donkeys	Mules	Camels
1951	1514	1249	61	600
1956	1484	1057	39	800
1961	1327	1096	53	900
1966	1148	1054	75	1000
1972	942	994	75	1100
1977	916	917	89	1100
1982	900	1024	131	1080
1987	784	960	169	1000
1992	800	1000	200	1030
1997	800	900	200	910
2003	800	700	200	640
2007	612	438	137	510
2012	625	319	198	400
2019	340 (-45.58%)	120 (-61.23%)	80 (-57.09%)	250 (-37.10%)

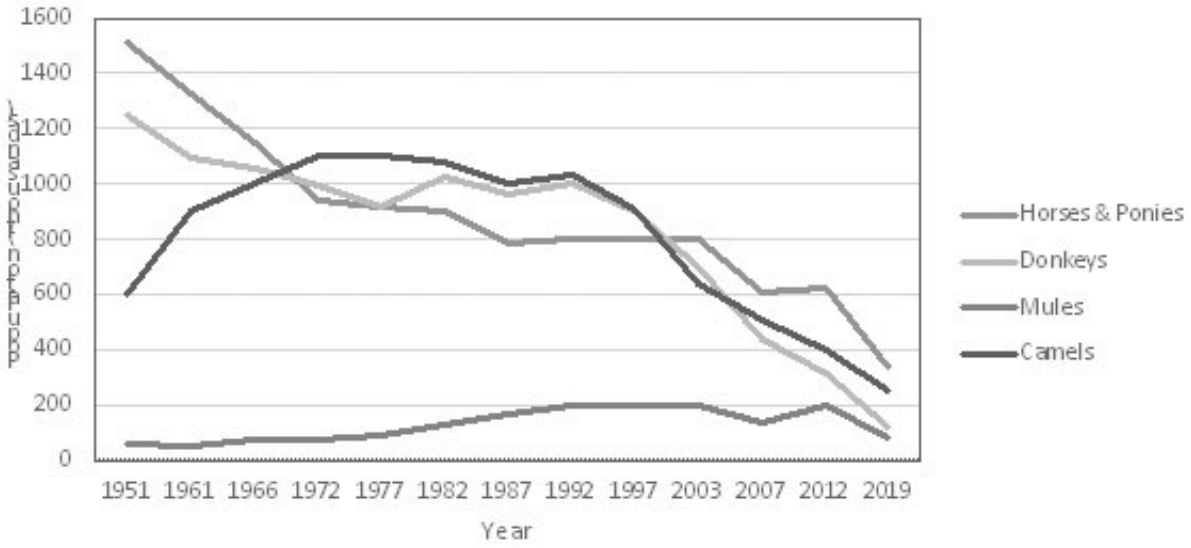

Fig.2. Population Trend : Equines and Camels in the Country (Livestock Census 1951-2019)

The states like Utter Pradesh, Jammu & Kashmir, Rajasthan, Bihar, Gujarat, Maharashtra and Punjab are among top states having sizable number of horses and ponies. Examination of the state-wise population of horses & ponies reveal that the population has declined significantly in the states like Uttar Pradesh and Jammu & Kashmir, where ponies are predominantly bred. The 20th livestock census data shows that the population of horses & ponies in UP has reduced from 1.52 lakhs to 0.76 lakhs (-50.14%) and that in J& K has reduced from 1.44 lakhs to 0.63 Lakhs (-56.17%). Still, these two states possess about 41% of the total population of horses and ponies in the country. The donkeys are most numerous in Rajasthan, Maharashtra, UP, Gujarat and Bihar states. The population of donkeys has declined significantly in the states like Rajasthan, UP and Gujarat. The Mules are most numerous in the states like Uttarakhand, Himachal Pradesh, J & K, Uttar Pradesh and Madhya Pradesh. The population of mules has declined significantly in UP and J & K. The population trend signifies that the draught use has gone down significantly leading to reduction in the population of ponies, donkeys and mules. The population of camel is chiefly concentrated in Rajasthan, which has about 85% of countries total camel population. A significant shift in the population of camel has been seen in 19th versus 20th livestock census i.e., the change in male to female ration. In 19th livestock census, the male to female ratio was 1:1.1, which has changed to 1: 2.125 in 20th livestock census, this shows significant reduction in the utility of male camels for draught power leading to a reduction rate which is more than twice than that of the females.

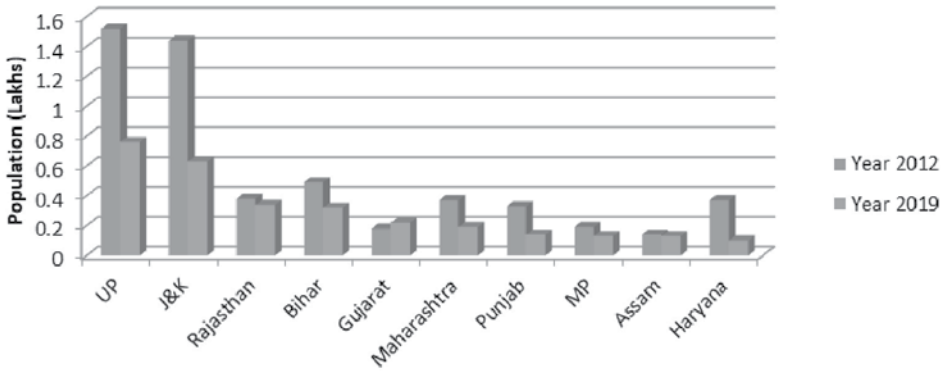

Fig. 3 : Population of Horses & Ponies (2012-2019)

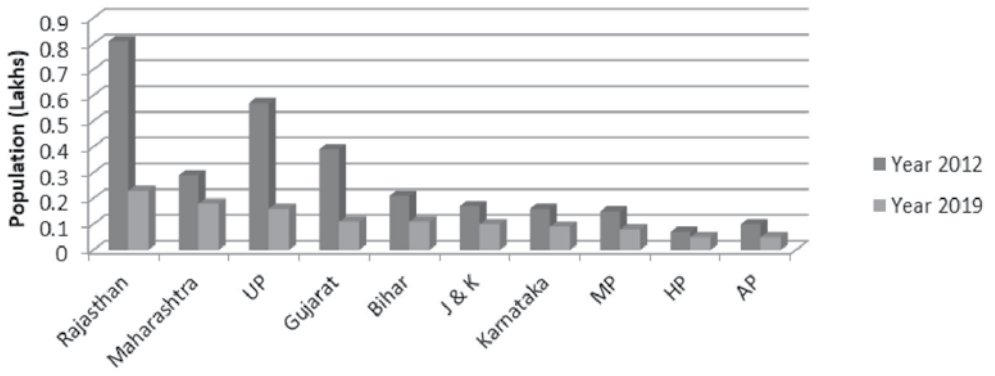

Fig. 4 : Population of Donkeys (2012-2019)

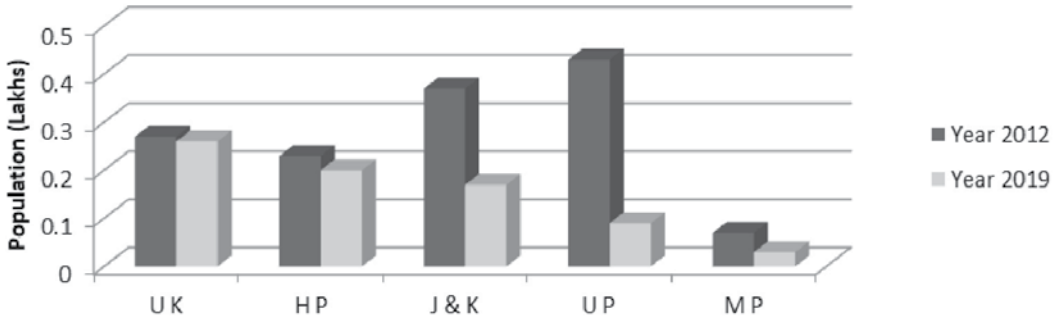

Fig. 5: Population of Mules (2012-2019)

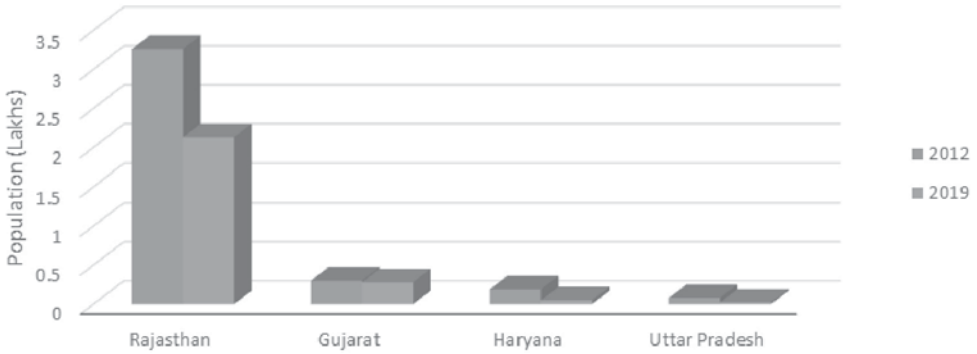

Fig. 6: Population of Camels (2012-2019)

Indian horse breeds

According to the Domestic Animal Biodiversity Diversity Information System of World Food Organization, India has 9 breeds of horses. These breeds are Arab, Bhutia Pony, Chummarti, Dakani, Kathiawari, Manipuri Pony, Marwari, Spiti Pony and Zanskari Pony. According to National Bureau of Animal Genetic Resources, Karnal, seven registered breeds of horses of India are Bhutia Pony, Kathiawari, Manipuri Pony, Marwari, Spiti Pony, Zanskari Pony and Sindhi (Kachchhi Sindhi). In addition, three other breeds viz. Charmarti, Dakani and Sikang are on the verge of extinction. The foreign breeds, such as English Thoroughbred, Water, Arab, Polish, Connemara and Haflinger were brought to India. It is believed that Arabic horses were first brought to India and this breed contributed in the creation of Kathiawari, Marwari (Malani), Sindhi and Manipuri breeds.

Indian Donkey Breeds

The origin of the asses is purely African and it is domesticated in the Neel Valley. Three wild species of them were seen in Nubian, Sudanese and Somali. Today's asses are considered related to Nubian species. According to the World Food Organization, Indian asses, Indian wild asses and kiang asses are found in India. Indian wild asses are found in Kutch region of Gujarat and Kiang asses are found in Sikkim and Ladakh. Spiti, Halari and Kachchhi are the registered breeds of donkey in the country.

Indian Camel Breeds

According to the Domestic Animal Biodiversity Diversity Information System of World Food Organization, India has 9 breeds of camels and the ICAR-National Bureau of Animal Genetic Resources, Karnal has also registered 9 breeds of Indian camel. Seven breeds viz. Bikaneri, Jaisalmeri, Kachchhi, Mewari, Marwari, Malvi and Mewati exists in both the lists, but the Sindhi and Shekhawati breeds of camel have been listed in DAD-IS and Jalori and Kharai have been listed in ICAR-NBAGR list of recognized breeds of camel.

Improvement of Efficiency: Identification of Traits

Present-day utility of Pack Animals: Global Versatility

Before the development of ammunition weapons (fire arms) in the world, the horse was the most important from view point of the war, even the donkeys were used in wars for carrying the wounded soldiers and riding. The donkeys were used as pack animal in day-to-day life of the human beings. Even today, they are still being used in hills and other places for the transport of man and material. However, invention of steam engine by James Watt in 1763 changed the entire scenario of transportation in the world. The animal driven carts were replaced by mechanized vehicles. Due to this, all draught species, e.g., horses, donkeys, bullocks, camels, mule etc. lost their utility. Still, the people in the world are versatile and they use most of the livestock species for everything that is possible, i.e., draught power, sport, meat, milk, skin, bone, urine, dung and other by-products. This is the main reason that the population of draught species is increasing globally, e.g., donkey, camel etc. Even now a days, the horses are used for sports, racing, games, rides, safaris etc. In approximately 55 countries around the world, 7,72,829 tonnes of horse meat is produced annually. In eight countries per annum 1,19,699 tonnes of donkey meat is produced and in two countries 12,087 tonnes of mule meat is produced annually. In Europe, the donkeys (small sized breeds) are also being reared as pet animal. In 36 countries 6,07,284 tonnes of camel meat is produced and in 27 countries 31,49,997 tonnes of camel milk is produced annually. There are well established camel

dairies and brands of camel milk products in Arab countries. The awareness about therapeutic utility of camel milk also has worldwide reputation due to international publications in research journals regarding diabetes, autism, cancer, various infections, heavy metal toxicity, colitis, and alcohol-induced toxicity (FAOSTAT data 2020). The asses and mules are being used exclusively for working in difficult situations and traveling to inaccessible places.

Present-day utility of Pack Animals: Indian Perspective

While the distribution of horses is quite uniform across the world, about 80 to 85% of the population of camels and donkeys' is concentrated in the underdeveloped countries of the world. The camels, donkeys, mules and ponies are still being used as pack animals for day-to-day transportation of man and material in plains as well as in hilly areas. In difficult terrains (hills and desert), even today there is no alternate transport system available to poor populations. Most of these animals are zero-input animals. People uses them and let them loose for grazing. The nomads in the country (India also) still use it to carry house hold material, ladies, kids, poultry, lambs etc. from one place to the other. In few pockets they are being used in agricultural operations, especially when the land holdings are very small and the farmer is very poor. Earlier, there used to be no data for the production of camel milk in the country. We did field survey during 2002 to 2007 and published a paper documenting the production of camel milk in the country. Since then there are several reports and now the FAO also shows annual production of 6640 tonnes of camel milk in India and the country ranks at 18th place in the world in terms of production of camel milk. However, it is well established that these species have been selected for their draught power for last several centuries by our ancestors. The present-day utility of equines and camels can be depicted as follows: -

1. Horses (Marwari and Kathiawari) – Show, Safari, Rides, Ceremonial use, Tourism and to lesser extent in endurance racing /sports
2. Horses (K-Sindhi) – *Rewal Chaal* (Endurance racing), Rides, Ceremonial use, Tourism
3. Ponies (Manipuri, Zanskari, Spiti, Bhutia) – Draught power in Hills
4. Donkeys – Draught, Milk
5. Camel – Draught, Safari, Rides, Tourism, Milk

It is very clear from above description that though there is a change in utility of the species but still the chief utility in India remains draught and the alternate utilities are yet to make a mark, though the awareness about the properties of camel milk has increased significantly and similar efforts are on for the donkey milk.

Traditional Animal Breeding Tools

The equines in this country were developed for endurance (the ability to finish in good condition) and at present also, the indigenous equine breeds are known for their endurance capacity. The present-day equine breeding of indigenous horses is focused on the improvement of endurance capacity in association with the increase in body height. Due consideration is also being given to the colour of the animals. In camels, the selection criteria have been shifted to milk but due consideration is being given to physical parameters associated with draught.

1. Accurate Performance data recording
2. Creation of databases
3. Estimation of inbreeding coefficient, heritability, genetic and phenotypic correlation etc.
4. Identification of trait(s) for selection

5. Basis of Selection
6. Methods of selection
7. Designing and implementing the breeding plan as per the requirement

Preparation of inventory of animals, creation of databases for biometry, growth, production parameters, reproductive performance and health (mortality and morbidity) are some of the basic requirements for carrying out selective breeding in equines. Using these databases, the breeding plans are prepared to improve the targeted traits by employing selection differential method or selection index method. The relationship or inbreeding coefficient is also paid due attention during the preparation of such plans. The pedigree is very important in equine breeding and when the animals are sold, the first thing the purchaser will ask is the pedigree of the animal. An animal belonging to higher performing ancestors or a particular bloodline will always be in higher demand, thus ensuring better returns to the owner.

Genome Analysis for Improving Livestock Productivity

Marker assisted selection is the need of the time as it is the only tool that is available to the geneticists to explain the production over and above that is possible by the phenotype. The phenotype and marker data put together can now explain the variability to the extent of 90% or even more. With the advancement in the technology, several throughput equipment like Illumina and MGI platforms have become available with advanced chemistries. The advancement in the field of bioinformatics has further revolutionized the field of molecular biology. Thus, application of Marker Assisted Selection in the improvement of livestock species is now being implemented. One can either go for Marker Discovery or can use already prepared SNP arrays –

1. Marker Discovery
    - Whole genome sequencing
    - Genotyping by Sequencing
    - Target Capture and Exome Sequencing
    - RNA seq / Transcriptome
2. SNP arrays / SNP chip
    - High, Medium, Low Density
    - Trait / Purpose Specific

Status in Equines

Several researchers across the world have studied different traits in equines and have worked out the association of the SNP markers with the traits of interest, including endurance and fertility. Since, these are quantitative traits with complex polygenic inheritance and low to medium heritability (h^2), the screening of animals at an early age using the polymorphic SNP markers can help the owner to do scientific selection of animals without waiting for long time till the trait is visible or expressed in terms of the phenotype.

By this time the whole genome sequencing of different livestock species and breeds has already been done. The whole genome of horse was first sequenced in the year 2006 and annotated subsequently. The Marwari horse genome was also sequenced in the year 2014. The Equine reference genome, EquCab 3.0 is now available in the Ensembl Genome Browser (http:// www.ensembl.org/ Equus_caballus/ Info/Index). Genome-wide Association Studies (GWAS) are possible and different SNP (Single Nucleotide Polymorphism) Chips are now available in the market. Initially 50K SNPs chip, followed by 75K SNPs chip were made available but now High-

Density Chip of 2 million SNPs (MNEc2M), in which whole genome sequence from 153 individuals representing 24 distinct breeds of horses was utilized, and a Low-Density Chip of 670 K SNPs (MNEc670K) is available for carrying out SNP genotyping of the animals for subsequent use in the breeding programme. The Donkey genome is also available in Ensembl Genome Browser (https://asia.ensembl.org/Equus_asinus_asinus/Info/Index?db=core) and can be used for genetic studies.

Indigenous Horse SNP Chip

The development of indigenous horse SNP chip is in progress. ICAR- NBAGR, Karnal has initiated this. The ICAR-NRCE has contributed the Marwari, Kathiawari, Manipuri and Zanskari samples. The Sindhi, Spiti and Bhutia breeds are also being included in the process of development of Marker Chip. The ICAR-NRCE is planning to record the performance data for subsequent use of the SNP chip for implementation of marker assisted selection in the breeding programme.

SNP markers for endurance and fertility

Several researchers across the world have studied different traits in equines and have worked out the association of the SNP markers with the traits of interest, including endurance and fertility. Since, these are quantitative traits with complex polygenic inheritance and low to medium heritability (h^2), the screening of animals at an early age using the polymorphic SNP markers can help the owner to do scientific selection of animals without waiting for long time till the trait is visible or expressed in terms of the phenotype. This investigation has also been carried out in Marwari, Kathiawari, K-Sindhi horses and Manipuri, Zanskari ponies. The endurance racing events of Tilwara, Jaisalmer, Surat, Bhuj, Pugal etc. were covered in the study.

iSCNT for Production of Horse Cloned Embryos

The intra and inter species somatic cell nuclear transfer (iSCNT) technique has also been explored for the production of horse cloned embryos. The protocol for isolation of oocytes from mare ovaries was standardized and maturation of iSCNT embryos was attempted in different media. The inter-species embryos matured up to 32 cell stage and intra-species embryos matured up to 64 cell stage.

Status in Camels

There are several reports of SNP discovery using WGS or GBS and using them in the selection programmes. In one of the important study a set of ~80,000 single nucleotide polymorphisms (SNPs) were developed for the dromedary camel. These SNPs are selected from whole genome sequencing (WGS) of 9 camels and Genotyping by sequencing (GBS) data of 244 dromedary camels. In another study, by using genotyping-by-sequencing (GBS) method 14,500 genome wide markers were identified to conduct a genome- wide association study (GWAS) for investigating the birth weight, daily gain, and body weight of 96 dromedaries in the Iranian central desert.

Indigenous Camel SNP Chip

A medium density SNP chip for Bactrian and dromedary camel involving indigenous breeds of camel has been developed by NBAGR and a patent for the same has been filed.

However, it is well known that the expression of same genome in different climates vary to a great extent. Defining micro-climates of each and every geographical location and finding out expression

of different genotypes (SNPs) is a very big challenge. Having sizable number of accurate records (phenotype recording) is also a big challenge because the livestock sector is an organized sector in this country. The animal holdings are very small and scattered. The poor animal keepers struggle for their own financial, nutritional, health and social security. Without accurate and sizable number of records, the validation of identified SNPs is not possible. Nevertheless, the phenotype is still the strongest guiding force and shall remain so for phenotypic selection or molecular selection. However, the molecular selection can add to it by identifying the genetic worth of an individual even when the trait is expressed at some later age or it is expressed in one sex.

Improvement of Profitability from Pack Animals

Entrepreneurship in Equines

Horse Safari: Our country is very rich in heritage. People from several countries visit India to look for the ancient art and culture. The horse safaris are being conducted in this country in different formats. Those, who have enough money can purchase horses, maintain them and conduct such safaris. Those who do not have enough resources can also come together in the form of a society, self-help group or FPO and organize such events. Tourism is a big business across the world and you can advertise yourself by having your own website, can launch your own App. and can also associate yourself with some other groups. Three to four successful safaris in a year give enough money to live a lavish life.

Horse Riding Institutions or Clubs: The metropolitan cities in the country already have race clubs where students and other citizens can go and learn riding or equestrian sports. However, in small cities this facility is not available. With the increase in per capita income, there are several aspirants, even in small cities, who wish to learn riding and giving them an avenue in the form of a riding school is a good idea. There can be batches, especially for summer and winter holidays. Recently, we had an exciting experience that an entrepreneur from Karnataka came to us and purchased Manipuri and Zanskari ponies from us. Upon enquiry about the uses of ponies in Karnataka, he replied that I am running a chain of international schools in Karnataka and these ponies, being smaller in size, would help us in staring the horse riding from smaller classes and thus we will have less risk but will have upper edge over other competing schools.

Endurance Racing or *Chal* : Most of the animal fairs are now turning into horse fairs. The number of horses is less but the participation in the fairs is more. This is mainly because of relative richness of horse owners. They visit the fairs for showcasing their horses in the rings and to take part in the race, endurance race or *chal*. The prizes are also very handsome. Wining a race, not only give the first or second prize to the owner but also increase the cost of animals genetically linked to the winning horse. The Sindhi horses are known for their *Rewal Chal* and there is lot of craze for the same. Probably because of the increased fascination for *Rewal Chal* in the state, Gujarat is the only state in the country which has shown an increase (19.42%) in the population of horses in the 20th livestock census. Though, much depends on the training of the horse and compatibility of the rider with the horse, the scientific intervention of selecting the animals at an early age by SNP genotyping either through customize endurance mini-chip or by using other techniques, would support in enhancing the income of the horse owners.

Horse Breeding: Breeding a mare with a prized stallion is a matter of money. The stallion can be a prized stallion due to its colour, height, racing potential etc. However, screening the colts or even male foals for fertility genes using customize SNP mini-chip or though other techniques, would help

the equine owners in making a better selection. Also, getting the stallions, screened for semen motility, sperm characteristics and associated parameters would help the equine owner in identifying highly fertile stallion. This will help in reducing the number of service per conception and thus would reduce the burden of transporting /bringing the mare again and again for breeding and would also reduce the inter-foaling period and thus increase in overall productivity from horse rearing.

Colour Prediction: The coat colour of the horse carries its own importance. The white horses are in great demand for the ceremonial functions. The inheritance of body colour in horses has been studied to a great extent. There are three base colors in horses. They are black, bay and red. They are controlled by the red or black extension factor and Agouti genes. The Extension gene controls the production of black or red pigment throughout the coat. The allele for black color (E) is dominant over the red allele (e), so a horse only needs one copy of the black allele to appear black-based. The Agouti gene can then modify black pigment and create bay. The Agouti gene is dominant, so a black pigmented horse only needs one copy of the Agouti gene (A) to appear bay. Agouti does not have any effect on red pigment.

There are genes that modify the base coat of the horse. They dilute the color of the horse. They are Cream, Pearl, Champagne, Silver, and Dun. The Dun, Champagne and Silver genes are dominant. The Cream gene is incompletely dominant and the Pearl Gene is recessive. Although, these genes function to dilute the pigment but they are not all expressed in the same manner. In addition to the modifiers, there are pattern genes which modify the colour by deleting (depigmentation) the colour. The experienced horse breeders have enough idea about this inheritance. However, for the newcomers, there are websites available on internet wherein one can define the colour of sire and dam using advanced option and can predict the colour of the offspring.

Polo: The history of polo suggests its origin in Persia during 6th Century BC to 1st Century AD. However, the modern game of polo was initiated in Manipur using Manipuri ponies during early part of 19th Century. However, this sport is now being played in several states and lot many sponsors have interest in it so is the case with crazy youngsters. One can train horses for the game.

Arena Polo: Arena polo is a modified version of original polo. This can be played as an outdoor or indoor game. In this polo smaller field of 300 ft x150 ft is required. The ground is enclosed by walls and the game is played in four periods of 7 ½ minutes each. The ball is like a mini soccer ball and it can be played on normal ground without grass. The arena polo has been tried successfully in Udaipur and Jodhpur. The indigenous Marwari horses have also been tried in this game and they are being trained for this game.

Sports and Race: The indigenous breeds of horses are not preferred for short distance racing and sports; however, they are more suitable for endurance racing. The Thoroughbred and other warm-blooded horses like Haflinger, Holsteiner, Hanoverian etc. are more suitable for high-quality sports because they have been bred for speed and agility for a long time. Apart from local or regional events, the equestrian sports are there in National and International games and people have fascination for them. The race-clubs in the country have their business because of the equestrian sports. The NCC also trains the students for such sports. Lot many sponsors have interest in the equestrian sports and so is the case with several crazy people of the country.

Horse Serum: Horses are well known for the production of antisera against several antigens. They are being used or the production of antisera against snake venoms, tetanus, diphtheria, rabies and several other infections. There are entrepreneurs working in this field near Pune, Bangalore, Hyderabad etc.

Animal Power: Animals have been used for their draught power across the world for centuries but with the advent of mechanized means, the use animal power to carry man and material got restricted to the places where the mechanized means cannot reach. More specifically, the animal power is mainly being used in hills and desert areas. However, with the extension of metallic road to hills, the use of horses, mules and donkeys to carry loads across difficult terrains of hills has reduced significantly. The 20th livestock census data shows that the population of horses & ponies in UP has reduced from 1.52 lakhs to 0.76 lakhs (-50.14%) and that in J& K has reduced from 1.44 lakhs to 0.63 Lakhs (-56.17%). Still, these two states possess about 41% of the total population of horses and ponies in the country.

Donkey Milk - Cosmetic and Therapeutic Use: Looking at the use of donkey milk by the queen of ancient Egypt, Cleopatra to take care of her skin and preserve the beauty, the cosmetic properties of the donkey milk are being explored. Several products are being made and marketing is being done. It is said that the donkey milk is nutritious, it has anti-ageing and healing effect due to the kinds of essential Fatty acids it has, it is rich in antioxidants. It is also rich in Vitamins A, B1, B6, C, D, E; Amino acids, Omega 3, and 6 fatty acids. It is also being used as moisturizer and softener. Several milk products for day-to-day use are also being tried. The entrepreneurs like Dolphin iba are coming up and they are exploiting the properties of donkey milk for human health and preparation of various cosmetic products for human use. The Dolphin iba has so far launched a Firmness Cream for bed sores, a Facial Kit for glowing skin and a Shower Gel Shampoo for the treatment of dandruff etc.

Country-Wide Network for Propagation of Equines: Mating of mare to a priced stallion is a matter of money in equine industry. The stallion or jack semen is being cryo-preserved only at Bikaner campus of ICAR-NRCE and it is available to only those equine owners who are bringing their animals to this place. The artificial insemination and pregnancy diagnosis in mares is little different from that in the cattle and buffalo. The Veterinary graduates across the country do not have enough practical exposure of the equine health and management practices. In order to address these issues, at ICAR-NRCE, EPC, Bikaner an initiative has been taken to train the Veterinary Doctors of the country to in equine breeding, health, reproduction and production. Also, a network for the supply of semen across the country has been initiated. In this direction, so far, we have trained 44 veterinary officers of 11 states in the country and further programmes are in pipe line.

Equine Eco-tourism: The Equine Production Campus, Bikaner is committed for *in situ* conservation and propagation of the elite equines in the country. Due to rapid mechanization of transport system, population of horses in the country is dwindling. It has been felt that there is disconnect between man and its' age-old companion, the horse. In order to strengthen this relationship, the campus has taken an initiative to conserve and propagate equines by popularizing them through Equine Ecotourism. Several new attractions like the Souvenir Shop Complex, Herbal Park, Desert Photoshoot Point, Sand Dunes, Information Centre and the Museum have been created. The impact of this initiative has so far been excellent. Further, the campus achieved another landmark and the Horse Ecotourism that has been initiated at the Campus has been included in the official website of Department of tourism, Government of Rajasthan. Recently, the Equine Ecotourism of the Bikaner Campus has been included by the website Tripadvisor, which is referred by the tourists across the globe. Hope, the innovative action would strengthen the relationship of the people with its very old and reliable companion, the horse.

Donkey Sanctuaries and Parks: Recently some Sanctuaries for the conservation and propagations of donkeys have also come up. Some of them are: -

1. Wild Ass Wildlife Sanctuary, Little Rann of Kutch, Gujarat

2. Donkey Sanctuary, Leh, Ladakh
3. Donkey Sanctuary Welfare Association, Ahmedabad, Gujarat
4. The Donkey Palace, Tirunelveli, Tamil Nadu
5. The Donkey Park, Tirunelveli, Tamil Nadu

Entrepreneurship in Camel

FSSAI approve sale of Camel Milk for Human Consumption: The Food Safety and Standards Authority of India under section 16 (5) of Food Safety and Standards Act 2006 operationalize the Standards for Camel milk on November 29, 2016. For the raw, pasteurized, boiled, flavoured and sterilized camel milk the standards are set to a minimum of 6.5% SNF and 3 % Fat.

Therapeutic use of camel milk: Camel milk has been considered unique in terms of having low fat (1.5 -3%) with much higher concentration of long chained fatty acids than short chained fatty acids and is therefore considered healthier. The protein content is low (1-2.5%). It has longer shelf life. The lactose content is 3.8 - 4.3%, ash is 0.79% and total solids are 8-11%. It is rich in minerals like Iron (0.32-0.36 mg/dl), Zn (1.2-6.3 mg/dl), Copper (0.09-0.5 mg/dl) and vitamin B_1 (0.03 mg %), B_2 (0.04 mg %), B_6 (0.05 mg %), B_{12} (0.0002 mg %) and vitamin C (40-50 mg/Kg). The essential fatty acids (linoleic and arachidic etc.) are available in adequate quantity. The camel milk acts as immunomodulatory due to the presence of high amount of lysozyme, lactoferrin, immunoglobulins and lactoperoxidase. The ratio of β-casein to □-casein is considerably higher in camel milk. Lysozyme C and β-lactoglobulin are absent and Whey Acidic Protein and Peptidoglycan Recognition Protein are present. The fresh and fermented camel milk has been found to provide potential health benefits including angiotension I-converting enzyme-inhibitory activity, hypocholesterolaemic effect, hypoglycaemic effect, antimicrobial and hypoallergenicity effect.

Therapeutic trial with human patients: The work carried out at the ICAR-National research Centre on Camel, Bikaner in collaboration with the SP Medical College, Bikaner and other institutes indicated that

1. The came milk can be used for the management of type I diabetes (The Type I diabetes results from the autoimmune destruction of the insulin-producing beta cell in the pancreas) mostly in the patients having inherent deficiency of beta –cells.
2. The camel milk is useful in the treatment of tuberculosis.
3. The camel milk has been found useful in the treatment of autism.
4. The camel milk acts as a functional food.

The world literature especially from Israel, UAE, UK and France indicated that camel milk is useful in the treatment of Jaundice, Kala-azar, tuberculosis, heart patients, high blood pressure, milk allergy in children etc.

Adaptation and single domain antibodies: Both *Camelus dromedarius* (single humped camel) and *Camelus bactrianus* (double humped camel) are the iconic animals for the mechanism of adaptation they have for the extremes of climatic situations. They survive in - 40 degree Celsius to +50 degree Celsius with scares of water and food resources. They are also known for the possession of single domain antibodies (12-15 kDa) and the unique defence mechanism against biotic stress (pathogens). They do not succumb to the diseases like foot and mouth disease and blue tongue.

Diagnostic Kit: The Bhabha Atomic Research Centre, Mumbai in collaboration with ICAR-National

Research Centre on Camel, Bikaner has developed a kit for the detection of thyroid cancer in human patients, utilizing the single domain antibodies of the camel.

Anti-Snake Venom: The production of Anti-Snake Venom against the local Snake (*Echis carinatus sochureki*) utilizing camel antibodies has been successful at experimental level. Further testing for commercial production is in progress.

Milk Products: The Centre has developed a variety of products from camel milk and most selling products are tea, coffee, kulfi, flavoured milk and lassi. Camel milk powder, ghee, ice-cream, chocolate, biscuits, peda, barfi are some other products.

Eco-tourism: The ecotourism with regard to camel is well established by this time. The camel safaris, camel riding, camel racing, camel dancing, camel decoration etc. are commonly seen in the entire western part of Rajasthan especially the Jodhpur, Bikaner, Jaisalmer and surrounding area. The camel ecotourism at ICAR-National Research Centre on Camel, Bikaner is also well established. There are several entrepreneurs engaged in this business. It can be said that eco-tourism is contributing significantly in conserving the camel under changed scenario.

Camels in Border Security Force: The BSF is still using the camels for safeguarding the international border but at the same time they are also developing border tourism like Wagah border involving camels at Babliyan in Jaisalmer and Sanchu & Khajuwala in Bikaner district of Rajasthan. border posts.

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STATISTICAL MODELLING FOR GENOME-WIDE ASSOCIATION WITH MILK PHENOTYPES IN DAIRY CATTLE

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Milk and milk products are integral part of human nutrition in many countries all over the world. The composition of milk reflects the physical, chemical and nutritional properties of milk products (Heck et al., 2009). India is the largest milk producer in the world with annual milk production of 209.96 million tonnes (NDDB, 2020-21), contributes about 22 percent of global milk production (FAO, 2021). The per capita availability of milk is increased to 427 gm/day in 2020-21 which was only 124 gm/day in 1950-51 after independence. About 45 % of the India's total milk production is contributed by indigenous buffaloes followed by 28 % by crossbred cattle and 20% by indigenous/Non-descript cattle (DAHD&F, 2020-21). The major components of bovine milk are water, fat, protein and carbohydrate, along with minor proportion of certain bioactive elements such as mineral, vitamins, peptides and immunoglobulins (Foroutan et al., 2019). These components determine the quality based pricing of the milk in several countries of the world. However, in India till now the quantity of milk is considered as the only important characteristic for dairy animals. Recently, other characteristics such as fat content, protein content, lactose content, solid-not-fat etc. were also prioritized as the demand for quality milk is expanding among customers. Knowledge about the milk composition of indigenous animals will help modify our breeding strategies for optimised milk quality production. The rearing of indigenous cattle is getting uneconomical as there is no price difference between Buffalo milk and cow milk. There is a need to valorise the milk of indigenous cattle and to sell this milk at higher prices because of its better nutritional value. Thus, milk composition is of great significance to the dairy industry. After exploring the genetic polymorphism of beta casein protein (A2 allele) in indigenous cattle and buffalo, and its positive association with human health (Kumar et al., 2019); the new area to unravel is milk minerals and fatty acid compositions in different breed of cattle and buffaloes. Identifying the variation in the fatty acid and protein content in indigenous dairy animals and crossbred cattle can be utilized for selective breeding. The fatty acid and mineral profile of indigenous bovine animals would also provide scientific data for ascertaining superiority of indigenous animal milk in terms of their milk constituents, if any. The bovine milk fatty acid fraction is characterized by a 50–70 percent of saturated fatty acids (SFA), 20–40 percent monounsaturated (MUFA) and low amount (1–5 percent) of polyunsaturated fatty acids (PUFA) (Jensen, 2002). Studies suggest that combination of about 30 percent SFAs, 60 percent MUFAs and 10 percent PUFAs in milk lipid is beneficial for human health (Soyeurt et al., 2008). Thus, the fatty acids profile of bovine milk is having still scope of selection/improvement for higher PUFAs and MUFAs. The observed difference in SFAs, MUFAs and PUFAs can be modified by different factors such as feed and genetics to get closer to the ideal fatty acid profile (Palmquist et al., 2009). The high level of dietary SFAs in humans is often associated with increase in blood cholesterol level and, subsequently an increased risk of atherosclerosis and heart diseases (Pulina et al., 2017). While, PUFAs such as conjugated linoleic acid, arachidonic acid, eicosapentaenoic acid and docosahexaenoic acid are correlated with various positive human health conditions such as anticancer effects, anti-adipogenic, anti-atherogenic, anti-diabetogenic and anti-inflammatory properties due to its cholesterol declining properties along with role in prevention and treatment of various immune disorders (Park et al.,2013). Apart from fatty acids (FAs), bovine milk is also an important source of essential minerals accounting for approximately 10 to 20 percent of daily requirement and 4 percent of body mass (Zamberlin et al., 2012). Minerals consist around 6 percent of the total milk solid and present in various chemical forms including inorganic ions and salts, and complex with organic elements such as nucleic acid, fat and carbohydrate (Summer et al., 2010).

Minerals are categorised as macro minerals which are required for human being in concentration more than 50 mg/day including Sodium (Na), Potassium (K), Chloride (Cl), Calcium (Ca), Magnesium (Mg) and Phosphorus (P) and trace elements which are required in amount less than 50mg/day including Iron (Fe), Copper (Cu), Zinc (Zn), Manganese (Mn), Selenium (Se), Iodine (I). All of these mineral elements are stated to present at some concentration in milk of bovines (Cashman, 2006). Variation in individual FAs composition and mineral concentration in milk exist between and among bovine breeds, which is further influenced by environmental as well as physiological factors (Hauget al.,2007). The effect of various genetic and non-genetic factor on milk fatty acid and minerals has been well described in literature (Buitenhuis et al., 2015; Patel et al., 2017; Gottardo et al., 2017). Genetic variation in milk constituent traits has been seen, with heritability varying from 0.22 to 0.71 for FAs (Stoop et al., 2009) and from 0.49 to 0.72 for minerals (Buitenhuis et al., 2015) Identification of genes and genomic regions that determine the variance in FAs and minerals concentration in bovine milk, may refine our understanding of their synthesis pathways This will also provide the opportunities to improve their composition via selective breeding (Tavakoli et al., 2016). Candidate gene studies have shown that polymorphisms in several genes including DGAT1(Diacylglycerol O-Acyltransferase 1), ABCG2 (ATP-binding cassette super-family G member 2) and SCD1(Stearoyl-CoA Desaturase), that are well known for their association with FAs and mineral traits in several bovine breeds (Tantia et al., 2006; Moioli et al., 2007, Buitenhuis et al., 2015; Bovenhuis et al., 2016). However, due to complexity of the underlying mechanism that influences FAs and minerals biosynthesis in milk, these major genes cannot explain all the variability in milk. Recently, with the advancements in genotyping technologies Genome-wide association study (GWAS) have emerged as a powerful method to resolve constraints of conventional Quantitative trait loci (QTL) mapping. GWAS utilises large amount of SNP markers to detect their association with economic traits based on linkage disequilibrium (Davey et al., 2011). Earlier, a total of 1,500 SNPs (Single nucleotide polymorphisms) was used to detect loci for FAs in cattle milk using family based linkage studies (Schennink et al., 2009). However, since last decade GWAS has been extensively used to investigate the genetic architecture of complex phenotypes such as milk fatty acids (Knutsen et al., 2018; Gebreyesus et al., 2019) and minerals (Buitenhuis et al., 2015) in various populations. The major advantage of GWAS is that it can even detect smaller loci associated with trait. The SNP chips with high marker density provide the opportunity to perform GWAS for complex traits (Bovenhuis et al., 2016). Genome-wide association studies (GWAS) have evolved over the last few years into a powerful tool for investigating the genetic architecture of novel phenomics. Unlike Mendelian disorders caused by a single genetic defect, most complex phenomics such as fatty acid profile in milk and carcass trait relies on multiple genetic variants and their interaction with social and environmental factors. A genome-wide association study is an approach that involves rapidly scanning markers across the complete sets genomes, to find genetic variations associated with a complex trait. With the availability of single nucleotide polymorphism(SNP)chip of various densities it is possible to identify regions, QTL and genes on the genome that explain the association and its effect on the phenotype under consideration. Remarkable advancement in dissection of the genetic mechanisms of complex traits has resulted the application of GWAS in the field of domestic animal breeding and genetics. The quantitative or polygenic traits are controlled by many genes as well as environmental factors. Most economic traits in livestock breeding are quantitative traits, and there is a tremendous interest in analysing these traits, e.g., to estimate breeding values of selection candidates or to map the underlying genes or chromosomal regions (quantitative trait loci, QTL). In 90's QTL mapping was largely based on microsatellite markers (Lipkin *et al*., 1998) whereas, now-a-days with the advent of whole genome sequencing technologies SNP along with the phenotype and pedigree information are utilized for mapping. Till date thousands of QTLs have been identified for various traits have been reported in database (http://www.animalgenome.org/QTLdb) maintained by United States Department of Agriculture(Hu *et al*., 2018). The genome wide association study (GWAS) utilises

the sequence variations (mainly SNPs) across whole genome, along with its phenotype to identify genomic regions that are truly associated with the desired trait of interest (Stranger *et al.*,2011). As compared to traditional QTL mapping strategies, GWAS covers the major advantages both in the power to detect causal variants with modest effects and indicating the narrower genomic regions that harbor causal variants (Greely, 2007; Zhang *et al.,*2012). Thus, GWAS is a new ideal technique to discover the major genes for complex traits and is a main way to study the genetic mechanism of complex traits of livestock (Ikram *et al*., 2010). Through GWAS, several novel loci and candidate genes such as FASN, LIPJ, AGPT4, DGAT1, SCD1 and GHR were identified that will provide us better insight in network and pathways for these traits (Li et al., 2014), that could be used to modify the composition of milk to according to the customer demand (MacLeod et al., 2016).

The fundamental concept of GWAS implementation is based on the assumption that a significant association can be detected between the genetic variants and the economic trait of interest because the SNPs are in LD with the QTL(Korte and Farlow.,2013). The high density of SNP markers in the chip used in GWAS was sufficient to identify the LD between SNP markers and causative mutations (Barsh *et al*., 2012; Danesh and Pepys, 2009). GWAS has become feasible in most of the livestock species with the development of new technologies in molecular genetics as well as affordable genotyping cost associated with it.

Statistical Methods for Genome-Wide Association Studies (GWAS)

Genome-wide association studies (GWAS) exploit linkage disequilibrium, which are population-level associations between markers and causative mutations. There are a number of statistical methodologies which exploit these associations. The simplest of these is the genome-wide association test using single marker regression.

Model for GWAS using single marker regression:

$$y = Wb + Xg + e$$

where y is a vector of phenotypes, W is a design matrix assigning records to phenotypes fixed effects, b is a vector of fixed effects (e.g., the mean, population structure effects, and age), X is a design matrix allocating records to the marker effect, g is the effect of the marker and e is a vetor of random deviates eij~N(0, σ^2e). In this model the effect of the marker is treated as a fixed effect, and the model is additive. The underlying assumption here is that the marker will only affect the trait if it is in linkage disequilibrium with an unobserved QTL (Gondro *et al.*,2015).

Model to remove the effect of population structure using a mixed model:

$$y = 1n \text{ ` } \mu + Xg + Zu + e$$

where u is a vector of polygenic effect in the model with a covariance structure ui N ð0; Aσ2 a Þ, where A is the average relationship matrix built from the pedigree of the population, and σ2 a is the polygenic variance. Z is a design matrix allocating animals to records. In other words, the pedigree structure of the population is accounted for in the model. Note that this is BLUP, with the marker effect and the mean as fixed effects and the polygenic effects as random effects

Model for GWAS is correcting population substructure using principal components:

$$y_i = \boldsymbol{x_i b} + \sum_k PC_k \gamma_k + m_{ij} q_j + e_i$$

where y is a vector of phenotypes, P is the matrix for principal componenet of G, C is a design matrix assigning records to phenotypes fixed effects, γ is a vector of fixed effects (e.g., the mean, population structure effects, and age), mis a design matrix allocating records to the marker effect, q is the effect of the marker and e is a vetor of random deviates eij~N(0, σ^2e). The PC of G can be computed using the function eigen in R. And the loadings are the regressors that can be used (Janss et al.,2012).

Model for GWAS from GBLUP-

y = Xb +a1 +a2+ e

where $\boldsymbol{a}_1$ is the vector of additive random effects associated with those SNP located in the segment, such that a1~N (0, G1 $\sigma^2_{A1)}$ and $\boldsymbol{a}_2$ is the vector of additive random effects associated with all SNPs except those involved with $\boldsymbol{a}_1$, such that a2~N (0, G2 $\sigma^2_{A2).}$ This model assesses the proportion of variance explained by the segment of interest (local variance) from the genome variance explained by all SNPs (global variance) (Gualdron *et al*., 2014, Gondro *et al*.,2015).

GWAS has proved to be an ideal method to identify genes associated with various phenotypes and to elucidate the mechanisms of the complex traits.The results have provided unprecedented views into the contribution of common variants to complex traits, illuminated genome function, and have opened new possibilities for the development of therapeutic interventions. In future, further, understanding of the roles of epistasis (gene–gene interactions), gene–environment interactions, and copy number variants are anticipated to provide additional insights into our understanding of complex human and animal disorders.

Steps for GWAS in R environment-

Recording of phenotypic data and genotyping.
Quality control of genotyping data for Minor allele frequency, Hardy Weinberg, heterozygosity, GC score etc. via PLINK or snpQC software.
Basic association study using R packages (snpMatrix)
Graphics via R/gap

Useful R Packages for GWAS-

Packages at BioConductor, an open source and open development software project for the analysis and comprehension of genomic data.

- *snpSTAT*, for simple regression model
- *GenABEL*, a comprehensive suite of functions for GWAS and one of the most widely used
- *fdrtool*, handy functions for false discovery rates
- *multtest*, yes you guessed it—multiple testing
- *qtl* for analyzing QTL projects and *bim* for a Bayesian approach
- *GeneticsPed*, some nice functions for handling pedigrees
- *beadarraySNP* has lots of functions and reporting options for Illumina data
- *haplo.stats* for haplotypes
- *snpMatrix* is a flexible package with many functions for association studies and imputation

Genome-Wide Association Study with milk phenotypes: At our laboratory, a study was aimed to identify candidate genes associated with milk fat percent, protein percent, individual fatty acid (FA)

and mineral composition in Vrindavani cattle using the Illumina 50K single nucleotide polymorphism (SNP) array (Singh et al., 2021). After quality control, a total of 41,427 informative and high-quality SNPs were used for a genome-wide association study (GWAS) for milk fat percentage and 16 different types of fatty acids. Lactation stage, parity, test day milk yield, and proportion of exotic inheritance were included as fixed effects in the GWAS model. A total of 67 genome-wide significant SNPs and 176 suggestive significant SNPs were identified. Out of these, 15 SNPs were associated with more than one trait. The strongest associations were found on BTA14 for milk fat percentage (Figure 1), and on BTA2 and BTA16 for polyunsaturated fatty acids. Several significant SNPs were identified close to or within the genes *ELOVL6, FABP4, PMP2, PLIN1, MFGE8, GHRL2, and LDLRAD3 which are known to be associated with fat percentage and FA composition in dairy cattle breeds.* A total of 45 and 65 significant SNPs were detected for monounsaturated and polyunsaturated fatty acids, respectively. A total of 28, 5 and 12 SNPs were associated with C14:1, C16:1 and, C18:1n9c, respectively. On BTA 6, two significant SNPs associated with C14:1 were detected 1.2 Mb downstream from the Fatty acid-binding protein 2 (*FABP2*) and 1.5 Mb downstream from the ELOVL fatty acid elongase 6 (*ELOVL 6*) gene. The strongest association for C16:1 was SNPs BovineHD0600018691 on BTA6 and for C18:1n9c it was BTB-01351221 on BTA4.

For PUFA, 13 SNPs for C20:2, 34 SNPs for C20:4n6, 2 SNPs for C22:2 and 16 SNPs for C22:6n3 were identified as significantly associated. For C20:0 and C20:4n6, a cluster of six and 25 significant SNPs was found on BTA2, respectively. The strongest association for C22:6n3 was identified as SNP Hapmap30788-BTA-130706 located at 38.2 Mb on BTA 16. For C22:2, the most significant SNP, ARS-BFGL-BAC-34040, located on BTA17 only reached a suggestive significance level.

Across all milk mineral traits, 13 genome-wide significant and 49 suggestive SNPs were identified which were located on 18 different autosomes (Singh et al., 2022). The strongest association for protein percentage, calcium (Ca), phosphorus (P), copper (Cu), zinc (Zn), and iron (Fe) were found on BTA 18, 7, 2, 3, 14, and 2, respectively. No significant SNP was detected for manganese (Mn). Several significant SNPs identified were within or close proximity to CDH13, BHLHE40, EDIL3, HAPLN1, INHBB, USP24, ZFAT, and IKZF2 gene, respectively. Enrichment analysis of the identified candidate genes elucidated biological processes, cellular components, and molecular functions involved in metal ion binding, ion transportation, transmembrane protein, and signaling pathways. This study provided a groundwork to characterize the molecular mechanism for the phenotypic variation in milk protein percentage and minerals in crossbred cattle. Further work is required on a larger sample size with fine mapping of identified QTL to validate potential candidate regions. For protein percentage, the significant 1.9 Mb region (8.03- 9.94 Mb) on BTA 18 was partly overlapping with previously reported QTLs associated with milk coagulation (Figure 2). The milk coagulation is directly influenced by the casein composition, which indicates that this region may have the potential to influence the protein percentage in milk. This region includes the CDH 13 (Cadherin-13) gene which is expressed in mammary tissues and associated with the protein content of the milk. Among studied minerals, the strongest association for Ca, P, Cu, Zn, and Fe were found on BTA 7, 2, 3, 14, and 2, respectively.

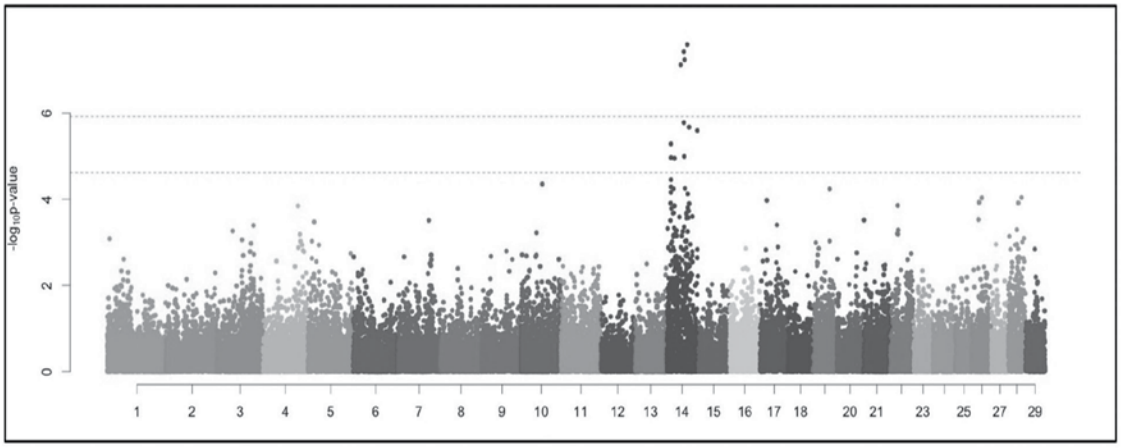

Figure 1: Manhattan plot for fat milk percentage in Vrindavani cattle. The red line represents genome-wide significance level (P<1.20x10^{-06}), and the blue line represents the suggestive significance level (P<2.41x10^{-05})

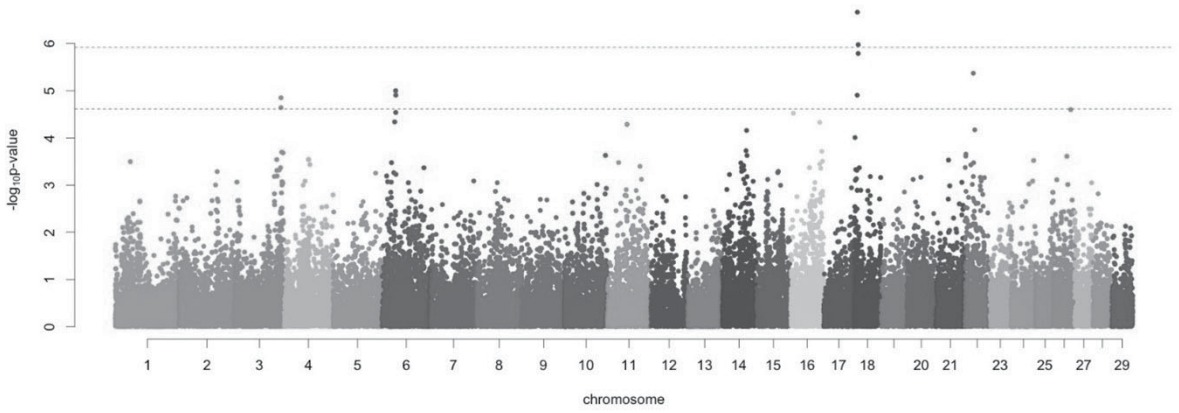

Figure 2: Manhattan plots for protein percentage in Vrindavani cattle milk. The red line represents genome-wide significant level (p<1.20 x10^{-06}), and the blue line represents suggestive significant level (p<2.41 x10^{-05})

Genome-Wide Copy Number Variations and its association with milk production in *Vrindavani* cattle: Copy number Variations (CNVs) are a type of structural variants that involve fragments whose size varies from few kilobases to around five megabases (Zhou et al., 2016). In humans, CNVs cover around 77.97% of the total genome size (Silva et al., 2016). The changes in CNV regions can be copy number gain or copy number loss or mixed type (with both gain and loss) (Butty et al., 2020). Therefore, the CNVs change the gene dosage or cause gene disruption and ultimately affect the gene expression levels. CNVs at genomic level have also been reported to additionally possess evolutionary and functional significance (Jakobsson et al., 2008). Traditionally, karyotyping and fluorescent in-situ hybridization (FISH) procedures were used for detection of CNVs at cytogenetic levels. Currently, different arrays and NGS platforms are available for elucidation of CNVs and CNVRs in human and animal genomes.

A study at our laboratory it was aimed to analyze the genome-wide copy number variation (CNVs) in *Vrindavani* composite cattle and concatenate them into CNV regions (CNVRs), and finally test their association of CNVRs with different production and reproduction traits (Ahmad et al., 2021).

Genotypic data generated on BovineSNP50 Beadchip (v3) array for 96 Vrindavani animals was used to elucidate the CNVs at genome level. Intensity data covering over 53,218 SNP genotypes on bovine genome was used. Algorithm based on Hidden Markov Model was employed in PennCNV program to detect, normalize and filter CNVs across the genome.

The GenomeStudio v2.0.5 software (Illumina) was used to retrieve the information related to signal intensity ratios or log R ratio (LRR), B-allele frequency (BAF) and population frequency of B-allele (PFB) from signal intensity data of genotyped samples. The PennCNV program (Wang et al., 2007) was employed for the detection of CNVs. CNVs were called from intensity files using detect_cnv perl script inbuild with PennCNV software. Quality control of CNVs was based on the following criteria: LRR standard deviation <0.3; BAF_drift <0.01 and GC wave factor <0.05. Though PennCNV program was originally devised for human genome, appropriate and recommended modifications were used during the present analysis to cater to additional somes present in bovine species. Other settings and parameters were kept as default in PennCNV program. Downstream analysis of CNVs detected above was performed in CNVRuler program (Kim et al., 2012) with default parameters. Three types of CNVRs were detected *i.e.,* gain, loss and mixed (gain and losses at same region). Association analysis of CNVRs with production and reproduction traits was done using linear regression following a univariate model:

$$Y_i = \sum_{j=1}^{m} X_{ij}\beta_j + e_i$$

where Y_i is the phenotypic observation on i^{th} individual, X_{ij} is the type of j^{th} CNVR on i^{th} individual (gain, loss or mixed), $\hat{a}_j$ pertains to the effect of CNVR, M is the total number of CNVRs and e_i refers to the residual/ error term in the analysis.

The CNV regions were not present uniformly across the bovine genome and were stratified in an irregular manner with maximum CNVRs present on Btau_7 (7 CNVRs). Single CNV regions were present each on Btau_10, _18, _19, _21, _25 and _26. The 208.264 kb long CNVR_45_1 on Btau_12 was present in maximum number of genotyped individuals (82 animals). CNVR_69 covers a 695.73 kb region on chromosome 29. The CNVR_69 was found to be associated with service period, and test-day milk yield at days 6 and 306. The 252 putative CNVs, detected via PennCNV program, in different individuals were concatenated into 69 CNV regions (CNVRs) using CNVRuler program. The Association of CNVRs with important (re)production traits in Vrindavani animals was assessed using linear regression. Five CNVRs were found to be significantly associated with ten important (re) production traits. Among 69 CNVRs detected in the study, five CNVRs were significantly associated with ten important production and reproduction traits that included peak yield (in second lactation), lactation length (1st lactation), test day milk yield (at 6th, 66th, 96th and 306th days of lactation), service period (first and second), inter-calving period (first and second). The chromosomal coordinates of these CNVRs harbor important genes and QTLs that have earlier been reported to be associated with important traits related to milk production, milk constituents, fertility and other traits. A 141.43 kb region on CNVR_22 associated with peak yield in second lactation, lactation length in first lactation and first inter-calving period harbors three important genes *viz., WASHC4;* ALDH1L2; and C5H12orf45. Among these, WASHC4 gene expression is reported to modulate the metabolic profile across different phases of lactation cycle in bovines during prepartum and postpartum stages. The genes harbored in these regions provided useful insights into the association of CNVRs with genes and ultimately the variation at phenotype level. Important genes that overlapped with CNVRs included WASHC4, HS6ST3, MBNL2, TOLLIP, PIDD1 and TSPAN4. Furthermore, the CNVRs were found to overlap with important QTLs available in AnimalQTL database which affect milk yield and composition along with reproduction and immune function traits. The results from the present study

significantly enhance the understanding about CNVs in Vrindavani cattle and should help establish its CNV map.

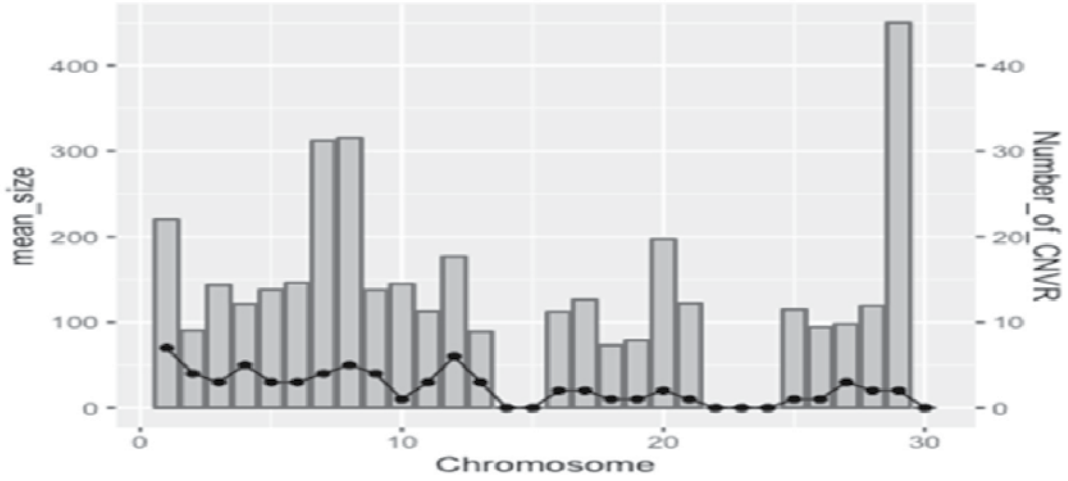

Figure 3: Plot depicting mean size (kb) and distribution of CNVRs across different chromosomes in Vrindavani population.

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LP-7

APPLICATION OF GENOMIC DATA IN LIVESTOCK AND POULTRY

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Abstract
Availability of genomic information, along with the advancement in sequencing technology holds the key to transform the future of poultry and livestock research. This transformation provides solution to increasing demand of animal source food in developing countries. Sequencing platforms produce massive amounts of biological data in various file formats, which may then be analyzed using a variety of computational tools. The data analysis includes whole genome sequencing data analysis, genomic selection, genome wide association studies, signature selection, genome and transcriptome-based assemblies, gene prediction, metagenome analysis and annotation along with identification of genic marker. This genomic data has applications in the field of evolutionary biology, comparative genomics, animal breeding, biotic and abiotic stress tolerance, immunogenetics and medicine. This review provides information related to functional genomic resources, tools available and challenges of genomics in enhancing the health and well-being of poultry animals.

Key words: Livestock, next generation sequencing, genomics

Introduction

The greatest challenge of 21st century is faced by scientist is to meet the hunger of the growing human population in developing countries. The statistics suggest an estimate of about 7.3 to 9.6 billion people (at time of publication, https://www.worldometers.info/world-population) in 2050 along with 50-70% increase in food production as compared to the present. In India, livestock plays an important role enhancing the socio-economic and cultural development of many landless and marginal farmers as well. Livestock abreast of food production and nutritional security, provides various products such as fertilizer, skin, fuel etc. Another factor responsible for reduction in genetic potential of poultry constitutes challenges from biotic and abiotic stresses. In developing countries, upto 25 % of potential profit is lost because of diseases while huge economic loss due to thermal stress has been reported in livestock (Rist et al., 2015).

Hence, there is a need to restore animal health and implement measures to resolve these issues. Therefore, the increase in production has been managed by developed countries with help of advanced genetics and genomics resource with the belief to support and provide efficiency for increased demand of animal-based foods. Genomes of livestock have become an important resource for addressing the challenges in domestication. Next generation sequencing (NGS) technology elucidate DNA/RNA sequences from whole genome/exome sequence at much lesser cost than traditional sequencing methods. When combined with other sequencing technologies such as enrichment for exome, RNA, or other genomic regions. With the availability of genomic data and development of sequencing technologies combined with the applied tools and protocols holds applications in the field of genomics, transcriptomics, and metabolomics. The objectives describe some of the opportunities to utilize genomic data and challenges faced while using these improved tools.

Types of genomic data used for analysis

Researchers may now examine the complete genome or exome since NGS can detect mutations that traditional sequencing technologies are unable to identify. Structural variation can be discovered using whole genome NGS data or "targeted" data such as exomes. Hence, targeting of sequencing

greatly increases sequencing depth or coverage of individual genes and can introduce biases in the data for further computational analysis. Analysis of whole genome sequencing data involves examining the targeted genome of specific animals for the detection of variants, which can be a valuable source for further data mining of the percentage of sequence reads that are still unmapped to the relevant reference genome. However, 2-10% of the sequencing data is left uncharacterized that constitutes unassembled regions of the animal genome, archaea, bacterial and viral DNA which can be sequenced through shot-gun sequencing approach. Availability of WGS based tools to animal scientists has led to large scale analysis of data involving genome resequencing, SNP genotyping, RNA interference and gene expression profiling. Moreover, high-throughput whole genome has been sequenced for duck (Zhang et al., 2022), cattle (Stothard et al., 2015), chicken (Fulton lucinda et al., 2004), pig (Gronen, 2016), buffalo and goat (Low et al., 2019) within last 10 years and commercial SNP chips are available for chicken (Liu et al., 2019), buffalo (Iamartino et al., 2017), etc (**Figure 1**).

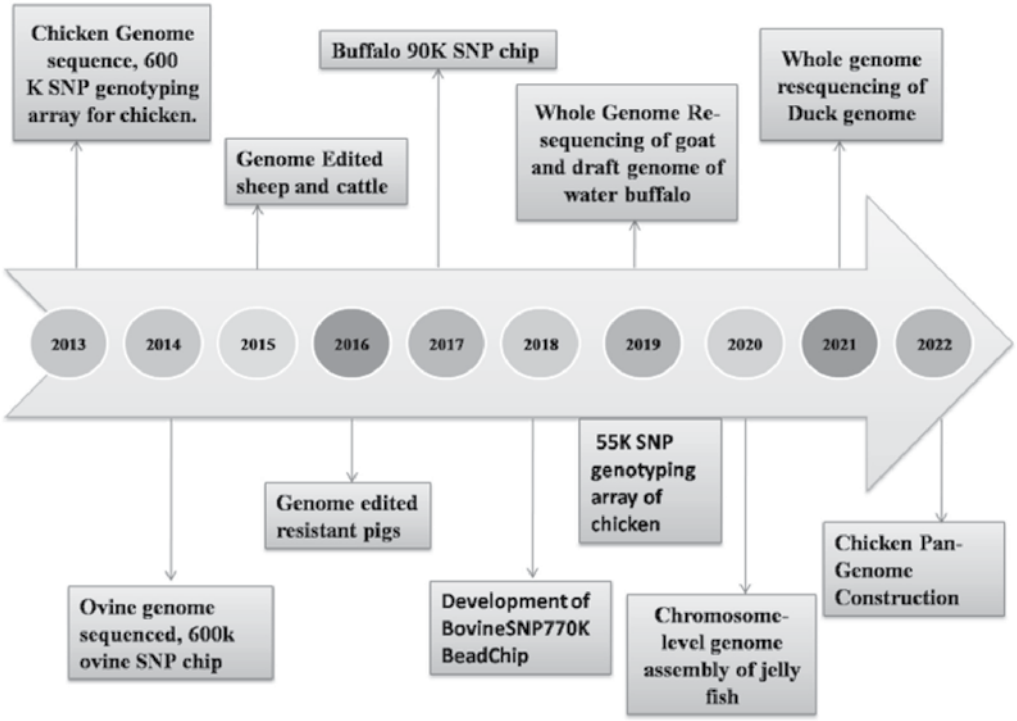

Figure1: Time line of development in genomic research in livestock and poultry

Further, attempts are made to improve the quality of these assembled genomes and assign gene information. Also, genome-wide scans for selection signatures can be performed that enhances the search for genomic variants and selection signals across the entire genome that can reveal new information about genes. Along with the advancement in high-throughput DNA sequencing technologies, transcriptome sequencing (RNA-seq) data analysis in animals has quickly overtaken microarray technology by sequencing cDNAs and thereby identifying alternative splicing events (Wang et al. 2008), novel genes (Denoeud et al., 2008), and fusion transcripts (Maher et al., 2009) Nonetheless, data generated through meta-genomic sequencing offers opportunity to differentiate different class of microbes, gene mutations, antibiotic gene resistance along with reconstruction of smaller genomes (viruses) and find early diagnosis of infectious diseases. Metagenomics aids in identifying variety, studying population structure, and isolating genes of interest from members that have not yet been cultivated. The process involves identification and genetic characterization of candidate pathogens is not enough to establish causal relationships or understand how they may be

associated with disease. It is therefore necessary to use a synergistic approach combining molecular diagnostic tools, such as NGS-based metagenomics and follow-up PCR-based assays targeting detected pathogen sequences, with more conventional diagnostic methods, including isolation and characterization. This is crucially important in situations where metagenomic data indicate the potential presence of multiple pathogens.

Genomic data analysis

Using DNA markers to discover genes or genomic areas that regulate desirable traits, livestock breeding programmes can now be developed. This is thanks to the development of molecular genetics in the 1970s. Marker-assisted selection replaced traditional selective breeding as a result of the discovery of QTLs in animals (MAS). The creation of PCR and sequencing techniques during the 1980s set the stage for the rise of genomics as a discipline. From identifying small DNA nucleotides to decoding an organism's full genome, the field has advanced greatly. Various kind of analysis can be performed using genomic data. A list of various databases related to livestock are depicted in **Table 1**

Analysis of Whole Genome and Exome Sequencing Data

Genetic variation can be determined using a variety of methods for diagnostic purposes. The bioinformatics techniques utilised in the study of whole genome and exome sequencing will be discussed further. The sequencing instrument's creation of the FASTQ files constitutes primary analysis. Secondary analysis involves the cleaning/trimming of raw read sequences and then locating genetic variations by connecting these shorter reads to the target genome. Tertiary analysis involves collecting data on each detected genetic variation and using this data to produce a subset of relevant variants.

Various studies have been conducted using whole genome resequencing platform such as the Author Li et al., (2020) performed whole-genome resequencing analysis in wild and domestic sheep has revealed genes associated with morphological and agronomic traits. Another study by Luo et al., (2020) identified positive selection regions harboring genes in Xiangxi cattle, which were related to reproduction, growth, meat quality, heat tolerance, and immune responses. The methodology for DNA-seq is represented in **Figure 2.** The list of softwares used in the methodology are showed in **Table 2**

Genomic data can be used to investigate (a) genetic diversity and breed population structure (b) Identify genetic variants and QTLs related to economically important and ecological traits, genome-wide association studies (GWAS) and genomic signatures of selection (c) genomic selection to enhance breeding programs

Genome wide association studies

GWAS analyse the relationship between genotype and phenotype by searching the entire genome for genetic variations. Various GWAS studies have been conducted to identify the significant SNPs linked to crossbreed cattle's milk production for example Sahiwal cattle's fertility and growth qualities, pigs' immune responses, and Vrindavani cattle's coat colour reference (Illa et al., 2021). Using the genotyping-by-sequencing (ddRAD-GBS) method, Vohra et al. (2021) conducted GWAS to discover genomic areas linked to lactation and fertility variables in Murrah buffalo. Further, jasiwal et al., (2021) followed targeted gene panel approach to explore rare genetic variants associated with mastitis genes in water buffalo. The results reveal relatedness of these genetic variants with economically important traits. Also, a genome-wide association study conducted in chicken has identified for natural antibodies and resilience in a purebred layer chicken line by Doekes et al., (2022).

GWAS has accelerated the use of selection signatures to link candidate genes or variations under selection to desirable qualities, which can then be employed in genomic selection. The molecular mechanisms of adaptability and production in native breeds are better understood with the aid of selection signatures. These investigations help identify advantageous mutations that provide a selective advantage in a particular population or breed. For a better understanding of population origin and the genetic mechanisms that affect phenotypic difference across livestock breeds, the detection of selection signatures is essential.

Genomic selection

The concept of conventional breeding holds limitation with the traits linked to sex-chromosomes as they display low heritability in later stages of life, therefore accomplishing lesser genetic gain. By utilising the knowledge of polymorphic loci, the notion of marker-assisted selection (MAS) has allowed the selection of superior breeding animals. Genomic selection (GS) is anticipated to increase selection accuracy and shorten the generation interval due to early selection in contrast to traditional approaches. GS measures genetic variances within every individual based on the prediction of breeding values by associating traits with genomic dataset (Heffner et al., 2009).

In last few years, genomic selection has been applied in several significant livestock species pig (Knol et al., 2016), cattle (Hayes et al., 2009) Genomic selection in developed countries has resulted in early genetic gains, particularly in dairy cattle, because of a well-established genetic evaluation system, ongoing breeding programmes that have received funding from both the for-profit breeding businesses and public sector. To carry out these development programmes, however, breed groups or associations are still lacking in developing nation due to insufficient routine recording of phenotypes, no reliable tools to synthesise the data, inaccurate pedigree and performance documentation, and variations in production settings. Genetic improvement based on genomic analysis has thus far been impossible.

Various studies have revealed positive selections and genotype value by using different prediction models such as random regression model, single step Genomic Best Linear Unbiased Prediction model (ssGBLUP), GBLUP, parametric (RR- Ridge Regression, LASSO- Least Absolute Shrinkage and Selection Operator, Elasticnet, Bayes A and Bayes B), semi-parametric (RKHS- Reproducing Kernel Hilbert Space), and non-parametric (RF- Random Forest). A study conducted by Nayee et al., (2018) using ssGBLUP model has reported to enhance the prediction accuracy in both cow and sire.

A study conducted by Tan et al., (2022) on the effect of genomic selection and detection of selection signatures has led to the improvements in body weight and meat production in chicken. There are examples where non-government organisations like BAIF (http://www.baif.org.in) are involved in genomic selection of *Bos indicus* where smartphones are used for phenotypic recording. Such kind of programmers is initiated in six different states where SNP chip is used to obtain genomic breeding values. A programme started by NBBD (https://www.nddbdairyservices.com/) has made 59K SNP BUFFCHIP for genotyping indigenous breeds of buffaloes that can be utilised for genomic selection studies.

Genome wide selection sweep

With whole-genome resequencing data, selective sweeps analysis can also be performed to identify candidate genetic sequences that underlie complex traits. It is a process where a new mutation increases in frequency and becomes fixed in the population leading to elimination of genetic variants among nucleotide sequences which are present near the mutation. In case of positive selection, the

mutation reaches fixation and the near gene exhibits hitchhiking effect and becomes fixed in nature. Therefore, a region of the genome with a significant reduction in genetic variation in that chromosome region is the result of a selective sweep caused by a strongly selected allele that emerged on a single genomic background (Barrett R. D. and Schluter D, 2008). A particular advantage of this method is that it allows the discovery of many breed-specific mutations. In 1974, John Maynard-Smith and John Haigh proposed the hypothesis that strong positive selection could lessen local genetic variation brought on by hitchhiking.

Approaches for genome wide scan to identify signature genes

Recent selection in a population can also result in significant levels of genetic divergence between groups. Two approaches can be explored to identify signatures of positive selection between different populations. Fst (F statistic) is a popular method for determining genetic difference across populations. First, identification of selective sweeps is performed by calculating pairwise Fst between breeds. It is performed by calculating the genetic differentiation (Fst) value for each window using VCFtools (http://vcftools.sourceforge.net/; last accessed September 12, 2017) (Danecek et al., 2011). For example, a sliding window of 40-kb window with 20-kb step size can be used to determine pairwise-Fixation index (FST) between populations. Therefore, a Z transformation of Fst can be used to find genome-wide outliers with high degrees of differentiation in whole-genome resequencing data.

Further, heterozygosity (ZHp) is an alternate way to estimate nucleotide diversity (Rubin et al., 2012). To identify regions with high levels of homozygosity and genomic sequences that can influence phenotypic traits of a particular group. Therefore, whole genome sequencing data can be used to identify cross-group comparison through ZHp. Genes that partially or completely spanned the window regions will be regarded as putative candidate genes under positive selection. The pipeline used for this analysis in depicted in (**Figure 2**). Annotation of the genes showed enrichment of pathways related to fat and starch metabolism. Recent study on genomic selection for meat quality in duck conducted by Zhang et al. 2022 revealed high prediction accuracy results from Bayesian R model.

Transcriptome analysis

The typical RNA-seq analysis workflow may include the following steps as shown in (Figure 2) (i) quality check, (ii) pre-processing of raw reads, (iii) read alignment and mapping, (iv) transcriptome reconstruction, (v) transcript abundance estimation, and (vi) differential expression analysis

The pipeline includes use of FastQC and Trimmomatic tools which are primarily used for quality assessment and pre-processing. Clean reads must first be aligned or mapped to a reference genome or transcriptome to identify the exact genomic positions (origin) with respect to that reference. Further, transcript abundance and differential gene expression are calculated followed by KEGG pathway and gene ontology analysis. A detailed information of tools used for this pipeline are listed in **Table 2.** Various findings in livestock research involving transcriptome studies have revealed important pathways regulated during postpartum disease *viz.* enrichment of Parathyroid hormone synthesis pathway and stem cell differentiation function-related pathways in beef cow (Yang et al., 2022). A study by Dickson et al., 2022 studied the endometrial transcriptomic response to pregnancy is altered in cows after uterine infection. The results reveal genes responsible for uterine bacterial infection alter the endometrial transcriptomic signature of pregnancy after the resolution of disease.

Metagenomic analysis

We should evaluate the quality of raw reads before data analysis. Like whole genome sequencing data, thereafter read alignment can be done to map the reads to the reference genome. The next step is transcript reconstruction in which we identify the transcripts that are expressed in the samples. Based on the availability and unavailability of reference genome, transcriptome reconstruction

can be categorized into two parts *viz.,* reference-based and *de novo* (reference-free) assembly approach. *De novo* assembly approach is used when the reference genome is not available. Once assembled transcripts have been identified, their abundance can then be estimated. Metagenome analysis involves binning where DNA sequences are grouped that could represent a single genome or genomes from closely related organisms. Contigs are grouped by binning into classes to represent a biological taxon. Software used for binning analysis are MetaWatt (Strous et al., 2012) and CONCOCT (Alneberg et al., 2014).

Sequence analysis is used to compare the sequences of various types of organisms using simple alignment and multiple alignments. The most used tool is BLAST (Basic Local Alignment Search Tool). The alignments are scored statistically based on expectation value (e-value) (Altschul et al., 1990). Further the sequences are analysed for taxonomic profiles, COGs (cluster of orthologous genes) and KEGG pathways. Pfam database is used for Protein family identification. Also, protein structure prediction is necessary to understand the structure and functioning of proteins. The primary structure of proteins comes from the sequences of the genes that encode it. Bioinformatics' prediction study of protein structure can assist in comprehending a protein's physical properties and functions (Raza, 2012). In order to reconstruct the evolutionary links between groups of protein molecules and to forecast certain properties of a molecule, phylogenetic analysis is performed. The tools widely used in phylogenetic analysis are MEGA (Molecular Evolutionary Genetics Analysis) (Tamura et al. 2011) and PHYLIP (Felsenstein, 1989). Furthermore, differential expression analysis can be performed using different available softwares. (**Table 2)**

A study by Xue et al., (2022) identified individual microbes involved in fiber digestion and fermentation in the rumen of dairy cow through meta-genome assembled genome. The results reveal there are still many microbial genomes yet to be sequenced and assembled for greater understanding the function of rumen microbes. Moreover, a metagenome assembly was performed on sheep, cow, rein deer and red deer genomes to identify CAZymes as they tend to organise into Polysaccharide Utilization Loci (PUL) that comprise a set of genes which enable the binding and degradation of specific or multiple carbohydrates (Glendinning et al., 2021)

Abiotic stress and biotic stress in livestock

The mass production of chicken meat and eggs on an industrial scale creates an environment where infections can spread easily and cause significant disease outbreaks with corresponding financial losses. Viral disease and heat stress make it harder for livestock to operate to their true genetic potential. In case of abiotic stresses, such as heat, which constitutes high temperature, solar radiation, humidity, and wind speed are responsible to decrease the genetic potential of birds and cattles. Since, most of the world's poultry is produced in hot climates, this stress costs the chicken industry millions of dollars each year (St. Pierre et al., 2003). High exposure results in production loss from egg production, body weight, feed intake, reduces fertility and modifies animal behaviour (Sohail et al, 2012, thornton et al.,). However, a study by Liu et al., (2020) identified four genes (OAS2, MX2, IFIT5, and TGFB2) associated with heat tolerance involved in the immune effector process following heat-tolerant mechanisms in dairy cows. In case of biotic stress, lumpy skin disease (LSD) is a threat to Indian livestock industry and is quite prevalent in middle-eastern countries (Yeruham et al., 1995). In 2019, a report from a district in Odisha shows a concern where control and surveillance are needed to curb the disease. LSD is caused by a virus which shows similarity with pseudo-lumpy disease (PLSD) from bovine herpesvirus-2. Differentiating the viruses through serological methods is quite difficult therefore, NGS has been applied for quick diagnosis and screening of diseased sample of cattle affected from BHV-2. Another study by Saelao et al., (2021) performed global transcriptome analysis in chicken during heat stress and new castle disease

caused by respiratory virus. The results reveal robust response at 6 dips per inoculation activates immune response which can be further investigated to identify resistance genes.

Applications

These applications offer new perspectives and demonstrate how new technologies have an immediate influence on how we comprehend and combat infectious diseases in animals (Bai et al., 2012), and traits that affect poultry interact with microbial populations and are resistant to pathogens (Diaz-Sanchez et al., 2013). The most important step in comprehending the biology of parasites is to understand the properties of gene expression, regulation, and function by transcriptome analysis of various parasite species and/or developmental stages. A study reported identification of important genes involved in anthelmintic resistance and the prediction of possible therapeutic targets have both been done using RNA-Seq data (Tritt et al., 2012)

The genomic data from NGS could be of help at different levels in vaccine industry. In case of bacterial vaccines, the whole genome sequencing can establish the identity of the bacterial strain used in the vaccine. Bacterial strains can also be verified for batch-to-batch consistency as well as to validate the absence of extraneous agents. When compared to bacterial vaccines, NGS has a wider application in viral vaccines. First, the vaccine material is supposed to be devoid of anything other than the antigenic material. To avoid the unintentional introduction of adventitious agents in the vaccine manufacturing process, detailed characterization of seed stocks, final bulk and formulated vaccine is necessary (Kumar et al., 2012). We could identify the genomes of some of the live vaccines used in poultry. Lojkić et al., (2018) reported use of vaccine against lumpy skin disease of cattle. The strain for vaccination was isolated from infected animal of skin with LSD virus. Hence, stable results were reported after first vaccination. Genomic data is useful for identifying mixed infections, particularly those that impair production or have immunosuppressive effects but lack obvious clinical symptoms. Another study by Sun et al., (2022) reported nanopore sequencing method for detecting variations in a live attenuated chicken vaccination for Newcastle disease.

Using genomic technologies to guide selective breeding in livestock can be helpful in examining the genetic underpinnings of resistance to Eimeria and cestode parasitism in two indigenous chicken ecotypes from Ethiopia (Psifidi et al. 2016). These diseases included infectious bursal disease, Marek's disease, fowl typhoid, and fowl cholera. The authors of this study discovered SNPs that were strongly correlated with attributes related to immunity, illness, and production. Additionally, they discovered no genetic relationships that were statistically significant between these features, supporting the idea that selection for disease resistance or altered antibody response had little impact on production. Another study in the field of reproductive technologies highlighted the role of semen quality biomarkers for improving production in livestock (Vasisth et al., 2022)

Advances in DNA sequencing methods and bioinformatics are shaping our perception of microbial diverse communities like the mammalian gastrointestinal tract. Research on the microbiome is becoming more popular in animal goods as it explains diseases and efficiency processes. The rumen microbiota in cattle is thought to be responsible for breaking down millions of tonnes of cellulosic material globally to produce milk and meat, and it is directly linked to the digestion of feed and accessibility of host nutrients (Hackmann and Spain et al., 2010). Hence, the microbiota rapidly digests plant material and can be used as cost-effective system for converting lignocellulosic plant material into biofuel. Further, the microbiota was outlined using 16S rRNA sequencing. To comprehend the microbial diversity of both avian animals, the gastrointestinal tract microbial profiles of chicken and Guinea fowl were examined using a metagenomic approach. DNA was gathered from the gastrointestinal tracts of chicken and Guinea fowl for this investigation. Using the metagenomics,

the area encoding hypervariable 16s rRNA was targeted to determine the make-up of microbial communities in organisms (Fadiji and Babalola, 2020).

Future prospects

The livestock genomics research community is undoubtedly prepared to advance in coming future still there is a need to effectively integrate, analyse, and interpret enormous amounts of data from various sources that will replace technology availability as the limiting factor in research discovery. Fortunately, researchers studying model animal and human species encounter the same issues and have easier access to resources to find answers. As a result, we estimate that the next ten years will see more changes and obstacles to livestock improvement systems than there have been since artificial insemination was invented.

Table 1: Public Databases available for livestock data

Database	Description	URL
ChickNET	The chicken Genome information network	https://www.chicken-genome.org/
Chicken database	Online public database browser	http://www.thearkdb.org/browser ?species=chicken
Wellcome trust chicken genome browser	Provides annotation of the first draft chicken genome assembly	http://www.ensembl.org/Gallus_gallus/
Pig QTL database	The database makes it possible to compare on pig chromosomes the most feasible location for a gene responsible for quantitative trait important to pig production	http://www.animalgenome.org /QTLdb/
Pig EST database	Pig EST database accommodates 98,988 pig ESTs, which were obtained from various sources	https://www.animalgenome.org/pig /projects/pigESTdb/doc/
PigVar	Variation information (SNPs and structural variations (SVs) and selection signatures of pigs	http://202.200.112.245/pigvar/
Bovaine genome database	Data mining, genome navigation and annotation tools for the bovine reference genome	https://bovinegenome.elsiklab.missouri.edu/
Cow genome browser	UCSC genome browser created by the genome bioinformatics group of UC Santa Cruz	http://genome.ucsc.edu/cgi-bin/ hgGateway?clade=vertebrate&org =Cow
NCBI SNP database	Cattle single nucleotide polymorphism database	http://www.ncbi.nlm.nih.gov/SNP/snp_ batchSearch.cgi?org=9913&type=SNP
Sheep genomedb	The genome database of the sheep	https://sheepgenomesdb.org/

Sheep genome resources	Genome effort will generate an important resource for gene discovery, affecting health and biology and the growing	http://www.ncbi.nlm.nih.gov/ genome/guide/sheep/
Sheep genetics	Genetic evaluation service of australian sheep and goat industry	https://www.sheepgenetics.org.au/
Fishdb	functional genomics database for fishes	https://fishdb.sinica.edu.tw/eng/ fishquer.php
FishBase	Description of fish species	http://www.fishbase.org/search.cfm
Goatmap	Mapping the goat genome and Genomic mapping	https://animalhealthaustralia.com.au/ goatmap/
GoSh	A goat and sheep ESTs database	http://www.itb.cnr.it/gosh/
BuffSatDb	Buffalo MicroSatellite Database	http://webapp.cabgrid.res.in/buffsatdb/
Buffalo database	Bibliographic and abstract database collecting information in buffalo from world wide. It provides bibliographic records, abstract and full text in Thai and English	https://agkb.lib.ku.ac.th/buffalo/index

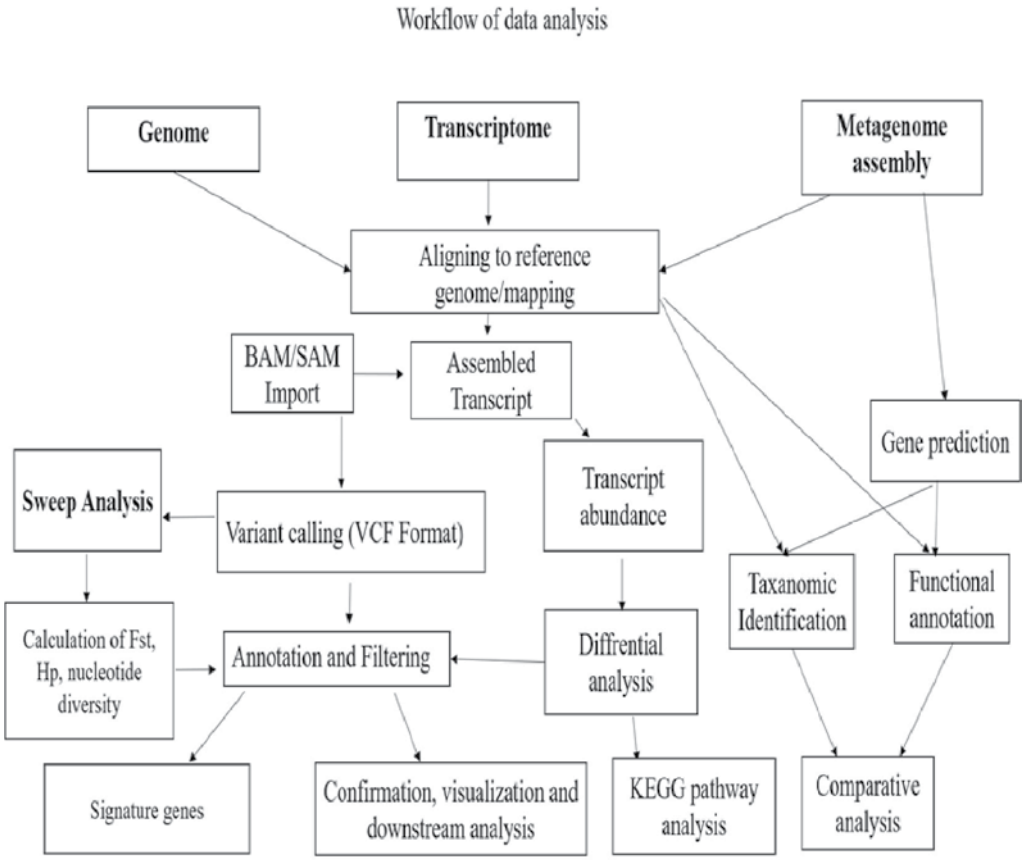

Figure 2: Pipeline of various analysis which can be performed on NGS data

Table 2: Softwares available for data analysis.

Tools	Description	References
Fastqc	Quality assessment	Leggett et al., 2013
NGSQC-Toolkit		Patel and Jain, 2012
Cutadapt	FASTQ Pre-processing	Martin, 2011
Trimmomatic	(Remove adapter sequences, contamination and low-quality reads)	Bolger, 2014
SOAPdenovo-Trans	Denovo transcriptome assembly	Xie et al., 2014
Trinity		Haas et al., 2014
Bowtie	Mapping of RNA-seq reads	Langmead, 2010
BWA		Li and Durbin, 2010
Hisat		Kim et al., 2015
Tophat		Trapnell et al., 2012
Cufflinks package	Transcript assembly, transcript abundance estimation, and differential expression analysis	Trapnell et al., 2012
RSEM	Transcript abundance estimation	Li and Dewey, 2011
DESeq2	differential expression analysis	Love et al., 2014
edgeR		Robinson et al., 2010
Blast2GO	Gene ontology annotation and pathway enrichment analysis	Conesa et al., 2005
DAVID		Sherman et al., 2022
Novoalign	Aligner for denovo assembly	Yu et al., 2012
Soap-denovo		Liang et al., 2012
Samtools mpileup	Summarizes of the coverage of mapped reads on a reference sequence at a single base pair resolution	Li et al., 2009
Freebayes	Variant Caller	Marth et al., 1999
GATK	Identifies SNPs and indels in germline DNA and RNAseq data.	McKenna et al., 2010

SnpEff	Genetic variant annotation and functional effect prediction toolbox	Cingolani et al. 2012
SNVer	calling common and rare variants in analysis	Wei et al., 2011
Variant effect predictor	determines the effect of variants (SNPs, insertions, deletions, CNVs or structural variants)	McLaren et al., 2016
MetaVelvet	Metagenomic assembly	Namiki et al., 2012
MetaQuast		Alla et al., 2016
MetaBAT	Binning	Kang et al., 2015
MetaWatt		Strous et al., 2012
CONCOCT		https://arxiv.org/abs/1312.4038
MetaGeneAnnotator	Gene Prediction	Hideki et al., 2008
Orphelia		Hoff et al., 2009
InterPro	A consortium of 14 protein/domain/ family databases	https://www.ebi.ac.uk/interpro/
InterProScan	Available as Linux/Unix command-line ; or web-interface; or via API	Quevillon et al., 2005
KEGG	Pathway Databases	Ogata et al.,1999
MG-RAST	Analysis Pipeline	Keegan et al., 2019
MEGAN		Huson and Weber, 2013

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LP-8

HANDLING BIG DATA TO UNDERSTAND PHENOMICS

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Decoding the functional information hidden in DNA and RNA sequences demands generation of large volumes of big data using new biomedical techniques, such as next-generation genome sequencing. Powerful computational and statistical methods are being used to decipher and unravel information hidden in the genome. Big data generation involves both DNA sequencing and RNA sequencing. DNA sequencing is used to de-novo sequence or re-sequence the whole genome(s) and to explore single nucleotide polymorphism(s) across the genome. The need for whole genome sequencing varies from species to species. Further, the need to dig and explore the importance of polymorphisms depend on the species and economic importance of the trait/phenotype in the concerned species. RNA – sequencing is used to understand the systems biology behind a phenotype. Systems biology, also referred to as network biology, is powered by the fact that a discrete biological function is seldom determined by a single gene. Oligonucleotide microarray is another technique to generate data under systems biology.

DNA sequencing

1. **Need to develop an SNP Chip, its development, data generation and its downstream analysis**

India has a wide variety of indigenous cattle breeds distributed throughout its agro climatic zones. These are known for their natural tolerance to tropical heat and disease resistance with sustainable milk production. To meet the growing demand of milk in India several crossbreeding programmes were taken up. Every state has its own crossbreeding policy which is agro climatic and breed specific. This resulted in breed dilution of valuable indigenous cattle in their native breeding tract leaving behind very few purebreds in comparison to graded cattle. Also, our indigenous breeds have not been exploited to their potential because of slow genetic gain through generations using conventional breeding policies. With the crossbreds not withstanding harsh climate, being susceptible to tropical diseases and requiring constant input of good managemental conditions, conserving our indigenous cattle genetic resources which are far superior in these aspects is the need of the hour. To strike a balance between the increasing demand for milk at 180 mn tonnes by 2022/ 330 mn tonnes by 2022 and change in environment due to global warming conserving our indigenous cattle breeds becomes all the more important. For conserving these breeds the first and foremost requirement is identification of purebreds. The advent of DNA sequencing and high-throughput genomic technologies together with the automated SNP genotyping resulted in a paradigm shift in identification and selection of animals vis - a - vis the phenotype under consideration.

Though there are several Bovine SNP Chips available in the market, literature shows that these chips would partially cover the *Bos indicus* genome. Dash et al., (2018), genotyped three Indigenous dairy breeds (Sahiwal(19), Tharparkar(17) and Gir(16)) using the available Illumina Bovine HDchip and found only 40%−50% SNPs, informative for genetic analysis in these cattle breeds. Similarly at BAIF genotyping of Gir showed only 50% of the SNPs in Bovine 50KChip to be polymorphic (Hidalgo et al.,2016). In Pakistan, the performance of bovine high density SNPs genotyping array on indigenous Pakistani cattle breeds was evaluated and out of 777, 962 SNPs only 500, 939 SNPs were found polymorphic in Achi (18), Bhagnari (14), Cholistani (13), Dajal (10), Dhanni (10), Kankraj (12), Lohani (19), Red Sindhi (13), Sahiwal (14), and Tharparkar (13). These

findings indicate that the available SNP chips truly do not represent our indigenous breeds. The availability of high-density chip with improved mapping resolution across indigenous breeds would further result in better imputation. This would further help in screening the indigenous breeds for their purity vis - a - vis admixture.

Genomic research in developing countries moved at a rapid pace (Fig 1) and a high-density chip has been recommended to improve the accuracy in multi-breed approach (Gautier et al., 2007, de Roos et al.,2008, Gibbs et al., 2009 and de Roos et al. 2009). However, In India no program with an effort to conserve genetic makeup for any breed using genomic signatures of the breeds has yet been undertaken.

A pre-requisite for developing an SNP chip for indigenous cattle, where huge diversity (50 breeds of cattle) exists is selection of unrelated animals within a breed. After having met this challenge, the DNA isolated from these unrelated animals (n=20 per breed) is whole genome sequenced at a minimum coverage of 50X. This ensures that the SNPs called at a site are called with great reliability.The data generated should be run using at least two pipelines to explore the SNPs across all the breeds. However, selection of a proper reference against which the SNPs are identified is the key while running the data through these pipelines.The SNPs identified commonly across both the pipelines are filtered through the plink pipeline and finally placed on the SNP chip ensuring homogenous distribution of SNPs across the genome. The chip so designed and manufactured should be validated before the release. Inclusion of trios and duplicates in the process of validation would stake a better claim in using the chip for commercial purposes. A high-density chip should be employed initially to identify genetic signatures specific to a breed and this can further lead to development of breed specific / group specific low-density chips. Further, the SNP chips in the long run can be used for GWAS and genomic selection.

2. **Diversity analysis - Observed and Expected heterozygozity**

Heterozygosity is the classical measures of genetic diversity estimated from molecular information. Out of the observed and expected heterozygosity the most widely used is the expected heterozygosity (*He*). Which is the probability that two alleles chosen at random from a population are different. Alternatively, it may also be defined as the proportion of heterozygous individuals. The classical formula to estimate it is: $H_e = 1 - p^2$, where *p* is the frequency of all the alleles at that locus. It is assumed that populations with higher *He* are genetically more diverse and hence, more capable to adapt to changes and to respond to selection (natural or artificial).

3. **Linkage disequilibrium as a demographic processes**

Non-random association between alleles at different loci within a population is linkage disequilibrium(LD). This results in higher frequency of certain haplotypes at a locus than expected by chance. Genomic linkage disequilibrium is a consequence of different genetic forces, such as selection, mutation, drift and non-random mating, and can also be due to non-genetic causes. Studies in livestock populations have shown that LD in them is more extensive than in human populations due to smaller effective population size and directional selection. The advent of high-throughput SNP arrays have resulted in identifying LD patterns across the genome. Further studies are now focused on LD patterns and effective population size (Ne) and their relationships with demographic processes, such as migration and admixture.

4. **Runs of Homozygosity as a measure of Inbreeding**

The use of high-density SNP arrays opened the possibility to develop new approaches to identify uninterrupted long runs of homozygous genotypes, commonly known as runs of homozygosity

(ROH) defined as continuous and uninterrupted stretches of DNA sequences without heterozygosity in the diploid state. In outbred populations, the number of ROH is associated with the effective population size, with smaller populations tending to have more ROH and larger populations fewer. On the contrary, populations with high inbreeding rates have much longer ROHs segments because of deep parental relatedness. Admixed populations have fewer ROH segments comparing with their respective parental populations.

Note : Further analysis is given in Figure 2

Transcriptome analysis

Transcriptome analysis to decipher systems biology is give in Figure 3. The subheads under this section include:-

1. Experimental considerations for an RNA-seq experiment
2. Data generation and platforms available for data generation
3. Data quality check and considerations
4. Differential expression analysis
5. Functional annotation of differentially expressed genes
6. Interactome analysis
7. Identification of Transcription factors and miRNA
8. Importance of IPA
9. Example of transcriptome analysis with (pestis des petits ruminants) PPR as a model

1. **Experimental considerations for an RNA-seq experiment**

The change in biological function that can be reflected by the dysregulation of the transcriptome not only involves mRNA, but also other RNA types such as lncRNAs , miRNAs and circRNAs. The interplay among them influences RNA metabolism and in turn the biological and pathological conditions. Different types of strategies are being employed to profile the global change in different types of RNA. Considering the fact that rRNA accounts for 85% of total RNA level, under-representation of mRNA , lncRNAs , miRNAs and circRNAs is inevitable when whole transcriptome sequencing (total RNA sequencing) is carried out. To overcome this caveat, two strategies are followed - 1. Isolating the mRNA using oligodT probes attached to beads as all the mRNAs have a Poly (A) tail, and 2. Using a Ribozero Kit initially, to eliminate all the rRNA from the total RNA before sequencing. However, both the strategies have their own limitations. In the former, though all the differentially expressed mRNA could be identified, identification of differentially expressed lncRNAs is beyond the scope of this strategy. This is because some of lncRNA would not have a polyA tail (Zhang et al., 2014). This makes the later strategy an ideal choice, though, the Ribozero kits available in the market are only 60 - 70 % efficient. This strategy has enabled researchers to identify mRNA and lncRNA using appropriate tools for analysis.

In general, the integrity of RNA is critical for total RNA sequencing. The RNA integrity can be evaluated by carrying out denaturing or nondenaturing agarose gel electrophoresis. Many instruments viz. Bioanalyzer, Tapestation, Femto pulse systems, etc. based on capillary gel electrophoresis are currently in vogue to evaluate RNA integrity. RNA integrity is evaluated by a parameter called RIN (RNA Integrity Number). RIN greater than 7 is considered ideal for downstream processing and sequencing (Jahn et al., 2008). For miRNA sequencing specialized kits are used to recover pure miRNAs compatible for sequencing.

2. **Data generation and platforms available for data generation**

For an RNA–Seq experiment, advances in sequencing technology have led to the production of millions of relatively short reads. Illumina platforms are most commonly used for generation of RNA -

Seq data. However, the introduction of BGI sequencers in the market has put forth a tough challenge. Different read lengths generated by different platforms are given in Table 1. The ideal read length for mRNA and lncRNA sequencing varies from 75bp - 150bp and for miRNA sequencing varies from 25 bp - 50 bp.

Table 1. Sequencing platforms with read length(s)

Sequencing Platform	Read lengths	Maximum Output (Million Single Reads)*
iSeq™ 100	1 × 36 bp,1 × 50 bp,1 × 75 bp, 2 × 75 bp and 2 × 150 bp	4
MiniSeq™	2 × 150 bp,2 × 75 bp,1 × 75 bp, 1 × 100 bp	25
MiSeq™	2 × 25 bp, 2×150bp,2×250bp, 2×75bp,2×300bp and 2×150bp	25
NextSeq™ 500	2×150bp, 2×75bp and 1×75bp	130
NextSeq™ 550	2×150bp and 2×75bp	400
NextSeq 1000	2 × 50 bp,2 × 100 bp and 2 × 150 bp	400
NextSeq 2000	2 × 25 bp, 2 × 50 bp,2 × 100 bp and 2 × 150 bp	1100
HiSeq™ 1000	1 × 36 bp,1 × 50 bp,1 × 75 bp,2 × 75 bp and 2 × 150 bp	3000
HiSeq™1500	1 × 36 bp,2 × 50 bp and 2 × 100 bp	1000
HiSeq™ 2000	1 × 35 bp,2 × 50 bp, 2 × 100 bp and 2 × 150 bp	1500
HiSeq™ 2500	2 × 36 bp,2 × 50 bp,2 × 100 bp, and 2 × 125 bp	3000
HiSeq 3000	1 × 50 bp,2 × 75 bp, and 2 × 150 bp	2500
HiSeq 4000	1 × 50 bp,2 × 75 bp, and 2 × 150 bp	5000
HiSeq X	2 × 150 bp	6000
NovaSeq™ 6000	1 × 35 bp,2 × 50 bp, 2 × 100 bp, 2 × 150 bp and 2 × 250 bp	20000
BGI500	2 x 100 bp, 2 x 150bp	2000

*The output (Reads passing filter) varies from kit to kit used for the same platform. The output given here is the maximum output got with high output kit used on the platform

However, the main question in hand is the quantum of data that needs to be generated for an RNA seq experiment. As the quantum of data generated increases, the cost incurred per sample increases. Therefore, it is important to understand the minimum required data for proper inferences to be made from an experiment. For e.g. Assuming 2% of the genome is transcribed to mRNA, the number of bases that correspond to this 2% would be 6×10^7 bp (3×10^9 bp × 0.02). The thumb rule for a transcriptome experiment is to have a coverage of at least 50X. This means that we should have at least 3×10^9 bases (6×10^7 bp × 50) sequenced. This accounts to 3Gb (3 giga bases) of data to be generated. If the read length is 1 × 100 bp then a total of 30 million reads of 100bp each would cover 3 Gb of data ((3×10^9 bases) / 100). Therefore, it is mandatory to generate at least 3 Gb of data per sample for mRNA sequencing. However, for whole transcriptome data generation it is recommended to generate 60 million reads per sample as from the same data both the mRNA and lncRNA are

identified for their differential expression. The number of samples to be considered for differential expression should be at least six for an in vitro experiment and at least 15 for an in vivo experiment.

3. **Data quality check and considerations**

Once the data is generated for each sample, the data needs to be checked for quality and uniqueness. The quality of the data can be checked by using the FASTQC tool (Andrews, 2010). This tool gives the basic statistics (viz Total number of reads,Read length and GC content), per base sequence quality (quality in phred score), per sequence quality score, per base sequence content, per sequence GC content, sequence length distribution, overrepresented sequences (viz. Adapter sequences), duplicate sequences and overrepresented Kmers. The uniqueness of the data is checked by calling the checksum value. This value is used to verify the validity of data, typically to make sure that any two data sets are not the same. The data so checked is then trimmed using tools like prinseq-lite or trimmomatic to remove either the adapter sequences or the bases with poor quality at the ends of the reads.

4. **Differential expression analysis**

The major goal of an RNA-Seq experiment is to determine which genes are differentially expressed between the treated and control. The reads generated in an RNA-Seq experiment can be used for transcript quantification, differential expression testing, reference-based gene annotation, and de novo transcript assembly. The tools for RNA-Seq analysis are categorized into, those for mapping the reads; those for assembly of transcripts and annotation of the genome; and those for quantification of transcripts and genes to arrive at differentially expressed genes (DEGs) across conditions. HISAT2 (Kim et al., 2015) in combination with Cufflinks packages (Trapnell et al., 2010) takes care of all these and gives a list of differentially expressed genes. RSEM (RNA-Seq by Expectation Maximization), is another user-friendly software package for quantifying abundances of genes and isoforms, from the data generated (Li and Dewey, 2011). The counts obtained from RSEM can be used for identifying DEGs in an RNA-Seq experiment using DEpackages viz. DESeq (Love et al., 2014), edgeR (Robinson et al., 2010), baySeq (Hardcastle and Kelly, 2010), BBSeq (Zhou et al., 2011) , EBSeq (Leng et al., 2013) etc.. The counts obtained are normalized for factors like gene length, library size and transcript composition bias to yield metrics like FPKM (Fragments per kilobase of gene length per millions of reads)/ RPKM (Reads per per kilobase of gene length per millions of reads), CPM (counts per million), TPM (Transcripts per million) and TMM (Trimmed Mean of M Values). FPKM is a term used for paired end reads and RPKM for single end reads. The detail on these metrics is given in Table 2.

Table 2. Metrics used in RNA-Seq data analysis*

Metric	Normalization	Remarks	Package that gives the parameter
RPKM/ FPKM	Library size (Sequencing depth) and gene length	Should not be used for between sample comparisons and DE analysis Should be used only for comparison of genes within a sample	Cufflinks and RSEM
TPM	Library size (Sequencing depth) and gene length	Should not be used for between sample comparisons and DE analysis Should be used only for comparison of genes within a sample	RSEM

CPM	Library size (Sequencing depth)	Should not be used for between sample comparisons and DE analysis Should be used only for comparison of genes within a sample	CLC genomics workbench
Size factor (Median of ratios)	Library size (Sequencing depth) and transcript composition bias	Should not be used for comparison of genes within a sample Should be used for between sample comparisons and DE analysis	DESeq2
TMM	Library size (Sequencing depth), transcript composition bias and gene length	Should be used for between sample comparisons, DE analysis and for comparison of genes within a sample	EdgeR

* The ideal workflow (Figure 3) for identifying differentially expressed genes is by choosing the common differentially expressed genes (DEGs) identified across packages.

Functional annotation of differentially expressed genes (DEGs)

The first step after identification of DEGs is functional annotation of the DEGs. Gene Ontology refers to categorizing the genes into the biological processes in which they are involved; into the basic molecular function, they determine, and; into the cellular component that they are localized in. For eg., DNA polymerase is involved in the biological processes – replication; molecular function - polymerization and ; cellular component – nucleus. The functional enrichment of the differentially expressed genes in different categories (i.e Biological processes, Molecular function and Cellular component) would help in identifying the pathways and networks that are dysregulated. This functional annotation/enrichment can be done by using the DAVID (Dennis et al., 2003), g:Profiler (Reimand et al., 2007), AmiGO 2 (Carbon et al., 2009), PROSITE (Sigrist et al., 2002), PRINTS (Attwood et al., 2003), Pfam (Finn et al., 2007), ProDom (Bru et al., 2005), SMART (Letunic et al., 2006), TIGRFAMs (Haft et al., 2003), PIR superfamily (Nikolskaya et al., 2006), SUPERFAMILY (Wilson et al., 2007), Gene3D (Yeats et al., 2007), PANTHER (Mi et al., 2007), BLAST2GO (Conesa et al., 2005) and HAMAP (Lima et al., 2009), etc.

Interactome analysis

The study of interactions between the biological molecules on a comprehensive scale in the cell is otherwise called Interactome analysis. This analysis involves high-throughput mapping of protein interactions to construct protein-protein interaction networks. The topology of these networks reflects the functionality of the interacting genes thus helping the researcher to place the genes identified in microarray/RNA-seq experiments in a broader biological context. This functional grouping of interacting or coordinately induced/repressed genes, help in deciphering the roles of the subsets of co-expressed genes. This would result in framing biological hypotheses with increased confidence. The molecular interactions between transcription factors (TFs) and the genes that they regulate can also be mapped for identifying cell or tissue-specific regulatory networks.

The Biological General Repository for Interaction Datasets (BioGRID) is a curated biological database of protein-protein and genetic interactions (Stark et al., 2006). It provides a comprehensive resource of protein-protein and genetic interactions for all major model organism species. BioGRID currently holds 2005220 interactions curated from both high-throughput data sets and individual focused studies derived from over 75988 publications in the primary literature. In this repository,

protein-protein interactions in humans are well defined to construct the protein-protein interaction network with the differentially expressed genes. For any other species in question, the orthologs of the DEGs in humans can be considered to fish out the interactions using customized Perl scripts. The other alternative for identifying the protein-protein interaction networks is the STRING database (Szklarczyk et al., 2019). The interactions thus obtained can be visualized in Cytoscape 3.8.2 (Shannon et al., 2003).

Identification of Transcription factors, miRNA

Prediction of transcription factors binding to upstream regions of important differentially expressed genes would help in establishing a strong hypothesis for the biological question(s) in hand. As transcription factors bind upstream to the genes, the first major step towards identifying the TFs is the extraction of all the upstream regions of the genes in question. For this extraction of sequences, Ensembl database forms a very strong resource. Ensembl is a comprehensive database that provides access to an ocean of data to decode eukaryotic genomes. The upstream regions extracted from Ensembl can be fed into MEME (Multiple EM for Motif Elicitation) suite to identify common motifs across the upstream regions of the DEGs (Bailey et al., 2006). These motifs are then put into TOMTOM tool in the MEME suite that allows identification of transcription factors that bind to these motifs. TOMTOM compares the identified motif to a database of motifs in JASPAR (Fornes et al., 2020), JOLMA, Uni-PROBE (Newburger et al., 2009), etc., and finds matches.

Importance of IPA

A robust alternative to all this analysis is QIAGEN's Ingenuity Pathway Analysis (IPA) (QIAGEN, Redwood City, USA) with its database: Ingenuity Pathways Knowledge Base (IKB). IPA takes the input of DEGs and predicts the canonical pathways, Diseases and Functions, Upstream regulators, Molecular activated pathways, miRNAs etc. Core analysis in IPA is performed to know activated (Z score > 2) or inactivated (Z score < −2) canonical pathways along with their p-value. The canonical pathways from core analysis predict the changes in cells vis-a-vis the different physiological or pathological insults. The comparison analysis in IPA helps to give an insight into the molecular changes across the groups considered in the study. Also, upstream regulators (transcription factors, cytokines, and other molecules) identified in IPA help to chalk out the most important regulators or modulators in the study. IPA is thus an advanced stand-alone tool for data interpretation to delineate the changes at the systems biology level.

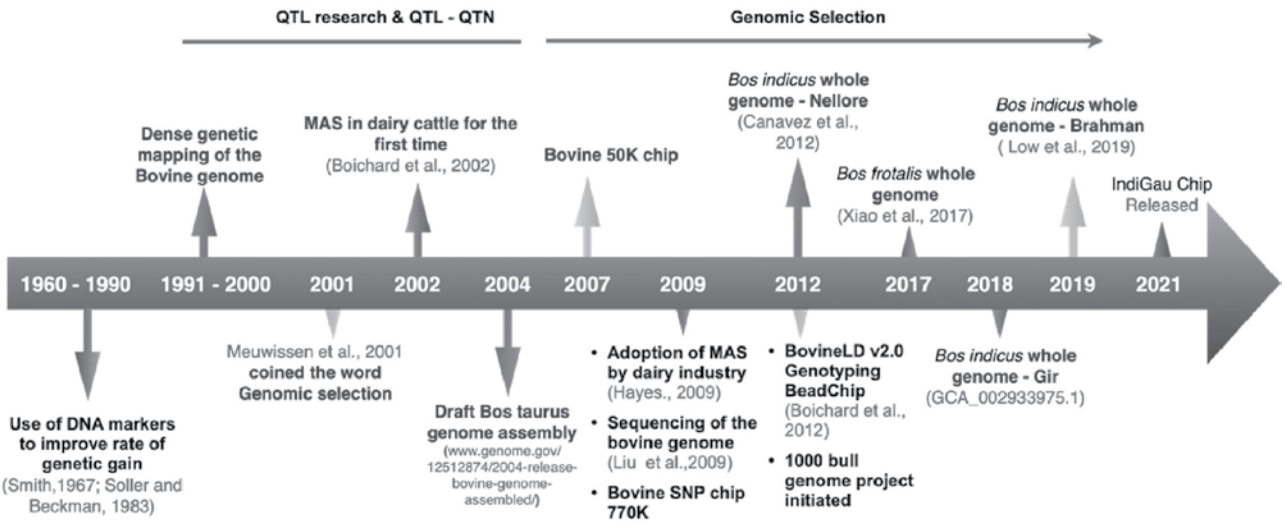

Fig 1. Genome Research in cattle world over

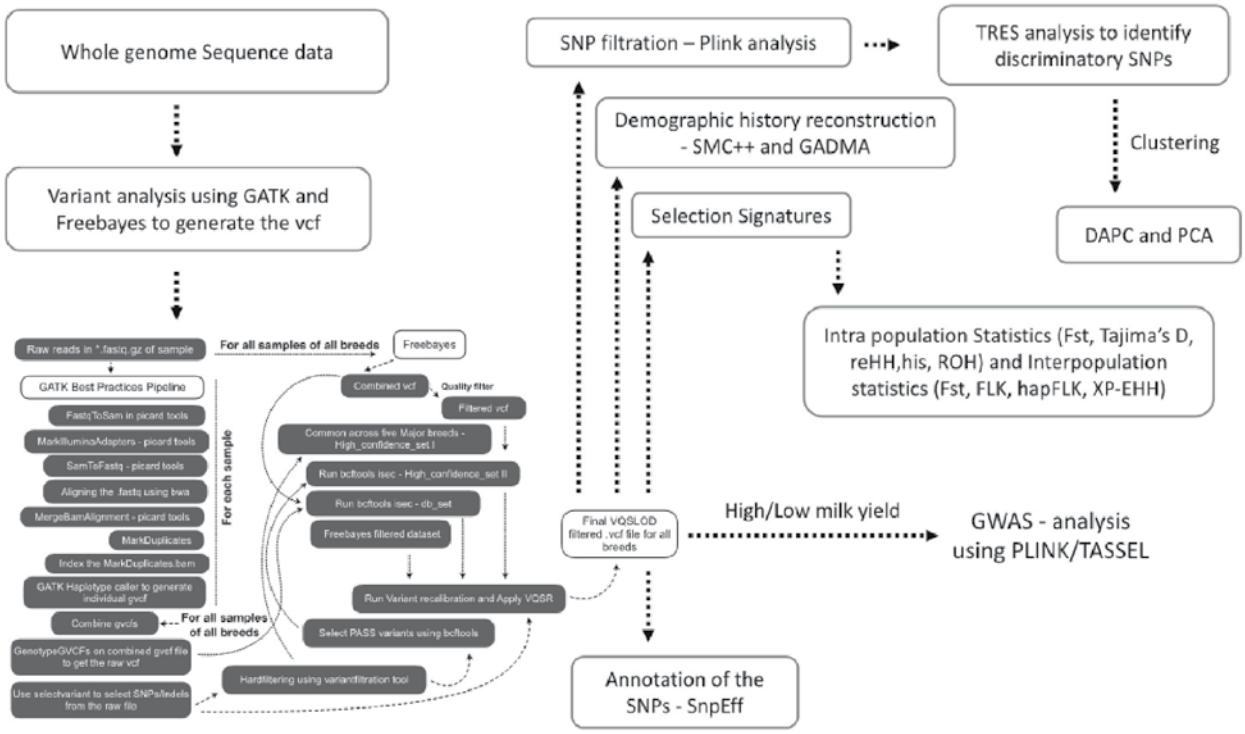

Figure 2. – SNP data analysis workflow

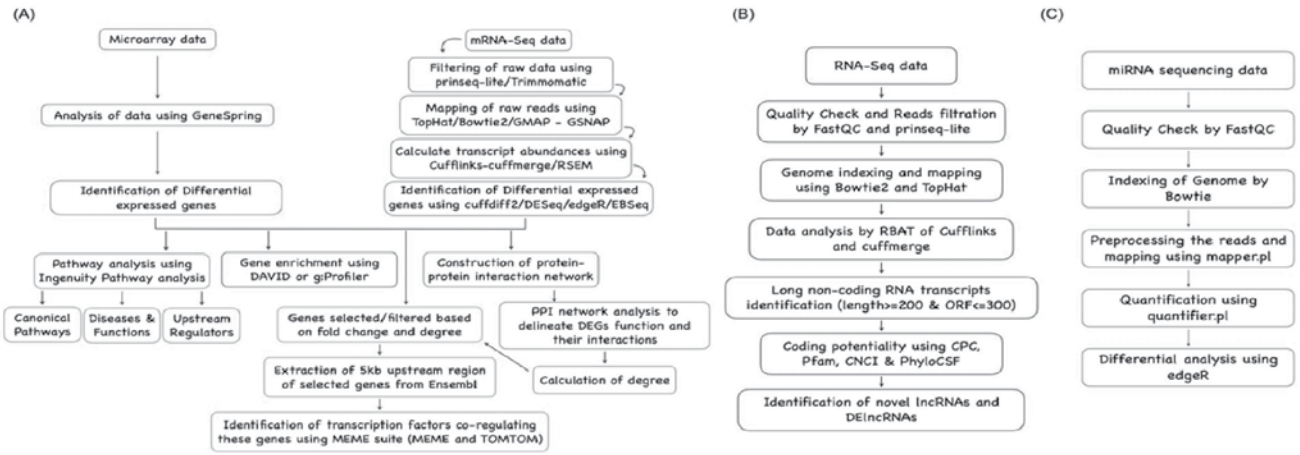

Figure 3: Workflow for the analysis of data from Microarray and RNA-Seq. (A) Data analysis pipeline for analyzing microarray and RNA-Seq data to identify dysregulated genes (B) Data analysis pipeline for analyzing RNA-Seq data to identify the dysregulated lncRNAs (C) Data analysis pipeline for analyzing miRNA-Seq data to identify the dysregulated miRNAs

Example : - Deciphering systems biology using Transcriptome analysis in Peste des Petitis Virus infection

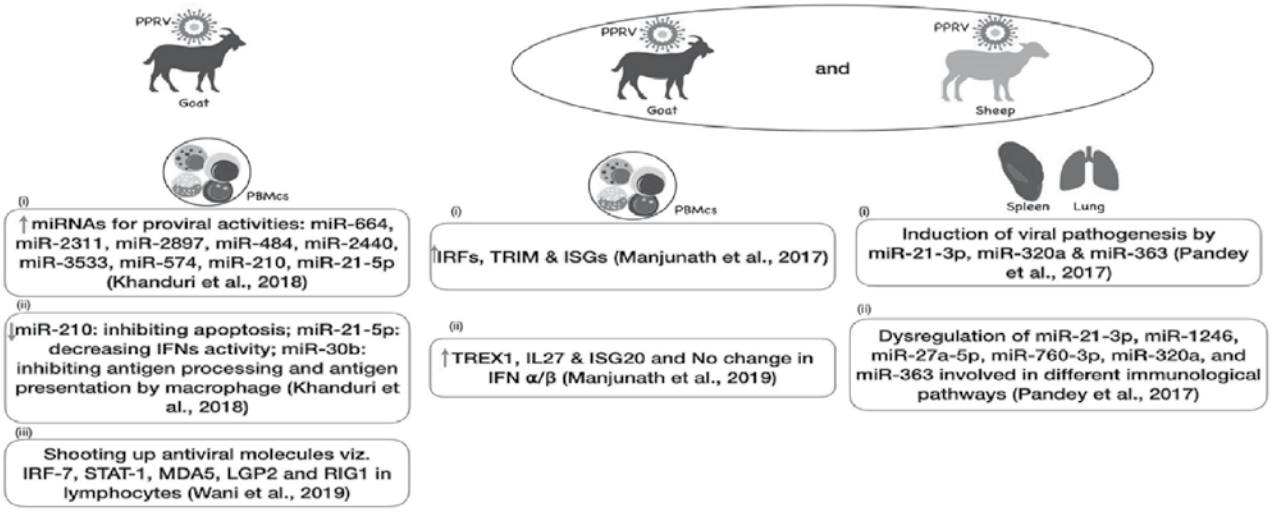

Figure 4: The picture depicts the dysregulation of Genes/miRNAs upon Peste des Petits Virus (Sungri/96 or Izatnagar/94) infection in Goat and Sheep. The dysregulation is shown with the green arrow as downregulated and the red arrow as upregulated.

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LP-9

EPIGENETICS FOR IMPROVING PRODUCTION AND ADAPTIVE TRAITS IN LIVESTOCK AND POULTRY

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The improvement of livestock has been a central paradigm in the evolution of human civilization with the phenotypic traits initially employed, being the most preliminary method for livestock breeding and improvement. With the advent of the Mendelian theory post 1865, thereafter the classical genetics has been instrumental in the livestock breeding and improvement. With the advent of molecular genetics after 1970s, enabling marker assisted selection and mapping of QTLs, revolutionizing the field. In recent times, the high-density SNP chips and the whole genome sequencing platforms have hastened the exploration of candidate genes enabling breeding for low heritable traits. Despite the progress from classical to molecular genetics, the 'genetic gain' still equated on the basis of genetic variance which is assumed to be an indicator of phenotypic variance. The phenotypic traits, particularly the adaptive ones are the factor of environmental influence the existing concept of 'genetic gain' exclude the interaction between the environment and genetic variance. This missing link highlights the epigenetics concept, referred as 'black box' in recent literature (Ibeagha-Awemu and Yu, 2021). Today, variations in the genome are gaining increasing importance in livestock improvement strategies. Genomic variation alone, however, explains only a part of the phenotypic variance in traits of interest. It is possible that part of the unaccounted variance is governed by the epigenome also, encompassing the epigenetic marks such as DNA methylation, histone modifications, chromatin remodeling, and other molecules such as non-coding RNA species. Epigenetic factors respond to external or internal stimuli such as nutrition, pathogens, and climate, and have the ability to alter the gene expression and emergence of specific phenotypes. Accumulating evidences indicate that epigenetic marks listed can influence the gene expression and phenotype in the form of trait variation in the livestock species.

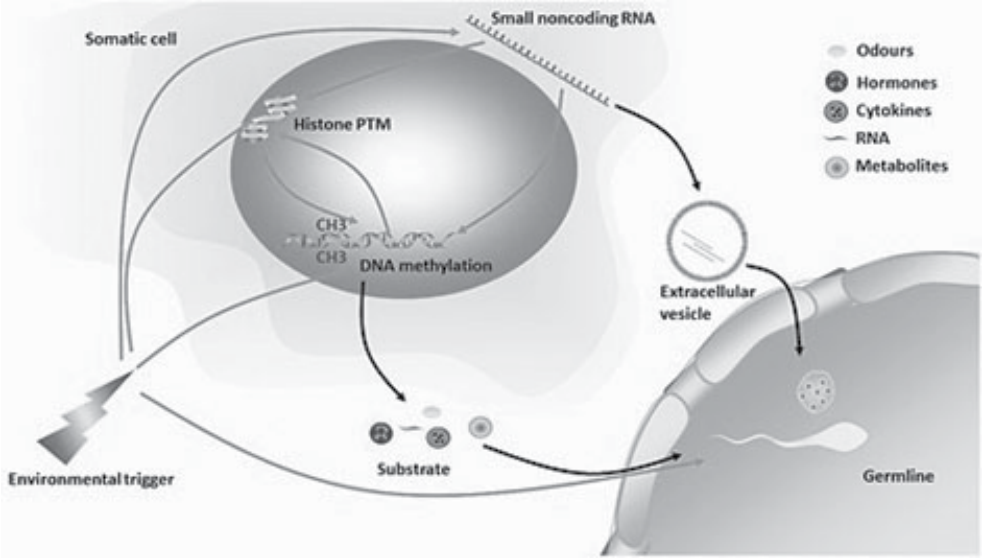
Rollin Hotchkiss made the epigenetics (DNA methylation) breakthrough in 1948, and there are now a wide variety of faculties in this field. If we assume that the chromatin mesh in the nucleus starts unwinding, numerous layers of epigenetics that act in various ways would be apparent. Genetic changes at nucleotide levels can alter the protein sequence and structure as well as function, whereas epigenetic changes affect the gene expression by turning it “on” and “off”. Epigenetic changes are greatly influenced by the environment and the behaviors, such as diet, exercise etc., and it is possible to correlate the gene expression and behaviors and environment. There are epigenetic changes taking place during the process of embryo development, aging etc. also. Various mechanisms through which epigenetic regulation displays changes in gene regulation are listed below.

1. Topological elements at chromatin compartmentalization: At the level of chromatin, the spatial arrangement of coding genes and associated regulatory elements within the three-dimensional (3D) space of the nucleus regulates the accessibility of transcript regulatory elements and therefore the gene expression.
2. Histone modifications: The post-translational modifications of histone at the core and tail parts by various covalently attached moieties (acetylation, methylation, phosphorylation, ubiquitination, glycosylation and ADP ribosylation) bring about a change in the binding affinity of the nucleosomes for regulatory complexes by virtue of stereochemical property alterations. Histone variants encoded by various genes contribute towards the change in physiochemical properties of the nucleosome, and these variants have been implicated as being key in several epigenetic modifications during

biological processes.

3. Covalent modifications on coding and non-coding DNA stretches: The covalent modification of DNA strands by the methyl group at the CpG islands at the promoter site has been extensively studied in livestock epigenetics for highly heritable traits as well as lowly heritable traits like reproduction. The key enzymes involved are DNA methyltransferases (DNMT1—maintenance methylation; DNMT3a and DNMT3b—de novo methylation).

4. Non-coding RNAs: The regulatory non-coding RNAs (iRNAs, miRNAs, piRNAs, and lncRNAs) determine the expression of genes at the post-transcriptional level without any changes in the genome sequence. Among the epigenetic mechanisms of gene regulations studied, DNA methylation and non-coding RNAs have emerged as the most important one, being exploited for understanding the non-genetic factors impacting the traits of economic importance.



Potential pathways for epigenetic information flow (Zhang and Sirard, 2021).

Epigenetic mechanisms impacting different traits studied among various livestock and poultry species are listed below.

A. Disease-resistance:

The transcriptome and methylome of *S. uberis* infected and non-infected Holstein cow's milk somatic cells have been recently studied, and the association of either data could identify genes involved in host immune response during *S. uberis* via various pathways, including cytokine pathways, the nuclear factor-kappa B (NF-B) signaling pathway, and candidate biomarkers such as *SLC40A1, SMPD3, TCF7L2*, etc. (Wang et al., 2022a). Considering, another aspect of epigenetics– 'histone methylation' which majorly controls the expression of NF-κB-dependent genes- which regulate the induction of a very large fraction of the inflammatory transcriptome has been studied. The pace at which the various inflammatory genes respond to the NF-κB is the key to the effective immune response against the stimulus such as LPS. The fast responding and slow responding genes of the pathway have been reported to have various degree of accessibility, governed by the histone modification stereochemistry, to the transcriptional factor (Natoli, 2009). Certain histone marks also contribute towards bringing down the inflammatory response elicited by LPS during mastitis infection. In rodents, the GSK-J1- an inhibitor of *JMJD3* (a histone demethylase encoding gene) has

been reported to reduce expression of *TLR*s and subsequently cease the NF-κB signaling pathway, a unique therapeutic solution for reducing mastitis related inflammation (Wang et al., 2022b).

In poultry, infectious bursitis has been reported to be a consequence of demethylation in one of the miRNA precursors (pre-miR-16-2) promoter demethylation. The demethylation of pre-miR-16-2 occurring during the IBDV or bursitis infection in fowl, increases the expression of the miRNA, gga-miR-16-5p, and subsequently the miRNA pace up apoptosis and viral replication. Such kind of epigenetic regulation of miRNA expression in poultry might be an impetus behind the avian infectious diseases such as Marek's disease, avian influenza, mycoplasma infections, and avian leucosis, which have been reported earlier (Duan et al., 2020; Zhang et al., 2019). Workers have also pointed towards the possibility of involvement of such epigenetic regulation of miRNAs during the pathogenic infections in wide range of species and also the type of demethylase enzyme involved in this regulation need to be explored.

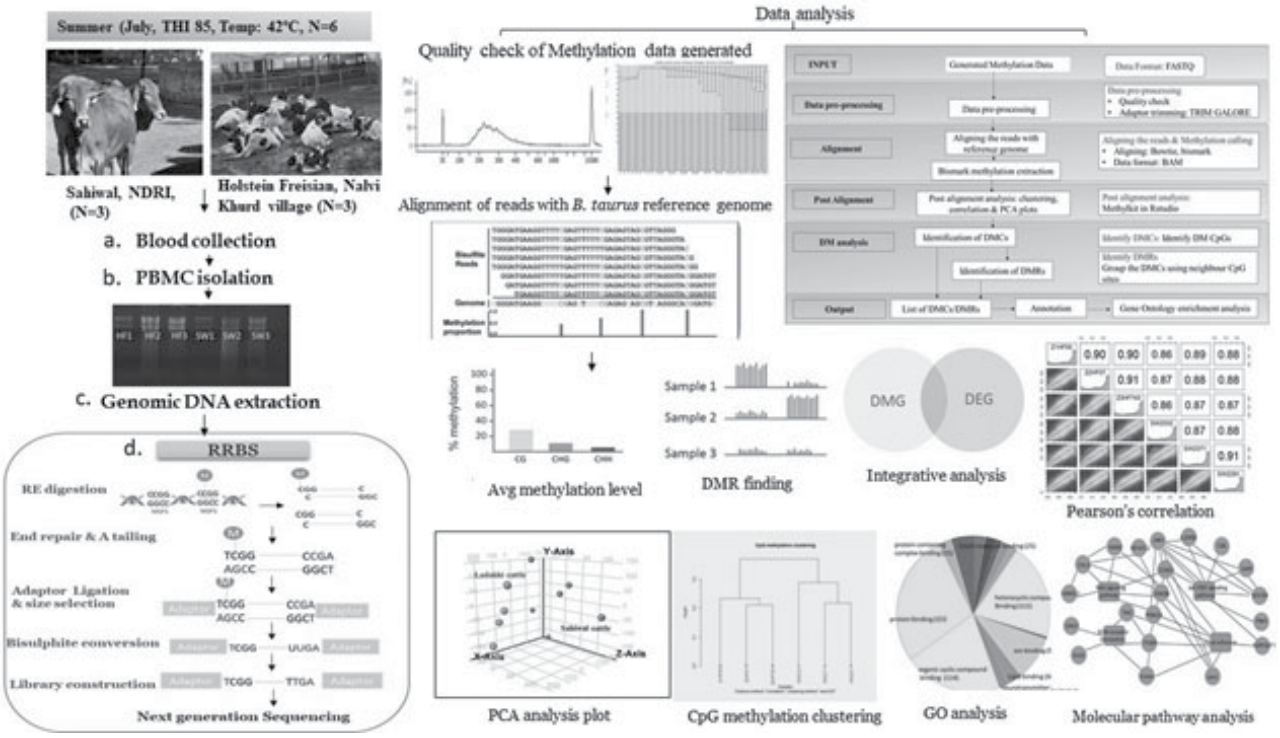
The role of epigenetics phenomenon in the infection mechanisms, makes it an obvious choice to study the post-vaccination changes occurring in an organism against corresponding infections. In porcine, recent research has demonstrated the role of epigenetics in imparting the immunity against PRRS disease (Zhang et al., 2021). The inherited methylome in the piglets from the vaccinated sow and classified based on high and low antibody titers were found to have differentially methylated genes such as *MX1* and *GNG11,* which are located in quantitative trait loci related with PRRSV antibody titer and susceptibility. Conclusively, the role of epigenetics can be inferred to play myriads of roles in various spheres of immunogenomics and opens the avenue for new age immunotherapeutics.

B. <u>Adaptation Traits</u>:

The adaptation traits have been defined very broadly in this era of 'omics'. The classical thought on the phenotype as an interaction of genotype and environment has been elaborated in the form of the role of vertically transmitted as well as acquired changes in the methylome and microbiomics in an organism. The huge impact of the aforesaid in shaping the adaptive traits of an organism during the lifetime as well as inter-generationally has been documented (David et al., 2019; Ibeagha-Awemu and Yu, 2021). Converging the focus on adaptive traits in the sub-tropical and tropical countries like Indian sub-continent lead us to realize that reducing or overcoming the heat stress for the major forms of livestock has been the prime focus for the animal breeders. The degree of impact of the heat stress varies from species to species. In the recent study at ICAR-National Bureau of Animal Genetics Bureau workers have investigated the DNA methylation pattern in response to heat stress in heat tolerant cattle (Indigenous breed- Sahiwal; *n*=3) and heat sensitive cattle (Exotic breed- Holstein Friesian; *n*=3) using the reduced representation bisulfite sequencing approach of the DNA isolated from PBMCs. The overall CpG methylation were almost same, 61.1% and 60.6% in Sahiwal and Holstein Friesian groups respectively, but the study could identify 4433 hypermethylated and 2661 hypomethylated differentially methylated cytosines in Sahiwal breed on the basis of the magnitude of differential methylation in comparison to the Holstein Friesian group. The gene ontology analysis found at least 38 and 81 genes differentially methylated in the gene body to be linked with response to stress in Sahiwal group and Holstein Friesian group respectively. Several members of heat shock protein family were methylated in HF (*HSPA13*, *HSP90AB1*, *HSP90AA1*, and *HSPA8*) and in Sahiwal (*HSPA5* and *HSPA14*). The master regulator of the heat shock genes, *HSF-1* was differentially methylated in the two breeds investigated.

The confluence of epigenetics and biotic effects have been elucidated in the nutritional-epigenomics of livestock. The Lvliang Black goat breed from China known for its ability to thrive on the sparse vegetated mountains and well-documented for its ability to survive in the hostile extremities of

temperatures has been investigated. Wang and co-workers (2020) studies the methylome of the grazed and confinement fed groups of the goats to understand the role of the feeding pattern in the goat breed's survival abilities. The authors concluded the lower expression of the *PLCL1* (Phospholipase C Like 1) gene in the grazing group than the confinement feeding group to be linked with the differential methylation of *PLCL1* and this epigenetic regulation is enabling the grazed group of goats to cope up with the extremities in the ambient temperature. This articulates the importance of free range grazing in providing the edge to the indigenous livestock to sustain their adaptational qualities through epigenetic changes. The studies of similar kind can provide more scientific backing to the peculiar adaptations of indigenous livestock of India, known for thriving on poor quality roughages and better feed utilization. The epigenetics also have imparts on the adaptational advantage for livestock introduced to the newer environmental conditions. Sevane and co-workers (2019) demonstrated the epigenetic regulation of long-term adaptation of the livestock to the newer environmental conditions in the cattle imported from Spain during the Columbian era to the South American continent. The research group concluded the epigenetic regulation of genes such as *CYB561* to be involved in bringing out the heat stress related adaptive phenotype changes during the generations.



Workflow of generation of DNA methylation in heat tolerant Sahiwal cows and heat sensitive HF cows.

C. <u>Production Traits</u>:

Globally, the farm animals including cattle, buffalo, goat, sheep etc. accounts for 87% of dietary animal-origin protein for human population (Thilsted et al., 2014). Among various production traits, the milk, beef/meat, and egg production are prime focus owing to the surplus demand of ever-growing human population. In this context, understanding the epigenetic regulation of these traits will certainly gear up the genetic improvement programmes, amalgamating epigenetics and genetic basis of variations. In dairy livestock, the lactation period has been implicated in the negative energy balance during a span of time before and after parturition. Poirier and coworkers (2020) have reported the epigenetic marks in the genes involved in metabolism and development in the post-partum (early and mid-

phase) Holstein Friesian cow. The oocytes collected from early, mid-phase of post-partum, and cyclic heifers were sequenced for whole genome methylome, the methylome revealed the occurrence of differentially methylated region of gene bodies in the CpG islands of paternally imprinted genes such as *MEST* and *GNAS* in early post-partum samples, and not in the mid-phase post-partum and cyclic heifers. The imprinted genes have been linked with the non-esterified fatty acid concentrations in milk, which indicates that if the methylation in gene bodies regulate these imprinted genes-they could influence the milk quality in post-partum cattle (Reik et al., 2001).

The role of epigenetic marks have been also implicated in the multiparous mammals, the epigenetic memory generated during the first parity in rodent has been reported to influence lactations in the subsequent parities (Dos Santos et al., 2015). This clearly emphasizes the role of epigenetics marks acquired during the lifetime of an individual in regulating the imprinted genes. Such studies are lacking in the livestock, and can be targeted to optimize the physiological experiences gained by the lactating animals. Further, the role of miRNAs in the regulation of the lactation-related genes, such as *CSN1S1*, *EIF5*, *PPARγ*, *SREBP1*, and *GLUT1* has been reported by Bian and research group (2015). The workers delineated the miRNA (miR-29) to be negatively regulating the de- novo DNA methyltransferase encoding genes- *DNMT3A* and *DNMT3B*, therefore the inhibition of the miR-29 led to hypermethylation of lactation related genes. Additionally, the miR-29 also promotes the cell proliferation, hence lactation is supposed to increase upon mammary epithelial cells' proliferation (Yang et al., 2013). An elaborative integrated study involving methylome, transcriptome, and genome-wide association data identified the candidate genes such as *DOCK1*, *PTK2* and *PIK3R1* in high milk and low milk production Holstein cattle (Dong et al., 2021).

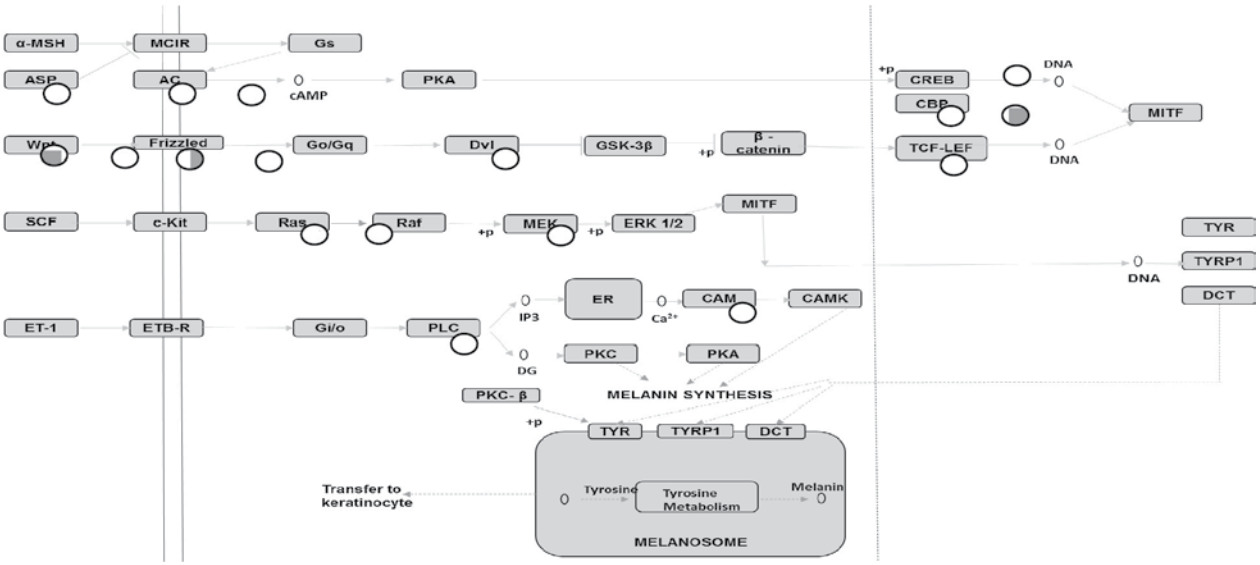
Wool is another important livestock produce that contributes to a significant fraction of the country's export- worth US$ 1.64 billion (https://www.ibef.org/exports/wool-industry-india). One of the prime aspects in the mass production of wool (sheep and goat) is the hair follicle cycling, the follicle cycling involves three steps rapid growth phase called as anagen, regression phase called as catagen, and quiescence phase of telogen. In rodents, the crucial role of maintenance DNA methyltransferase has been reported where the inhibition of *DNMT1* gene led to the reduction in number of hair follicles (Li et al., 2012). A whole genome bisulfite sequencing study on the Cashmere goat has demonstrated the further role of differential methylation in keratinocytes structure formation, ceramide biosynthesis pathway, and hair follicle development when compared the anagen phase tissues with the telogen phase tissues (Li et al., 2018). Trans-generational epigenetics has been studied for the epigenetics variance in Quail for egg quality traits. For egg quality traits such as egg length and width, albumen weight, shell weight, yolk weight and egg weight epigenetic heritability was reported to be non-significant on the basis mixed model analysis, where the random effect was considered as epigenetic effect (Paiva et al., 2018). The study of epigenetics heritance using the mixed model may be an ineffective way to look at the global methylation changes. In an effort to understand the embryonic development in eggs at the level of DNA methylation in the broilers Sun and coworkers (2018) studied inorganic zinc and organic supplemented groups. The methylation of the global DNA and H3K9 acetylation of MT4 promoter in the liver samples of embryo (E20) was higher in the organic zinc group than the inorganic zinc group. The MT4 encodes for metallothionein protein which is crucial for the binding of zinc ions, the acetylation of histone must be promoting the binding of transcriptional regulators to the MT4's promoter region. The study drops clue about the source of mineral supplements in boosting the productivity, such kind of scenarios dietary factors influencing the production through epigenetic modifications, could also influence the milk, meat, and wool productivity. This branch of epigenetics has been termed as 'nutritional epigenetics' widely studied in human subjects (Kaja., et al., 2022). The sustainable goals for enhancing productivity in livestock could actually be revised by conducting epigenetic pilot experiments to scan the cheapest and locally

available dietary supplemental sources for our country's colossal agro-ecosystem diversity.

In Northern India, the Nili Ravi water buffalo is known for its peculiar pigmentation pattern. The over-white trait of Nili Ravi buffalo is assumed as a negative trait by their owners and leads to economic losses to the marginal farmers. In an effort to delineate the epigenetic background of this typical pigmentation pattern, the group of workers at ICAR-NBAGR, has studied the DNA methylation events mark as major epigenetic change in the genome, reflecting the varied phenotypes (Gurao et al., 2022). For deconstructing this research question, DNA extracted from skin tissue of three different groups of water buffalo, white Nili Ravi, black Nili Ravi, and black Murrah, 3 from each group, was explored. The skin tissue bisulfite treated DNA sequenced using the reduced representation bisulfite sequencing (RRBS). The study is first of its kind in water buffalo providing insights into the epigenetic regulation of skin pigmentation in Nili Ravi buffalo. Results of the study indicated the variation in the methylation pattern among the three groups of buffalo with varying coat color. Major genes associated with skin pigmentation, were found to be having the varying levels of methylation in Nili Ravi's over-white and under-white skin tissues. The methylation in specific genes (SNAI2, HERC2, and TBX2) need to studied at gene expression level for formation of white patches in Nili Ravi sub-types. This information can be used to demonstrate the unique breed characteristics in Nili Ravi.

D. **Reproduction Traits:**

Heat stress has been known for decades to adversely affect animal productivity and reproductive potential. Buffalo bulls have poor thermoregulatory capabilities as compared to cattle, and it has been reported earlier that due to heat stress, semen quality goes down during the summer. DNA methylation is an epigenetic phenomenon affected by various environmental stimuli. In the context of livestock breeding, genomic selection and the use of elite sires are important tools for improving production traits. However, performances are also impacted by environmental factors, thus limiting the efficiency of genomic selection. Environmental heat stress could manipulate the DNA



Nili Ravi buffalo skin methylome: Differentially methylated cytosines ($p < 0.05$) enriched for pigmentation pathway and the bar plot at right corner depict the number of genes enriched for pigmentation pathway in the promoter region of Nili Ravi-Over White (G2) and Nili Ravi-Under White (G3) when compared with Murrah (G1).

methylation pattern, and the changes in methylation pattern at CpG sites, particularly at the promoter region, may determine the fate of semen quality, meiosis, and spermiogenesis-related genes. Group of workers at ICAR-NBAGR has identified DNA methylome signatures in buffalo bull spermatozoa under summer heat stress that could delineate the epigenetic regulation responsible for poor sperm quality during heat stress or during the hot summer season. Based on the seasonal semen quality parameters, bulls were classified as seasonally affected and non-affected, and the RRBS-based methylome study was conducted. The functional enrichment of the differentially methylated cytosine data identified several pathways involved in spermatogenesis (oocyte meiosis, oxytocin signaling, and MAPK signaling), heat stress, and chromatin remodeling that were significantly enriched. The workers could identify some spermatogenesis-associated genes, including *TEX29, SEPT9-SEPT6-SEPT4, and CCR7* in the top hypomethylated CpGs and *NPTN, CEP170B, ANO1, RPL31,* and *GRAMD4* in the top hypermethylated CpGs in the promoter region of seasonally affected animals. The study is the first of its kind to generate the methylome data of sperm cells from the heat stress-affected Murrah buffalo bulls. This data potentially paves the path to understanding the epigenetic regulation of heat stress on altered sperm function and semen quality. Future work on correlating the epigenetic data with transcriptome-level gene expression as well as targeting the bull fertility trait is suggested.

Diaz and co-workers (2021) investigated the global methylation level of 5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5 hmC) at various stages of oocyte developmental stages in bovines (primary oocyte and matured ovum) didn't vary but the transcriptomics could delineate changes in the transcript level of genes involved in glucocorticoid biosynthesis, apoptosis signaling, and HIPPO signaling pathway during the various stages of oocyte maturation influenced by heat stress. This potentiates the necessity to consider genome-wide bisulfite sequencing approach to understand the DNA methylation at gene specific loci.

The interaction of environmental factors not only determines the fertility of the animals, but also the vertical transmission of these epigenetic marks regulate the embryonic development. This is brought about by the epigenetic reprogramming occurring during the embryonic development. The most prominent aspect of this epigenetic reprogramming is the methylation events. Just after the fertilization, the zygote has intact pronucleus from both parents and this stage exhibits two extremely mystified preferences. While the global methylation marks are actively erased, the germline specific methylation patterns are conserved (Breton-Larrivée et al., 2019).

This assisted reproductive technologies used in livestock production are implicated in altering these epigenetic reprogramming in embryos. Superovulation has been widely used in the production of bovine in-vitro embryos from elite animals for assisted reproduction. Superovulation can amend epigenetic profiles in embryos (Camargo et al., 2019). Similarly, altered epigenetic profiles in embryos have been reported in the in-vitro environment produced during in-vitro maturation, fertilization, and embryo culture (Beaujean, 2018). Therefore, apart from emphasizing the nature of gamete epigenetics, priority must be given to profiling the epigenetic marks determining the health of the progeny.

To conclude, the epigenetics is an emerging area of research in livestock nutrition, genetics and breeding. It deals with the modifications that occur in the epi-genome (without changing DNA sequence) contributing significantly to phenotypic variability of a population. As epigenome information may add to the knowledge on the association between genotype and phenotype, there is need to discover the causal relationship of genome–epigenome–phenotype for effective improvement of livestock production. However, at present the research on epigenetics in livestock species is limited

partly due to lack of recognition, funding and a global network of workers. Exploring the epigenetic determinants of animal diseases and complex traits may represent one of the principal challenges to use epigenetic markers for future improvement of animal productivity. There are growing prospects for exploring into the direct and indirect associations between environment, epigenome, genome and the phenotypes. Whole genome based data generated using RRBS and whole genome methylome sequencing will definitely help in understanding the role of epigenetics in governing the traits of interest in future.

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TECHNICAL SESSION-I

Innovative breeding technologies- Current trends and future scope

ISAGBCON 2022, ICAR-DPR, Hyderabad

XVI Annual Convention of Indian Society of Animal Genetics and Breeding

and

National Conference on

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ABST-1-001

A PLATFORM-INDEPENDENT ONLINE FIELD DATA COLLECTION SOFTWARE SOLUTION FOR THE MULTI-TRAIT AND MULTI-BREED GENOMIC SELECTION PROGRAM UNDER SMALLHOLDER DAIRY SYSTEM OF INDIA

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The program aimed at creating an efficient, platform-independent online field data collection software solution for the multi-trait& multi-breedgenomic selection under the smallholder dairy system of India. This software solution is an upgraded version of our earlier windows based online-offline digital tablet-based software solution. The salient feature of this newer version of software solution is: platform independent supporting HTML 5 standard and integrated with consoles not just to the enumerators but also artificial insemination (AI) technicians, supervisory staff, farmers and molecular laboratory for processing samples for genotyping.To bring more accuracy to the performance recording data collection in the smallholder dairy system of India, the solution brought more validation, data entry check restriction to avoid typographical errors and an automated monitoring system, while introducing real-time GPS enabled data entry to keep a track of performance recording. In addition to this, the Bluetooth-enabled milk analyser and weighing scale for accurate & automated data recording added more value to the efficiency of accurate data collection. The enumerator collects the data on production (test day milk yield and milk components like fat, SNF etc.), reproduction (breeding history), health related trait (somatic cell score), mastitis and general disease incidences, body weight and dairy type traits (26 characters) on crossbreds, indigenous cattle and buffalo population. Considering the cost of the performance recording, we are promoting farmers to collect their own animals' records by providing them separate access for data collection. A total of more than 40,000 animals were recorded in over the period of 7 years. The information collected through this software solution will be utilised for creating a large female reference population for genomic selection.

ABST-1-002

GENETIC EVALUATION OF GROWTH TRAITS USING RANDOM REGRESSION MODELS IN JERSEY CROSSBRED CATTLE

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A total of around 34,726 number of body weight records collected at repeated intervals from birth to 54 months of age *i.e*. BW0, BW6, BW12, BW18, BW24, BW30, BW36, BW42, BW48 and BW54 pertaining to 7363 Jersey crossbred cattle, belonging to 108 sires, 7363 dams under Progeny Testing programme of APLDA were subjected to Random regression analysis for additive genetic, individual permanent environmental, maternal genetic and maternal permanent environmental effects by using different Legendre polynomials like quadratic, cubic and quartic *etc*. Preliminary analysis revealed significant ($P<0.01$) influence of all fixed effects on the body weight and were included in estimation of random regression coefficients. The mean value for body weight at birth, 6, 12, 18, 24, 30, 36, 42, 48 and 54 months of age in females were 23.17±0.02, 79.19±0.10, 122.50±0.20, 174.90±0.47, 215.40±0.65, 275.20±1.05, 300.30±2.27, 323.30±5.92, 317.10±11.84 and 368.15±44.98 kg, whereas in males were 26.36±0.18, 83.30±0.63, 144.60±1.19, 205.90±2.17, 277.30±3.56, 328.90±4.66, 377.40±9.40, 414.90±12.79 and 452.20 kg respectively. Results revealed that models using residual heterogeneous error variance were found to be significantly ($P\leq0.01$) superior over homogenous error variance. Comparison among 26 models revealed that smaller AIC & BIC values observed at model 4 (3333B), but highest likelihood value occurred at model 23 (5554B) with minimum number of 33 and 64 parameters respectively. The large Eigen value was recorded for intercept (L0) followed by linear (L1), whereas for quadratic coefficient it was found to be zero for all random effects. The trajectories for 1st and 2nd Eigen function accounting for >98 & 1.26% of total genetic variation and was zero for 3rd Eigen function. Among all

effects the highest covariance value was noted between intercept (L0) and linear (L1) (1134.30, 118.20, 117.63 and 1765.50) for direct additive genetic (G), maternal genetic (M), maternal permanent environmental (C) and animal permanent environmental effects (P) respectively. The average breeding value for birth weight was found to be 23.24 kg, which improved to 321.10 kg at 48 months of age.

ABST-1-003

GENETIC GAIN IN ECONOMIC TRAITS THROUGH SELECTION INDICES IN HF X GIR HALFBREDS

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The present investigation was undertaken to assess the magnitude of different factors along with generations affecting the age at first calving, service period, lactation length, lactation milk yield, dry period, calving interval, milk yield per day of calving interval (MY/CI), milk yield per day lactation length (MY/LL) of HF x Gir halfbreds. The data pertaining to HF x Gir halfbreds maintained from year 1972 to 2016 at RCDP on cattle, MPKV, Rahuri were used for present investigation. The data were analyzed by least squares technique and means were compared by DMRT. Heritability of traits and genetic correlation, phenotypic correlations between reproductive and productive traits were also studied. The overall age at first calving, service period, calving interval, lactation milk yield, lactation length, dry period, peak milk yield, (MY/CI) and (MY/LL) of HF x Gir halfbreds recorded were 983.69 8.64 days, 130.80 ± 4.88 days, 421.10 3.77 days, 3068.48 ± 38.57 kg. 328.50 2.39 days, 105.64 ± 5.33 days, 15.39 ± 0.10 kg. 7.70±0.09 kg and 9.33 ± 0.10 kg, respectively. The non-genetic factors had significant effect on most of the reproductive and productive traits, which indicated that to obtain better performance management plays vital role in addition to genetic improvement of the animals. A significant genetic and phenotypic correlation observed among reproductive and productive traits indicated genetic improvement in late observed economic traits like milk yield, animals can be selected on the basis of AFC or SP or CI. In HF x Gir halfbred cows the heritability of AFC, SP, PMY, LMY, LL. DP, CI, MY/CI, MY/LL was 0.521 ± 0.517, 0.132 ± 0.104, 0.432 ± 0.433, 0.259 +0.227, 0.330 ± 0.031, 0.430 ± 0.430, 0.087 ± 0.066, 0.077 ± 0.060 and 0.056 ± 0.061, respectively. Out of 28 selection indices constructed for HF x Gir halfbreds, index I_{24} to I_{28} from four traits combination were found to be relatively efficient indices and rated as the most useful indices for their high reliability and expected genetic gain.

ABST-1-004

KAIKADI DONKEYS: AN IMPORTANT EQUINE GERMPLASM OF WESTERN VIDARBHA REGION

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The non descript domestic donkeys in Western Vidarbha region of Maharashtra are one of the important non dairy domestic livestock species, which are being reared by poor and weaker communities as an ancestral profession of local society viz. Kaikadi, Bhoi (river sand and soil carriers), Kumbhar (Pot makers), Vadar or Vadari (makers of stone articles) and some minor communities like Vaidu and Dhobi etc. The donkey stakeholders popularly identify local domestic donkeys as “Kaikadi” or “Gavran” and primarily used for transportation of goods and as pack animals at brick kilns. medium sized with compactly build body and strong and straight back, efficiently working animals. The coat of hair was thin all over the body except mane and around ears and face in some cases. The prominent coat colour of donkey was grey followed by dark brown or black, roan (mixture of black and brown) and grey and white (light grey). Typical white band around muzzle, a strip of dark shade across the shoulder and back were observed in majority of the donkeys. The drastic decline in population has been highlighted in recent Livestock census. The major constraints faced by donkey owners have been noticed as unemployment and theft of free ranging animals. Also, the lack of knowledge of management, altered rural practices due to mechanization and socio-political ignorance towards donkey

owner etc. as major reasons of declining donkeys in this region. There is a need to evaluate its potentials and assess whether it is a distinct population/breed from other adjoining donkey population.

ABST-1-005

POULTRY LITTER COMPOST WITH SAW CHIPS – WEALTH OUT OF WASTE

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One of the major issues the poultry industry is currently facing is the accumulation of large amount of wastes, especially manure and litter, generated by intensive production, which is causing major environmental problem. To overcome environmental issues related to pollution, environmentally and economically sustainable management technologies are to be evolved to mitigate the adverse effect of poultry waste and evolve the means to utilize those for producing the meaningful by products, which can be used by other stakeholders. The compost was prepared having C/N ratio of 35:1 by mixing poultry litter with saw chips having Relative Humidity 50%, pH 5.0 and Temperature 34^{0}C. 15 Kg of litter was mixed with 48 Kg of saw chips. The humidity was maintained at around 50%. The temperature was changing due to the growth of the microbes inside the pile. The compost was ready on 70th day. The compost was prepared having C/N ratio of 30:1 by mixing litter with saw chips as supplement having Relative Humidity 50%, pH 5.0 and Temperature 34^{0}C. 18 Kg of litter was mixed with 42 Kg of saw chips. The compost was ready on 70th day. The compost was prepared having C/N ratio of 25:1 by mixing litter with saw chips as supplement having Relative Humidity 50%, pH 5.0 and Temperature 25^{0}C. 25 Kg of litter was mixed with 36 Kg of saw chips. The compost was ready on 70th day.

ABST-1-006

STUDIES ON GENETIC AND NON-GENETIC FACTORS AFFECTING FIRST LACTATION TRAITS IN CROSSBRED CATTLE

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Data on first lactation records of 529 crossbred animals available from organised herd of Instructional dairy farm of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar spread over a period of 30 years (1990-2019) were analysed to determine the effect of several genetic and non-genetic factors on production and reproduction traits of first lactation. The overall least-squares mean of age at first calving (AFC), first service period (FSP), first dry period (FDP), first calving interval (FCI), first lactation period (FLP), first lactation milk yield (FLMY), first lactation 305 days milk yield (FL305DMY), first lactation peak yield (FLPY) and first lactation days to attain peak yield (FLDAPY) were estimated as 1170.62±31.50 days, 263.94±3.40 days, 115.90±19.84 days, 513.00±22.60 days, 397.25±9.19 days, 3584.92±118.42 kg, 2854.26±59.61 kg, 14.18±0.27 kg and 48.42±0.87 days, respectively. The data were clustered into different classes according to genetic groups of animals, season of calving and period of calving. The random effect ofsire had statistically significant (P< 0.01) effect on AFC, FLMY, FL305DMY and FLPY.Genetic group had statistically significant effect onFSP (P< 0.05), FL305DMY (P< 0.01)and FLDAPY (P< 0.05).Season of calving significantly (P< 0.05) affected FL305DMY and FLDAPY. The significant differences of period of calving were observed onAFC (P< 0.01), FSP (P< 0.05), FLP (P< 0.01), FLMY (P< 0.01), FL305DMY (P< 0.01)and FLDAPY (P< 0.01). Variability in the traits due to various factors might be attributed to the differences in genetic and non-genetic factors. Therefore, satisfactory management and appropriate genetic improvement strategies would result in ameliorating the performance of animals.

ABST-1-007

APPLICATION OF MATHEMATICAL EQUATIONS TO DESCRIBE LACTATION CURVES IN MARATHWADI BUFFALOES OF WESTERN INDIA

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The present study was carried out to investigate the efficacy of fitting three different lactation curve models using monthly milk yield records of Marathwadi buffaloes maintained at College of Veterinary and Animal Sciences, Udgir Dist- Latur Maharashtra spread over a period of nine years. The monthly milk yield was recorded at 6th, 36th, 66th and so on till standard lactation with thirty days interval. The three different lactation curve models *viz*. exponential decline function, gamma-type function and parabolic exponential were used on monthly milk yields in Marathwadi buffaloes. It was inferred that the highest coefficient of determination for fitting of lactation curves models was with gamma-type function (98.82%), followed by parabolic exponential model (98.60%) and least by exponential decline function (94.79%). Further, the root mean square error was found least for gamma-type function (1.20), followed by parabolic exponential function (1.31) and highest by exponential decline function (2.53). It is therefore inferred that mixed log function fitted best in Marathwadi buffalo for prediction and modeling of lactation curves based upon monthly milk yields.

ABST-1-008

CONSERVATION AND MULTIPLICATION OF INDIGENOUS ANIMALS (BOSINDICUS) THROUGH IN VITRO EMBRYO PRODUCTION

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The objective of the study were Conservation and Multiplication of Superior Germplasm in Cattle by OPU-IVF Technology, Standardization of OPU process and Standardization of IVF Techniques/process. For this purpose, indigenous breeds viz. Dangi, Deoni, Gaolao, Gir, Red Kandhari, Sahiwalreared in BAIF's Central Cattle Breeding Farm and were selected on the basis of Minimum Standard Protocol set by Govt. of India. Ovum Pick up (OPU) was performed to aspirate the oocytes followed by In vitro Maturation (IVM) and the matured oocytes were processed for In Vitro Fertilization (IVF) which then kept for In Vitro Culture (IVC).A total of 891 ovum pick up (OPU) sessions were carried out. Totally 6416 oocytes were processed for in vitro culture and 2016 embryos were produced. The effect of breed, age of the animal and interval between two OPU sessions were evaluated for both number of oocyte and embryos produced per session.The average breed wise oocyte recovery was 6.585 ±0.451 (Mean±SE) and the average breed wise embryo production was 2.11 ±0.337 (Mean±SE) per session. Breed of cow and age at collection of oocyte were found to be significantly affecting the oocyte and embryo production. It was found that Gir breed has better oocyte recovery and embryo production efficiency in our study. Gir, Dangi and Sahiwal presented higher oocyte recovery and embryo production followed by Deoni, Gaolao and Red Kandhari.In conclusion, the process is standardized for Ovum Pick Up, In Vitro Maturation, In Vitro Fertilization, and In Vitro Culture. Embryo production thorough this standardized process supports the conservation and multiplication of the indigenous cattle breeds in native habitats.

ABST-1-009

ESTABLISHMENT OF GOAT RESEARCH CENTRE AT CHINNAKOVILANKULAM, SANKARANKOIL TALUK IN TENKASI DISTRICT, TAMIL NADU

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Goat rearing is considered as a profitable occupation among the small, landless and poor rural farmers. Tamil

Nadu has 9.89 million goats contributing to 15 per cent of the goat population in the country. Out of 34 goat breeds registered in India, the state of Tamil Nadu possesses three breeds, viz. Kanni Aadu, Kodi Aadu and Salem Black. But the vast majority of the population is of non-descript type of goats. Importantly, southern part of Tami Nadu has two popular breeds of goats, Kanni Aadu and Kodi Aadu. In order to take up genetic research on production of superior germplasm, production of seedlings of improved fodder varieties and legumes and to improve the socio-economic status of the goat farmers, a Goat Research Centre has been established for Rs. 151 lakhs in 128.44 acres of land at Tenkasi District of Tamil Nadu. And the station would help to maintain a nucleus stock of pure indigenous breeds of Kanni Aadu and Kodi Aadu goat breeds, whose productivity can be enhanced by selection over the years. High genetic merit bucks of indigenous goats born to superior parents would be supplied to the farmers for propagation of the breed.

ABST-1-010

EVALUATION OF THE PERFORMANCE OF THE SEX-SORTED SEMEN IN BUFFALOES MAINTAINED UNDER THE SMALLHOLDER DAIRY SYSTEM OF UTTAR PRADESH

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The objective of the study was to evaluate the performance of sex-sorted semen in buffalo population maintained by smallholder dairy farmers and to determine the factors influencing the conception rate. The data on 21,422 artificial inseminations on follow-up basis and 1,400 calving's were used to study conception rate and female calf sex percentage. The effects studied were agro-climatic zones, order of lactation and month of insemination. The conception rate, a binomial trait was categorized as "*0*" for not conceived and "*1*" for conceived and the pregnancy diagnosis for call the cows were carried out by per-rectal examination post 60-90 days after insemination. The agro-climatic zones were categorized as seven agro-climatic zones *viz.* Eastern plains, Bundelkhand, Central western plains, Central plains, North-eastern plains, Western plains, and south western semi-arid plains. While order of lactation were grouped in six as Heifer and 1 to 5 and above. The statistical analysis was performed using the binary logistic regression model to estimate the effect of factors on the conception rate. The overall mean of conception rate was 43.04 ± 0.34 percent, while the female calf sex percentage was found to be 91.20%. All of the effects included in the study significantly ($P<0.05$) influenced the conception rate. The probability of conception rate was higher in central western plains while low probability for conception rate was found in North-eastern Plain. The conception rate increased gradually from February and declined in July 39.13. The odds of conception were comparatively lower in heifers than multiparous buffaloes. The reason for the low conception rate in heifers was due to preferential treatment given by farmers to milking animals. The performance in terms of conception rate and sex ratio of sex-sorted semen in buffaloes maintained under smallholder dairy system were encouraging and could be replicated with good management practices.

ABST-1-011

GENETIC EVALUATION OF REPRODUCTIVE AND LITTER TRAITS IN CROSSBRED LARGE WHITE YORKSHIRE PIGS (SVVU-T17)

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The present investigation was carried out on farm bred 75% crossbred LWY Pigs (SVVU-T17), maintained at ICAR- All India Coordinated Research Project on pigs, Tirupati, Chittoor district, Andhra Pradesh. The data on 343 reproduction records (from 2005 to 2020) were utilized to assess the effect of various genetic and non-

genetic factors including inbreeding on reproductive and litter traits. Single trait analysis was done by fitting a general linear model (GLM) to study the effect of various non-genetic factors (fixed factors) on each trait. The (co)variance components for different reproduction traits were estimated by Restricted Maximum Likelihood Method (REML) using WOMBAT programme of Mayer (2007).The overall least squares means for age at first farrowing (AFF) and farrowing interval (FI) in 75% crossbred LWY (SVVU-T17) pigs were 352.59 ± 6.42 and 249.14 ±2.15 days, respectively. The effect of period, season and inbreeding were significant on reproductive traits. The overall least squares means for litter size at birth (LSAB),litter size at weaning (LSAW), litter weight at birth (LWAB) and litter weight at weaning (LWAW) in 75% crossbred LWY (SVVU-T17) pigs were 7.71 ± 0.10, 7.44 ± 0.10, 8.58 ± 0.13 kg and 55.42 ± 0.91 kg, respectively. The effect of period and parity were significant (P<0.05) on majority of the litter traits. Effect of level of inbreeding on all litter traits was also found to be significant. Inbreeding co-efficient (Fx) values in the population varied from 0 to 25.5 percent with an overall mean of 0.36 percent. Heritability estimates for AFF, LSAB, LWAB, LSAW, LWAW and FI were 0.70, 0.96, 0.95, 0.87, 0.93 and 0.70, respectively. The repeatability estimates for LSAB, LWAB, LSAW, LWAW and FI were 0.97, 0.96, 0.88, 0.94 and 0.80, respectively. Phenotypic correlations among litter traits were positive and ranged from 0.11 ± 0.10 to 0.91± 0.01. Phenotypic correlations between AFF and FI was low and positive (0.05±0.01) in direction.

ABST-1-012

GENETIC PARAMETERS OF GROWTH TRAITS IN BLACK BENGAL GOAT MAINTAINED UNDER NATURAL FARMING SYSTEM IN DIFFERENT AGRO-CLIMATIC ZONES OF WEST BENGAL

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The genetic parameters of body weights of Black Bengal goat were estimated at different ages including 3872 Kids born from 2151 Does reared by 685 traditional goat keepers of four Agro-Climatic Zones of West Bengal under the project “All India Co-ordinated Research Project on Goat Improvement, Black Bengal Field Unit, Kolkata” during 2015-2021. A moderate heritability of body weight was estimated at 3rd and 12th month of age (0.327±0.034 and 0.215±0.026 respectively) which were low at 6th and 9th month of age (0.134±0.019 and 0.115±0.017 respectively). The estimated genetic and phenotypic correlations between 3rd and 6th month body weight was found to be positive and medium (0.227±0.098 vs 0.213±0.098), whereas these were positive and low for the ages between 3rd and 9th month as well as 3rd and 12th month (0.145±0.103 vs 0.184±0.103 and 0.101±0.098 vs 0.110±0.109 respectively). The calculated genetic and phonotypic correlations of body weight between 6th and 9th month as well as 6th and 12 month were found to be positive and high (0.903±0.020 vs 0.931±0.020 and 0.724±0.055 vs 0.390±0.055 respectively). Whereas, the estimated genetic and phonotypic correlations of body weight between 9th and 12th month age was positive and medium (0.482±0.085 vs 0.265±0.085). Therefore, it can be concluded that for getting desirable body weights in Black Bengal goats a strategic plan for two stage selction of kids at 3rd and 6th month of age may be performed without linger further. In addittion to this proper care and management of goats with maintenance of existing biomass should also be considered to avoid irrepressible situations.

ABST-1-013

GENETIC PARAMETERS OF GROWTH TRAITS OF MECHERI SHEEP OF TAMIL NADU

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Mecheri sheep is a hairy-type sheep breed of India, reared for meat, and they play a vital part in the economic well-being of farmers. The present study aimed to estimate the (co)variance components and genetic parameters of Mecheri sheep by fitting six different animal models in the restricted maximum likelihood

method, with a preliminary investigation on the performance of animals for non-genetic sources of variation. The growth performance of Mecheri sheep was assessed for the body weight traits recorded at birth (BW), three (3MW), six (6MW), nine (9MW) and twelve months (12MW) of age. A data set on growth information of 2616 lambs with pedigree details was created after eliminating the outliers. These lambs were produced by involving 226 sires and 1044 dams. The coefficients of variation in growth traits were above 16 per cent, and the most significant variation was seen in 3MW at 24.70 per cent. The mean values of body weight of Mecheri sheep at birth, three, six, nine, and 12 months were 2.35, 9.76, 13.72, 16.68 and 19.46 kg, respectively. On least-square analysis, the influence of the period of birth on all the body weight traits; sex on 9MW and 12MW; birth type on birth weight, parity on BW and 6MW; and the season of birth on 3MW and 12MW (Table 1 and Figure 1a, b) were found to be significant ($P<0.05$). Direct heritability estimates derived from the best animal model for body weight at birth, 3 months, 6 months, 9 months and 12 months were 0.21, 0.24, 0.10, 0.15 and 0.09, respectively, and maternal heritabilities of the corresponding traits were 0.12, 0.05, 0.04, 0.04 and 0.04, respectively. The genetic correlations between body weight traits were all positive and moderate to strong except for birth weight with the other body weight traits. The significance of non-genetic factors studied in this work demanded a correction to improve the accuracy of the direct selection of lambs for body weight traits. The estimated direct heritabilities for growth traits were lower in post-weaning age groups compared to pre-weaning stages. The intermediate heritability and moderate to high genetic correlations observed for the weaning weight indicated that the trait could be employed as a selection criterion for enhancing later-age body weight traits.

ABST-1-014

MORPHOMETRIC CHARACTERIZATION OF ADULT GIR CATTLE IN SAURASHTRA REGION OF GUJARAT

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The lactating female population selected for study was 693 animals belongs to 234 keepers in Amreli in 65 villages, 281 animals belongs to 136 keepers in Bhavnagar in 26 villages, 256 animals belongs to 189 keepers in Rajkot in 42 villages and 77 animals belongs to 12 keepers in Surendranagar in 4 villages. The average herd size was found to be 23.4, with minimum and maximum of 1 and 150 animals belongs to single herd respectively. The survey was done in local language in breeding track on all the multiple sub types found in selected characters with the help of native breeders and traditional gir keepers The attempt is made to define pure breed characters of gir cattle breed with the help of 27 morphometric characters (Qualitative traits) wise body coat colour, body length, lion length, forehead height, forehead breadth, ear shape, colour of nostrils (Muzzle), Eye type, dewlap, horn shape, horn tip orientation, hump size, skin smoothness, tail length, tail switch colour, naval flap size, milk vein, udder type, teat shape, teat type, legs thickness, legs colour, hooves colour, vulvar colour, milking behaviour, herd behaviour, temperament in correlation with 9 quantitative characters wise hump circumference, forehead height, forehead breadth, dewlap length, tail length dewlap width, body surface area, peak milk yield . The study includes correlations and ranking of the subtype with production performance to know economic values of the traits. The total variance caused by Principal component is 43.45%. Moreover, its corresponding eigenvalue 62.25 is highest amongst all the other principle components. The 11 traits having correlating more than 40% were selected for the ranking.

ABST-1-015

PERFORMANCE OF H.F. CROSSBRED- “FREISWAL” UNDER FIELD PROGENY TESTING IN TARAI REGION OF UTTARAKHAND

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Field progeny testing (FPT) programme was started by ICAR – CIRC, Meerut in 8th five year plan to improve the performance of crossbred cattle through utilization of high yielding genetically superior bulls under field

conditions at four different ecological regions of the country. Presently the programme is implemented at BAIF Pune, KVASU Mannuthy, GADVSAU Ludhiana & GBPUA&T Pantnagar. The programme at Pantnagar was initiated during January 2010, which encompasses 5229 beneficiaries spread over 270 villages, clubbed into 8 clusters of U.S. Nagar & Nanital districts of Uttarakhand. In order to have a strong hold on field a total of 51 training program (covering 3686 farmers beneficiaries), 10 Heifers show, 13 Animal Health camps, 18 Kisan choupal, 03 Refresher training programmes for field inseminator were organized to keep them update with the latest know howwith various scientific techniques. Till August 2022, a total of 47045 test inseminations were carried outand 26115 pregnancies were confirmed, leading to 55.51% conception rate. A total of 20010calving occurred leading to birth of 9146 female progenies.A total of 1900 heifers reached at age at first calvingand 1548 of them completed their first lactation with 305 days milk yield as3310.60 kg and 3.5% fat. The remarkable increase of 41.95% in first lactation yield (305 days) was found; first set of bulls (2010-11) as 2494.8 kg and current set (sixth set) of bulls (2020-21) was3541.47 kg.The age at first calving was reduced significantly by 99 days i.e., 1149 days in first set of data and 1049 days ,in current set (sixth set) of data. The farm beneficiaries have been benefitted in different ways by the program.

ABST-1-016

PRODUCTION PERFORMANCE AND CARCASS TRAITS OF DUAL PURPOSE CROSSES OF TWO INDIGENOUS WITH IMPROVED CHICKEN VARIETY OF BIHAR

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Broiler meat production in India is around 3 million metric tons while the return from broiler meat market is estimated around Rs. 30,000 crores. The present experiment was conducted on Vanaraja (VR) and its crosses with Desi fowl native to Bihar at Institutional Livestock Farm Complex, BVC, Patna, Bihar. Vanaraja was received from PDP, Hyderabad and Desi males were collected from Muzaffarpur (MUZ) and Gaya (GAYA) districts of Bihar. Males were crossed with the females of Vanaraja in the sex ratio of 1:5. Body weight of the chicks at 0 day, 5, 10, 15, 20 week was taken. Besides, 24 males and 24 females from each genetic group were taken randomly to study various carcass traits. Effect of Genetic Groups on Body weight at various ages and various carcass traits like Dressed weight, Eviscerated weight, Giblet Weight, Leg Weight, Thigh Weight and Breast Weight was studied. The least squares means; standard error and coefficient of correlation were calculated through least squares models (Harvey, 1990). The phenotypic correlation coefficients of between the traits have been estimated. It was recorded that the genetic group had significant ($P<0.05$) effect on body weight at all the ages. VR♂♂ x VR ♀♀ (Vanaraja) excelled over all the genetic groups where as GAYA♂♂ x VR ♀♀ had the lowest body weight at all the age groups. Sex also had significant ($P<0.05$) influence on the body weight at all the age groups and males were heavier than the females. Significant ($P<0.05$) effect of genetic group was also observed on carcass traits at 20 weeks of age. VR♂♂ x VR ♀♀ genetic group excelled over all the genetic groups for dressed weight, eviscerated weight, giblets weight, legs weight, thighs weight and breast weight followed by MUZ♂♂ x VR ♀♀and GAYA♂♂ x VR ♀♀. Sex had significant ($P<0.05$) influence on slaughter traits, and males were observed to have heavier dressed weight, eviscerated weight, giblets weight, legs weight, thigh weight and breast weight. Positive and significant correlation coefficients of high magnitude among body weights and among carcass traits suggested that selection for improvement in any one of the traits would also lead to the simultaneous improvement of other correlated traits.

ABST-1-017

QUANTITATIVE GENETIC METRICS FOR SELECTION AND CONSERVATION OF MECHERI SHEEP OF TAMIL NADU

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The primary goal of population management is to maximize a breed's long-term competitiveness. Hence, monitoring the rate of change in inbreeding and genetic diversity within a population is critical for guiding

breeding programmes.For the purpose of estimating the inbreeding coefficient, a total of 4168 Mecheri sheep, including pedigreed individuals and their sire and dams, were used. The pedigree analysis was carried out in ENDOG software, version 4.8. The study revelaed that the pedigree completeness level recorded for different generations ranged from 78.95 per cent in the first generation to 0.00001 per cent in the twelfth generation. The population of Mecheri sheep had an average equivalent generation of 1.74. The effective number of founder animals (f_e) and effective number of ancestors (f_a) for the pedigreed population were determined to be 117 and 99, respectively. It was predicted that the founders' uneven contributions would increase inbreeding by 0.27 per cent. A significant subset of founders accounted for 50% of the population's genetic diversity. The effective number of founder animals (f_e) to the effective number of ancestor animals (f_a) ratio was 1.18., and the mean value of the genetic conservation index (GCI) was 3.001. The mean generation interval (GI) for the gametic pathways, Sire-Ram lamb, Sire-Ewe lamb, Dam-Ram lamb and Dam-Ewe lamb were 3.022, 3.036, 3.593 and 3.451 years, respectively. The GI recorded for the entire population was 3.26 years. The average percentages of inbreeding for the whole population, pedigreed population and inbred animals were 0.45, 0.61 and 3.41 per cent, respectively. In the whole population, only 1.65 per cent of the animals had more than 10 per cent inbreeding. The mean inbreeding values in the population ranged from 0.005 to 0.010 over generations. The generation-wise inbreeding increased from the second generation (0.5 %) to subsequent generations and reached its maximum in the fifth generation (1.00 %). Thereafter, it decreased and fluctuated between 0.86 per cent to 0.44 per cent across sixth to twelfth generations. A total of 13.00 per cent of the Mecheri sheep population was inbred. The range of the mean average relatedness was 0.001 to 0.014 across generations. The average relatedness coefficient between individuals was estimated to be 0.89 and 1.1 per cent for the entire population and pedigreed population, respectively. The analysis of pedigree information and genetic differences in the population revealed a high level of intra-flock diversity, with the effective population size exceeding the critical point, indicating sufficient genetic diversity for breed conservation. The population's generation interval is at an intermediate stage, indicating that there is room for improvement in genetics and management aspects of sheep reproduction. The rate of inbreeding in the population was under control, and the introduction of genetically superior rams from other populations to reduce inbreeding could be balanced by the flock's selection and mating of superior breeding animals with a high genetic conservation index, which may maintain the founders' balanced contribution.

ABST-1-018

CALF REARING SECTOR IN INDIA

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Indian Dairy farming operation involves traditional and scientific knowledge, wherein farmers use their family based knowledge obtained through ages, and combine with all modern findings and find their own path of milk production, which is working well when it comes to milk production and make good use of available resources. Dairy farming is complex because it involves the mobilization of raw material, procurement of milking cows and buffaloes, feeding, breeding, housing, milking, sale of milk, human resource management, record keeping and cleaning of dung. In the whole operation, their calves get neglected and are not taken care of and are fed inadequately, and hence lose the precious germplasm either by their mortality or poor health. In our field experience of more than 25 years, it is found that calves are highly neglected and mortality ranges more than 30 per cent. The calf rearing sector is very well developed in other countries, and there is tremendous scope in our country as well, since male calves can be successfully reared for meat purpose and females for milk, provided they are well taken care of from day one. This can be achieved by feeding the calves ad libitum colostrum as early as possible in order to achieve passive transfer of immunolglobulins, one month compulsory feeding of milk at the rate of one tenth BW, and then can be weaned from milk and put to cooked gruel grains, concentrates and forages thereby preventing the acute starvation and optimal daily gain be achieved. This sector is yet to see its growth and promotion, hence is the abstract presented for information.

ABST-1-019

IMPACT OF VARYING STOCKING DENSITIES ON THE PERFORMANCE OF BROILER CHICKENS

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The goal of the present study was to investigate the effects of stocking density on performance of broiler chickens raised under intensive rearing systems. Present investigation was conducted on broilers aged 6 weeks at poultry unit of Livestock farm complex, College of Veterinary and Animal Science, Navania, Udaipur (Rajasthan University of Veterinary and Animal Sciences) India. There were three treatment groups consisting of four replicates each of eight, ten, and twelve chicks respectively, i.e., D1 (8 birds/m^2), D2 (10 birds/m^2), D3 (12 birds/m^2). Each treatment group showed a statistically significant (p <0.05) effect on body weights, growth, and feed conversion efficiency (p <0.05). Treatment group D1 had the highest body weight, body weight gain, better FCR, followed by control groups D2 and D3 at 42 days of age. The results of this study revealed that having a higher live body weight in a smaller space increases productivity when it comes to profitably rearing birds and keeping them for longer than 40 days.

ABST-1-020

EFFECT OF BULL AGE ON SEMEN CHARACTERS OF HF BULLS

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Increasing need to enhance field conception rate through Artificial insemination in HF cross breds under changing climate warrants regular asses of seminal characters and factors influencing them. The present study was under taken to assess the effect of bull age (2 years to 8 years normally used for semen collection) on seminal parameters. Data on nineteen HF bulls maintained at State Semen Collection Center (SSCC), Hesaraghatta, Bengaluru were collected. The overall average values and standard errors of sperm phenotypic characters of HF bulls under study were 4.4 ± 0.19, 6.9 ± 0.02, 1078.5 ± 52.01, 76.5 ± 0.65, 85.8 ± 0.77 and 91.8 ± 0.87 for volume(ml), pH, Concentration(10^6), % Motility, % Live and % Acrosome integrity respectively. Similarly, the average values for abnormal sperm characters as abnormal head, proximal droplet, abnormal mid piece, abnormal tail, distal droplet and loose normal head were 7.2 ± 0.61%, 1.1 ± 0.41%, 2.7 ± 0.22%, 1.5 ± 0.29%, 0.9 ± 0.10% and 1.8 ± 0.19% respectively. General linear model - univariate analysis revealed significantly higher Semen volume (p=0.049) and semen pH (p=0.011) was observed in bull above 5.5 years of age. However, no significant effect of age on semen concentration (p=0.236), mass motility (P=0.214), Live sperm percent (p =0.359) and acrosome integrity (P=0.522) as well on sperm defects as abnormal head defects (p=0.206), Proximal Droplet (p=0.844), Abnormal mid piece (p=0.541), Abnormal tail (p=0.531), Distal droplet (p=0.520) and Loose normal head (p=0.915) was observed. Further, no correlation of seminal parameters with sire conception variation was established. Results indicate that non seminal parameters are more likely responsible for differential sire conception rate among the in service bulls of semen station.

ABST-1-021

EFFECT OF BULL AGE ON SIRE CONCEPTION RATE UNDER AI IN HF BULLS

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The effect of various factors as age group of the bull, parity number of the cow inseminated, number of insemination, inseminator or institution on the Sire Conception Rate of HF bulls through Artificial Insemination under field conditions was evaluated using Binary Logistic regression. A total of 2850 semen straws from 19 HF bulls stationed at State Semen Collection Center (SSCC), Hesaraghatta, Bengaluru were supplied to six

selected Veterinary Institutions with experienced Artificial Inseminators. HF crossbred cows within first three services were randomly inseminated with 19 Holstein Friesian bull semen straws. HF crossbred cows within first three services were randomly inseminated and pregnancy was confirmed by per rectal examination post 90 day insemination. Overall average sir conception rate in HF bulls in the present study was 50.61 ± 1.17%. The least square means and standard errors for Sire conception rate among bull age groups 2-3 years (G-I), 3-5.5 years (G-II) and >5.5 years (G-III) were 45.0 ± 0.01%, 54.0 ± 0.017% and 53.0 ± 0.017% respectively and differed significantly (p = 0.003). The least square means and standard errors for Sire conception rate among different parity groups of the cows inseminated ie., Heifers, I, II, III, IV, V & above were 43.0 ± 0.05%, 54.0 ± 0.02%, 52.0 ± 0.02%, 49.0 ± 0.02%, 52.0 ± 0.03% and 51.0 ± 0.03%respectively and did not differ statistically (p=0.533). Institution / Inseminator was found to significantly influence conception rate, however, insemination number did not affect conception rate in HF cross bred cows under field conditions.

ABST-1-022

ASSESSMENT OF GROWTH PERFORMANCE OF OSMANABADI GOATS FED ON AZOLLA SUPPLEMENTATION-BASED DIET

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Azolla pinnata is an aquatic free-floating fern belonging to the family *Azollaceae* which nutritive value is well documented. As a good source of protein and essential minerals like Iron, Calcium, Magnesium, Potassium etc. and appreciable quantities of Vitamins A and Vitamin B-12, it is promoted as potential feed ingredient for livestock including small ruminants like goat. An experiment on feeding Azolla in 14 Osmanabadi adult goats of same age and body weight was carried out for a period of 90 days at BAIF Goat Farm based at Wagholi, Pune. Goats of divided into control and experimental groups. Same standard feeding regimen as per ICAR 2013 feeding standards was followed for all goats except experimental group supplemented with Azolla Feeding at the rate 250 g per day per goat as 15% dry matter replacement through total diet with other fodder and roughages like sorghum straw, maize, lucerne, concentrate mixture and mineral mixture. All the goats were provided liberal fresh, cool drinking water *ad-libitum*, throughout experimental period. Observations on total body weight gain and average daily gain in body weight were recorded and compared between control group and experimental group. The results of the experiment indicated that goats in experimental group fed with Azolla gained higher total body weight of 7.44 kg and average daily gain in body weight of 82.70 g/day over the control group where the values were 4.55 kg and 50.61 g/day. This study revealed that Azolla feeding in Osmanabadi goats enhances the growth performance of goats in terms of improved total body weight and average daily gain in body weight without any adverse effect. Azolla exhibits its acceptance and high palatability in goats and large quantities may be voluntarily consumed.

ABST-1-023

CHALLENGES AND GOALS IN BREEDING POLICY FOR DOMESTICS BREEDS IN INDIA

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Breeding policy statement for cattle and buffaloes is to be made, the stake holders need to be identified and provided a goal with specific objectives and a statement of assets. During the last couple of decades both production and consumption of animal products, such as milk, meat and egg has substantially increased and, likely growth in the livestock and poultry population is most urgent if a successful and implementable breeding policy is to be developed. The total population of cattle and buffaloes that need to be improved, including the infrastructure for their management, needs to be identified with quantifiable feed and fodder resources. The goal of the government is to ensure improvement of livestock sector for enhanced economic returns to the farmers or livestock keepers, so as to improve their life style and provide them a regular livelihood option within the possible economic frame work existing at the time. The inputs for improved technologies, health care,

reproductive cover, artificial insemination services, vaccinations against diseases, diagnostics medication and management need to be identified and provided. It is necessary that any breeding policy frame work should be able to meet out the required inputs in the area of implementation so that deliverables are available in the targeted time. Feed and fodder are the bedrock of any breeding plan because these play a central role in providing proper nutrition to livestock. The feeding of a balanced diet meets achieving high and sustained livestock productivity and the required genetic gain. Policy makers, scientists and livestock keepers need to take up the challenge to improve the Indian livestock by selecting the best of the cattle and buffaloes by the best method of genetic selection.

ABST-1-024

CHARA DUCK – A PROMOSING MEAT TYPE DUCK VARIETY

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A study was conducted to compare the growth pattern of two indigenous Kuttanad duck varieties of Kerala, *viz.*, *Chara* and *Chemballi*. Data were collected on body weight and measurements from hatch to 16 weeks of age at fortnightly intervals from 125 Chara and Chemballi ducks reared on slatted floor management system under standard management conditions. Chara and Chemballi were found to differ significantly for the body weight at almost all stages of growth ($p<0.05$). The mean body weight at hatch, 2, 4, 6, 8, 10, 12, 14 and 16 weeks of age were found to be 36.98 ±0.36 g, 255.84 ±5.64, 471.56 ±16.81g, 744.60 ±28.62g, 1080.55 ±29.94 g, 1333.33 ±23.66g, 1484.55 ±20.28 g, 1590.00 ±19.24g and 1660.73 ±17.04 g in Chara. The corresponding estimates in Chemballi were 36.01 ±0.30 g, 209.55 ±5.74g, 474.20 ±14.29 g, 765.07 ±31.02g, 1002.46 ±20.85g, 1177.20 ±24.02g, 1349.63 ±26.76 g, 1457.50 ±25.94g and 1575.22 ±24.09 g. The average weight gain at fortnightly intervals from 2 to 16 weeks of age ranged from 107 to 335 g in Chara and from 70 to 290 g in Chemballi. Chara had significantly higher weight gain than Chemballi from 8 to 16 weeks of age ($p<0.05$). Chara ducks had a dominant pattern of growth in terms of higher body weight and fortnightly weight gain compared to Chemballi ducks during the grower phase from 8 to 12 weeks of age. Chara ducks were also found to have longer breast bones and shanks as well as larger chest girth than Chemballi ducks. Hence the study points out that Chara ducks on account of their higher body weight, fortnightly weight gain and larger estimates of meat-type biometrics could be regarded as a more promising meat type duck than the Chemballi variety.

ABST-1-025

COMPARISON OF SIRE MODEL AND ANIMAL MODEL EFFICIENCY FOR FIRST LACTATION AND LIFETIME LACTATION TRAITS IN CROSSBREED CATTLE

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To investigate the present study, the data of 1029 crossbred cattle from 107 sires, distributed over a period of 49 years from 1966 to 2014 was collected from history sheets of crossbreed cattle at the dairy farm of G.B. Pant University of Agriculture and Technology, Pantnagar. Sire model and animal model were run to estimate the average breeding values of 107 sires by Sire Model and 91 sires by Animal Model to evaluate first lactation(AFC, FLMY, FLP, FDP, FCI) and lifetime lactation (LTMY and LTLL) traits. The average breeding values for AFC, FLMY, FLP, FDP, FCI, LTMY and LTLL were estimated by both the models and sires were ranked according to their breeding values for both the models which were not consistent for some traits. Comparison between Animal and Sire Model was done by estimating Akaike (AIC) and Bayesian (BIC) information criteria. The value of AIC and BIC for Animal Model was -39918.663 and -40111.128 respectively, whereas for Sire Model the

value of AIC and BIC was -39948.198 and -40140.663 respectively, indicating Animal Model(highest negative value for AIC and BIC) would be the adequate model for evaluation of genetic parameters over Sire Model.

ABST-1-026

CONSTRUCTION OF SELECTION INDEX FOR SIX-WEEK BODYWEIGHT AND SHANK LENGTH IN VANARAJA MALE LINE (PD-1) FOR IMPROVEMENT OF THE TRAITS

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The selection index is one of the best methods for estimating the breeding value of an animal combining all sources of information on the animal and its relatives on single or multiple traits. It is the best linear prediction of an individual breeding value. The selection index was constructed utilizing the five generations data of Vanaraja Male line (PD-1) for body weight (BW-6) and shank length (SL-6) at 6 weeks of age. The data generated on 13338 birds produced from 50 sires and 250 dams in each generation was analyzed using REML fitting in animal model. The data was rationalized for both body weight and shank length. The variance and covariance estimate and heritability of both the traits were utilized for the construction of index. The h^2 for BW-6 and SL-6 was 0.20 and 0.17, respectively. The genetic and phenotypic variance for BW-6 was 2566.28 and 13298.4 and for Sl-6 was 5.42 and 32.25, respectively. The covariance between the traits was 93.98 for Bw-6 and 520.06 for Sl-6. The economic value for each trait was given based on the market value of Rs. 120/ kg chicken meat. The average body weight and shank length at six weeks of age was 692.88±1.00 g and 77.44±0.05 mm, respectively. The economic value estimated was Rs. 0.12/ g for body weight and Rs. 1.074/ mm shank length. The final weightage for body weight and shank length was 1:8.95. Thus, the selection index constructed was **I= 0.2260*BW6(g) + 0.7717*SL6(mm).** The expected genetic gain utilizing the above index at different selection intensities with are detailed below.

Selection Intensity	Proportion selected (%)	BW-6, g	SL-6, mm
0.798	50	17.55	0.68
0.966	40	21.25	0.83
1.159	30	25.50	0.99
1.400	20	30.80	1.20

The above index will be utilized for selection in the PD-1 population in future breeding programs with about 30.8 g gain in body weight and 1.2 mm improvement in shank length with a selection intensity of 1.4 in each generation.

ABST-1-027

EFFECT OF AGE ON EGG QUALITY PARAMETERS OF HIMSAMRIDHI CHICKEN VARIETY UNDER INTENSIVE SYSTEM OF MANAGEMENT IN HIMACHAL PRADESH

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The present study was carried on Himsamridhi chicken variety to assess the effect of age on egg quality traits. A total of 300 eggs collected from birds at different age groups i.e. 24, 30, 36, 44 and 50 weeks of age for studying the external and internal egg quality parameters. The external egg quality parameters like egg weight, egg length, egg width and shell thickness were measured. The internal traits viz. albumen length, height and width, yolk height and width, shell thickness, albumen weight, yolk weight, shell weight were recorded using standard procedure. The derived traits like shape index, albumen index, yolk index albumen percentage, yolk

percentage, shell weight percentage and Haugh unit were estimated. Most of the egg quality traits differ (P< 0.05) significantly at different age of measurements. Egg weight increases as the age of bird advances and varied from 40.35±0.89 g at 24 week of age to 51.85±0.64 g at 50 week of age. Analysis of variance revealed that shape index did not differ significantly at different age of measurements. Length, width and height of albumen increases as the age of bird progresses. Albumin index was found to be significantly (P<0.05) higher at 24 weeks of age. Similarly yolk height and width increases as the age of bird advances. The yolk index found to be significantly (P<0.05) higher at 36 week of age. The differences for albumen percentage and yolk percentage were not significant among the different age groups. Albumen and yolk percentage varied within a very narrow range 57.76 to 60.01 % and 29.87 to 31.95 % respectively at different age of measurements. Haugh unit index was observed to be significantly higher at 24 weeks of age and ranging from 82.93 to 88.78 indicating uniform internal egg quality over the age. Average shell thickness ranged from 0.34 mm at 24 weeks of age to 0.38 mm at 50 week of age. The result indicates that the age of bird significantly affect egg quality parameters at different age of measurements.

ABST-1-028

EFFECT OF INTENSIVE AND EXTENSIVE HOUSING SYSTEM ON GROWTH PERFORMANCE OF NARMADANIDHI AND CROSSBRED KADAKNATH CHICKEN

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The dual type coloured bird Narmadanidhi and crossbred Kadaknath were produced by direct crossing and back crossing of Jabalpur colour(JBC) and Kadaknath(Kd) parent birds. The present investigation aimed at assessing the effects of intensive (deep litter) and extensive housing system (semi-intensive and free range) on growth, feed intake, survivability and carcass performance of Narmadanidhi and crossbred Kadaknath chicken. All the experimental chicks were brooded upto 6 weeks age under deep litter system of management on similar feeding and managemental conditions. Thereafter, randomly divided into three groups i.e. under Intensive (deep litter), semi-intensive and free-range housing system. During brooding period (dayold to 6 week) feed containing 20% CP and 2800 ME kcal/kg of diet and during growing from 7-14 weeks of age 16% CP and 2600 ME kcal/kg of diet was fed under intensive housing system. Only 40% of feed (16% CP and 2600 ME kcal/kg of diet) was offered to chicks under semi-intensive housing system. Under free range system chicks were fed with some amount of Supplementary feed in the form of kitchen waste, broken grains etc. in the night and morning, then allowed to walk a distance in search of feed in the area provided for feeding. The traits were measured include weekly body weight, from dayold to 6 weeks age and biweekly body weight from 7-14 weeks age, feedefficiency, mortality, conformation traits and carcass characteristics at 14 weeks of age. Narmdanidhi bird was heavier in body weight, gained body weight at faster rate, better in feed conversion ratio, superior in body conformation, less percent inedible losses, lowest abdominal fat percent, higher breast weight and back with neck weight than crossbred Kadaknath having 50% Kadaknath inheritance. Intensive housing system had significantly (P<0.05) higher bodyweight, higher feed intake and better feed conversion than semi intensive followed by free range system of management. Free range system exhibited lowest abdominal fat percent. Narmdanidhi variety showed little bit higher total meat yield in semiIntensive whereas crossbred Kadaknath in intensive housing system.Boththe varieties recorded 100% survivability under Intensive andextensive housing systems.The net income/ return per bird realized Rs. 128.66, 127.62, 109.84 for Narmadnidhi and Rs. 106.05, 103.91, 85.01 for crossbred Kadaknath under free range, semi-intensive and intensive housing systems, respectively. Free range housing system was found most economical among three housing systems.

ABST-1-029

EFFECT OF NON GENETIC FACTORS ON PRODUCTION AND REPRODUCTION TRAITS IN MURRAH BUFFALOES

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The data pertaining to 241 lactation records of 63 buffaloes maintained at Livestock Research Station, PV

Narasimha Rao Telangana Veterinary University, Mamnoor, Warangal were utilized to study the effect of parity and season of calving on various production traits *viz*. Lactation Length (LL), Total Lactation Milk Yield (TLMY), Standard Lactation Milk Yield (SLMY) & Peak Yield (PY) and reproduction traits *viz.* Birth Weight of calf (BW), Calving Interval (CI), Dry Period (DP) and Service Period (SP). The least square means of LL, TLMY, SLMY & PY were recorded as 285.15 ± 5.76, 1772.29 ± 40.82, 1870.38 ± 30.07 & 9.30 ± 0.15 and for BW, CI, DP & SP the estimates were recorded as 30.69 ± 0.29, 590.24 ± 19.05, 310.87 ± 19.91 & 276.95 ± 17.50, respectively. Parity showed a significant effect on LL, SLMY, CI, DP & SP. Buffaloes in the first parity had a longer lactation length (314.48 ± 15.04) but lower productivity (1729.43 ± 106.60) than the buffaloes with 2 or 3 or more calving, where as third and fourth parity buffaloes had significantly higher values for CI (672.75 ± 35.23 & 654.81 ± 39.95) and SP (338.38 ± 32.39 & 339.73 ± 36.72) and moderately significant values for SLMY (1803.79 ± 57.85 & 1969.43 ± 65.45) and LL (291.46 ± 11.08 284.91 ± 12.54) than 2nd, 5th, 6th & 7th parity buffaloes. The buffaloes in 5th and 6th parity showed significantly lower values for DP (275.47 ± 47.66 & 256.44 ± 53.08). Season of calving showed a significant effect on SLMY, PY & DP. The animals calved during winter season had higher SLMY (1946.47 ± 38.94) and lower DP (260.05 ± 25.60), whereas the animals which calved during summer showed higher peak yield (9.88 ± 0.35). In conclusion, buffalo breeders must consider the animal's parity and the season of calving in their managemental plans since they are essential to the productive and financial success of the farm and also play a major part in the selective breeding of the animals.

ABST-1-030

EFFECT OF NON-GENETIC FACTORS ON SEMEN CHARACTERISTICS OF MURRAH BULL UNDER TROPICAL CONDITION

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The objective of this study was to assess the effect of non-genetic factors on semen characteristics of 22479 ejaculates from 139 Murrah bulls during the period of 2017-2020 was analyzed under tropical conditions, maintained and recorded at Frozen Semen Bank (FSB), Bassi, Rajasthan Cooperative Dairy Federation, (India) as well as in Information Network for Animal Productivity & Health (INAPH) application maintained at National Dairy Development Board (NDDB). Results were recorded as 2.94±0.03 mL for volume, 1234.72±13.51million/ mL for sperm concentration and 68.44±0.25 percentage for motility. Statistical analysis presented a significant difference for all semen parameters with studied non-genetic factors except semen collector for motility traits. Also, seasonal dynamics presented winter as the most suitable season for semen collection under tropical conditions. Age of bull showed significantly increased values for all semen traits with the increasing age of bull except motility traits. Data analysis in this regard may be utilized to enhance the fertility rate by increasing the semen quality.

ABST-1-031

ESTIMATION OF GENETIC PARAMETERS OF PRODUCTION EFFICIENCY TRAITS IN MURRAH BUFFALOES

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The data of 614 Murrah buffaloes pertaining to performance efficiency traits viz. milk yield per day of calving interval (MCI) and milk yield per day of age at second calving (MSC) was collected from the history-cum-pedigree sheets maintained at Buffalo farm, Department of Livestock Production Management, Lala Lajpat Rai University of Veterinary and Animal sciences, Hisar over a period of 24 years from 1996 to 2019. The data was classified into classified into six periods and four seasons. Milk yield per day of calving interval was calculated by dividing total lactation milk by calving interval and milk yield per day of age at second calving was the daily outcome of milk yield upto the second calving interval, was calculated by dividing the total lactation

milk yield by total age in days upto second calving. The least squares means of MCI and MSC were 5.57±0.06 kg/day and 1.33±0.02 kg/day, respectively. Period of calving had highly significant (p<0.01) effect on MCI and significant (p<0.05) effect on MSC. Non-significant effect of season of calving on MCI but significantly (p<0.05) influenced the MSC. The heritability estimates of MCI and MSC were moderate, valued as 0.25±0.11 and 0.21±0.02, respectively. The genetic (0.73±0.05) and phenotypic (0.51±0.19) correlation was found between MCI and MSC which was high and positive. Selection based on MSC would result in improvement in desirable direction as it can be used as index trait in selection programme because it includes both age at first calving and milk yield of the animal and had moderate heritability, thus determines the economic merit of the animals.

ABST-1-032

EVALUATION OF LAMB SURVIVAL TIME FROM BIRTH TO YEARLING IN HARNALI SHEEP

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The current study used data records of 2057 Harnali lambs born to 134 sires and 623 dams between 2001 and 2020 to estimate the survival time (days) from birth to weaning (T1), birth to 6 months of age (T2), and birth to 12 months of age (T3) and also factors affecting these survival times. Under survival analysis, the cox proportional hazards model was used to analyse the targeted traits. According to the descriptive analysis, lambs had survival rates of 91.59, 85.91, and 82.31 percent for the T1, T2, and T3 time periods, respectively. Kaplan-Meier estimates of mean survival time for respective traits were observed as 85.77, 161.54 and 276.37 days, respectively. Cox-proportional hazard modelling revealed female (T1=0.60, T2=0.57 and T3=0.59) had lower hazards of death than male (1.00). When compared according to birth weight of lambs, lambs with lower birth weights, had lower hazard than in bigger lambs, with dangers of mortality ranging from 0.32 to 0.63. (1.00). Therefore, it had been suggested that adoption of improved managerial practices, especially during first three months and obtaining higher birth weights, may increase the lamb survival and subsequently farm profitability.

ABST-1-033

EVALUATION OF THE PERFORMANCE OF FUNCTIONAL TRAITS IN SALEM BLACK GOAT UNDER FARM CONDITIONS

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Goats forms the integral part of the rural livelihood in India and considerably improves the source of revenue of a large number of small, marginal farmers and landless labourers involved in goat husbandry through production of meat, milk, skin, and manure. Salem Black goats are one among the 37 registered breeds of goats in India having considerable production potential under semi-arid, tropical conditions of north-western agro-climatic zone of Tamil Nadu. The native tract of this breed is the Salem, Dharmapuri, Krishnagiri, Erode, Karur and Namakkal districts of Tamil Nadu. Evaluation of functional traits is important since they impact fitness indirectly. Functional traits include traits of reproduction and survivability. Data on functional traits (n=1014) *viz*., age at first kidding, kidding interval, incidence of multiple birth, litter size, pre-weaning survivability (0-3 months) and post-weaning survivability (3-6, 6-9, 9-12 and 3-12 months) accrued over 19 years at Mecheri Sheep Research Station, Pottaneri, Salem district, Tamil Nadu were analysed using SPSS (v.26.0). Least squares mean for age at first kidding (in days), kidding interval (in days) and litter size were 658.486 ± 31.357, 249.134 ± 43.225 and 1.638 ± 0.066 respectively. Out of total number of kidding (n=694) recorded 39.42 per cent were twins, 2.44 and 0.14 per cent were triplets and quadruplets respectively. Pre-weaning survivability (0-3 months) and post-weaning survivability at 3-6, 6-9, 9-12 and 3-12 months of age in Salem Black goat 87.9 ± 0.020, 99.8 ± 0.019, 99.9 ± 0.008, 99.7 ± 0.008, 93.0 ± 0.036 respectively. High survivability in the farm indicated better management practices of the farm.

ABST-1-034

GENETIC ANALYSIS OF RETAINED PLACENTA IN JERSEY CROSSBRED CATTLE

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Data on Retained Placenta (RP) of Jersey crossbred cattle, maintained at the Eastern Regional Station of ICAR-National Dairy Research Institute, Kalyani, Nadia, West Bengal over a period of 39 years (1980-2018) were collected to estimate the variance and (co)variance components and genetic parameters and to study the relationships with production viz. 305 days milk yield (305DMY), total milk yield (TMY), lactation length and reproductive traits viz. days open, gestation period, calving interval of cattle. A total of 1822 calving records were included for the present study. (Co)variance components of RP were estimated by applying a series of univariate animal models using a derivative free REML algorithm (DFREML). By ignoring or including maternal genetic or environmental effects, a total of six animal models were fitted. Direct heritability (h^2) estimates for RP ranged from 0.003-0.05 in different animals models. Maternal heritability (m^2) varied from 0.02-0.05 in different models. Permanent maternal environment effect (c^2) contributed 1% to the total phenotypic variance in different models. The genetic correlations between direct and maternal effect in most comprehensive model were all negative (-0.57 to -0.79) in the present study. Low heritability estimates of RP indicates slow genetic improvement may be possible through selection under prevalent management system. Correlation coefficients with production traits showed the antagonistic relationships of RP with 305DMY and TMY indicating that animals having lower RP problems would produce higher production. Correlation coefficients with reproductive traits showed the existence of negative genetic correlations of RP with all reproductive traits of animals. The existence of significant relationship between with reproductive traits indicate that calving traits should be taken into consideration for improving the fertility of animals.

ABST-1-035

GENETIC AND NON-GENETIC FACTORS AFFECTING SEMEN PRODUCTION AND QUALITY CHARACTERISTICS OF SAHIWAL CATTLE BREED UNDER SEMI-ARID CLIMATE

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Present study aims to evaluate genetic and non-genetic factors influencing semen production potential of Sahiwal bulls. Semen ejaculate information on semen production traits *viz.*ejaculate volume (VOL): 13186, sperm concentration per ml (CONC): 13084, total sperm per ejaculate (TS): 13130, initial motility (INIT): 13077 and post thaw motility (PT): 12157; and semen quality traits *viz.*hypo osmotic swelling test (HOST): 601 and acrosome integrity of frozen semen (AIFS): 594,belonging to 52 Sahiwal bulls, available from January 2011 to December 2018 at BAIF's frozen semen station, Jind, Haryana, India, were used for the study. The observations beyond mean±4 standard deviations (S.D.) were considered as outliers and removed from the study. The various factors influencing semen characteristics considered in the study were season (winter, summer, and monsoon) and age (classified as 12 months interval class, from less than 36 months to 156 months) at collection. To study the bull correlation (Genetic + Permanent environmental correlation) on the semen parameters, a repeatability animal model with bull as a random effect was used in WOMBAT software. The observation we found is the season of semen collection had a very high significant ($P < 0.01$) effect on VOL, CONC, TS and PT while INIT, HOST, and AIFS didn't influenced ($P > 0.05$) by season of collection. All the semen characters were significantly affected by age at semen collection. The VOL and TS showed increasing trend up to 72 to 84 months and declined till 96 to 108 months.

ABST-1-036

GENETIC AND PHENOTYPIC TRENDS OF PRODUCTION PERFORMANCE TRAITS IN MURRAH BUFFALOES

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The data of production performance traits of 614 Murrah buffaloes was gathered from the history-cum-pedigree sheets of Buffalo farm, Department of Livestock Production Management, Lala Lajpat Rai University of Veterinary and Animal sciences, Hisar over a period of 24 years from 1996 to 2019 which were divided into six periods having four years interval each. The least squares means of 305 days milk yield (305DMY), peak yield (PY), lactation length (LL) and dry period (DP) were 2258.28±26.25 kg, 11.59±0.09 kg/day, 302.07±2.78 days and 148.18±3.32 days, respectively. The genetic trends of production performance traits were estimated by taking regression of weighted average of sire's estimated breeding value (WAEBV) for each year on year and the phenotypic trends for each trait was estimated as linear regression of performance of population on year. The year wise genetic trends of 305DMY, PY, LL and DP were 1.472 kg, 0.010 kg/day, -0.216 days and -0.287 days having R^2 as 9%, 13%, 14% and 18% and the phenotypic trends were 59.86 kg, 0.199 kg/day, 1.358 days and -2.206 days having R^2 valued as 74%, 65%, 19% and 47%, respectively. The period wise genetic trends of 305DMY, PY, LL and DP were 7.45 kg, 0.045 kg/day, -0.94 days and -1.257 days having R^2 valued as 30%, 35%, 43% and 52% and period wise phenotypic trends were 243.6 kg, 0.803 kg/day, 5.888 days and -8.269 days having R^2 valued as 88%, 75%, 73% and 79%, respectively. Critical appraisal of genetic and phenotypic trends of production performance traits dictated that selective breeding and managemental practices directed the performance in desirable direction as yielding traits were found raised round the years and dry period was found dropped which shows the enhancement in regularly improving herds.

ABST-1-037

GENETIC CHARACTERIZATION OF NATIVE CHICKEN POPULATION USING MICROSATELLITE MARKERS

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The present study was planned to characterize native chicken population of North Gujarat by using microsatellite markers. Chicken specific 25 microsatellite markers were selected using 7 multiplexed PCR panels. Blood samples were collected randomly from 60 unrelated chickens from different villages of North Gujarat area. DNA was extracted and amplified for selected microsatellite markers using PCR. Genotyping of the obtained product was done by capillary electrophoresis. Results showed that a total of 240 alleles were identified wherein number of alleles per locus varied from 6 (ADL 172, MCW 43) to 15 (ADL 136). Mean observed numbers of alleles were found to be 9.60. Overall mean for observed heterozygosoties was 0.531 ranging from 0.067 (ADL 172) to 0.800 (ADL 23) whereas overall mean for expected heterozygosities was 0.771 ranging from 0.518 (ADL 158) to 0.892 (ADL 136). High number of observed alleles as well as heterozygosity value indicates high genetic variability in native chicken population. The Fixation index (F_{IS}) value for all 25 microsatellites loci ranging from 0.075 (MCW 59) to 0.683 (MCW 73) with mean value of 0.309 revealed considerable level of inbreeding present in native chicken population. Polymorphic Information Content (PIC) value ranging from 0.494 (ADL 158) to 0.883 (ADL 136) with a mean value of 0.747 indicated informativeness of the markers used. It was concluded that these microsatellites were highly polymorphic and proved very useful for breed characterization.

ABST-1-038

GENETIC EVALUATION OF JUVENILE AND PRODUCTION TRAITS IN VANARAJA MALE LINE (PD-1) CHICKEN

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A study was conducted to evaluate the performance of Vanaraja male line chicken (PD-1) by collecting data on 2,538 chicks, progeny of 50 sires and 250 dams produced in a pedigreed full sib mating at the Directorate of Poultry Research, Hyderabad in five hatches during 12th generation.The mean fertility was 84.79 percent. The mean hatchability percentage on total egg set (TES) was 77.71 and on fertile egg set (FES) was 91.64 percent. Highly significant (P≤0.01) differences among all hatches were observed for body weights and shank length. The overall least squares means of body weight at day old, 2, 4, 6, 20, 40 and 52 weeks of age were found to be 40.50 ± 1.46, 149.46± 1.04, 405.71 ± 2.65, 804.27 ± 5.17, 2086.77 ± 0.96, 2772.04 ± 0.99 and 2780.97 ± 1.28 g, respectively. The overall least squares means of shank length at 4 and 6 weeks of age were 62.61 ± 1.78 and 82.41 ± 2.26 mm. Significant (P≤0.01) hatch effect was observed for egg weight at 32 and 40 weeks of age. The corresponding least square means were 52.67 ± 1.47 and 56.90 ± 0.01 g. Significant (P≤0.05) hatch effect was observed for shell weight, shell thickness and haugh unit and the corresponding means were5.07 ± 0.11 g, 0.32 ± 0.0013 mm and 84.88 ±0.49. While highly significant hatch effect was observed for albumin weight (P≤0.01) and egg weight, yolk colour and yolk weight. Heritability estimates for juvenile body weights were moderate and ranged from0.08 ± 0.11 to 0.36 ± 0.07.High heritability estimates of 4 week weight (0.34 to 0.28) indicate scope for genetic improvement on 4 week body weight is the primary trait for selection for improving body weight. In general, the heritability estimates for adult body weights were low to moderate. Heritability estimates based on sire, dam and S+D component ranged from0.18 ± 0.26 to 0.48 ± 0.31;0.05 ± 0.29 to 0.47 ± 0.25; 0.16 ± 0.20 to 0.44 ± 0.17respectively.The sire component of heritability for ASM was 0.15 ± 0.25, while the heritability estimates based on sire, dam and S+D component for EP40were 0.17 ± 0.28, 0.10 ± 0.27 and 0.14 ± 0.20, for EP52 were 0.04 ± 0.16, 0.17 ± 0.21 and 0.09 ± 0.11respectively. The h^2_S, h^2_D and h^2_{S+D} for EW28 were 0.43 ± 0.26, 0.56 ± 0.39 and 0.49 ± 0.25 and for EW40 were0.12 ± 0.28, 0.36 ± 0.31 and 0.24 ± 0.23, respectively. Heritability estimates for shank length were low to moderate and varied from0.17 ± 0.06 to 0.33 ± 0.08. Higher dam component of heritability was noticed for at 4 and 6 week shank length. Correlations among juvenile body weights were positive, medium to high in magnitude and ranged from0.25 ± 0.12 to 0.93 ± 0.01. High and positive correlations were observed between body weights and shank length at various ages ranging from0.22 ± 0.13 to 0.82 ± 0.05.Genetic correlation estimates ASM with body weights and egg weights studied were positive and low too high in magnitude, while ASM with EP40 was negative. The genetic correlation of body weights with egg weights was positive and high in magnitude, while that of BW20 with EP40 was positive and BW40 with EP40 was negative. Genetic correlation estimates among egg weights were positive and low too high in magnitude, while with egg weights with egg production were negative. Genetic correlations of bw52 with EW52 and EP52 were positive, while EW52 with EP52 were negative. Phenotypic correlations show the similar trend. The results of the study conclude that the PD-1 population has the reasonable variability in both juvenile and production traits. The heritability estimates are moderate to high for body weights shank length, the production trait of selection for improvement. The gradual improvement in production traits in parent line will improve the performance in terminal cross Vanaraja with respect to shank length and body weight which ultimately benefit the farmer.

ABST-1-039

INSIGHTS INTO THE BUFFALO BREEDING PRACTICES IN RELATION TO HERD SIZE ADOPTED BY FARMERS OF CHITTORGARH DISTRICT IN RAJASTHAN

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A total of 160 buffalo rearers were randomly selected and investigated from eight villages of Begun and

Kapasan tehsils of Chittorgarh district of Rajasthan. Among the buffalo rearers under study, 53.12 per cent of the respondents got conceived their buffalo by natural method whereas A.I. service was followed by 46.88 per cent only. Nearly half 50.62 per cent of the buffalo keepers used non-descriptive buffalo bull for service. It was found that 47.50 per cent of the respondents inseminated/crossed their buffalo at mid heat stage. Pregnancy diagnosis of buffalo was practiced by 56.22 per cent of the respondents. Practice of treatment of anoestrus and repeat breeding by veterinarian was followed by 73.75 per cent of the respondents. Washing of hind quarters of their buffalo after the drop of placenta was followed by 79.37 per cent of the respondents.It is found that 41.25 per cent farmers bred their buffalo at 3 to 5 months after calving. Calving interval of more than 18 months is observed in 50.00 per cent of buffalos this point indicate that repeat breeding is major problem in this area.

ABST-1-40

INVESTIGATION ON ASSOCIATION OF SOME TYPE TRAITS WITH LIVE WEIGHT AND BIOMETRY OF GANJAM GOATS

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Data on live weight and 11 biometric traits from 262 Ganjam goats were collected along with three type traits on Ear type (long, medium and short), beard (present, absent) and wattle (present, absent). The data pertained to adult female Ganjam goats more than 2 years of age, raised at three different locations viz. Chhatrapur, Rambha and Khallikote cluster by the registered farmers of AICRP on goat improvement in Ganjam district of Odisha. The biometric traits recorded were body weight in kg, body length, wither height, chest girth, brisket height, horn length, ear length, tail length, rump height, rump width and neck circumference head length in cm. The least squares means were 30.32±.57kg of body weight, 63.59±.79cm of body length, 71.93±.80cm of wither height, 74.04±.77cm of chest girth, 43.07±.52cm of BH, 18.75±.27cm of head length, 15.71±.61cm of horn length, 14.08± .23cm of ear length, 15.34 ± .28 cm of tail length, 75.24 ±.75 cm of Rump Height, 15.42 ±.25 cm of Rump Width and 32.74 ±.42 cm of Neck circumference. Out of the total 18.7% and 9.5% of Ganjam goats were having wattles and beard respectively. Ganjam goats having long and pendulous ears constituted 25.6%, whereas goats with medium and short ears were 61.8% and 12.6% respectively. Goats having wattles and beard formed 18.7% and 9.5% of the total respectively. There was significant effect of location on almost all the trait studied except on the horn length and tail length of animals. Presence and absence of the wattles and beard did not influence the morphometric traits. Ear type did not have significant effect on nay of the morphometric trait studied except on the ear length for obvious reason.

ABST-1-041

MONTH WISE SURVIVABILITY OF SIROHI GOAT KIDS UNDER FARM AND FIELD CONDITION

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Survivability is an important phenomenon to enhance the economic viability of goats breed. The present study was conducted to find out the month wise survivability of Sirohi goat kids at 0-3 month, 3-6 months and 6-12 months of age under farm and field condition. Under this study data were collected from 504 records of Sirohi kids died out of 21,790 total available Sirohi kids up to age of 0-12 months, maintained at livestock research station, Bojunda, Chittorgarh as farm unit and field unit of AICRP, Vallabhnagar during year 2015-2021. This study reveals that least-squares means of survivability was highest in February (98.17±0.438 %), January

(97.70±2.910%) and April (99.00±12.580%) during 0-3, 3-6, 6-12 months of age, respectively. Whereas, lowest in August (88.00±3.023%), December (55.14±5.389%) and July (87.75±3.631%) during 0-3, 3-6 and 6-12 months of age, respectively.

ABST-1-042

MORPHOMETRIC CHARACTERISTIC OF DESI CHICKEN IN INDIA

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Indigenous poultry farming plays a vital role in development of Indian economy. It helps in reducing malnutrition and creates employment opportunity at rural area and provides nutritional stability. Indigenous chicken are known for disease resistance and can adapt to harsh humid climatic conditions. Native chicken production has got huge demand for their meat and egg because of their nutritional and medicinal values. It is found that phenotypic characteristics of native chickens have an impact on production performance. The phenotypic characteristics includes both qualitative and quantitative traits in which native chickens shows great morphological variation in their qualitative traits like feather morphomology, feather distribution, plumage colour, skin colour, shank colour, earlobe colour, eye colour, comb colour and comb types. The important quantitative traits namely body weight, shank length, shank width, beat length & keel length. In India almost all desi birds have normal feather morphology and frizzle feather pattern is comparatively less. Fast growing feathers are predominant over slow feathering pattern. In plumage colour black, brown, white, gold, red and multicolour are commonly found in desi birds. Majority of the desi birds have yellow skin colour comparatively yellow. The predominant shank colours are yellow, white, green and black. Most of the birds have single combs over pea and rose type and majority of the birds found to be red coloured comb. The predominant ear lobe colours are red, white, and mixed colour. The quantitative traits help in prediction of age based on its body measure.

ABST-1-043

MORPHOMETRIC CHARACTERIZATION OF JANWAL PASHMI DOGS IN MARATHWADA REGION OF MAHARASHTRA

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Janwal Pashmi is the medium sized dog found predominantly in black colour. However the colours like fawn, grey, brown, white are also found rarely. This dog population has been identified as Janwal Pashmi, the feathered variety. This dog is mainly found in the villages of Chakur Tahsil of Latur District and surrounding area in Marathwada region of Maharashtra State. There is no any research work conducted on this dog up till now. Considering this fact, the present investigation has been carried out by collecting morphometric data on 200 Janwal Pashmi dogs from its breeding tract. The data collection was classified into two age groups i.e. 0-1 year (Puppies) & above one year (Adults). Further the sex wise distribution of the data was done for each age group. The morphometric characters studied were body weight (BW) in kg and height at weather (HW), chest girth (CG), paunch girth (PG), tail length (TL), head length (HL), height at base of tail (HBT), neck length (NL), neck girth (NG), ear length (EL), ear width (EW), eye width (EYW), hind foot length (HFL), Upper hind leg length (UHLL), Lower hind leg length (LHLL), fore foot length (FFL), Upper fore leg length (UFLL) and Lower fore leg length (LFLL) in centimetre. The estimated mean of the morphometric traits for puppies were found to be 18.68±0.90, 62.62±0.51, 43.15±0.71, 59.81±0.93, 45.41±0.90, 46.67±0.50, 21.87±0.17, 62.87±0.81,

20.06±0.19, 30.75±0.71, 13.70±0.35, 7.25±0.09, 4.93±0.02, 19.18±0.23, 29.02±0.23, 26.87±0.25, 16.37±0.19, 21.83±0.29, 22.41±0.31 whereas for one year and above dogs, those were 26.00±0.26, 67.64±0.25, 48.30±0.29, 67.58±0.36, 47.63±0.44, 47.94±0.31, 22.24±0.05, 68.19±0.27, 20.17±0.14, 36.37±0.22, 13.70±0.10, 7.45±0.04, 5.07±0.009, 19.84±0.11, 29.90±0.27, 28.19±0.24, 16.25±0.10, 24.15±1.13, 24.17±0.1, respectively. The effect of sex was found to be non-significant on all the traits in puppies. However, BW, HW, BL, HL, HBT, NL, EL, HFL, FFL were found significantly higher in males of adult age group. It was concluded from the above study that Janwal Pashmi dog is a medium-sized indigenous dog mainly used for guarding purpose and hunting in Marathwada region of Maharashtra State.

ABST-1-044

NON GENETIC FACTORS AFFECTING THE PRODUCTION AND REPRODUCTION PERFORMANCE OF CROSSBRED PIGS

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In the present study, data on crossbred pig was collected from PGRIAS, Kattupakkam, Tamil Nadu for a period of 20 years from 2001 to 2021. The data were analyzed by Univariate General Linear Model for determining the fixed effects of period, season, sex and parity of 7456 birth and 955 farrowing of the animals. The overall least-squares mean for birth weight, weaning weight and pre-weaning average daily gain were 1.107 kg, 7.849 kg and 150.36 g respectively. The period, season and sex were found to have high significant effects on birth weight. The period, season and sex have significant effect ($p<0.05$) on weaning weight. The period and season have significant influence on pre-weaning average daily gain. The least-squares mean age at first farrowing (AFF) and farrowing intervals (FI) were 481.440 days and 196.175 days respectively. The period, and season were found to have high significant effects ($p<0.01$) and genetic group have no significant effect on AFF. The AFF was shortest and longest in the genetic group 50% LWY and 75% LWY respectively and vice versa for farrowing intervals. The overall mean litter size at birth (LSB), litter size at weaning (LSW), litter weight at birth (LWB), and litter weight at weaning (LWW) were 7.541 ± 0.324, 7.103 ± 0.340, 8.886 ± 0.426kg and 53.058 ± 3.158 kg respectively. The genetic group and parity were noticed high significant effects on LSB, LSW, LWB and LWW. The season have no significant effect ($p>0.05$) on all the litter traits. Significantly highest LSB, LSW, LWB and LWW were noticed in the genetic group 75% LWY than 50% LWY. Based on this study we concluded that, overall period, season and sex had significant effect on production and reproduction performance of crossbred pigs and 75% LWY had higher performance value than 50% LWY.

ABST-1-045

PERFORMANCE EVALUATION OF MAGRA SHEEP FOR GROWTH TRAITS AND IMPACT OF INBREEDING

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The objective of this study was to measure the impact of inbreeding on growth traits in Magra sheep. The data of growth traits of 5059 animals were collected from 22 years (1998 to 2019) records of Magra sheep maintained at ICAR-CSWRI-ARC, Beechwal, Bikaner, Rajasthan. The inbreeding coefficient (F) was computed using pedigree viewer software. The linear regression analysis of all the growth traits on inbreeding was performed using SPSS. The mean inbreeding coefficient (F %) for whole population, male and female were 0.89, respectively. The overall proportion (%) of inbred animals was 46.39 in which most of animals (37.22 %) had fewer than 3 % level of inbreeding. The linear regression had highly significant and positive effect on

all growth traits except KR2 (weaning to 6 months) where it was highly significant but negative effect. The non-significant and positive effect of linear regression was seen on KR3 (6 months to 12 months) while non-significant and negative effect was observed on ADG2 (weaning to 6 months). The rate of inbreeding increased slowly under a prescribed criterion. This study indicated that inbreeding over the period of time had positive effect on all the growth traits and enhances the growth performance because of scientific selection and careful mating among animals. The steady increase in the level of inbreeding over the years alerts that subsequent mating should be more carefully prepared to prevent mating of close relatives

ABST-1-046

PHENOTYPIC CHARACTERIZATION OF NATIVE SHEEP PREVALENT IN NAGARJUNA SAGAR AREA OF TELANGANA

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A study was undertaken to characterize the native sheep prevalent in Nagarjuna sagar area of Nalgonda, Nagarkurnool and Suryapet districts of Telangana based on the morphological features and production performance by recording the data on 1000 sheep from 89 farmers in a total of 30 villages of 10 mandals under field conditions. The predominant coat colour pattern was bi-colour of brown and white (48.1%), followed by black and white (37.6%). The predominant features were convex head, pendulous ears, black coloured muzzle, brown eyelid colour, slender type of tail and black coloured hooves. Horns were oriented in backward, downward and forward direction in 44.33% sheep and 75.6% of the sheep had wattles. The morphological features were found to be distinct and different from the other breeds in the region such as Deccani and Nellore in comparison to the literature studied. The overall mean values for body weight, height at withers, chest girth, paunch girth and body length at 8 teeth age in males were 45.08 ± 1.09 kg, 84.08 ± 0.94 cm, 91.59 ± 0.82 cm, 94.42 ± 0.85 cm and 77.51 ± 0.49 cm, respectively and in females were 43.63 ± 0.26 kg, 79.29 ± 0.31 cm, 88.98 ± 0.19 cm, 90.85 ± 0.32 cm and 72.10 ± 0.65 cm, respectively. The overall means of age at first mating in ewes, age at first lambing, litter size and twinning percentage were 358.47 ± 5.64 days, 508.26 ± 3.57 days, 1.53 ± 0.04 and 52.5%, respectively.

ABST-1-047

PRODUCTION PERFORMANCE OF TAMIL NADU BLACK PIGS UNDER FARM-BRED CONDITION

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Black pig is a native breed of Tamil Nadu and it was commonly reared by rural poor and socio economically weaker section peoples of Tamil Nadu. Even though there are so many exotic breeds available, tribal peoples are more interested in rearing Black pigs because of most suitability in tribal areas. The present study is framed to evaluate the production performance of black pigs in an organized farm. The data was obtained from Pig Breeding Unit, Post Graduate Research Institute in Animal Sciences, TANUVAS, Kattupakkam, Tamil Nadu for the period of 2018 to 2022. The least squares analysis was carried out to study the effect of sex, season and period on production performance by using SPSS software. The overall mean birth weight, weaning weight and pre weaning average daily gain were found to be 0.66 ± 0.014 kg, 4.855 ± 0.164 kg and 59.54 ± 2.384 g respectively. Comparatively highest birth weight was noticed in male piglets, whereas female pigs showed highest weaning weight and pre-weaning average daily gain. The period and season of birth had highly significant source of variation ($p<0.01$) and sex had no significant variation on birth weight. Significantly highest birth weight was noticed on season of south west monsoon and period of 2020. The weaning weight had highly significant effect ($p<0.01$) in period and season of birth than sex. The period and season were found to have high significant effects ($p<0.01$) on pre-weaning average daily gain. The result concluded that the season factor influence the birth weight and weaning weight of piglets.

ABST-1-048

SOW TRAITS OF TAMIL NADU BLACK PIGS IN AN ORGANIZED FARM

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Pigs are reared only for the purpose of meat to meet out the protein demand in India. The production of pigs decide the profitability of the farm. This study was conducted to evaluate the performance of black pig sows in an organized farm. The data was collected from Pig Breeding Unit, Post Graduate Research Institute in Animal Sciences, TANUVAS, Kattupakkam, Tamil Nadu for the period of 2018 to 2022. The least squares analysis was carried out to study the effect of sex, season and period on sow traits by using SPSS software. The overall mean litter size at birth, litter size at weaning, litter weight at birth and litter weight at weaning were found as 5.597 ± 1.08, 5.557 ± 0.591, 4.363 ± 0.712 kg and 26.17 ± 3.162 g respectively. The period of farrowing had highly significant effect ($p<0.01$) on all the sow traits. The period of 2020 had highest values on all the sow traits (8.514 ± 1.09, 7.569 ± 1.01, 7.765 ± 0.72 kg and 44.692 ± 5.46 kg respectively). The season of birth had no significant influence on sow traits except litter weight at birth. The parity of sow had significant variation in sow traits except litter weight at weaning. Among three numbers of parity, third parity had higher values in all the sow traits and lowest in first parity. Overall effect of season not influence the performance the animals than other non-genetic factors. Period of farrowing had high significant variation in period of farrowing may be due to management effect. The result concluded that the season factor not influence the black pigs.

ABST-1-049

STUDIES ON EGG PRODUCTION AND EGG QUALITY TRAITS OF KADAKNATH BREED OF CHICKEN

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Kadaknath breed, (Kalamashi) is famous for its black-coloured meat, reared by tribal communities in Jhabua and Dhar (M.P.). Native rural chicken are valuable genetic resources due to their adaptability to local conditions and resistance against common diseases. the present investigation was undertaken with objectives to assess the egg production performance and various egg quality characteristics of Kadaknath breed of poultry. Day old, 50 female chicks of Kadaknath birds were obtained from the Hatchery Unit of the College of Veterinary Science and Animal Husbandry, Rewa. All the chicks were reared up to the age of 40 weeks on deep litter following standard managemental practices for chick, grower and laying stages. Birds were fed standard feed during chick, grower and laying stage having CP20%, 14% and 18% and ME 2600 Kcal/Kg feed, 2400 Kcal/ Kg feed and 2600 Kcal/Kg feed, respectively. The egg collection period was divided in to three different age groups i.e. 20-26th weeks, 27-33th weeks, 34- 40th weeks of age. The body weight, growth rate, egg production, egg quality, FCR, Mortality and cost economics were estimated. The body weight at first egg was 1124 gm at 22 weeks of age. The growth rate was highest during 8-12th week. During 28-32nd and 32-36th & 36-40th weeks the growth rate was very less. The egg production was highest during 2nd Interval then it decreases during 3rd Interval. The FCR for production of one dozen eggs was very poor during first interval. The egg weight was increasing with age and reached upto 47.07 gm during 3rd interval. The egg shell percentage was highest during 2nd interval whereas the albumen percentage was slightly decreasing however the yolk percentage was increasing with age. The yolk index and albumen index was found decreasing with age. The total mortality was only 12% from day old to 40th week of age. The cost of production for 20-40th week was Rs. 15.38 per egg.

ABST-1-050

STUDY ON GROWTH AND REPRODUCTIVE PARAMETERS OF KARKAMBI PIGS UNDER FIELD CONDITIONS OF MAHARASHTRA

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Pigs are traditionally reared by the socio-economically backward and downtrodden sections of the society. It plays crucial role as an insurance coverage and employment generation to the weaker section of the society. Majority of pig in India belongs to non-descript class; Karkambi pigs are amongst them found in Maharashtra state managed under extensive scavenging system in Solapur, Pune and Satara district of Western Maharashtra. In the present study, the performance of Karkambi pigs (N=642) under field condition in respect to growth (381/642) and reproductive (261/642) parameters were recorded and further studied scientifically with respect to age, sex and reproductive parameters. Descriptive statistics was employed to study the respective parameters. The body weight at different age groups was classified according to the sex of the animals. The average body weights of Karkambi pigs were found to be 0.50±0.01, 3.30±0.05 and 43.17±0.50 kg at birth, weaning and adult respectively. The corresponding values in male and female pigs were 0.497± 0.01 and 0.496±0.01; 3.08±0.06 and 3.50±0.07 and 44.11±0.61 and 42.44±0.73 kg at birth, weaning and adult respectively. The average age at first estrus, age at first fertile service, age at first farrowing and farrowing interval were found to be 225.51±1.56, 293.90± 2.11, 383.92±1.76 and 211.61±1.52 days respectively. The average litter sizes at birth, litter weight at birth and litter size at weaning were 5.77±0.14, 3.15±0.07 kg and 4.45 ±0.11 respectively. Study of these growth and reproductive performance may be useful in selection of superior animals for development of suitable breeding programme and conservation policy for Karkambi pigs of Maharashtra.

ABST-1-051

ESTIMATION OF COMBINING ABILITY AND GENETIC PARAMETERS FOR GROWTH TRAITS OF ROHU CARP (*LABEO ROHITA*) FROM DIALLEL CROSS

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The experiment of two 3X3 partial diallel crosses was carried out between four hatchery-bred stocks of rohu, assuming that the hatchery-bred stocks are inbred. The effects of non-genetic factors on five growth traits and genetic combining abilities among four rohu stocks were estimated. Four stocks were bred in a 3 X 3 partial diallel mating design, and 37 full-sib families were produced in two batches. In total, 1129 fish were individually PIT-tagged at six months of age and body weights were recorded at stocking and up to four months of pond age at monthly intervals. A total of 2104 observations were recorded. At four months of pond age, the least-squares mean body weight was 62.18 ± 1.07 g. The effects of non-genetic factors like batch, rearing system and ponds were found to be significant on body weight. Heritability of body weight at four months of the pond age was 0.05 ± 0.03, and the genetic and phenotypic correlation with body weight at stocking was -0.06±0.08 and -0.06±0.01, respectively. Griffing's method-3, models I and II, were employed to estimate the combining abilities for body weight. The General Combining Ability (GCA) for the body weight at four months of pond age ranged from -0.6 to 7.6 per cent. The highest Specific Combining Ability (SCA) was found for the cross between the males of Stock-2 and the females of Stock-1. The overall heterosis effects for body weight ranged from -5.7 to 7.5 per cent. The result suggests that with a suitable mating design, the heterosis effect can be exploited to enhance the growth rate in rohu.

ABST-1-052

EVALUATION OF COMPARATIVE STUDIES ON PRODUCTION PERFORMANCE OF FOUR GENERATIONS OF RAJASRI BACKYARD CHICKEN

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Backyard poultry is recognized as a tool for improving the nutritional standards of the rural poor. However, desi birds are poor egg producers and commercial birds will not fit as they are both capital and technology intensive. Keeping in view of the above PV Narsimha Rao Telangana Veterinary University had developed Rajasri, A dual purpose backyard variety which is suitable to rear under free range system. These birds can survive under low plane of nutrition, easily escape from predators. The genetic makeup of Rajasri involves 56.25% RIR, 25% Native breed, 12.5% Delham Red and 6.25% WLH. Improvement in performance of Rajasri birds is done by selective breeding. For this purpose, females (based on EP40) are selected and used for production of next generation. The data on production records of 7098 female birds belongs to four generation (S4 to S7) were analyzed. The estimated average age at sexual maturity for the four generations was 162.5, 161.2, 160.5 and 160.1.Individual egg production was recorded from 18 to 40 weeks of age,corresponding egg weights in grams at 28th weeks of age was 42.65, 47.87, 42.76 and 44.32 respectively and at 40 weeks of age was 51.26, 49.79, 47.56 and 49.07 respectively. Egg productions up to 40th weeks of age on hen day egg production, the estimates were 64.97, 72.09, 73.72 and 80.02 respectively. The overall least square mean body weights at 20thand 40th week of age were 1365.36 ± 2.65 g and 1602.13 ± 2.94 g respectively.The overall least square mean egg weights at 28th and 40th weeks of age were 45.12 ± 0.05 g and 49.06 ± 0.04 g respectively. The overall least square mean egg production at 40th week of age was 70.57 ± 0.18. It was observed that the effect of generation and hatch was highly significant on the parameters studied.

ABST-1-053

GROWTH AND PRODUCTION PERFORMANCE OF BLACK ROCK CHICKEN REARED AT HIGH-ALTITUDE

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Leh-Ladakh is located at 3500 meter hight which comes under high-altitude region. This region possess harsh climatic condition charecterized by hypobaric-hypoxia, low humidity, and adverse temperature which poses difficulty to animals, birds and humans. Successful poultry farming is a huge challenge here and there is also unavailability of native chicken germplasm. Therefore, it becomes utmost important to study the survivability and performance of different chicken breeds at high-altitude region in order to meet the increasing demand of fresh chicken meat and egg especially during the winter season. The present study was performed to compare the growth and production performance of Black Rock (BR) chicken for three subsequent generations at high-altitude. Growth performance like weekly body weight of the bird was recorded. Production related parameters like age at first egg laying, body weight of the hen at first egg, pubic bone distance and egg weight were recorded and compared among three generations. It was observed that BR started laying egg at high-altitude quite late compare to chickens reared in lowlands. The body weight of parental, first and second generation of BR was 674g, 704.9g, and 744.8g respectively at 7th week. The first egg of parental, first, and second generation of BR was obtained at 185 days, 159 days and 157 days respectively, which shows that with the advancing generation egg laying age of the hen has been reduced. The body weight of the hen at the first egg laying of the three lines was 2.45kg, 2.38kg, and 2.26kg, similarly, the pubic distance of laying hen during laying was 5.27cm, 5.15cm and 5.32cm and the egg weight was 49.25g, 49.39g, and 49.77g repectively. The preliminary data on growth and production performances of BR shows that with subsequent generation rearing at high-altitude indicates the adapting nature of these chickens at high-altitude and to perform better in the existing environmental condition. However, an extensive work is required to better understand the physiological and genetic changes regarding the adaptation of these birds at high-altitude.

ABST-1-054

IDENTIFICATION AND CHARACTERIZATION OF INDIAN DOG POPULATIONS: PRESENT STATUS AND FUTURE PROSPECTS

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India is a rich country for its biodiversity of flora and fauna, as blessed with different types of soils, climate conditions and physical features. As per 20th livestock census domestic dog population is 9.7 million while according to one of the official record stray dog's population is estimated around 17.14 million in India. These Indigenous dog breeds were once kept by the royal families' rulers and Mughals. Through many years, the popularity of Indian dogs has severely declined and most of these breeds heading towards extinction, due to increased demand for the foreign dog breeds as a status symbol and our tendency of never fully embraced domestic breeds. This trend has led to the dilution of gene pool of native lineage through crossbreeding. For sustainable use, improvement and preservation of these high valued indigenous dog populations, identification, characterization and documentation is the first and foremost priority. Recognizing this, NBAGR, Karnal initiated the process and recently registered three Indian dog breeds viz., Rajapalayam and Chippiparai from Tamil Nadu and Mudhol Hound belonging to Karnataka. The Rajapalayam is medium sized, white coat coloured dog, used for guarding purpose while Chippiparai is medium sized with coat colours varied from fawn to dark brown, brownish black and black, used for guarding and hunting purpose. Mudhol Hound dogs are strongly built, having high stamina and endurance with aerodynamic body for effortless stride and giving flying appearance. Found in many coat colours mainly white, brown, patchy, brindle, black, fawn along with spots. Mudhol Hound dogs are used for guarding and shepherding with high in obedience. Indian dog breeds include the Indian Spitz, Gaddi, Bully Kutta, Indian Pariah, Kaikadi, Taji, Pandikona, Jonangi, Bakharwal, Tangkhul, Combai, Rampur Greyhound, Vikhan Sheepdog, Mahratta, Sinhala Hound, Kumaon Mastiff, Pashmini, Karwan, Gull Dong, Gull Terrier and many other lesser-known needs urgent attention toward their characterization and preservation. As they are better adopted to the Indian environment and cost less for their raising, a policy decision for characterization, not to neuter pure male, avoid crossbreeding and registered them as a breed at national level would allow conservation of these ancient lineage and will preserve their beauty and temperament.

ABST-1-055

PHENOTYPE AND MORPHOMETRIC ATTRIBUTES OF LOCAL BUFFALOES IN GADCHIROLI DISTRICT OF MAHARASHTRA

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A study was conducted to document the phenotype and morphometric attributes of 106 local buffaloes in Gadchiroli district of Maharashtra during August to October, 2022. These buffaloes are popularly known as "Gondi buffalo" locally and phenotypically distinct from adjoining buffaloes. The data was collected by using preformed questionnaire and the morphometric measurements were recorded individually. These local buffaloes were of medium sized, black coloured (skin, coat, muzzle, eyelid, hoof and tail switch etc.) having horns with upward pointing orientation, small dewlap and hump. The udder was bowl shaped, teat shape was cylindrical and the teat tip was round in female. The mean values for various morphometric traits recorded in adult animals (n=106) were as Height at wither as 120.38± 11.69 cm; Height at croup as 126.26±12.26 cm; Body length as 103.42±10.04 cm; Chest girth as 159.27±15.47 cm; Paunch girth as 152.73±14.83 cm; Face length as 45.36±4.41cm; Face width as 19.25±1.87cm; Ear length as 26.36±2.56 cm; Horn length as 42.09±4.09 cm and Tail length as 64.74±6.29 cm, respectively. The study suggested that there is need of further detailed characterization and differentiation at molecular level of local Gondi buffaloes.

ABST-1-056

PHENOTYPIC CHARACTERIZATION OF JANWAL PASHMI DOG

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The Janwal Pashmi is a medium sized local dog found in villages of Chakur Tahsil of Latur District and surrounding area in Marathwada region of Maharashtra State. There was no research work conducted on this dog population up till now. A survey was conducted to study the morphological features of this dog population. The present investigation is based on data of 200 Janwal Pashmi dogs collected from its breeding tract. Majority of the dogs were found to be black in color (79.5%). However, the other colors include Fawn (11.5%), Brown (5%), Grey (2.5 %) and White (1.5 %). Maximum dogs were found to have medium hairs length (53%) followed by long hairs (44.5 %) and rarely small hair length (2.5%). The shape of the head was straight and wedge shaped with 69 % and 31 %, respectively in Janwal Pashmi dogs. The color of nostrils in the majority of dogs was black (95 %) and very few dogs had brown (4%) and pinkish (1%) color nostrils. The eyes were light brown (46%) or dark brown (54%) in colour. The small ear length was observed in 2 % dogs only. Majority of dogs were having long ear length (57 %) while 41 % of dogs were having medium sized ears. They have tucked-up abdomen, deep chest. Feathery hairs were observed predominantly at ears, tail, head, shoulder, thigh and abdomen. The shoulder blades were well defined and set obliquely. The hind limbs were thin and strongly muscled with well angulated stifles. The feet have close set oval foot pads turning neither in nor out. Thick hairs on their paws resemble winter shoes. A unique feature of Janwal Pashmi dog is a rolled-up ring at the end of its tail. It is actually the jointed vertebras of the ring that do not make it unrollable. They have a whip-like tail with a natural bend at the end that is situated high on their hindquarters. Janwal Pashmi dogs were mainly used for guarding and hunting purposes. There is wide scope for this unique canine germplasm to be documented and registered at National level to characterize this as a distinct breed.

ABST-1-057

EFFECT OF SILVER NANOPARTICLES AS DISINFECTANT AND AS FEED ADDITIVE ON GROWTH, IMMUNESTATUS AND GUT HISTOPATHOLOGY IN BROILERS

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The quest for alternatives for antibiotics has been going on for decades. The usage of antibiotics has resulted in developing resistance against them by various microbes posing a global threat, one alternative is the emerging innovative technology called as Nanotechnology which includes Nanoparticles of silver which is an emerging alternative feed supplement for poultry. Its antimicrobial property is becoming increasingly important due to their wide range of applications. Despite the widespread use of nano silver products, relatively few studies have been undertaken to determine the biological effects of nanosilver exposure. The objective of this study is to clarify the potential of nano-Ag as an alternative growth promoting supplement for chicken. Day old commercial broilers (225) were randomly segregated into 3 treatment groups with 5 replicates in each group and 15 birds in each replicate (75 birds in each treatment). The experimental groups which include control group T_1 (Basal diet + conventional disinfection), and case groups T_2(Basal diet + 0.05 ml of AgNPs / ltr drinking water + disinfection using AgNPs), T_3 (Basal diet + 0.1 ml of AgNPs / ltr drinking water + disinfection using AgNPs). Growth performance, carcass traits, serum biochemical profile and survivability was studied.A significant improvement ($P \leq 0.05$) in body weight in case groups was observed compared to control group, the same results were reflected in case of feed intake and feed efficiency also, indicating that silver nanoparticles have positive effect on performance traits. Serum biochemical profile viz., serum cholesterol, triglycerides, HDL remained unaffected. Carcass traits were significantly ($P \leq 0.05$) affected and survivability in silver nanoparticles fed groups were improved compared to control.It was concluded that inclusion of silver nanoparticles in broilers can be advantageous in poultry. Since, it improves growth performance and reduces

mortality rates by providing immunity against various infections. Silver nanoparticles improves feed efficiency thereby reducing the expenditure on feed which can be helpful for farmers who are involved in poultry rearing as an alternative source of income.

ABST-1-058

EXPLORING THE GENETIC DIVERSITY IN A CLOSED NUCLEUS FLOCK OF SIROHI GOATS THROUGH PEDIGREE ANALYSIS

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Sirohi is a highly popular goat breed famous for its meat and milk production potential, found mostly in the semi-arid climate of Rajasthan, but presently distributed all over Rajasthan and adjoining areas of the neighbouring states. The genetic diversity was explored by using pedigree analysis in a closed nucleus flock of Sirohi goats maintained under All India Coordinated Research Project (AICRP) on Goat Improvement scheme located at ICAR - Central Sheep & Wool Research Institute (CSWRI), Avikanagar to find out different parameters like generation interval (GI), inbreeding coefficient (F), average relatedness (AR), effective population size (Ne), effective number of founders (fe), effective number of ancestors (fa) in the population. The complete data set consisted of 8895 animals spread over 46 years (1976–2021). Whereas the inbreeding coefficient and average relatedness were calculated from the data of the whole population, the other parameters of genetic diversity were generated from a reference population of 1359 animals born during 2011-15 using ENDOG v4.8 software. The mean inbreeding was 1.99% and the mean average relatedness was 3.39%. The average generation interval was 3.49 ±0.05 years; the pathway of buck to daughter was least (2.73 years) and it was highest for doe to son (4.32 years). The mean maximum generations, mean complete generations and mean equivalent generations were 9.25, 2.32 and 4.66, respectively. The realized effective population size (Ne) computed via individual increase in inbreeding was 148.04. The effective number of founders (fe) and effective number of ancestors (fa) were 50 and 40, respectively. The ratio of fe/fa, indicating the effect of population bottlenecks, was 1.25. The number of ancestors explaining 50% genetic variability was 14. The different parameters of genetic diversity generated from the present study in Sirohi goats can be useful in devising appropriate breeding and management strategies for restricting inbreeding and maintaining ample genetic variability in the flock so that the desired genetic improvement can be achieved.

ABST-1-059

TOXICITY EVALUATION OF SYNTHETIC INDIGO DYES IN ZEBRAFISH (*DANIO RERIO*)

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Textile dyeing wastewater is considered one of the most important environmental pollution and degradation sources. Indigo dye wastewater from the blue denim jeans manufacturing industries poses a significant threat to the environment due to the release of untreated wastewater into the water bodies, thereby affecting aquatic ecosystems. The present study assessed the toxicity of synthetic indigo dyes in zebrafish (*Danio rerio*) embryos up to 120 h post-fertilization (hpf) using biomarkers such as acute toxicity test, teratogenicity, and histology. The acute toxicity of the dye was assessed by performing the zebrafish embryo toxicity test (ZFET) using ten different concentrations. A total of 24 embryos were exposed to each concentration, and mortality was recorded at different time intervals up to 120 h. The highest mortality was observed in zebrafish embryos exposed to the indigo dye at 800 mg/l concentration after 120 h. The Proc Probit procedure determined the LC50 values for synthetic indigo dyes as 304 mg/l. Various teratogenic effects such as egg coagulation, tail

detachment, yolk sac edema, pericardial edema, and tail bend were observed in zebrafish embryos following exposure to the synthetic indigo dyes at different concentrations and time intervals. The data analysis revealed that teratogenicity was induced by synthetic indigo dyes in the zebrafish embryos. Thehistological investigation of the zebrafish embryos revealed morphological alterations followingexposure to the synthetic indigo dyes. The present study thus indicated that the synthetic indigo dyes used in the textile industries could induce teratogenic effects in aquatic organisms.

ABST-1-060

NON-GENETIC FACTORS AFFECTING BODY WEIGHTS IN KADAKNATH CHICKEN REARED UNDER INTENSIVE SYSTEM IN CHHATTISGARH

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The present investigation was carried out on 3000 Kadaknath birds to study the non-genetic factors affecting body weights in Kadaknath chicken reared under deep litter system.Chicks were fed standard balanced feed as per recommendations. Around 3000 birds divided in 3 generations and 3-4 hatches in each of the 3 generations were raised and recorded for the study. The mean weekly body weights with standard error in three generations and also overall means of Kadaknath birds from 0 to 20 weeks of age, are presented in table 4.4. The overall means of the Kadaknath chicken at 0, 4, 8, 12, 16 and 20 weeks of age were recorded as 26.73 ± 0.06, 92.60 ± 0.52, 228.22 ± 1.45, 414.82 ± 2.68, 624.70 ± 3.55 and 844.00± 4.56 g, respectively. There was significant differences between generations across the age periods and the body weight at all age, G2 generation is on higher side followed by G3 and G1. This is mainly due to selection performed in the Generation 1. It can not be denied that the significant difference is not only due to genetic but also because of environmental reasons which indicate that there is a scope for improvement of performance of the flock.It was noticed that the difference at earlier ages is less and this difference becomes more with increasing age. Due to sexual dimorphism, males grow faster than females leading to significant differences between them. At 20 weeks of age the difference between male and female body weight is to the tune of 228g. The hatch effect was highly significant in the parent generation and the two progeny generations. The probable reason might be the variation of environmental factors over three generations as the performance varied with one another.

ABST-1-061

REPRODUCTIVE PERFORMANCE OF SANGAMNERI GOATS UNDER FIELD CONDITIONS

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The experiment entitled, "Reproductive performance of Sangamneri goats under field conditions," was conducted by All India Co-ordinated Research Project on Goat improvement, MPKV, Rahuri (Maharashtra) to investigate the reproductive performance of does, reproductive performance of progeny of the bucks supplied by the project under field condition and factors that affects the reproductive performance of Sangamneri goats breed at field condition.In the pre - partum reproductive performance of progeny of Sangamneri bucks under field conditions (days). The overall means age at maturity, age at first conception and age at first kidding were 257.36±4.85 (1701), 301.54±9.38 (1708) and 452.77± 9.86 (1667) days, respectively. The non-genetic factors i.e. village clusters, year of birth and season of birth had significant influence and type of birth had non-significant influence on pre-partum traits. In the Post - partum reproduction performance of Sangamneri goats under field conditions (days). The overall mean of service period and kidding interval were 122.06±5.27 (2217) and 270.33±7.17 (2176) days, respectively. The number of kids per kidding were 1.67±0.07 (2818) days. While the post-partum reproductive traits i.e. service period, kidding interval and number of kids per kidding were significantly influenced by village cluster, year of kidding, season of kidding and kidding order, except season of kidding had non significant influence on number of kis per kidding.

ABST-1-062

EFFECTS OF NON – GENETIC FACTORS ON GROWTH PERFORMANCE OF OSMANABADI GOAT BREED

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The experiment entitled 'Effects of non – genetic factors on growth performance of Osmanabadi goat breed' was invoked to investigate the growth and productionperformance and effect of non – genetic factors on growth performance of Osmanabadi goats. The data on growth and production performance of Osmanabadi goats maintained at Osmanabadi goat unit, Rahuri were collected and statistically analysed by LSQ model. The data during the period of 10 years (2010-2019) was tabulated and it was statistically analysed to estimate least square mean of the body weight (Kg). At different stages of growth i.e. at birth, 3 months, 6 months, 9 months and 12 months of age of animal, it was observed that mean birth weight of 498 number of animals was 2.22 ± 0.01, at the age of 3 months mean weight of 365 animals was 8.35 ± 0.11, at the age of 6 months mean weight of 307 animals was 11.24± 0.28, at the age of 9 months mean weight of 245 animals was 13.30 ± 0.27 and at the age of 12 months mean weight of 178 animals was 17.24 ± 0.26.The year of birth and sex significantly influences body weight at all the ages. The type of birth significantly affects the body weights at all the ages except 9 and 12 months of age. While, season of birth exerts significant influence on only birth weight.

ABST-1-063

COMPARATIVE EVALUATION OF FERTILITY AND HATCHABILITY OF DIFFERENT CHICKEN BREEDS/ VARIETIES/CROSSES IN HOT HUMID CLIMATIC CONDITION OF TRIPURA

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A study was undertaken to evaluate the fertility and hatchability of different chicken breeds/varieties/crosses in hot humid condition of Tripura. For this, hatching eggs were collected from different breeder stocks of poultry farm of ICAR-Research complex, Tripura Centre, Lembucherra and brought to the hatchery unit. After proper cleaning and fumigation, the hatching eggs were stored in the egg holding room at 65^{o}F (18^{0}C) and relative humidity 75-80% to curtail embryonic development completely. A total 11093 eggs of Dahlem Red (3030 nos.), Coloured Broiler (1792 nos.), Tripura Black (1951 nos.), Kadaknath (869 nos.), BN Cross (50%) (1396 nos.) and BND Cross chicken (2055 nos.) were set for hatching in four different batches in the hatchery unit. Hatching eggs was kept in incubator for first 18 days and then transferred to the hatcher for last 3 days during incubation period. Proper temperature, relative humidity and ventilation were maintained in incubator as well as in hatcher during the period. A total of 7120 chicks of different breeds / varieties / lines were hatched out at 21th day. The results revealed that the significantly ($P<0.01$) highest fertility was found in BND Cross (88.69%) and lowest fertility was found in Kadaknath (72.88 %). The hatchability on total egg set (TES) was significantly ($P<0.01$) highest in BND Cross (69.5%), then followed by Dahlem red (65.81%) and lowest in Kadaknath (53.13%). However there was no significant different observed in hatchability on fertile egg set (FES). The hatchability on fertile egg set (FES) was highest in BN Cross (79.68%) and lowest in Kadaknath (72.91%). Thus, it was concluded that significant differences were observed in fertility ($P<0.01$) and hatchability on total egg set ($P<0.01$), however there was no significant different observed in hatchability on fertile egg set (FES) among different chicken breeds/varieties/crosses in hot humid climatic condition of Tripura.

ABST-1-064

FATTY ACID PROFILES AND MINERALS COMPOSITION OF EGGS IN KADAKNATH CHICKEN

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The role of egg and its nutritional value in every day to day life is very crucial. The National Egg Coordination Committee states that a single egg contributes 12 % of the daily value for protein and edible supply of Omega-3 fatty acid (180mg). As per the recommendation of the National Nutrition of India, a person should consume one egg per day on an average. Considering the above facts, the nutritional value of egg was studied for fatty acid and mineral profiles of eggs in Kadaknath chicken. The Kadaknath (black chicken) a native chicken of Madhya Pradesh is well known to have higher nutritional value and low cholesterol content in its meat and egg. Here, in this study the fatty acid profiles by Gas chromatography and mineral content by ICP-OES spectrophotometer were estimated in 400 birds of Kadaknath chicken maintained at the Institute farm of ICAR-Directorate of Poultry research, Rajendranagar, Hyderabad. The recorded egg weights at 40 weeks and 64 weeks were 45.7±4.0 g and 47.89±4.10 g, respectively, which has shown slight increase over 24 weeks. Whereas, the length and width of eggs were observed as 53±3.1mm and 55±2.87mm, respectively. The fatty acid composition of egg at 40 weeks of age revealed that mono and poly unsaturated fatty acids (Oleic acid was 50±3.8 %, Linoleic acid was 15±4.6% and Linolenic Acid was 1.6±1.9%) accounted for 67% of total fatty acids and rest were saturated fats such as Palmitic acid (21.5±0.8%), Steric Acid (7±0.9%). The egg mineral content in Kadaknath chicken at 40 weeks of age were estimated as Phosphorus (150±24mg) being the highest quantity and followed by Sulphur (126±21mg), Potassium (78±39mg), Sodium (73±11mg), Magnesium (6.1±2.5mg), Iron (2.9±2.8mg), and Zinc (0.9±0.3mg). Finally, it was concluded that eggs of Kadaknath chicken contained more than 65% unsaturated fatty acids and very high iron content suggesting an excellent source of unsaturated fatty acid and organic iron for human being.

ABST-1-065

PHENOTYPIC CHARACTERIZATION OF INDIGENOUS CHICKEN OF BELAGAUM DIVISION OF KARNATAKA STATE, INDIA.

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The study was undertaken to characterize the indigenous chicken of Belagaum division of Karnataka State, based on some phenotypic traits. The study included two parts I. Survey study and II. Evaluation under farm conditions. In the survey study a total of eight hundred and ten birds (810), 270 males and 540 females, mature indigenous chicken were randomly sampled from the study area and in the evaluation under farm conditions a total of one hundred and sixty birds (160), 24 males and 136 females from each district were selected for morphological characterization. The study covered three districts (Bijapur, Belagaum and Dharawad).The parameters included feather morphology, feather distribution, plumage colour , primary plumage pattern, secondary plumage pattern , skin colour, shank colour, ear lobe colour, comb type and colour and eye colour as per NBAGR proforma . The most predominant feather type, plumage colour, skin colour, shank colour, comb type, ear lobe colour were normal feather (94.44 %), brown plumage (29.26%), yellow skin (95.45%), yellow shank (88.69 %), single comb(73.42 %) , brown eye colour (56.10 %) and red ear lobe (100%) in field conditions and in farm conditions it was normal feather (92.15%),brown plumage (34.44%), yellow skin (93.87%), yellow shank (87.37%), single comb (83.28%), brown eye colour (57.55%) and red ear lobe (100%) .The study revealed that most of the parameters measured revealed distinctive variations among the birds of three districts of Belagaum division, providing the basis for further characterization of indigenous chicken; therefore further study can be concentrated towards selection for qualitative traits of interest and conservation of these breeds for future poultry development.

ABST-1-066

PERFORMANCE EVALUATION OF INDIGENOUS CHICKEN OF BELAGAUM DIVISION OF KARNATAKA STATE, INDIA

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A study was undertaken to evaluate the indigenous chicken of Belagaum division of Karnataka State, India for performance and morphological characters pertaining to three districts namely; Bijapur, Belagaum and Dharawad, both under field conditions and under farm conditions. Survey was conducted in three districts and the data was recorded as per NBAGR proforma. The evaluation of birds under farm conditions revealed that, the bodyweight ofbirds belongingto Bijapurand Belagaum weresignificantly higher at all age groups compared to Dharawad district. Significant differences were noticed in hen housed egg production and in survivor's egg production up to 52 weeks of age. The birds of Bijapur district showed good survivability compared to other two districts. The birds of all the three districts under study showed very good ELISA titres against New Castle disease at all the stages of life.

ABST-1-067

STUDY ON INHERITANCE PATTERN OF DIFFERENT ECONOMIC TRAITS IN CROSSBRED CATTLE

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The present study was undertaken utilizing the records of 567 daughter progeny of 55 sires, distributed over a period of 30 years from 1990 to 2019 in crossbred cattle maintained at Instructional Dairy Farm of G.B Pant University of Agriculture and Technology, Pantnagar, Uttarakhand to study the inheritance pattern of different economic traits in crossbred cattle. The Least squares mean (LSM) along with their standard errors of age at first calving (AFC), first service period (FSP), first dry period (FDP), first lactation length (FLL), first calving interval (FCI), first lactation peak yield (FLPY), days to attend peak yield (DPY), first lactation milk yield (FLMY) and first lactation 305-day milk yield (FL305DMY) were observed as 1268.85 ±16.75 days, 267.51 ± 1.93 days, 91.56 ± 1.86 days, 369.41 ± 6.68 days, 465.80 ± 6.64 days, 13.88 ± 0.17 kg, 39.76 ± 0.78 days, 3294.64 ± 77.93 kg and 2570.74 ± 38.30 kg, respectively. Significant effects of sire were found on AFC, FLPY, DPY, FLMY and FL305DMY. Significant effect of period of calving was observed on AFC, FSP, DPY, FLMY, and FL305DMY while non-significant effect was found on FDP, FLL, and FCI. The effect of season of calving was found non-significant for all the first lactation traits under study. The heritability estimates for the traits under study AFC, FSP, FDP, FLL, FCI, FLPY, DPY, FLMY and FL305DMY were observed as 0.34 ± 0.21, 0.10 ± 0.1, 0.12 ± 0.11, 0.45 ± 0.16, 0.32 ± 0.17, 0.42 ± 0.22, 0.40 ± 0.20, 0.54±0.19 and 0.59±0.20, respectively. The genetic and phenotypic correlations between first lactation traits were found to vary from range low to high. The ranking of sires for estimated breeding values (EBV) was compared for all animals using Pearson's correlations or Spearman's rank order correlations. Spearman's rank correlations between sire estimated breeding values ranged between 0.05 and 0.78. The selection of the superior sires with maximum accuracy is important for any breed improvement programme.

ABST-1-068

EFFECT OF CLIMATIC PARAMETERS ON DOE PRODUCTIVE EFFICIENCY OF SANGAMNERI DOE UNDER FIELD CONDITIONS

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The research entitled "Effect of climatic parameters on doe productive efficiency of Sangamneri doe under

field conditions". The doe productive efficiency (DPE) on doe kidded basis in terms of total litter weight at birth (TLWB), total litter weight at weaning (TLWW), total litter weight at 6 months of age (TLWS), total litter weight at 12 months age (TLWY) were calculated as sum total of kids weight harvested at birth, weaning, 6 months age or 12 months age divided by number of does kidded. Data on DPE were classified according to year of kidding, season of kidding, the maximum temperature, the minimum temperature and THI to notice its effect during particular stage on doe productive efficiency of Sangamneri goat. The overall least squares means for doe productive efficiency in terms of total litter weight at birth (TLWB), total litter weight at weaning (TLWW), total litter weight at 6 months of age (TLWS) and total litter weight at 12 months age (TLWY) of Sangamneri goat was 2.9810.033 kg. 11.59+0.116 kg. 20.04+0.287 kg and 29.02-0.317 kg, respectively. Year of kidding significantly (P<0.01) affected the doe productive efficiency in terms of TLWB of Sangamneri goat. The season of kidding had non-significant effect on doe productive efficiency of Sangamneri goat. Rainy season showed higher doe productive efficiency than other seasons at each stage studied. The maximum temperature, minimum temperature and THI had non-significant effect on doe productive efficiency in terms of total kilograms of kids harvested by Sangamneri doe at all stages studied. This implies that Sangamneri goat is well acclimatized to adverse climatic conditions especially higher temperature.

ABST-1-069

SIRE EVALUATION STRATEGY TO COMBAT THE IMPACT OF HEAT STRESS ON FAT PERCENTAGE IN MEHSANA BUFFALOES UNDER FIELD PROGENY TESTING PROGRAMME

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The first lactation records of 7791Mehsana buffaloes sired by 182 sires on average fat percentage (AFP) spread over a period of 24 years (1989 to 2012), collected from Dudhsagar Research and Development Association (DURDA), Dudhsagar Dairy, Mehsana.Meteorological data of the region (where field progeny testing was undergoing), were collected from one of the center ofIMD, Pune to know the association of AFP with heat stress indicators. The mean along withheritability ofAFPwas estimated.Various heat stress models were screened foroptimization (Based on value of R2, adjusted R2, AIC and BIC) and effect of heat stress was quantified.Depending on the estimate of AFP and THI, year was classified in to various heat stress zones. Sires were evaluated (both by BLUP-SM and BLUP-AM) for AFPin different HSZ, in order to identify optimum sire for each of the zone. The least squares mean estimate for AFPwas7.13±0.01 %. The heritabilityestimates were obtained as0.14±0.02 (LSML),0.038±0.007(BLUP-SM) and 0.451±0.052(BLUP-AM). THI 6model (Yousef, 1985) was found to be the best suited model and it was observed that AFPwasincreased significantly (p<0.05) by 0.048% with per unit rise in THI. Year was classified in to NHSZ (non heat stress zone – November to March), HSZ (heat stress zone- April to October) and CHSZ (critical heat stress zone- June to August). The average breeding values of Mehsana buffalo bulls evaluated for AFP by BLUP-SM and BLUP-AM in NHSZ, HSZ and in CHSZ were estimated to be 7.1281, 7.1476and 7.1315% and 7.1267, 7.1379and 7.1263%, respectively. It was also indicated that the bulls having superior performance in NHSZ were not as superior in HSZ and CHSZ. This warrants that evaluation of bulls may be done separately in each heat stress zone.

ABST-1-070

EFFECT OF GENOTYPE AND ANATOMICAL REGION ON TICK DISTRIBUTION IN CATTLE OF DANTIWADA REGION OF BANASKANTHA, GUJARAT

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Tick infestation contributing significantlyin economic losses to cattle industry. The judicious use of acaricidesand selection of resistant animals can minimize the economic losses. This study aimed to determine the anatomical distribution of ticks in cattle in the Dantiwada region of Banaskantha district of Gujarat state. This study was

conducted by using a total 116 cattle (27 Kankrej and 89 Crossbred HF cattle). Tick counts were conducted at monthly interval under natural challenges over a 3 months period (Summer- May 2021 to July 2021). The whole cattle body was divided into three regions *viz.* Region-I (ear, head, neck, dewlap, and hump), Region-II (cranial limb, thorax, flank, abdomen, and naval), Region-III (rump, caudal limb, udder, crotch, and tail). Female ticks with greater than 4 mm size, present on the left side of the animal body were counted and then the number was multiplied by two to get the tick count of the whole body. The generalized linear model procedure of the R programme was used to analyse the data. Kankrej cattle (Mean tick count: 6.69) had significantly lower tick count then HF cross (Mean tick count: 18.03). The region-III (rump, caudal limb, udder, crotch, and tail) had the highest mean tick number ($p<0.01$) as compared to another`r region. The tick numbers of the R3 had showed strong correlation (0.965) with the total tick count.

ABST-1-071

PRIMODIAL GERM CELLS (PGC) CRYOPRESERVATION OF NATIVE CHICKEN BREED FOR BIOBANKING

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In chickens and other animals, primordial germ cells (PGCs) are precursors to the development of functional gametes, so they can be used as genetic resources to resurrect live chickens. Indian poultry breeds possess a large genetic diversity, but some are threatened by extinction. The conservation of these endangered breeds is extremely important for maintaining biodiversity and for mitigating the ever-increasing demand for animal proteins. Cryopreservation of primordial germ cells (PGCs) is a crucial technique in ex situ conservation of chicken breeds and lines. In this study, we collected PGCs from Ghagus native chicken embryos of HH stage 15 and standardized the protocol for culturing these cells on feeder cells derived from fibroblasts. We analysed the expression of marker genes such as VASA, SOX, Nanog, BLIMP etc. in PGCs and cryopreserved with 3%DMSO in liquid nitrogen for biobanking of the chicken breeds. Three months after cryopreservation, we checked PGC viability and gene expression. We observed 70% viability of PGCs after cryopreserving PGCs for three months. For repeatability, we repeated this experiment. The results were highly repeatable. It is concluded that the PGCs of Ghagus native chicken breed have been cryopreserved in liquid nitrogen for biobanking, which would be used further for resurrecting the breed during exigencies.

ABST-1-072

GENETIC CHARACTERIZATION FOR GROWTH TRAITS AND PERFORMANCE OF KUZI DUCKS BEING SELECTED FOR HIGHER EIGHT WEEK BODY WEIGHT

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A study was conducted to evaluate genetic parameters of growth traits of Kuzi ducks of Odisha, and its performance in respect to growth and production traits under intensive system of rearing. Sexual dimorphism was evident in these ducks at 5 weeks of age. The ducklings recorded more than 1 kg body weight at 6 weeks of age. The primary traits of selection 8-week body weight were 1474 and 1383 g, in male and female respectively. The heritability for the body weight were moderate to high in magnitude and the heritability estimates at 6 and 7 weeks of age were 0.44±0.14 and 0.45±0.14, respectively and the estimates for 8 weeks was 0.22±0.09. Genetic correlations between body weights were high in magnitude after initial 3 weeks of age. Growing period body weight revealed not much increase after 16 weeks of age. Multicolour plumage was dominant in the flock whereas brown and pink were found more in respect to bill and shank colour. The ducks reached 50 % hen housed egg production at 133 days of age. The egg production of the ducks up to 72 weeks of age was 251 eggs. The egg weight increases as the age advances and recorded more than 70 g from 36 weeks onwards. The results revealed that the Kuzi ducks can be subject for higher growth rate through selection; however, the egg production was quite encouraging indicating a suitable breeding strategy to be followed for this indigenous duck for its further improvement and commercial use.

TECHNICAL SESSION-II

Genomics: Phenotype variability and trait expression in animals

ISAGBCON 2022, ICAR-DPR, Hyderabad

XVI Annual Convention of Indian Society of Animal Genetics and Breeding

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ICAR-DPR, Hyderabad | December 2-3, 2022

ABST-2-001

IDENTIFYING FOOTPRINTS OF FRIESWAL USING DIFFERENT SUMMARY STATISTICS

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The Frieswal cow strain was developed in 1987 at the Project Directorate on Cattle (PDC), Meerut (U.P.), in partnership in conjunction with Military Dairy Farms (MDF), with about 5/8 exotic inheritance from the Holstein Friesian breed and the remaining from the Sahiwal cattle breed. The animals in this study (n=14) were genotyped using the Illumina Bovine SNP50 Bead Chip from Frieswal cattle. Other data from an online database were used in our study, includingGir (n = 24); Sahiwal (n = 17); Red Sindhi (n = 10); Kankrej (n = 10); Ongole (n = 20); Hariana (n = 10), Nellore (n = 24) and taurine cattle breeds like Holstein Friesian (n = 63); Jersey (n = 28); Ayrshire (n = 18); Guernsey (n = 21); Brown Swiss (n = 24). Additionally, we included laboratory data that was already produced during earlier trials. Those are Frieswal (n=14) and Vrindavani (n=72). We employed a total of nine summary statistics, including both intra-population statistics (Tajima's D, CLR, iHS, and ROH) and inter-population statistics (FST, FLK, XP-EHH, hapFLK, and Rsb). We found a total of 20, 11, 6, 15 overlapping genes using Tajima's D, CLR, iHS, ROH, and 10, 10, 6, 17, 19 overlapping genes using F_{ST}, FLK, hapFLK, Rsb, and XP-EHH, respectively, in the Frieswal cattle. The UGDH gene in Frieswal, which is related to milk fat percentage, the PMM2 gene related to conception rate, the LETM1 gene related to somatic cell score, the CHCHD7 gene controls age at puberty, the LYN gene has an effect on innate immune response, and the CLPB gene related to cellular response to heat are some significant candidate genes identified in Frieswal. This research adds to our understanding of the Frieswal cattle's selection footprints, but we need to validate the result in a larger sample.

ABST-2-002

IDENTIFYING FOOTPRINTS OF THARPARKAR USING DIFFERENT SUMMARY STATISTICS

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Tharparkar is a well-known dual-purpose indigenous breed, which is bred primarily for its milking abilities. They have unique characteristics and are widely renowned for their resistance to various diseases and heat tolerance among cattle breeds. In our research, we used 72 Tharparkar cattle, which have been generated from earlier research projects carried out in our lab. Other data from an online database were used in our study, includingGir (n = 24); Sahiwal (n = 17); Red Sindhi (n = 10); Kankrej (n = 10); Ongole (n = 20); Hariana (n = 10), Nellore (n = 24) and taurine cattle breeds like Holstein Friesian (n = 63); Jersey (n = 28); Ayrshire (n = 18); Guernsey (n = 21); Brown Swiss (n = 24). Additionally, we included laboratory data that was already produced during earlier trials. Those are Frieswal (n=14) and Vrindavani (n=72). We employed a total of nine summary statistics, including both intra-population statistics (Tajima's D, CLR, iHS, and ROH) and inter-population statistics (FST, FLK, XP-EHH, hapFLK, and Rsb). We found a total of 16, 21, 7, 1 overlapping genes using Tajima's D, CLR, iHS, ROH, and 15, 10, 6, 26, 47 overlapping genes using F_{ST}, FLK, hapFLK, Rsb, and XP-EHH, respectively in the Tharparkar cattle. A few significant candidate genes were revealed, including GCK, COA1, SLC16A7, TMCC3, KCNIP4, SEC14L1 and APBB2, which are connected to milk yield, milk calcium content, milk protein percentage, milk fat yield, somatic cell score, first service at conception, daughter pregnancy rate, age at puberty, inseminations per conception, and conception rate. Additional immune-related genes, such as CCR2, CCRL2, CCR5, SEC14L1, and CCR5, have been identified. This can aid in our perception of how locally bred cattle respond to adverse environmental conditions, inferior nutrition, endemic diseases, and challenging reproductive conditions.

ABST-2-003

INVESTIGATING SIGNALS OF POSITIVE SELECTION IN THE GENES INFLUENCING COAT COLOUR IN DIFFERENT INDIGENOUS CATTLE BREEDS

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The selective sweep events in the genes responsible for normal coat colour in Indian cattle groups are still mostly unknown. In order to find coat colour genes displaying potential signs of selective sweeps in the Indigenous cattle population, we performed a genome-wide scan of positive selection signatures using the BovineSNP50K Bead Chip in 187 individuals of seven indigenous breeds. We applied a wide range of methods to find evidence of selection, such as 1) tests to deviations from the Site Frequency Spectrum (SFS) from neutral (Tajima's D and CLR), 2) tests to find high-frequency haplotypes with extended linkage disequilibrium (iHS and varLD), 3) Test based on reduced local variability (ROH) and 4) tests based on genetic differentiation between populations (F_{ST}). We identified outlier-distributed pigmentation genes based on the empirical distribution for each statistic over all windows. In method-wise analysis, a total of 67,158, 92, 42, 37, and 32 regions were found in Tajima's D, CLR, F_{ST}, iHS, ROH, and varLD respectively. We found a total of sixteen genes that were involved in coat colour and pigmentation physiology such as *MC1R* in Sahiwal, *PMEL* and *POMC* in Tharparkar, *TYRP1, ERBB2,* and *ASIP* in Red Sindhi, *PAX3* and *TYR* in Ongole, and *SDR165* and *KIT* in Nelore. These genes are related to melanin synthesis, the biology of melanocytes and melanosomes, and the migration and survival of melanocytes during development. The majority of these genes had already been identified in prior genomic studies. However, to show the role of these genes in coat colour biology, different association, and functional studies would be required.

ABST-2-004

IDENTIFICATION OF PUTATIVE GENES AND PATHWAYS RESPONSIBLE FOR REGRESSION OF RIGHT OVARY DURING EMBRYONIC AND POST HATCH PERIOD IN CHICKEN

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In the present study, the transcriptome datasets (SRR4029458, SRR4029457, SRR4029464, SRR4029463, SRR4029460, SRR4029459) from NCBI were used to identify the putative genes responsible for regression of right ovary during Embryonic 6th day (E6), Embryonic 12th day (E12) and Post hatch Day 1 (D1) in chicken. HSD17B1 gene is involved in the synthesis of 11beta hydroxytestosterone and estradiol 17 beta. This gene was up-regulated (0.685248) in the early embryonic stage (E6 to E12), and then down-regulated (-5.58248) in the late embryonic stages (E12-D1) suggesting the regression of the right ovary. STEAP3 was down-regulated (-4.76293) in the E6 to E12, and then up-regulated (1.387534) in the E12 to D1. STEAP3 is involved in fenton reaction triggering feroptosis suggesting its role in the oxidative damage to the cell membrane which further leads to the cell death in the right ovary at the E6 to E12. NME7 is involved in phosphorylation of dADP to dATP, dGDP to dGTP, dIDP to dITP, ADP to ATP, GDP to GTP, IDP to ITP and vice versa. The NME7was up-regulated (7.082978) in the E6 to E12, and then down-regulated (-1.75833) in the E12 to D1 suggesting limited energy production leading to apoptosis of the cells. CALML3was down regulated (-4.57281) in the E6 to E12 than the E12 to D1 (-2.41755). Down-regulation of CALML3 during the embryonic stages leads to apoptosis of the cells and reduced gonadotropin secretion. In Early Embryonic Stages CALML3 is highly down-regulated

preventing the contraction of vascular smooth muscles, thereby enabling better blood circulation to the ovarian tissue than the later stages. PROCA1was up-regulated (4.013282) in the E6 to E12, and is then down-regulated (-3.83398) in the E12 to D1. In later embryonic stages down-regulation of PROCA1 leading to Ca+2 influx into vascular smooth muscle cells enhancing its contraction which may further prevent the blood supply to the ovarian tissue. The up regulation (4.902271) of MLKL during E6 to E12 resulted in dephosphorylation of DRPL leading to the mitochondrial fission and further necroptosis. This study identified the putative genes involved in the various pathways leading to the right ovary regression.

ABST-2-005

SCREENING OF GAOLAO CATTLE FOR BOVINE LEUKOCYTE ADHESION DEFICIENCY (BLAD)

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There are several established inherited disorders were reported in Holstein Friesian cattle and its crosses, considered as breed specific disorders. viz. FXI deficiency, BC , BLAD, CVM and DUMPS. BLAD is characterized by greatly reduced expression of the heterodimeric β2 integrin adhesion molecules on leukocytes resulting in multiple defects in leukocyte function. Defective leukocyte adherence leads to inadequate mucosal immunity. BLAD affected cattle have severe and recurrent mucosal infections such as pneumonia, gingivitis, periodontitis, loss of teeth, papillomatosis, dermatophytosis, impaired pus formation, delayed wound healing, and stunted growth . Most of the cattle with BLAD die without having the diagnosis established, probably before one year of age. Some cows survive for more than two years. The research was carried out with the genotyping of 50 Gaolao male from Bull mother farm, Hetikundi of Wardha and Pohara of Amravati District of Maharashtra State using PCR-RFLP. DNA extraction of all the samples was done by Phenol Chloroform Isoamyl Alcohol Method and the samples were subjected for PCR-RFLP. The amplified fragments for BLAD expected to present 357 bp with the annealing temperature of 64.5^{o}C for 45 seconds.The amplified PCR products upon digestion revealed two bands of 156 bp and 201 bp size however the carrier animals represent 156 bp, 201 bp and 357 bp and homozygous recessive represents 357 bp. The findings revealed that all the Gaolao males were found normal for BLAD.

ABST-2-006

GENETIC CHARACTERIZATION OF INDIGENOUS DUCK OF TRIPURA USING 25 MICROSATELLITE MARKERS

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Investigating genetic variation is important for genetic improvement, the preservation of native breeds, and the generation of high-quality progeny. Microsatellites are the marker of interest in polymorphism study for their high polymorphic nature and random dispersion throughout the genome. Lack of knowledge on microsatellite profile of Tripura's native duck has endorsed curiosity in the current study. A total thirty-six (36) blood samples of random bred indigenous duck were collected from different districts of Tripura. Genomic DNA samples were isolated and PCR was performed using primers for twenty-five (25) duck specific microsatellite (M.S) loci. Alleles were separated on 3.4% MetaPhore^{TM} agarose and molecular size of alleles approximated by Image Lab software. Genotypic data was analyzed through POPGENE version 1.31. All the studied loci demonstrated polymorphic patterns resolving 112 alleles. The number of alleles varied from two (2) to fifteen (15) at different polymorphic M.S loci with an average of 4.48±0.6586. Allele sizes and allele frequency per locus ranged from 96 to 357 bp and 0.0139 to 0.8194, respectively. Estimated polymorphic information content (PIC) was ranged from 0.2522 (CAUD020) to 0.911 (CAUD019) and sixteen loci were highly polymorphic (PIC>0.5) and informative. Averaged Nei's heterozygosity and Shannon's Information index (I) were 0.6169±0.03552 and 1.1836±0.1123, respectively. The mean observed (N_a) and effective number (N_e) of alleles was 4.48±0.6586

and 3.5384± 0.52746, respectively. N_e was less than N_a at most of the studied loci, indicating occurrence heterozygosity at these M.S loci. Chi-square and G-square test revealed that all studied 25 microsatellite loci were found Hardy-Weingberg disequilibrium in native duck of Tripura. All examined microsatellite loci had moderate to high levels of polymorphism, indicating that these markers might be useful for genetic characterization and the development of suitable conservation methods to fully use the genetic potentiality of Tripura's native duck.

ABST-2-007

GENOMIC SCANS FOR SIGNATURES OF SELECTION REVEALING PUTATIVE GENOMIC REGIONS AND CANDIDATE GENES FOR ADAPTATION AND PRODUCTION TRAITS IN CATTLE BREEDS OF TAMIL NADU

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Domestication and selection are the major driving forces responsible for genetic variability in livestock. These selection patterns create unique genetic signatures within the genome. Whole genome sequence data from 79 animals (Pooled into 15 samples from five cattle breeds of Tamil Nadu- Alambadi, Bargur, Kangayam, Pulikulam and Umblachery) were analyzed in the present study. Two approaches viz. CLR and FST, were utilized to detect selection signatures from the filtered 13,90,449 SNPs. A total of 7,250 and 806 genomic regions revealed 1,238 and 101 candidate genes identified by CLR and F_{ST} methods, respectively and are related to production, adaptation of indigenous breeds to tropical climatic conditions and disease resistance. Of the total selective sweep regions, six regions shared among all the five cattle breeds; of which, five regions were intergenic and one region had a candidate gene,*GALNTL6,* which is associated with susceptibility to bovine tuberculosis. A total of 12 candidate genes were identified by both CLR and FST methods (e.g., *GABRG1, GABRA4, USP46, RASL11B, SCFD2, FIP1L1, LNX1, FRYL, LOC109560438, GAS8, CBFA2T3* and *NNT*), mostly related to production, disease resistance traits and emotional and behavioural control of these cattle. NETWORK analysis revealed that six candidate genes were associated with calving ease (*JAK1* and *DOCK1*), milk fat yield (*ITGA1*), bovine respiratory disease susceptibility (*ITGA3* and *ITGAL*) and meat and carcass (*EPS15L1*) traits. The knowledge about signatures of selection and candidate genes affecting phenotypes have provided a background information that can be further utilized to understand the underlying mechanisms involved in these traits in cattle breeds of Tamil Nadu.

ABST-2-008

POLYMORPHISM AT THE 5'UTR REGION OF THE *ACACB* GENE AND ITS ASSOCIATION WITH BODY WEIGHTS AND HDL CONCENTRATION IN LAYER CHICKENS

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The present study was carried out to identify the polymorphism at the 5'UTR region of the Acetyl-CoA Carboxylase Beta (*ACACB*) gene and its association with body weights and High Density Lipoprotein (HDL) concentration in IWI and IWK lines of White Leghorn layer chicken. A total of 500 birds comprising of 250 IWI line and 250 IWK line were included in Single Stranded Conformation Polymorphism (SSCP) data analysis. Results reviled that in IWI lines within group there is a significant (P≤0.05) effect on body weights at 8th week and 16th week of age. Whereas In IWK lines within group there is a significant (P≤0.05) effect on body weights at day old and 20th week of age was observed. In general h8h8 showed the highest body weights was observed in both the lines. The association analysis of serum concentration of HDL in IWI line revealed that h12h12 haplogroup birds was the highest (61.64±2.99) and in the h1h2 haplogroup it was found to be the lowest (42.72±7.23). Incase of IWK, the h8h8 haplogroup birds were the highest (62.47±6.06) serum concentration of HDL and in the h7h7 haplogroup it was found to be the lowest (44.85±2.64) serum concentration of HDL. In IWI lines within group there is a non-significant (P≤0.05) effect on serum concentration of HDL. Where as in IWK lines within group there is a significant (P≤0.05) effect on serum concentration of HDL was observed. It is concluded that promotor of the *ACACB* gene is highly polymorphic and have a significant effect on body weights and serum concentration of HDL in White Leghorn layer chicken.

ABST-2-009

TAPASIN, TAP1 AND TAP2 GENE HAPLOGROUPS ASSOCIATION WITH IMMUNE TRAITS IN CHICKEN

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Immune response in animals is a highly coordinated and synchronized process that responds to the infection in a consecutive and coordinated way. Several genes including Tapasin and Transporter associated with antigen processing (TAP) plays a pivotal role in the immune surveillance of the avian species. In the present study the Brown Nicobari, Dahlem Red and Ghagus chicken breeds haplogroups were associated with the immune, serum and body weight parameters. The haplogroups having less than five birds were excluded for the association study. In Tapasin gene brown Nicobari Cytotoxic T cell, Hemagglutination inhibition titer (log2) and serum creatinine were significantly higher in h1h3 while monocytes was higher in h1h4 haplogroup. In TAP1 gene Brown Nicobari haplogroup h1h2 had significantly higher Hemagglutination inhibition titer (log2) and total serum protein while in haplogroup h1h9 day old chick weight was observed to be significantly higher. In Ghagus TAP2 Haplogroup h2h3 showed significantly higher serum cholesterol level while in Brown Nicobari the haplogroup h1h2 has significantly higher egg weight. The study revealed that the TAP1, TAP2 and Tapasin genes have important roles in chicken immune responses and serum parameters.

ABST-2-010

GENOME WIDE ASSOCIATION STUDY REVEALED SUGGESTIVE QTLS FOR PRODUCTION AND REPRODUCTION TRAITS IN INDIAN MURRAH BUFFALO

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The present study was aimed to identify the genome wide SNPs associated with production and reproduction traits in 96 Indian Murrah buffalo genotyped based on ddRAD approach using Genome Wide Association Study (GWAS) along with phenotypes of contemporary animals (born between 1996 and 2010) using Mixed linear model for production and reproduction traits. A total of 27,735 SNPs identified using ddRAD approach in 96 Indian Murrah buffaloes was used for GWAS. A total of 28 SNPs was found to be associated with production and reproductive traits. Among these, 14 SNPs were present in the intronic region of AK5, BACH2, DIRC2,

ECPAS, MPZL1, MYO16, QRFPR, RASGRF1, SLC9A4, TANC1 and TRIM67 genes and one SNP in long non-coding region of LOC102414911. Out of these 28 SNPs, 9 SNPs were found to have pleiotropic effect over milk production traits and were present in chromosome number BBU 1, 2, 4, 6, 9, 10, 12, 19 and 20. SNPs in the intronic region of AK5, TRIM67 genes were found to be associated with milk production traits. Eleven and five SNPs in the intergenic region were associated with milk production and reproduction traits respectively. The above genomic information may be used for selection of Murrah animals for genetic improvement.

ABST-2-011

CONGRUENT SELECTIVE SWEEP REGIONS ADDRESSED IN GIR AND THARPARKAR CATTLE

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Anthropogenic activities are posing threats to nature which is evident in the form of climate change. These climate changes may be seen as change in radiations, soil, water stress, temperature and increased infections. Thus, performance traits should be selected parallel to the environmental changes so as to incorporate plasticity and robustness, in order to further the biodiversity. Such trends in traits were seen by exploring the genetic architecture of Gir and Tharparkar cattle (n=7+7), maintained at LRC-NDRI, Karnal for common selective sweep regions. The samples were sequenced using ddRAD (Double Digest Restriction Associated DNA) approach. A total of 13.4 and 12.1 million reads passed the quality control, respectively. A total of 19,127 SNPs, passed the quality control. In all, 191 Selective sweep regions were found by CLR approach in Gir and Tharparkar in top 1 percentile of the empirical distribution. *ARHGEF4, MUM1, FSTL4, GCFC2, TMEM132C, GINS3* and *MAP4* genes were commonly found under selection in Gir and Tharparkar cattle by employing CLR approach. *ARHGEF4* is related to milk yield, *MUM1* is disease-related, *FSTL4* is reproduction-related, *GCFC2* is related to nervous system, *TMEM132C* is carcass-related, *GINS3* is DNA replication related and *MAP4* is mastitis-related. The study aims to decipher the thermos-excellence of the two breeds besides ecological challenges.

ABST-2-012

PRDM6 GENE INDEL VARIANTS WITHIN THE INTRON 1 REGION AND ITS EFFECTS ON BODY MEASUREMENT TRAITS IN NATIVE GOAT BREEDS OF KERALA

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A goat is generally considered a multipurpose animal that contributes to the economy and helps with food production in rural areas. Goat meat (chevon) is in high demand in India. Kerala is home to two goat breeds - Attappady Black, which is known for its disease resistance and Malabari, which is known for its prolificacy. In goat breeding programs, molecular markers are imperative for selecting growth traits. In goats, PR/SET Domain 6 (PRDM6) gene mutations were associated with bone development, bone density, and body mass index. Therefore, the gene serves as a conformational marker that is pleiotropic. The study identified a deletion of 12bp in the intron 1 region of the PRDM6 gene among 237 goats (110 Attappady Black and 127 Malabari). However, the association between 12bp indel variants and body conformation traits was examined. It was

found that body height, cannon circumference and cannon circumference index was significantly associated with the identified InDel($p \leq 0.05$). The frequency of deletion (D) allele was higher than the insertion (I) allele in both breeds. Also found that the identified 12bp deletion was deviate from Hardy-Weinberg equilibrium ($p < 0.05$) among those breeds due to absence of population stratification, non-random mating, and migration. A large proportion of inbreeding in the population of the native goat breeds was suggested by the expected heterozygosity considerably higher than the observed heterozygosity. The study on PIC revealed that the population under study had a low level of genetic diversity (0<PIC<0.25) in Attappady Black goat and medium level of genetic diversity in case of Malabari goat breeds (0.25<PIC<0.5). These findings show that the 12bp InDel within the goat PRDM6 gene plays an important role in the growth and development of goats and hence, based on thisInDel marker breeders can quickly and effectively select animals for body conformation traits.

ABST-2-013

REDUCED-REPRESENTATION SEQUENCING BASED ANALYSIS OF GENETIC DIVERSITY IN INDIAN CATTLE BREEDS

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Livestock diversity is shrinking rapidly among pure indigenous cattle breeds because of genetic dilution using a few selected exotic breeds. In livestock populations, approximately half of the genetic diversity is shared across breeds while the other half is observed within single breeds. A total of 8 cattle breeds (n=38) were taken in consideration in the current study. Alignment rates above 99.1% were obtained against reference sequences of ARS_UCD-1.2 were subjected to quality check. After bioinformatics analysis, 3,61,296 SNPs (RD=10) were processed for Biodiversity analysis. Genetic diversity analyses (F_{ST}, F_{IS}, number of polymorphic sites, observed and expected heterozygosity) among the breeds was carried out using population STACKS, from the set of SNPs. The pairwise F_{ST} value was found to be the highest between Holstein Friesan and Ongole cattle. The differences may be on the grounds of lineages and utility. Friesan cows have exotic inheritance and serve dairy utilities, while Ongole is indigenous and draught purpose breed. Minimum values were reported in between Gir and Tharparkar. This may be due to overlapping ecological niches and milch utilities of the two breeds. The F_{IS} was maximum in Tharparkar cattle (0.06). The average observed heterozygosity was higher than expected heterozygosity in all the breeds except Gir and Tharparkar where they were equal. This is indicative of high diversity with a hint of isolating breaking effect in the former. These studies can be undertaken in larger herds and larger number of breeds for validation.

ABST-2-014

IMMUNOINFORMATIC ANALYSIS OF OVALBUMIN GENE REVEALS POTENTIAL EPITOPES OF IMMUNOGLOBULINS AND MHC BINDING LIGANDS

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Ovalbumin is the most abundant protein in egg white which contributes up to 54%. It is a storage protein and major source of amino acids for the developing embryo. Sequencing of ovalbumin CDS from IWI and IWK lines of white leghorn chicken revealed that both the products were 1161bp in length. Comparison of obtained nucleotide sequence and deduced amino acid sequence with that of available sequences of reference genome confirmed that the sequence was of ovalbumin gene encoding a peptide of 386 amino acid sequence in both the cases. At 15th position T>C transition and at 237th position C>T transitional mutations were observed in both the lines. At 291st position, T>C transition and 562nd position G>A transitional mutations were observed

in IWI line. 562nd G>A transition had changed the amino acid alanine to threonine at 188th position in amino acid sequence, while other mutations did not change any of the amino acids. Based on the predicted structure of protein using coding sequence it is found that molecular weight of Ovalbumin protein from IWI and IWK lines were 42.91 KDa and 42.55 KDa respectively. Immunoinformatic analysis revealed potential epitopes for IgE, IgG and MHC binding ligands. The antigenic index also revealed the potential antigenic determinant candidates can be present in this genic region, which may bear association with consumer egg protein allergy. These results can be further validated through invitro and invivo before including in breeding for less allergic egg production.

ABST-2-015

IDENTIFYING FOOTPRINTS OF VRINDAVANI USING DIFFERENT SUMMARY STATISTICS

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Vrindavani is an Indian synthetic cattle breed that has been developed by crossing exotic dairy breeds with indigenous Indian cattle. According to various research, crossbred cows have various advantages, like better calving rate, calf survival rate, efficiency, longevity, and lifelong productivity. Therefore, in addition to native breeds, we should concentrate on crossbreds also. In our research, we used 72 Vrindavani cattle, which have been generated from earlier research projects carried out in our lab. Other data from an online database were used in our study, includingGir (n = 24); Sahiwal (n = 17); Red Sindhi (n = 10); Kankrej (n = 10); Ongole (n = 20); Hariana (n = 10), Nellore (n = 24) and taurine cattle breeds like Holstein Friesian (n = 63); Jersey (n = 28); Ayrshire (n = 18); Guernsey (n = 21); Brown Swiss (n = 24). Additionally, we included laboratory data that was already produced during earlier trials. Those are Frieswal (n=14) and Tharparkar (n=72). We employed a total of nine summary statistics, including both intra-population statistics (Tajima's D, CLR, iHS, and ROH) and inter-population statistics (FST, FLK, XP-EHH, hapFLK, and Rsb). We found a total of 3, 24, 4 overlapping genes using Tajima's D, CLR, iHS, and 21, 10, 6, and 33 overlapping genes using F_{ST}, FLK, hapFLK, and Rsb, respectively, in the Vrindavani cattle. Certain significant immune-related genes, such as CD28, GSDMB, and CTLA4, are linked to immunological response. Other significant genes, such as HSPB1, which stands for Heat Shock Protein Beta 1, have an effect on heat response. In our investigation, we identified several genes associated with production and reproduction in Vrindavani cattle, including COBLL1, RAB4A, ERBB2, CTNNA2, FTO, and RABGAP1 by using different summary statistics. Our study's findings can aid in the comprehension of the production, reproduction, and environmental adaption of Vrindavani cattle.

ABST-2-016

NOVEL VARIANTS IN 5'UTR REGION OF DAZL GENE SPECIFIC TO NARI SUWARNA SHEEP

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Prolificacy in sheep is the major economic trait which is polygenetic in inheritance. Several major genes such as BMPR-1B, BMP15 and GDF9 are extensively studied for their role in fecundity. Of the several genes *Deleted in azoospermia-like* (Dazl) is one which is said to have a role in determining the quality and quantity of the ovarian reserve which may have significant impact on reproductive outcome. The present study was undertaken to know the difference in nucleotide polymorphism in 5 prime UTR region of Dazl gene between Mandya breed of sheep (a non prolific sheep breed) and Narisuwarna sheep breed (prolific sheep breed). Polymorphism was studied in fifty unrelated sheep from each breed by PCR SSCP analysis followed by DNA sequencing of the samples exhibiting unique SSCP banding patterns. We could identify six polymorphism against 13 reported for the same region in Ensemble gene variants database. The proportion of three substitution variants ie., rs414492975 (A/T), rs409843899 (G/C) and one triple nucleotide insertion variant rs590749171 (-/GAG) was

not significantly different between two breeds. At rs415881546 (T/C), the frequency of allele T was significantly less in Mandya (0.31) compared to NariSuwarna (0.68). Two novel variants observed were specific to NariSuwarna breed ie., a substitution variant at nucleotide position 271715485 (A/G) with G allelic frequency of 0.26 and a deletion variant at 271715711(A/-) with 100% deletion in all Narisuwarna animals studied. The observation of variants unique to Narisuwarna breed warrants further study to elucidate its probable role in prolificacy traits.

ABST-2-017

PROTAMINE EXPRESSION AND FIELD FERTILITY IN HF BULLS

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Understanding the changes in the protamine expression, and field fertility during bull aging is indispensable for increasing the efficiency of artificial insemination. Therefore, the present study was undertaken to study the association of age with PRM1:PRM2 expression ratio and field fertility in nineteen Holstein Friesian bulls maintained at State Semen Collection Center(SSCC), Hesaraghatta, Bengaluru. The field fertility of bulls was evaluated under uniform field conditions at six different veterinary dispensaries. PRM1 and PRM2 expression levels by quantifying mRNA using real time PCR, Sperm DNA integrity by flow cytomerty and SNP's in protamine 1 by PCR and sequencing were recorded. The average PRM1 to PRM2 ratio and DNA Fragment Index% (DFI) observed in the HF bulls were 1 : 0.06 and 8.88 ± 0.22%, respectively. Expression of PRM1 was significantly lower in the younger (G-I) bulls and expression increased with age of the bulls however, PRM2 expression decreased with age. The PRM1 expression (r=0.569) and PRM1:PRM2 ratio (r=0.597) exhibited a significant positive correlation with the field fertility. On contrary, no significant correlation was observed between the PRM2 expression and fertility. Further, the Single Nucleotide Polymorphism (SNP) analysis of Protamine 1 gene revealed the presence of six different SNPs in the promoter region and no SNPs in the exonic and intronic region of Protamine 1 gene. A novel SNP in the TATA box TT > TG (TATATAA), which is 30 bp upstream from exon 1 was found related to lower expression of PRM1 gene and lower field fertility. These results provided new insights into the understanding the age-related changes in the PRM1 and PRM2 expression and its association with the field fertility.

ABST-2-018

ASSOCIATION OF GENETIC VARIANTS WITH REPRODUCTION TRAITS IN VRINDAVANI CATTLE USING BOVINE 50K BEADCHIP DATA AND GWAS METHODOLOGY

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The genetics of reproduction traits is poorly known since the heritability of this type of trait is reported to be low. To elucidate the genetics underlying reproduction in Vrindavani cattle, a total of 96 Vrindavani cattle were genotyped using the Illumina Bovine 50K BeadChip technique for revealing genome-wide association of SNPs with age at first calving (AFC), inter calving period (ICP), dry days (DD), and service period (SP) during the first three lactations. After quality control, 41,414 SNPs were filtered from total of 53,218 markers based on HWE, location on the X chromosome and call rate thresholds. The association study was performed using a linear regression model between phenotype and genotype data using PLINK program. A total of 06, 07, 09, and 17 SNPs were significant ($p<0.01$) associated with AFC, ICP, DD, and SP, respectively, which were located on different chromosomes. The QTL overlapping significant SNPs from each chromosome were annotated and

the nearby genes on each chromosome within 500 bp range on each side of the significant SNP were identified as affecting the reproductive parameters. These genes included: ITGB5 (first service conception), UMPS (fertility index), and UPK1B (insemination per conception). The present study provides important insights into the genetic variants associated with different reproduction traits which may be explored further for incorporation in the breeding program for Vrindavani cattle.

ABST-2-019

ASSOCIATION OF *SPEF2* AND *PLCZ1* POLYMORPHISMS WITH SPERM MOTILITY AND PLASMA MEMBRANE INTEGRITY IN BULLS OF ANDHRA PRADESH

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Bull fertility is a crucial component of increasing the herd's economic value because a single bull can artificially inseminate numerous cows. Semen quality traits, such as sperm motility, sperm concentration, sperm abnormalities, and plasma membrane integrity of semen, which were influenced by both genetic and non-genetic factors, were used to measure the bull's fertility. Using Chilibot and Connected paper web-based bioinformatic tools, the genes *SPEF2* and *PLCZ1* influencing the semen quality traits such as sperm motility and plasma membrane integrity of semen were discovered. In the current study, information from 239 bulls of various breeds living in FSBS of Andhra Pradesh was used. *HpyCH4*V and *Ava*II restriction enzymes were used for PCR-RFLP assay for *SPEF2* and *PLCZ1* genes respectively. The presence of the C allele was almost insignificant in the *SPEF2/HpyCH4*V assay for cattle, and fixation of the T allele was seen in both the exotic pure breeds (HF and Jersey). Heterozygotes were found to be prevalent in Murrah. In the *PLCZ1/Ava*II assay for Ongole cattle, the GG (0.64) genotype frequency was higher than the CG (0.22) genotype frequency. In the Murrah population, it was discovered that there was an excess of heterozygosity and low genetic diversity at this locus. In both cattle and buffaloes, the association of the *SPEF2/HpyCH4*V polymorphism had no significant impact on the pre- and post-thaw sperm motility. The plasma membrane integrity of the semen from Holstein Friesian, Jersey ($P<0.05$) and Ongole bulls ($P<0.01$) is significantly influenced by the *PLCZ1/Ava*II genotypes. In heterozygotes (CG) of Jersey and Ongole cattle, the plasma membrane integrity of the semen was reported to be high. Genotypes in Murrah have no significant influence on the semen's plasma membrane integrity. The results of the current study highlight the significance of the *PLCZ1* gene as a marker for selection of bulls for high semen quality and fertility.

ABST-2-020

EXPRESSION PROFILE OF HOXA10 IN INDIGENOUS GOAT BREEDS IN KERALA

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Homeobox (Hox) genes all encode a conserved homeodomain and were first discovered in Drosophila melanogaster, where they function as transcription factors in the control of embryonic morphogenesis. It comprises of 16 members with *HOXA10* gene being one of the most important. Homeobox A10 (HOXA10), a member of Hoxa gene family, is necessary for the endometrial receptivity and embryo implantation through activation and repression of various downstream targets. Hoxa10 has been reported to be expressed in uterine muscle, stromal and epithelial cells with increased expression observed during luteal phase and peaking at the time of implantation. Tissue samples of the ovary and uterus were collected from six Malabari and six Attappady Black goats. From these samples 100mg of tissue were used for RNA isolation following which

cDNA was synthesized. Using Quantitative Real Time Polymerase chain reaction, and with GAPDH as the reference gene the values for ΔCt, ΔΔCt and 2-ΔΔCt were calculated. It was found that the ovary of Attappady Black goat had 0.8 fold expression compared to Malabari goat breed and the uterus of Attappady Black had a 2.81 fold expression over Malabari goat. No significant difference was observed in the expression levels of HOXA10 in the ovary and the uterus of both the breeds ($p>0.05$). Keeping the uterus as a control it was observed that the ovary had a 0.12 fold expression. Significant difference was observed in the expression of *HOXA10* gene between uterus and ovary.

ABST-2-021

GENOME WIDE DNA METHYLATION: FUNCTIONAL PERSPECTIVE

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Epigenetics refers to stable heritable traits not explained by changes in DNA sequence of gene. DNA methylation is a major epigenetic modification involved in regulating gene expression which differs by genomic location and vary across species and environmental conditions. As the most stable epigenetic modification, DNA methylation can be a promising marker in animal breeding and it is the chemical modification of the cytosine base through the addition of methyl group at carbon fifth position and plays an important role in tissue differentiation and normal developmental processes like gene expression, genomic imprinting, X-chromosome inactivation and gametogenesis. These modifications mostly occur at CpG sites with a high frequency in genomic regions called CpG islands (CGIs). DNA methylation hinders the binding of transcription factors causing repressed transcription. There are several methods for validating DNA methylation pattern out of which Bisulphite conversion is considered as gold standard. Whole-genome bisulfite sequencing (WGBS) enables genome-wide analyses of cytosine methylation at single-nucleotide resolution while Reduced representation bisulphite sequencing (RRBS) uses specific restriction enzymes to enrich for CpGs**.** DNA methylation is consistent across cell generations for the lifetime of the animal and can be trans-generationally passed from parent to offspring. Significance of DNA methylation is evident from the fact that knowngenetic factors alone often do not account for the total heritability of many traits from parent to offspring. With the appearance of the first GWAS on domestic animals, many genetic variants associated with various complex traits, disease susceptibility and resistance were identified, the level of DNA methylation on each locus can be regarded as a quantitative trait but prior to determining the quantitative impact of DNA methylation on genetic variation, the distribution of DNA methylation must be established in tissues relevant to economically important traits. With the reduced cost of sequencing and the recent concerted effort of the FAANG and FarmGTEx projects to explain genome and epigenome in farm animals, the number of discovered epigenome QTLs will increase. The accurate molecular mechanisms of complex traits can be well elucidated through this epigenetic information and domesticated animal selection that involves DNA methylation may occur in the future.

ABST-2-022

LUTEINIZING HORMONE RECEPTOR (*LHR*) GENE POLYMORPHISM IN BUFFALOES USING PCR-RFLP METHOD

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The productivity of buffaloes is commonly affected due to many inherent disorders. Luteinizing hormone (LH) is a glycoprotein hormone of pituitary origin that regulates gonadal function, including steroidogenesis as well as

gametogenesis. LH is responsible for follicular wall rupture, ovulation and stimulates corpus luteum to produce progesterone in females. The aim of this study was to explore the Luteinizing hormone receptor (*LHR*) gene polymorphism in 203 Murrah / Graded Murrah buffaloes. Polymerase Chain Reaction - Restriction Fragment Length Polymorphism (PCR-RFLP) method was used to identify the polymorphism. A 303 bp fragment of exon 11 of *LHR* gene was amplified using specificforward and reverse primers were 5'- CAA ACT GAC AGT CCC CCG CTT T -3 and 5'- CCT CCG AGC ATG ACT GGA ATG GC -3' respectively. The restriction digestion was carried out with *Hha*I restriction enzyme at 37°C for overnight. In the present study, all the tested animals were found monomorphic for *LHR* / *Hha*I gene at 303 bp and genotyped as *TT*, which indicates the fixation of *T* allele and absence of *C* allele. Consequently, we could not perform association studies with reproductive traits.

ABST-2-023

MICROSATELLITE VARIANT ASSOCIATION WITH TRAITS RELATED TO MILK PRODUCTION IN MURRAH BUFFALOES

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Microsatellites markers are highly conserved in related species like cattle and buffaloes. The present study was undertaken to evaluate the association of microsatellite variants with milk production traits such as total lactation milk yield, 305-day milk yield, peak yield, lactation length and dry period of the second lactation in Murrah buffaloes. A total of 17 microsatellites viz. BMS713, BM6404, BM4513, BM121, BM6105, TGLA245, BL1100, BMS1948, BMS711, BM1443, BM1706, BM6438, BM143, BM415, ETH131, ETH2, and BM1329 were chosen for the study. Among them, nine were chosen based on the published literature and eight were selected from the cattle QTL database, and were amplified in 109 Murrah buffaloes. Molecular techniques such as PCR amplification and MetaPhor agarose gel electrophoresis were employed for the study following DNA isolation from blood. TGLA245 was found to be a monomorphic locus and all other loci were polymorphic. None of the microsatellites were found to be in Hardy-Weinberg equilibrium. Considering the polymorphic loci, the average polymorphism information content (PIC) value was 0.60±0.04, observed number of alleles (N_a) and effective number of alleles (N_e) were in the range of 3-6 and 1.10-4.68, respectively. The average observed (Ho) and expected (He) heterozogosities were found to be 0.34 ± 0.05 and 0.66 ± 0.03, respectively. Microsatellite loci BM1706 and ETH2 were found have a significant association with total lactation milk yield. Loci BL1100 and BMS711 exhibited significant association with peak yield. A significant association was observed between loci BM6438, ETH131, BM1443, BM415 and dry period. The remaining eight polymorphic microsatellite loci did not exhibit a significant association with any of the traits considered. The microsatellites with significant associations with milk production traits may be further evaluated and validated in large number of animals for their utilization as genetic markers.

ABST-2-024

RELATIVE EXPRESSION OF KITLG GENE IN MALABARI AND ATTAPPADY BLACK GOAT BREEDS

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KIT ligand (KITLG), also known as stem cell factor and mast cell growth factor is encoded by the *KITLG* gene and functions by triggering its receptor tyrosine kinase. This gene participates in the survival and proliferation of granulosa cells, in the recruitment of theca cells from ovary stroma and in the regulation of ovarian steroidogenesis. KITLG can be expressed as either a membrane-bound (KL-1) or a soluble protein

(KL-2) depending on the mRNA processing after transcription. In goats, the protein and mRNA for KITLG are expressed in granulosa cells during all stages of follicular development, and the KITLG system may play an important role in various processes including folliculogenesis and luteal activity. The present study was undertaken to compare the relative expression of KITLG gene in tissues of ovary and uterus of Attappady Black and Malabari goat breeds. Tissue samples were collected from the animals slaughtered at the Meat technology plant, Mannuthy. From these tissue samples, RNA was isolated and converted to cDNA using the Takara primescript 1st strand cDNA synthesis kit. Quantitative Real Time Polymerase Chain Reaction was carried out to find out the expression levels of *KITLG* gene in ovary and uterus. *GAPDH* was selected as the reference gene. For breed wise comparison Malabari breed was selected as the control. The expression of KITLG in the uterus of Attappady Black goats had a 2.70 fold increase over the uterus of Malabari goat breed. It was found that the ovary of Attappady Black had a 0.84 fold decrease of KITLG expression compared to the ovary of Malabari goat breed. Tissue wise comparison found higher expression of *KITLG* gene in the uterus compared to the ovary. Using t test no significant difference was observed between tissues. No significant difference was observed between the expression levels of the ovary and the uterus of both breeds ($p>0.05$).

ABST-2-025

SSCP POLYMORPHISM OF *HSP90AB1* GENE IN SAHIWAL AND CROSSBRED COWS

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The present study was aimed to study the genetic polymorphism in a 387 bp fragment of *HSP90AB1* gene through Polymerase Chain Reaction-Single-stranded conformation polymorphism (PCR-SSCP) technique. Genomic DNA of the experimental animals was isolated by phenol-chloroform extraction method and used for PCR after evaluating the quality and quantity. A 387 bp fragment of *HSP90AB1* gene was amplified and the amplified segment was subjected to Single-stranded conformation polymorphism (PCR-SSCP) technique to detect the polymorphism. The fragment was found to be polymorphic in both Sahiwal and crossbred cows. Four different SSCP patterns (AA, AB, AC, and BC) corresponding to three allelic variants (A, B, and C) were found in both the genetic groups studied. The frequencies of the alleles A, B and C were 0.78, 0.14 and 0.08 in Sahiwal and 0.59, 0.23 and 0.18 in crossbred cows, respectively.PCR-SSCP patterns were correlated with the physiological, productive, and reproductive traits. The association analysis of SSCP patterns revealed that cows with genotype BC had a longer calving interval in Sahiwal while BC genotype had higher total lactation milk yield and AA genotype had a lower age at first service in crossbred cows.

ABST-2-026

STUDY ON GENETIC VARIABILITY OF GROWTH AND REPRODUCTIVE TRAITS OF POLLED DORSET AND IT CROSSES UNDER TEMPERATE CLIMATIC CONDITIONS OF J &K.

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The present study was conducted to evaluate the performance of Polled Dorset Sheep and its Cross with Corriedale and local sheep using both quantitative and molecular genetics under farm flock system at Mountain Research Centre for Sheep and Goat (MRCSG), Shuhama.The results obtained were useful in formulating the future breeding policy for sheep development in farm system and for the local farmers.The data spread over a period of 18 years from (1999-2017) which was obtained from records maintained at sheep breeding farm (MRCSG). The growth traits studied were Birth weight (BW), Weaning Weight (WW), Six months body weight (6MW) and Yearling body weight (YW) and reproduction traits Such as Age at first lambing (AFL) and Inter lambing period (ILP) were included in present investigation. The molecular part of investigation pertains to the

study of polymorphism of three important candidate growth genes viz:*Growth hormone*, *Leptin* and *Calpastatin* gene with body weights such as Birth weight, Weaning weight, Six Months Weight and 12 months weight.The aim was to estimate the genetic parameters for growth and reproduction traits and also aimed at identifying the best genotypes, for three candidate growth genes viz., Calpastatin, Leptin and growth hormone gene in the two genetic groups . The mean, standard errors and coefficient of variations (CV) of all growth and reproduction traits were computed statistically. The effects of non-genetic factors such as period and gender on various normalized growth and reproduction traits were analyzed by least squares analysis using the technique developed by Harvey (1990). The overall means for BW, WW, 6MW and 12MW were found to be 3.49 ±0.04 kg, 12.63±0.28kg, 17.94 ± 0.28 kg, and 23.47±0.22 kg respectively. Age at first lambing (AFL) and Interlambing period (ILP) were found to be 731.75±29.83 days and 366.50±8.58 days respectively. Period of birth was found to have highly significant effect (P<0.01) on body weights except Birth Weight, Age at first lambing (AFL) and Interlambing period (ILP) under study. The effect of gender was found highly significant (p<0.01) on the Birth Weight (BW), Weaning Weight (WW), Six months body Weight (6-MW) and 12 months Weight (12-MW). Least square mean analysis revealed that males were heavier as compared to females in all the periods. Effect of breed was non-significant on the Birth Weight (BW), Weaning Weight (WW), Six months body Weight (6-MW), 12 months Weight (12-MWT), Age at first lambing (AFL) and Interlambing Period (IP).Moderate to high heritability estimates were observed for growth traits indicated moderate to high genetic variability. six months body weight was observed to be positively correlated with yearling body weight. Thus, selection for higher body weight at six months age will also improve yearling body weight as correlated response.The three candidate growth genes, viz; Calpastatin, growth hormone and Leptin gene were screened for polymorphisms using PCR-RFLP and SSCP technique.The associations of candidate genes with body weights revealed that MN genotypes of Calpastatin gene showed higher average body weights than MM in both Polled Dorset sheep and its Cross. The association of genotypes AA, AB, BB in Leptin gene were found to be non-significant (p >0.05) on all body weight in Polled Dorset Cross. The sheep population harbor a considerable amount of genetic variation with respect to gene polymorphism. Calpastatin and leptin gene stand strong candidate genes for selection of the lambs soon after birth for pre-defined breeding objectives, thereby reducing the generation interval and increasing the genetic gain.

ABST-2-027

THE STUDY ON GENETIC VARIABILITY AND BOTTLENECK ANALYSIS OF LOCAL BUFFALO POPULATION OF JABALPUR, MANDLA, DINDORI AND SEONI DISTRICTS AT MAHAKAUSHAL REGION OF MADHYA PRADESH

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The target districts of present study were Jabalpur, Mandla, Dindori and Seoni districts of Madhya Pradesh. The Mahakaushal region of Madhya Pradesh comprise all four districts. This part is found in central India. The local buffalo population is distributed in all four districts and adjoining parts of the other districts. This present study was the first attempt for genetic characterization and to explore genetic variability using STR markers. A total number of 48 unrelated buffaloes from the all four targeted district (native tract) were genotyped using 25 heterologous microsatellite markers. The Each microsatellite marker's was labeled with one of the fluorescent dyes to measure the fragment length of genotyped PCR product with automated DNA sequencer. All the heterologous markers were polymorphic and a total of 389 alleles were detected across 25 loci. All the microsatellite loci amplified successfully and adequately high allelic diversity (observed: 15.56 ± 0.777 and effected: 6.92 ± 0.647) was reported. Sufficient Shannon index and PIC indicated the suitability of markers to evaluate genetic diversity in buffalo population. The observed and expected heterozygosity values ranged from 0.167 (CSRM60) to 0.896 (ILSTS052) and from 0.507 (ILSTS019) to 0.941 (ILSTS052) with an overall mean of 0.659 ± 0.039 and 0.829 ± 0.018, respectively. The F-statistics varied from -0.099 (CSSM66) to 0.803 (CSRM60) with an overall mean of 0.207 ± 0.042. The overall conclusion of different tests (Sign, standardized difference test, Wilcoxon rank test and mode shift indication test) were that the buffalo population is not in

genetic bottleneck condition. The current findings will undoubtedly aid in the development of breeding plans for genetic improvement as well as conservation strategies for the buffalo population at Mahakaushal region of Madhya Pradesh.

ABST-2-028

BETA-CASEIN GENE POLYMORPHISM IN CROSSBRED CATTLE AT FARMERS HERD OF TAMIL NADU

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Milk is an important main source of nutrients containing proteins, carbohydrates, vitamins and minerals. In the recent decades have we much heard about the popularity of A2 milk, which is believed to have more nutritious with no health hazards than A1 milk. About 25-30 per cent casein in the milk is beta-casein-the protein that differentiates A1 from A2 milk. Due to point mutation in beta-casein gene, proline (A2 β-casein) converted into histidine (A1 β-casein) at 67th position of the resultant amino acid chain in 6th chromosome. The present study was conducted in 43 crossbred cattle of Tamil Nadu to analyse the frequency of the *A1* and *A2* allele. Phenol-chloroform method was performed to extract the genomic DNA. The mean yield of DNA isolated was 439.56 ng / µl. Polymerase Chain Reaction (PCR) was performed with allele specific primers to amplify a 244 bp long fragment of beta-casein gene and visualized in 2% agarose gel electrophoresis. The population genetic indices were calculated based on the formulas. The allelic frequency of *A1* and *A2* was 0.69 and 0.31 for jersey crossbred and 0.64 and 0.36 for HF crossbred cattle at farmer's herd. The observed frequency of *A1A1*, *A1A2* and *A2A2* genotypes were 0.38, 0.62 and 0.00 for jersey crossbred and 0.29, 0.71 and 0.00 for HF crossbred cattle. Heterozygotes were higher in number than homozygotes in Jersey and HF crossbred as expected. All the studied population was under Hardy Weinberg equilibrium which was confirmed using chi-square test ($p>0.5$). Expected and observed heterozygosity was highest in HF crossbred and lowest in Jersey crossbred cattle. The range of Expected homozygosity (0.54 to 0.57), polymorphism information content (0.34 to 0.35), effective number of alleles (1.75 to 1.85) and level of possible variability realization value (44.54% to 49.54%) noticed in studied population. In the present study revealed, *A1A1* and *A1A2* genotype alone noticed in crossbred cattle and not a single animal had *A2A2* genotype.

ABST-2-029

STUDY THE POLYMORPHISM OF FSHR GENE IN SAHIWAL CATTLE

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Follicle Stimulation Hormone Receptor (FSHR) is a gene that has function to regulate reproduction performance by controlling oogenesis in females and also spermatogenesis in male. Therefore, it's become a logical reason to use FSHR genes as part of selection criteria. The PCR - RFLP technique proved successful in identifying genetic polymorphism in population, which will be useful for selecting animals with desired genotype for better reproduction & production.In cattle, this gene has been mapped to exon 10 of chromosomes 11. The study was conducted on 60 lactating cows to identify the allelic variants of FSHR and to determine its frequency. The genomic DNA was extracted by HiElute Miniprep Spin column method and PCR was carried out with specific primers and 306 bp fragments was obtained under optimized PCR condition. The ampilcons were digested with *Alu*I restriction enzyme and kept at 37 ^{0}C for overnight and resultant fragments were resolved on 8 % PAGE. Based on the restriction pattern thus, three genotype and two alleles were detected with *Alu*I (CC, CG, GG; C and G). The genotype and allelic frequency with *Alu* I were calculated as 0.15, 0.57 and 0.28 for CC, CG

and GG genotypes and 0.43, 0.57 for C and G alleles, respectively. The reported frequency of C and G allele in exotic breeds are 0.449 and 0.551 respectively. So, this shows that variations exit between indigenous and exotic breeds, which warrants for further investigation.

ABST-2-030

GENOMIC DIVERGENCE IN HIGH AND LOW MILK YIELDING CATTLE BREED GROUPS FROM WHOLE GENOME SEQUENCING DATA

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Genome-wide association studies (GWAS) seek variations in the allele frequency of genetic variants amongst individuals with a common ancestor. However, they have different phenotypes to uncover connections between genotypes with phenotypes. This study aimed to identify genomic regions, genes, and pathways associated with the indigenous dairy cattle population. In this study, 114 cows (3 high milk yield groups (n=60) and 27 low milk yield groups (n=54)) were divided into two groups depending on the milk production. Through variant analysis using Freebayes and GATK on whole genome sequencing, over 6176954 SNPs were identified. Through initially stringent filtering in PLINK and further use of TRES, 628 candidate SNPs that discriminate the high and low milk yield groups were identified. GWAS was performed using a mixed linear regression analysis with PCA correlation in Golden Helix SNP & Variation Suite (SVS). Sixty-four SNPs on 19 chromosomes were found significantly associated with a cut off of 0.3 Fst. Some SNPs were located within or near known QTLs for milk production traits. The relationship between associated SNPs with neighbouring genes was investigated. These potential markers identified in the study can be helpful in the genetic improvement of milk production traits in indigenous cattle.

ABST-2-031

BIOLOGICAL VALIDATION OF BUBALINE AND OVINE ACE2 GENES FOR PREDICTION OF SUSCEPTIBILITY TO SARS-COV-2 AND IDENTIFICATION OF A NOVEL ACE2 VARIANT IN SHEEP

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Angiotensin converting enzyme 2 (ACE2), is the major receptor for SARS-CoV-2 virus hence the susceptibility of a species to SARS-CoV-2 can be predicted based on the sequence of the ACE2 expressed by the species. ACE2 gene of Buffalo and Sheep was sequenced and analysed to predict their susceptibility to SARS CoV-2. A set of 12 pairs of tiling primers were designed covering the complete ACE2 gene in Buffalo and Sheep. One step RT-PCR followed by gel electrophoresis revealed that ACE2 gene is expressed in the liver, lungs, kidney and testis of buffalo and liver, lungs and kidney of sheep. Amplicons from liver tissue were sequenced as a multiplex barcoded library on MinION. The data were analyzed by ont-guppy, minimap2, samtools, IGV to obtain ACE-2 gene consensus nucleotide sequence from buffalo and sheep. Variant X1 and X2in buffalo and X1, X2 and X3 in sheep were identified as predicted from their whole genome sequences. A novel X4 variant with 52 bp insert in the 3'UTR was identified in the present study. Phylogenic analysis reveals that ACE2 gene sequences of Buffalo and sheep are clustering with the predicted sequence of respective species. The structures of ACE-2 of Buffalo and Sheep were predicted by using SWISS-MODEL Homology Modelling. The interactivity between ACE2 Buffalo and Sheep variants and RBD-spike from Human coronavirus is determined using pyDockWeb webserver. Further susceptibility of these species to COVID-19 was assessed using RShinyApps application and Molecular Docking techniques based on the obtained sequences through sequence analysis. The score for sheep and buffalo ranged between 17 and 19. Based on this it can be predicted that these species are intermittently susceptible to SARS CoV2.

ABST-2-032

GENETIC DIVERSITY STATUS OF MALNAD GIDDA CATTLE BREED AND VALIDATION OF MICROSATELLITE MARKERS FOR PARENTAGE VERIFICATION

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Malnad Gidda cattle breed native of the Karnataka and is predominantly found in the Malnad area of Karnataka in the Western Ghats region. DNA isolated from twenty-seven samples collected from a closed herd maintained at the MalnadGidda Research and Information Centre at Veterinary College Shivamogga were screened using ISAG recommended microsatellite markers. The data obtained was analyzed using POPGENE software. The results indicated the heterozygous nature of the MalnadGidda herd. BMS-2847 and BM-6117 showed the highest number of 8 alleles each, BMS-518, BMS-1716, BMS-462 and BMS-922 marker showed 6 alleles each, BMS-511, SPS 115, RM-6, TGLA-227, BM-6548 and BMS-356 revealed 7 alleles each, MB-085 also had five alleles with a unique allele. A total of 68 alleles were identified in this study using 13 microsatellite markers and lesser allele number was reported in BMS 356 which seems to have been fixed in the herd. The number of alleles ranged from 1 (BMS 356) to 9 (BMS-2847) with a mean of 5.2308±2.0475alleles. The allele sizes ranged from 74 bp (BMS-922) to 262 bp (SPS-115). The percentage of polymorphic loci is 92.31%. The observed heterozygosity (Ho) of 13 markers ranged from 0.607 (TGLA53) to 0.904 (BM2113) while the expected heterozygosity (He) ranged from 0.581 (ETH225) to 0.873 (INRA23). Eleven out of 13 microsatellite loci revealed relatively high polymorphic information content (>0.6). The average PIC value was 0.6131$\pm$0.1893, average number of alleles and expected number of alleles were 5.3077$\pm$2.0569 and 2.9678 $\pm$0.9704 respectively. The observed and expected heterozygosity were 0.4231$\pm$0.2465 and 0.3773$\pm$0.2025 respectively. The F_{IS} was 0.054867$\pm$0.26168 and Shannon Index was 1.2017$\pm$0.4298. 11 dams and 2 sires' samples were matched for a total of 17 calves born to different Dam X Sire combinations. Out of these 17 (Dam X Sire) combination parentage was identified for 82.35 % (14 No.s) of the offspring and rest (3 No.s) could have been from unknown sire source. Based on the parentage testing it was identified that Six animals were sired by Bull number 11, Five animals were sired by bull number 12, remaining animals were born to earlier sire's that were removed from the herd. Hence this study gave an idea about the genetic diversity status of the herd and use of appropriate markers for parentage verification.

ABST-2-033

GENETIC IDENTITY AND DISTANCE BETWEEN CARPET WOOL BREED OF SHEEP IN TAMIL NADU

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Tiruchy Black and Coimbatore are the carpet wool breed of sheep in Tamil Nadu. Genetic differentiation or fixation indices F_{IS} and F_{ST} and genetic distance were assessed through the 25 recommended different microsatellite loci by FAO for both Tiruchy Black and Coimbatore sheep. The estimation of F_{IS} values for different markers revealed both positive and negative values. In Tiruchy Black sheep, negative F_{IS} values were observed in M1329, BM6506, CSSM31, ILSTO33, MAF65, OarFCB48, and OarFCB304 and SRCRS9 loci alone and all other markers showed positive values. In Coimbatore sheep, out of 25 microsatellite markers only BM6506 loci showed negative F_{IS} value. Comparatively Coimbatore sheep had more number of positive F_{IS} value than Tiruchy Black sheep. Genetic differentiation or fixation indices F_{IS} and F_{ST} values ranged from 0.0104 (BM8125) and 0.1417 (Oar FCB 20) with an average of 0.0624. The genetic identity and distance between Tiruchy Black and Coimbatore were 0.4727. and 0.6233 respectively. The cluster analysis showed in Tiruchy Black and Coimbatore breeds were formed from different clusters.

ABST-2-034

MOLECULAR CHARACTERIZATION OF THE PROMOTER REGION AND IN-SILICO TF BINDING SITES PREDICTION IN THE SPERM CELLS CHROMATIN REMODELING GENES OF MURRAH BULLS

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During spermatogenesis, the nucleus of a male's sperm undergoes major changes, including chromatin structural rearrangement. Tight packaging of DNA is essential for avoiding the DNA fragmentation caused by ROS. The replacement of histones by protamines provides a more compact packing of genomic material in sperm nuclei. Spermatozoa of Murrah buffalo bulls were classified as seasonally affected and non-affected by heat stress based on the semen quality parameters and characterization of the promoter regions of Protamines (*PRM1* and *PRM2*) and Transition nuclear proteins (*TNP1*, and *TNP2*) genes carried out. The current study sought to better understand the expression profiles of candidate genes involved in chromatin remodelling by promoter region sequence analysis of the target genes. The putative transcription factor (TF) binding sites for the promoter regions were analysed using a matrix search for TF binding sites and AliBaba2.1. The TF binding sites varied between the species in the promoter region. In buffalo, TFs such as CRE-BP1 (64G<T), SP1 (224C<A), C/EBP (62G<T) were located in the variable sites of the promoter. The *PRM1*, *PRM2*, *TNP1*, and *TNP2* promoter regions carried intraspecies variations of 5, 10, 13, and 2, respectively. The occurrence of transcription factor binding sites in the *PRM1* promoter region (305 nt region, -114 to -419) of the *Bubalusbubalis* consensus sequence and *Bos taurus*suggested a total of 32 and 39 putative TF binding sites, respectively. The TF binding site for GLI3 was found only in *Bubalusbubalis* and not in *Bos taurus.* In the *PRM2* promoter region (521 nt, -1 to -521), there were 32 and 39 putative TFs binding sites, predicted in *Bos taurus* and *Bubalusbubalis*, respectively. The GLI3 is regulated in response to the sonic hedgehog (Shh) signalling pathway, which is crucial for sperm motility. Furthermore, binding sites for TFs like AP-1 and C/EBP alpha were found only in the *Bubalusbubalis* promoter region and not in *Bos taurus*. These TFs might be playing an important role in species-specific regulation of PRMs and TNPs expression and could affect the tight packing of DNA at various levels. Correlation of variation with gene expression might confirm the role of TF sites with genetic variation identified in the study.

ABST-2-035

IDENTIFICATION AND CHARACTERIZATION OF DIFFERENTIALLY EXPRESSED MICRORNAS IN MILK EXOSOMES IN HEALTHY AND SUB-CLINICAL MASTITIC CROSSBRED CATTLE

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Exosomes are extracellular vesicles secreted by the bovine epithelial cells which plays empirical role in intercellular communication. Selectively wrapped microRNAs are protected in these milk exosomes and may reflect as biomarker for different patho-physiological states of the cells. Bovine mastitis, one of the most widely known inflammatory diseases in high-yielding dairy cows, has resulted in significant economic losses for the dairy industry. As a necessary consequence, the study aimed to investigate the identification and differential expression of miRNAs in milk derived-exosomes from sub-clinical mastitis and healthy crossbred cattle milk to explore biomarkers for early recognition of mastitis. We investigated the milk exosomal miRNA profile of three healthy (control group) and three sub-clinical mastitis (infected group) crossbred cattle using high-throughput small RNA sequencing. A total of 231 miRNAs were identified in both groups, with 180 miRNAs being shared by both. However, it was discovered that healthy cattle had 36 distinct miRNAs and crossbred cattle with sub-clinical mastitis had 15 distinct miRNAs. A total of 36 novel miRNAs were predicted in both groups, with 9 novel miRNAs in healthy cattle and 19 novel miRNAs in subclinical mastitis crossbred cattle being unique.

Among these identified miRNAs 12 known and 5 novel miRNAs were differentially expressed. 9 known and novels miRNAs were upregulated and 8 known and novels miRNAs were downregulated in the sub-clinical mastitis group of cattle by the with high read counts and log2 fold changes (> 2.0). Based on the findings, we speculated that these differentially expressed miRNAs could serve as biomarkers for the detection of mastitis-prone bovines and could represent as future indicators for the breeding and propagation of mastitis-resistant bovines to improve production efficiency in the dairy sector.

ABST-2-036

NUTRIGENETICS AND NUTRIGENOMICS IN LIVESTOCK

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The interaction of genetics and environment, nature and nurture, is the foundation for all health and disease. Genes define susceptibility to a disease or condition, and environmental factors such as diet and exercise determine who among the susceptible will develop the disease or condition and the nutrition is an environmental factor of major importance. Methodological advances in molecular biology and genetics have facilitated the study of inherited disease at the DNA level and of nutrients at the molecular level and the research has led to the development of concepts on genetic variation and dietary response, known as nutrigenetics and studies on the evolutionary aspects of diet and the role of nutrients in gene expression, known as nutrigenomics. Nutrigenetics or nutrigenomics could provide a framework for development of genotype-dependent novel foods for health promotion and for prevention and management of chronic diseases such as CHD, hypertension, diabetes, cancer, and obesity .Phenylketonuria (PKU) was the first “inborn error of metabolism” caused by a single-gene defect that responded to dietary treatment, employing a low phenylalanine containing diet for nutrigenetic management. There are about 6000 single-gene disorders, of which 2000 have been identified which are multigenetic and multifactorial. In future there is a need to learn in evaluating and to explain genetic knowledge about the affected individuals and combine it with an appropriate dietary regimen, the type, amount of physical activity and genotyping will become part of the routine management of an expanding range of human diseases over the next 5–10 years, and nutrigenetics will supplement pharmacogenetics in knowing who is at risk would be useful if it meant that one could avoid the environmental triggers that convert susceptibility into disease.

ABST-2-037

PHENOTYPIC AND GENETIC DIFFERENTIATION OF PURNATHADI BUFFALO

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Purnathadi buffalo is recently registered as 20th buffalo breed of India by NBAGR, Karnal. In the present study Purnathadi buffalo is differentiated phenotypically and genetically from other recognized breeds of adjoining region viz Nagpuri and Marathwadi breeds. Microsatellite data generated for Purnathadi and Nagpuri buffalo was compared with microsatellite data (19 loci) of Marathwadi buffaloes already available with buffalo genomics lab, NBAGR, Karnal to assess between breed genetic variability of three populations. Eighteen body biometric traits of three closely related buffalo populations were used to develop a suitable linear discriminate function having highest discriminating power to differentiate them phenotypically. Purnathadi, an excellent buffalo genetic resource maintained by the rural farmers of Vidarbha region, and receives its name as mostly found

along the bank of river Purna, Its native tract includes Akot, Akola and Telhara tehsils of Akola district; Daryapur, Anjangaon and Achalpur tehsils of Amravati district and adjoining villages of Buldhana district of Maharashtra state. Body coat colour in Purnathadi buffalo varied from whitish to light brown. Muzzles were either white, pinkish or black. Star white patch on forehead and in the lower extremities of all four legs and tail switch was common. Horns were long and tapering, seen up to the shoulder and were having upward orientation at the end like Hook. Step-wise discriminate procedure revealed Rump width (RW) as a most discriminating character. 71.7% Purnathadi, 79.6% Marathwadi and 61.7% Nagpuri buffalo's original observations were correctly classified. The dendogram based on the pairwise Mahalanobis distance also supports the results of discriminant analysis indicating uniqueness of Purnathadi buffalo. Genetic differentiation estimate (F_{ST}) ranged from 0.011 (CSSM066) to 0.252 (ILSTS019) with the overall average for all loci was 0.097± 0.015. The global average of 9.7% F_{ST} in the Purnathadi, Nagpuri and Marathwadi buffalo confirms the moderate breed differentiation. The pairwise genetic differentiation and gene flow estimated were 3.1% and 7.914 (between Purnathadi and Nagpuri), 9.4% and 2.422 (between Purnathadi and Marathwadi) and 8.4% and 2.727 (between Nagpuri and Marathwadi).The dendrogram based on Nei's genetic distance, Neighbour-Joining tree based on allele sharing distance, factorial correspondence analysis and admixture test of STRUCTURE analysis confirms the genetic structuring of buffalo population of Maharashtra.

ABST-2-038

CRISPR-CAS9 SYSTEM: A MOLECULAR TOOL FOR GENETIC IMPROVEMENT

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Gene editing or genome editing is a process consists of technologies to change organism's DNA. CRISPR Cas9 is considered as one of the modern technology or process, which lags in clustered regularly interspaced short palindromic repeats. It consists of two components a CAS9 protein and a guide RNA. This process is quicker, cost effective, efficient, and there is a less chance to detect error. We classify Cas9 process into three subtypes - type I, type II, type III.The use of CAS1 & CAS2 for the purpose of creation and incorporation of a unique spacer into DNA are considered as common whereas the complex involved in targeting a DNA are quite different. CRISPR-CAS9 includes CRISPR associated protein 9 having a nucleus activity and single guide RNA. CRISPR-CAS9 is one of the modern gene editing technology, yet it is not the first one. Processes like Zinc finger nucleases (ZFN) and Transciptor activator like effector nucleases (TALENS) were found before CRISPR-CAS9. In CRISPR-CAS9 technology, site recognition is maneuvered by RNA-DNA interaction. It provides advantage over earlier processes and technology, such as easier design of genome target, prediction of off-target sites, modifying multiple targets at the same time. This method is cost effective compare to historical technologies. CRISPR has wide range of applications across HIV treatment, Cancer treatment, anti-microbial resistance.

ABST-2-039

IDENTIFICATION OF SINGLE NUCLEOTIDE VARIANTS AND SELECTIVE SWEEP REGIONS IN ANKAMALI PIGS OF KERALA BY WHOLE GENOME SEQUENCING

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Ankamali pig is a domesticated native variety of Kerala, which is well known for its disease resistance, lean meat and adaptability to hot tropical environments. A study was conducted on Ankamali pigs of Kerala to

determine the genetic variations and to identify the selection signatures present in the genome of Ankamali pigs. Genomic DNA was isolated from 12 Ankamali pigs and was pooled for Whole Genome Sequencing. The GATK 'HaplotypeCaller' was used to identify the variants.Selective sweep regions in Ankamali pigs were identified using Tajima's D statistics. Annotation and enrichment analysis of the potential genes were done using Database for Annotation, Visualisation and Integrated discovery (DAVID). Genome sequencing yielded 1.36 billion (1,360,094,278) QC passed reads of which,1.357 billion (1,357,023,508) were mapped successfully to the reference genome (*Sus scrofa* 11.1). A total of 26.6 million (26,604,589) single nucleotide variants with 21.3 million (21,303,641) single nucleotide polymorphisms and 5.3 million (5,300,948) indels were obtained. Of the total number of SNPs obtained, total number of transitions and transversions obtained were more than 14 million (14,824,878) and 6 million (6,478,763), respectively. In Ankamali pigs, the total genome length obtained was more than 2.5 billion with an average variant rate of one variant in every 94 bases. A total of 437 selective signals were obtained (with a threshold of –ZTD ≤ -2.32) and 660 potential genes were annotated. Several candidate genes associated with body size (*PKPD1, MSNT*), fertility (*INHBB, CSMD1)*, erythrocyte stability (*GYPC*) and lipid metabolism (*REPIN1*) were identified. The results of this study may support the development of breeding programs for the effective conservation and to improve the production and performance traits of this indigenous desi variety.

ABST-2-040

POLYMORPHIC CHARACTERIZATION OF PARTIAL *TLR2* GENE IN MALNADGIDDA CATTLE

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The study was conducted in partial region exon-2 of *TLR2* gene covering 997bp region was characterized in Malnadgidda cattle which is one of the dwarf breeds of cattle which is famous for its disease resistance property. Toll like receptors (TLRs) are the cell surface receptors which mainly act by activating innate and adaptive immunity. These TLR's play very important role in disease resistance through the recognition of pathogen-associated molecular patterns (PAMPs). Among all the TLRs identified *TLR2* is mainly involved in the recognition of multiple pathogenic microorganisms. The partial exon-2 of *TLR2* gene is amplified using self designed primers and subjected for RFLP analysis using *BsaA1*restriction enzyme which revealed AB genotypes with fragments of sizes 71, 926 and 997bp exhibiting monomorphic pattern. The allelic frequency of A and B allele are 0.5 and the genotypic frequency of the AB genotyope is 1. Further, the observed heterozygositie, polymorphic information content (PIC) and allelic diversity are 1.0, 0.3750 and 0.5 respectively.Sequence analysis of Malnadgidda cattle revealed three SNPs when compared to *Bos Taurus* sequence.

ABST-2-041

GENETIC ADMIXTURE AND POPULATION STRUCTURE ANALYSIS OF SOUTH INDIAN CATTLE BREEDS

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According to FAO, about 300 out of 6000 breeds of farm animals have become extinct over the past 15 years and it is high time to identify the relationship of the indigenous cattle breeds for conservation. Hence, present study was conducted to analyze the genetic admixture in the South Indian cattle breeds at molecular level using microsatellite markers. A total of 542 unrelated animals representing 10 indigenous cattle populations:

Kangayam, Umblachery, Bargur, Alambadi, Pulikulam, Deoni, Ongole, Hallikar, Vechur, two exotic breeds: HF and Jersey and their crossbreds were collected from different regions of the native tract. The cattle genomic DNA was genotyped for 27 FAO recommended bovine specific microsatellite markers and Bayesian clustering analysis was employed using STRUCTURE version 2.3.4, assuming K=2 to K=15. The delta K versus K graph showed a peak at K=2, which represented the optimum K value for the investigated population. The HF and Jersey were assigned to the first cluster and all the indigenous breeds to the second cluster. Crossbreds showed admixture from both clusters. It was also observed that the level of exotic blood was beyond the permissible range (62.5 per cent) in some of the HF crossbreds and Jersey crossbreds. The Vechur cattle and crossbreds of Kerala showed similar clustering under Bayesian analysis. A sub-clustering was observed within the Vechur cattle indicating loss of purity despite the conservation measures undertaken. Further, breeds like Pulikulam, Umblachery and Alambadi showed high level of admixture with other south Indian breeds, despite sampling was done from animals with characterized morphological features. Breeds like Kangayam, Hallikar, Deoni and Ongole were comparatively pure to its type. Ongole as a breed with minimum taurine influence. The availability of purebred semen for artificial insemination can hence be a reason for maintaining the purity of breeds.

ABST-2-042

DEVELOPMENT OF GENE EDITED KADAKNATH CHICKEN FOR PROLACTIN GENE BY CRISPR/CAS9 MEDIATED GENOME EDITING

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The key factor in regulating reproductive physiology in birds is the prolactin (PRL) hormone, which is released from the anterior pituitary gland, restricts egg production in chicken. Therefore, we hypothesised that reducing the expression of this gene might increase egg laying in chicken. The goal of the current study was to use CRISPR/Cas9 gene editing tools to edit the prolactin gene *in vivo* in kadaknath chicken. A total of 4 CRISPR constructs were used to target exon 2 and exon 4 of prolactin gene. The sperm was collected from cocks and transfected with sgRNA-zsGreen1 clone by electroporation with Gene Pulser (Biorad) at 160 mV for 25 ms for 1 pulse. The transfected sperms were inseminated to each hen @ 0.25 ml for wo successive days. Eggs were collected and incubated at the incubator. Chicks were hatched and screened by PCR with a pair of primers (Forward: GACTATCATATGCTTACCGT and reverse: GTTGATAACGGACTAGCCT). Further, exon2 fragment of birds were amplified with exon specific primers and sequenced in both the directions. The sequencing results showed deletion of one nucleotide in exon 2 of the edited Kadaknath bird (Edited bird: ATC-AAAAGTTCCCCAAGGG). Age at first egg in the edited bird was 165 days as compared to control bird as 185 days. Finally, it is concluded that exon 2 of prolactin gene was edited in the Kadaknath chicken by CRISPR/Cas9 genome editing tool.

ABST-2-043

DIFFERENTIAL RESPONSE, MORBIDITY, MORTALITY PATTERN AND BACTERIAL LOAD TO EXPERIMENTAL AVIAN PATHOGENIC *E. COLI* (APEC) INFECTION IN COLORED BROILER AND VANARAJA CHICKEN

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Chicken breeds and varieties show different tolerance or resistance pattern to diseases owing to their genetic makeup. We investigated the tolerance / resistance to experimental *E. Coli* infection in two backyard chicken varieties (colored broiler &vanaraja). A total of 24 birds per variety (Total 48 birds) were divided into three groups of each 8 birds and were experimentally infected with 0.5 ml of 7 X 10^8 CFU/ml APEC isolate both by oral route and intraperitoneal route (IP) and one group (n=8) of each variety was kept as uninfected control. The APEC isolate from clinical cases of colibacillosis from ICAR-DPR flock was used. The birds were housed in isolator facility and observed for 10 days for the clinical signs, morbidity and mortality pattern. The deceased

birds were necropsied and lesion scoring was done based on the level of severity. All the surviving birds were sacrificed on 11th day post infection and bacterial load in liver was estimated. Colored broiler showed 75% and 37.5% mortality by IP and oral route respectively; whereas Vanaraja chicken showed 25% and no mortality by IP and oral route respectively. Control birds of both varieties were healthy and no symptoms were observed. Vanaraja chicken showed less morbidity, mortality, less lesion score upon death and less *E. coli* load in liver in comparison to colored broiler upon experimental infection. Vanaraja showed relative tolerance to APEC infection both by oral and systemic infection in comparison to colored broiler backyard variety.

ABST-2-044

PROTEOMIC AND GENOMIC DISSECTION OF (SEXED) SPERMATOZOA OF INDICUS CATTLE (BOS INDICUS)

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Sexed bovine semen, a disruptive change for Indian dairy sector, has thrown new challenges along with opportunities for development of alternate technology in view of restrictive nature of present one. There is a lack of proteomic and genomic resources of (sorted) spermatozoa of indicus cattle (Bos indicus) for comprehensive understanding. Here, we report proteome, specially plasma membrane (PM) proteins, and transcriptome of unsorted and sorted (X and Y) spermatozoa of indicus cattle. A rapid method for enrichment of PM fraction using percoll gradient has been developed, and is confirmed by significant enrichment of PM-associated proteins ($P<0.05$) as compared to total cell lysate using LC-MS/MS. High-throughput RNA sequencing was done for transcriptome analysis and differential gene expression profiling. Thirteen proteins were identified as differentially abundant between X- and Y-sorted spermatozoa. Two proteins were downregulated in Y-spermatozoa compared to the X-spermatozoa ($P<0.05$), while four and seven proteins could be noted in X- and Y-spermatozoa, respectively. Proteins that are presumed to support sperm capacitation and sperm migration velocity were found abundant in Y-spermatozoa while those associated with structural molecule activity were abundant in X-spermatozoa. The upregulation of 700+ transcripts in Y-spermatozoa as compared to X-spermatozoa was revealed while 1,000+ transcripts were downregulated. The common number of transcripts was 63% between X- and Y-spermatozoa while 16% was unique to X-spermatozoa and 21% to Y-spermatozoa. The resultant genomic and proteomic profiles of (sexed) spermatozoa of indicus cattle generated by us shall help a proteogenomics approach in biomarker discovery for immunosorting.

ABST-2-045

MOLECULAR CHARACTERIZATION OF SWINE LEUKOCYTE ANTIGEN (SLA) GENES IN INDIGENOUS PIGS (SUS DOMESTICUS)

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Swine Leukocyte Antigen (SLA), the Major Histocompatibility Complex (MHC) of domestic pig (Sus domesticus), plays a central role in the body defence and immunity. Recent outbreaks of Classical Swine Fever (CSF) and African Swine Fever (ASF) in different parts of India call for dissection of immunity at molecular level vis-à-vis (anecdotal) claim of disease resistance in indigenous domestic pigs. Here, we report the molecular characterization of the SLA genes of the indigenous pigs. The major constitutively expressed classical SLA

genes, namely SLA-I, SLA-II and SLA-III of Class-I and DRA, DRB, DQA and DQB of Class-II were cloned and sequenced followed by bioinformatic analysis. The PCR amplicons of 1,109 (SLA-1), 1,118 (SLA-2) and 1,728 bp (SLA-3) of Class-I and 799 (DRA), 907 (DRB), 793 (DQA) and 1,103 bp (DQB) of Class-II were produced, and we obtained ORF of 876 (SLA-1), 1,095 (SLA-2) and 927 bp (SLA-3) of Class-I and 759 (DRA), 801 (DRB), 765 and 768 (DQA) and 786 bp (DQB) of Class-II SLA genes. The sequence homologies varied between 90.39 and 99.91% for Class-I genes and 93.7 and 100% for Class-II genes when compared with respective gene of domestic and commercial pigs as well as closely related other pig species around the world. The SLA-1 gene of indigenous pigs was phylogenetically closer to Asian pig breeds and miniature pigs whereas SLA-2 and SLA-3 genes were closer to western pig breeds and their crosses. The Class-II genes were closer to western breeds and commercial crosses although DRB and DQA were also closer to few Asian native pigs. The information revealed by our study along with variation in peptide binding sites, allelic architecture, haplotypes and their inheritance vis-à-vis disease patterns shall guide breeding decisions for disease resilience in future.

ABST-2-046

DGAT1 AND STAT1 POLYMORPHISMS ASSOCIATED WITH MILK PRODUCTION TRAITS IN GAOLAO CATTLE

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Current dairy genomics research emphasizes on identification of polymorphisms within candidate genes and their association with economic traits. The current study was planned to detect polymorphisms within exon-8, exon-15, 16, 17 and intron-16 and exon-1,2 and intron-1 regions of DGAT1 and 3'UTR region of STAT1 candidate gene in Gaolao cattle population. The study included around 258 unrelated animals of Gaolao breed. The genomic DNA was isolated and the test day traits were recorded. The gene polymorphisms were explored using PCR-RFLP, PCR-SSCP & Direct DNA sequencing tools. *DGAT1G1-Cfrl* PCR-RFLP was monomorphic, however; *DGAT1G2-Bgl*I PCR-RFLP was polymorphic with frequency of A= 0.0568 and B=0.9432 in 258 animals. The association analysis revealed significant difference in Lactose% trait for 'AA' genotype (5.00±0.10*) as compared to other genotypes. Except *DGAT1G6* monomorphic PCR-SSCP; *DGAT1G4* with two patterns (A=0.678 & B=0.321) and *DGAT1G5* was highly polymorphic with 05 patterns (A=0.055, B=0.444, C=0.407, D=0.037, E=0.055) in random 56 animals. Direct sequencing of polymorphic *DGAT1G5-SSCP* variants revealed one transversion SNP G>C at 4th position and one computational SNP G>A at 260th position in the sequence. *STAT1G1 -Pag*I PCR-RFLP was polymorphic with frequency for A allele as 0.1573 and frequency for C allele as 0.8427 at the locus. The association study revealed significant difference in Fat % (5.16±0.83*) and Protein % (3.23±0.04*) trait for 'AC' genotype as compared to CC genotypes in 220 animals. *STAT1G4-SSCP* analysis revealed monomorphism. Results of the current study indicate existence of variation within different regions of functionally important DGAT1 and STAT1 candidate genes. The identified polymorphisms and association within DGAT1 and STAT1 candidate genes can be useful in selection and breeding for Gaolao cattle breed improvement.

ABST-2-047

COMPARATIVE GENE EXPRESSION PROFILING OF MILK SOMATIC CELLS OF SAHIWAL AND CROSSBRED CATTLE

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India is the world's largest milk producing country because of massive contribution made by the two major dairy species i.e., cattle and buffaloes. In the present investigation, comprehensive comparative profiling of

transcriptomic landscape of milk somatic cells of Sahiwal and crossbred cattle was carried out. Milk samples were collected from Sahiwal and crossbred cows during lactation period. RNA was extracted from the pelleted milk cells and Gene expression analysis was conducted by Illumina RNA sequencing. Sequence reads were assembled and analyzed in CLC Genomics Workbench. Gene Ontology (GO) and pathway analysis were performed using the Blast2GO program. RNA-Seq data was pre-processed and mapping was done to identify differentially expressed genes (DEG). A total of 10546 differentially expressed genes were identified. Analysis of differential expression identified 455 significantly up-regulated and 3 significantly down-regulated genes with fold change > 2. ALOX15, S100B, CSN2, PAEP, CSN1S2, CSN3, LALBA, GLYCAM1, FASN, RPS29, CSN1S1 and FABP3 were found to be top highly expressed genes. Genes encoding caseins, whey proteins and enzymes in lactose synthesis pathway showed higher expression in lactation. The genes and pathways delineated in this study have regulatory implications in cell morphogenesis, lipid droplet formation and protein synthesis in the course of lactation. The study provides an insight into the expression profile of genes influencing milk properties and lactation in Sahiwal and crossbred cattle.

ABST-2-048

PHENOTYPIC AND MOLECULAR CHARACTERIZATION USING MICROSATELLITE MARKERS OF VIZIANAGARAM (NAGAVALI) SHEEP

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Vizianagaram (Nagavali) sheep is alocally adopted sheep genetic group in north coastal region of Andhra Pradesh. The present study was carried out to establish breed characteristics of Vizianagaram (Nagavali) sheep and also to assess the genetic diversity at molecular level using thirty microsatellite markers recommended by FAO for genetic diversity studies in sheep. A total of 451 sheep of different age groups were used to study the morphometric characters of Vizianagaram (Nagavali) sheep and 56 blood samples from unrelated sheep were used for molecular studies. The predominant color of these animals is white with tan//brown/ black color patches on nose line, lateral face, neck/mane, perineum, back and lower extremities. The ears in this genetic group of sheep are observed to be either pendulous or tubular. Prominent occipital bone, black patches around the eye, hair on thigh, dewlap and neck/mane region are the important features of this genetic group. The overall least squares means of body weights (Kg), height at withers (cm), chest girth (cm) and body lengthy (cm) were 22.10±0.76, 64.96±0.48, 68.67±0.64, 62.30±0.42 at 2 teeth age, 26.03±0.75, 66.86±0.74, 72.33±0.78 and 65.76±0.81 at 4 teeth age, 28.89±1.21, 67.20±0.69, 74.75±1.07 and 65.76±0.81 at 6 teeth age and 28.09±0.62, 67.22±0.40, 76.76±0.51 and 65.89±0.37 at full mouth respectively. DNA isolated from 56 Vizianagaram (Nagavali) and 40 Nellore Jodipi blood samples was utilized for microsatellite analysis. A total of 377 and 321 alleles were observed across 30 loci in Vizianagaram (Nagavali) and Nellore Jodipi respectively. PIC of the markers ranged between 0.457 (OARCP38) and 0.861 (OARFCB304) in Vizianagaram (Nagavali) sheep while it was 0.345 (MAF214) and 0.866 (ILSTS11) in Nellore Jodepi sheep. The mean F_{IS}estimates among the two populations were 0.084 for Nellore Jodipi and 0.086 for Vizianagaram (Nagavali) sheep. The pairwise Nei's genetic distance and identify estimates were 1.6% and 98.5% respectively. The study concluded that Vizianagaram (Nagavali) sheep were phenotypically distinct from other breeds with low genetic diversity at molecular level.

ABST-2-049

INNATE IMMUNE RESPONSE GENES IDENTIFIED AGAINST *DUCK PLAGUE* INFESTATION IN *ANAS PLATYRYNCHOS*

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The present study depicts the host immune response at molecular level in duck model (*Anas platyrynchos*) against the DNA virus of the *Herpesviridae* family. Duck Plague (DP) or Duck viral enteritis is an acute

contagious and highly fatal disease in waterfowl and the causative agent is Anatidalphavirus-1 belonging to *Herpesviridae* family and contains double-stranded DNA as genetic material. *Gut Associated- Lymphoid Tissue (GALT)s* plays important role in immune response. Pathogen-associated molecular pattern (PAMP)s when identified by Pathogen Recognition Receptor (PRR)s acts as effective immunity system action against the pathogen. The current study depicts the important role of innate immune response genes as RIGI, MDA5, Mx, TLR7, PkR and OAS and INFalpha in duck plague infestation for the first time. *In silico* studies involve prediction of 3D structure prediction, post translational modification, important domain identification after gene sequencing followed by molecular docking with duck plague virus structural protein followed by differential mRNA expression profiling detect the effectiveness of gut associated immune responsiveness in the liver, where Kupfer cells are the major immune response cells. This was further confirmed through a histological section of liver, kupfer cell and immunohistochemistry. This will be helpful to identify the molecular mechanism of host innate immunity through duck plague virus infection in indigenous ducks. This information may be helpful for the production of duck with the inherent resistance against duck plague virus infection through suitable biotechnological approaches such as gene editing or genomic selection of DP resistant ducks.

ABST-2-050

ASSESSMENT OF GENOTOXICITY OF MITHI RIVER USING ZEBRAFISH (*DANIO RERIO*) AS A MODEL ORGANISM

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The Mithi River is also known as 'Mahim River,' and its length is 17.8 km. It has its flows through the heart of Mumbai and the discharge from various industries and domestic sewage contributes to the pollution of the River. The current study was conducted to determine the toxicity of Mithi River water in zebrafish (*Danio rerio*) embryos. Water samples were taken from three locations namely Saki vihar Lake (Upstream site; S1) Taximens Colony Road (Middle reaches; S2) and Mahim Causeway (Downstream site; S3). Zebrafish Embryo Toxicity Test (ZFET) was performed with 8 different dilutions for each site. After 120h, the LDil 50 values of 0.426, 3.648 & 2.458 was obtained for the S1, S2 & S3 respectively. Teratogenic endpoints such as egg coagulation, tail bend, body curvature, pericardial and yolk sac edema showed significant differences among the sites. The comet assay revealed a significant difference in DNA damage in terms of Olive tail moment (OTM) in the embroys exposed to the S1, S2 & S3 samples with OTM values of $2.3^{a}\pm$ 0.63, $4.03^{ab}\pm$ 0.91&$4.71^{b}\pm$ 0.59 respectively. The study found that pollution load is least in upstream site (S1), but the load increases as it flows along middle stretches (S2) and reaches maximum in downstream site (S3). The findings of this study indicated that Mithi River water is heavily polluted due to the presence of a wide range of pollutants and as such, the water may not be suitable for domestic or industrial use. Therefore, a mechanism for continuous monitoring of the quality of the water of River Mithi is required.

ABST-2-051

ROLE OF IMMUNE RESPONSE GENES AGAINST *HAEMONCHUS CONTORTUS* INFESTATION IN SHEEP MODEL CONFERRING HOST IMMUNITY

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Host immune response and its variability existing in the population play an important tool for controlling diseases

or development of disease resistant individuals. In the current study, we could explore a series of immune response genes responsible for innate resistance in sheep against deadly parasite *Haemonchuscontortus*. We characterized the immune response genes in sheep gut associated lymphoid tissue (RIGI, NFkβ, IL12, MyD88, MD2, LPB, IL-1β, IL-6 , IL-10, TNF-α , CD-14, TLR-4), some of them were characterized for the first time in sheep. These genes were earlier reported to be mostly antiviral or antibacterial in action. But this is the first report of antiparasitic effect of these genes from GALT. We employed the study initially through *in silico* approach of prediction of 3D structure prediction, post translational modification, important domain identification after gene sequencing followed by molecular docking with parasitic structural protein. Then we confirmed the study through differential mRNA expression profiling of the expressed gene and immunohistochemistry of the expressed protein in two groups of animals as *infected* with deadly parasite Haemonchuscontortus and *healthy* control. Simultaneously we assesed the findings and corelated with haematological and biochemical parameters of both groups of sheep (healthy vs. infected). The findings will be helpful for *genomic selection* of sheep resistant to H. contortus, which is a major treat to sheep industry. H.contortus resistant sheep may be developed in future through gene editing approach, that may save a huge loss of sheep industry.

ABST-2-052

IMPORTANCE OF BLACK SOLDIER FLY

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In India poultry production has developed as one of fast growing among various livestock sectors as its transformation from tradition backyard system to organized commercial farming over the last few decades. Due to increase in food demand of an over-growing human population, as well as the need to reduce the carbon footprint of agriculture and to introduce new protein sources for animal feeding. So the Black soldier fly (BSF) larvae are attracting the attention of researchers and livestock industry as an alternative source of protein. A larva seems to fulfill the requirements through low-cost, eco-friendly ingredient and by converting organic waste into larval biomass. BSFL reared on any type of organic wastes like rotting meat, decomposing fruit and vegetables waste, poultry waste, biogas digest, vegetable waste, and restaurant waste. They have high level of protein (32-58%) and fat sources (15-39%), essential amino acids, energy, and micronutrients. Mass production of BSF larvae requires less surface area than crops to produce the same amount of protein, whilst reducing the emission of greenhouse gases.BSFL farming is a zero waste solution, helps in uplifting the socio economic condition of the farmers, great solution to reduce the organic waste, initial investment is low and high income in the end. BSF larvae lives for about 5-6 weeks, it hasrapid growth rate, can easily manageable, has got high conversion rate, ideal for manure treatment and not a vector for any of the human diseases. Black Soldier Fly serves mainly 3 important values like Environmental, Nutritional and Economical.

ABST-2-053

POLYMORPHISM STUDY OF *BETA DEFENSIN 4* GENE IN CROSSBRED CATTLE OF KERALA

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The present study aimed to investigate single nucleotide polymorphisms in exon 1 and 2 regions of the bovine Beta defensin 4 gene (DEFB4) association with somatic cell score (SCS) in 200 crossbred cattle of Kerala using polymerase chain reaction-single stranded conformational polymorphisms (PCR-SSCP) method. Analysis shows the 192 bp fragment of exon 1 of the DEFB4 gene was found to be monomorphic. 229 bp fragment of exon 2 was found to be polymorphic with 3 genotypes viz. PP, QQ, and PR were obtained with frequencies of 54%, 34%, and 12%, respectively. The frequency of P, Q, and R alleles was found to be 0.60, 0.34, and

0.06, respectively. Sequencing analysis shows SNPs at five different locations, with four non-synonymous SNP (c.121T>A, c.131G>C, c.134T>G, and c.188G>C) and one stop-lost SNP (c.191A>G) was obtained at ORF positions. Cattle with PP and QQ genotypes were more related (p≤0.05) to lower SCS compared to PR genotypes. The association between DEFB4 polymorphism and SCS described in this study suggests the possible role of SNPs during mastitis infection. Thus, the SNPs present in the DEFB4 gene could be employed as a useful marker for genetic selection to promote mastitis resistance in dairy cattle.

ABST-2-054

PHENOTYPIC AND MOLECULAR CHARECTERIZATION OF MACHERLA SHEEP – A LESSER KNOWN SHEEP OF ANDRAPRDESH

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The status of lesser-known sheep cannot be ignored as they comprise 75 Per cent of the total Indian sheep population. The Macherla sheep is one of the lesser-known sheep breeds of Andhra Pradesh with medium to heavy sized body. Because of superior performance over Nellore and the characteristics such as good resistance and adaptability to local climatic conditions, the Macherla sheep attained considerable importance among sheep herders. The data was measured on 1279 sheep from 27 villages of nine mandals in four districts of two states. The predominant colour pattern in Macherla sheep was bicolour with combinations of white and black or brown and white. Rams are horned and ewes are polled. A gradual increase in the body measurements was observed from milk tooth to full mouth stage. Males recorded significantly higher body measurements than females. District has significant influence on the body measurements with higher recordings in Guntur district. Among sexes, males recorded heavier body weights compared to females. The reproductive performance of Macherla sheep was ideal and within the range of species. The lambing Percentage was quite good in Macherla sheep. The Phenotypic correlations of body weight with the linear body measurements were positive and high.Regression analysis revealed that the measurement of chest girth alone or a combination of chest girth, height at withers and body length are best suited for predicting body weights under field conditions. The present study was aimed to study Molecular characterization and to know the genetic differentiation of Macherla sheep with Nellore sheep. A total of 262 and 253 alleles were found in Macherla and Nellore sheep across the 27 microsatellite loci.On an average about 9.7 alleles per locus were observed in both the genetic groups. The private alleles observed in Macherla and Nellore Brown sheep were 91 and 81, respectively. The mean observed heterozygosity value was 0.593±0.039 in Macherla sheep while it was 0.593±0.043 in Nellore Brown. The PIC of different markers ranged between 0.640 (SRCRSP1) to 0.927 (DYMS1) in Macherla sheep, whereas the values range from 0.698 (BM8125) to 0.922 (DYMS1) for Nellore Brown genetic group. Bottleneck analysis revealed that abundance low frequency alleles suggesting the absence of recent bottleneck. The F_{ST} between the two genetic groups is 0.059 and the Nei's unbiased genetic distance is 0.212 suggesting that the two breeds are moderately differentiated.

ABST-2-055

TRANSCRIPTOME ANALYSIS REVEALS KEY GENES AND PATHWAYS ASSOCIATED WITH HEAT STRESS RESPONSE IN SAHIWAL CATTLE

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Our planet is warming at an alarming rate every decade. And due to the rise in heat stress on dairy animals, India is already losing part of its total milk production, which amounts to thousands of crores. That will be a blow to India's livestock industry in the long run if nothing is done. It necessitates the unravelling of the genetic basis of thermal stress tolerance mechanism of indigenous breeds, like Sahiwal, that have proved to be more climate-resilient than the exotic breeds and crossbreds. The transcriptome, which varies with conditions, was studied for its changes with seasons. Blood samples were collected from Sahiwal heifers in spring and summer

in the Livestock Research Centre, ICAR-NDRI, Karnal. The RNA isolated from the PBMCs were converted to cDNA library, which then underwent paired-end sequencing using the NovaSeq 6000. The gene counts of aligned files were generated. Overall, 9037 differentially expressed genes (DEGs) were obtained [log2(fold change)≤2; padj<0.05], of which 4948 were upregulated and 4089 were downregulated. Top 10 upregulated genes included CCNF, CAMK2A, EPHA10, GSTT4, SUSD2, KLF1, PHF21B, and LIMS2. Functional pathway analysis of the DEGs was done using iDEP.96. Top upregulated pathways obtained were chemical synaptic transmission, anterograde trans-synaptic signalling, trans-synaptic signalling, nervous system development, synaptic signalling, cell-cell signalling, animal organ morphogenesis and synapse organization. Downregulated pathways included RNA metabolic process, cellular protein metabolic process, immune system process, mRNA processing, translation, peptide biosynthetic process, peptide metabolic process, protein metabolic process, regulation of mRNA metabolic process, cellular protein modification process and protein modification process, suggesting suppression of various metabolic process and immune system. The findings of the present study will help to unravel the genetic basis of heat stress response in Sahiwal cattle. Moreover, it may aid in developing a genetic approach for developing heat-resilient dairy cattle breeds in India.

ABST-2-056

CHARACTERIZING BOVINE MILK-DERIVED EXOSOMES: AN APPROACHES FOR VALUE ADDITION

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Exosomes are nano-size extracellular vesiclesreleased by allprokaryotic and eukaryotic cells as a part of their normal physiology. They have complex cellular components with proteins, lipids, nucleic acidsas major contents and participate in intercellular signaling by delivering their cargo to recipient cells thereby modifying the target cells' signaling and function. Exosomes released by cells of different origins might have divergent functions depending upon the cargo these carry. The present study was planned to characterize the milk derived exosomes from Indigenous (*Bos indicus*), exotic (*Bos taurus*) and crossbred cows. Milk samples were collected from Sahiwal, *Holstein Friesian* and *Karan Fries* cows maintained at ICAR-NDRI and exosomes were isolated by different approaches including successive ultracentrifugation, isoelectric precipitation method and precipitation using kit-based methods.The exosomes were confirmed by western blot analysis for the presence of CD9, CD81 and CD63, the common surface marker present on the exosomes. The characteristic shape of the isolated exosomes was ensured by performing transmission electron microscopy. Maximum yield of exosomes was obtained through differential centrifugation coupled with ultracentrifugation whereashighest yields for microRNA and highest RNA to protein ratio were obtained when exosomes isolated from the ultracentrifugation were further purified by EQ reagent.Biophysical characterization revealed that the size of average exosomes from colostrum and mature milk was in the range of 30–150 nm in diameter. The mean size of the exosomes isolated from the colostrum was smaller (125 nm) than those of mature milk (176nm), however there was no size difference was observed across the three cattle types. Metabolome spectra generated using1H NMR spectroscopy,for the milk derived exosomes from all the three cattle types was analyzed to identify the possible presence of metabolites andexplorative data analysis was performed using heatmaps. In total, 46 metabolites from different classes could be identified.The complete composition of different classes of metabolites in milk exosomes revealed that profile was specific to cattle type used as milk resource with a total of 23 metabolites differentially regulated between the Indicus, taurine and crossbred cows.Presence of metabolites with positive health attributes in Indigenous cow's milk derived exosomes can add great commercial significance to their milk leading to their sustainable utilization.

ABST-2-057

IDENTIFICATION OF DIFFERENTIAL RESPONSES IN CHICKEN TO DIFFERENT CLADES OF HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS H5N1 USING OMICS APPROACH

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Influenza viruses cause severe respiratory infections in humans and birds, triggering global health concerns

and economic burden. Over the past years the risk of an influenza pandemic has grown, as an exceptionally virulent form of the H5N1 avian influenza virus has circulated widely among domestic poultry and wild migratory birds in Asia, Eastern Europe, the Middle East, and Africa. Influenza infection is a dynamic process involving complex biological host responses. In this study chicken upper repiratory tract (Trachea) infected with two different clades of HPAIV i.e, clade 2.2 clade 2.3 at 24hr post infection were taken to see the differences in host response through transcriptome analysis. Total RNA isolated from non-infected and infected birds in triplicate were used for RNA sequencing analyses to characterize differentially expressed genes and overrepresented pathways. Analysis was done by using the free open-source software tools like HISAT, StringTie and Ballgown, they allow to align reads to a genome, assemble transcripts including novel splice variants, compute the abundance of these transcripts in each sample and compare experiments to identify differentially expressed genes and transcripts. It was observed that at 24hr post infection (clade 2.2) the genes like FNDC1, SPTBN2, CEP250, TECTA, HK1, NOTCH2, VH26L1 and ALB upregulated and genes like AvBD7, 7044,JPH2, MKRN2OS, RAB18L, ENTPPL, SLC41A3,HEXDCL,FAM204A and MBL2 were downregulated, on the other hand at 24hr post infection (clade 2.3) genes like BDKRB1, PITPNM2, CPE, COL11A1, SLC40A1, ADARB1,DCX, ITGBL1, VWF, FAM172A, C2CD2L and MY06 were upregulated and genes like LOC770450, IFI27L2, NUSAP1, KRT80, ANKRD49 and PRELID3A were found to be downregulated. This transcriptomics study help us in understanding the differences in pathogenecity and host-pathogen interaction that occurs from different HPAIV infections.

ABST-2-058

GUT MICROBIAL DIVERSITY ANALYSIS IN PRE-HATCH AND POST-HATCH CHICKS

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The gastro-intestinal tract of the chicken is home to a diverse microbial assemblage involved in maintaining gut health, physiology, and productivity. It is well known that mammals acquire the gut microbiome in utero, but in oviparous birds, how the maternal microbiome influences commercially hatched chicks is still unclear. Therefore, this study was performed to assess the vertically acquired microflora in the chicken and to understand its probable implications through in silico analysis. The Cobb broiler eggs were set for incubation. The intestinal contents were collected from three embryoson day 18 of incubation (Pre_hatch) and from chicks immediately after hatching (Post_hatch). The metagenomic DNA was isolated from the intestinal contents using the ZymoFecal DNA mini prep kit. The V3-V4 region of the 16S rRNA gene was sequenced using Illumina 2x300 bp chemistry on MiSeq (Illumina) to generate 0.2 million PE reads. The metagenomic amplicons were analyzed using QIIME2 and visualised using the MicrobiomeAnalyst web portal. The GC content of the sequence data revealed the presence of low GC containing microbes in the pre-hatch group suggesting the presence of small genome pathogens belonging to Firmicutes. The microbial diversity in the Pre_hatch gut was also higher than the Post_hatch as revealed by the Shannon diversity index. At the phylum level, the Pre_hatch microbiome was dominated by *Proteobacteria*, *Firmicutes*and *Bacteroidota*comprising around 75% of the diversity, however, the same proportion in Post_hatch chicks was dominated by *Proteobacteria* alone. The higher diversity of the microbiome during the Pre_hatch stage is also related to development and training of the immune system as other studies have demonstrated effect of maternal microbiome on innate immunity development (Mei, 2019). At the genus level, the Pre_hatch microbiome was dominated by *Lactobacillus*, but the Post_hatch gut had predominance of the genus *Dickeya*, a group of known plant pathogens known to produce pectinases. With the current feeding trend of raisingpoultry on only vegetable protein sources mainly soybean mealcontaining pectin and low/no antibiotics, the genus *Dikeya* could have a role in ameliorating the negative effects of pectin-induced viscosity and improving feed efficiency (Dittoe et al., 2020). However, it needs to be seen if the same genus is maintained in the later life of the birds or could be supplemented to improve feed efficiency in poultry.

ABST-2-059

HIGHER ABUNDANCE OF IMMUNOGLOBULINS, ANTIMICROBIAL PROTEINS AND GROWTH FACTORS IN MILK COLOSTRUM *VIS* A *VIS* TRANSITION AND MATURE MILK OF NATIVE CATTLE AND YAK POPULATIONS

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The native cattle and yak populations of Leh-Ladakh are naturally adapted to hypobaric hypoxia condition prevalent in highland plateau. These two livestock species have been the integral component of daily life of rural as well as nomadic populations of Ladakh region. The milk of Ladakhi cows and yak, along with other related products like churpi, butter provides the nutritional security to the local Ladakhi populations. Since these animals are genetically unique and maintain under low input system with extensive grazing on local grasses and herbs, we hypothesized that the milk and colostrum of native cattle and yak are enriched with different biomolecules and immunoglobulins. In the present study, an effort was made to estimate the concentration of Immunoglobulins (IgG1, IgA, IgM) and two major whey proteins with antimicrobial properties (Lactoferrin and Lysozyme) and growth factor (insulin growth factor) in colostrum, transition and mature milk of Ladakhi cows (LAC) and yak (LAY)using bovine specific ELISA kits. For comparison with lowland cattle, the samples of Sahiwal cows (SAC) were also included. A total of 80 samples belonging to 0 day (colostrum, n=20), 2 day (transition milk, n=20), 4 day (transition milk, n=20) and >30 days (mature milk, n=20) of LAC, LAY and SAC were included. The analysis of data showed that concentration of IgG1 was maximum in colostrum samples across LAC, LAY and SAC. The IgG1concentration in0-daysamples was 30mg/ml, 17mg/mland 49 mg/ml in LAC, LAY and SAC, respectively. Its level reduced substantially in transition and mature milk samples across the three animal types. Similar to IgG1, the IgA level was also highest in colostrum samples across LAC (488.07ng/ml), LAY 465.53ng/ml) and SAC (500.05ng/ml) and its level declined in subsequent days of lactation.The IgM concentrations in colostrum, transition and mature milk samples of LAC (0 day: 2.41µg/ml, LAY (0 day: 4.11µg/ml) and SAC (0 day: 3.62µg/ml) also showed the similar trend as observed for IgG1 and IgA. Additionally, the lactoferrin (LTF) concentration in the 0-day samples were: LAC (614.43ng/ml), LAY (640ng/ml)and SAC (545.7ng/ml). While in 2-day samples, its value was: LAC (555.57ng/ml), LAY (611.5ng/ml), SAC (531.2ng/ml). In 4 day and mature milk samples its value decreased only marginally across all the three populations.The lysozyme (LYZ) concentration was also relatively high in colostrum samples**(**LAC:1130.20ng/ml, LAY:1124 ng/ml,SAC:1144.0 ng/ml), and then slightly reduced on 2day (LAC:1100.9ng/ml, LAY:1067.8ng/ml, and SAC:1097.43ng/ml),4day (LAC:1033.6ng/ml, SAC:1069.8ng/ml and LAY:1061.0ng/ml)and that in >30 milk was (LAC:1024.68ng/ml, SAC:1118.2ng/ml and LAY:1046.24ng/ml).The Insulin growth factor (IGF1) concentration varied from 125.33 ng/ml to 120.94 ng/ml in LAC colostrum and mature milk, 122.56 ng/ml to 118.0 ng/ml in LAY and 122.41ng/ml to 115.92ng/ml in SAC, respectively. Such kind of studies will be helpful in quantifying various biomolecules, growth factors and immunomodulators in milk and colostrum of native animals for their utilization and value addition.

ABST-2-060

MORPHOLOGICAL AND ZOOMETRIC TRAITS OF NATIVE GEESE IN NORTH BANK PLAINS OF ASSAM, INDIA

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The present study was conducted in different districts of North Bank plain agroclimatic zone of Assam, India. The state is privileged to possess the valuable germplasm of native geese, whose rearing goes back to very olden times. The exploratory approach was undertaken and data pertaining to 553 birds were collected. The morphological attributes and zoometry at adult stage were studied. In matured birds, two plumage varities were observed, *i.e.,* cinnamon and white. There was no sexual dimorphism in terms of plumage. The bill colour was black, orange, yellow and, mixture of black and orange. The shank and feet colour were predominantly orange followed by yellow and, mixture of black and orange. The eye colour was found to be black, brown and

blue. The LSM ± SE for various morphometric traits at 12 months of age were recorded. The overall mean for bill length, bill width, knob diameter, head length, head width, neck length, neck girth, breast length, keel length, body length, body circumference, shank length and wingspan were found to be 8.56 ± 0.009 cm, 2.86 ± 0.011 cm, 2.94 ± 0.016 cm, 11.58 ± 0.035 cm, 4.19 ± 0.012 cm, 22.83 ± 0.031 cm, 11.44 ± 0.031 cm, 30.17 ± 0.033 cm, 15.59 ± 0.084 cm, 49.22 ± 0.057 cm, 51.02 ± 0.019 cm, 7.12 ± 0.008 cm and 115.32 ± 0.042 cm, respectively. The present documentation of morphology and zoometry of native geese will help in developing breeding and conservation strategies for this precious germplasm.

ABST-2-061

STUDIES ON PCR-RFLP OF LEPTIN GENE IN MURRAH BUFFALO

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Leptin (LEP) is one of the candidate gene involved in regulation of feed intake, energy balance, fertility and immune functions in buffaloes.In the present study 50 unrelated Murrah buffaloe blood was collected to extract DNA and elucidate the genetic polymorphism in two exons of LEP gene through Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) technique and the data on milk production and reproductive traits were correlated if any polymorphism were identified.The exon-2 (289 bp) and exon-3 (405 bp) of gene were amplified with specific primers and were subjected to restriction enzyme digestion by using *Msp I* and *Hind III* . The exon-2 (289 bp) digestion with *Msp I* yielded two fragments of 79 bp and 210 bp and the exon-3 (405 bp) produced fragments of 255 bp and 150 bp with a single recognition site. Whereas, *Hind III* did not reveal any restriction sites in both the exons.Hence, PCR-RFLP revealed the monomorphic nature of the LEP gene in studied two exons indicating its conserved nature in the buffaloes.Therefore, correlation study was not possible,however data was analysed for various production and reproduction traits.The overall least squares means for total lactation milk yield, standard lactation milk yield, lactation length, peak yield, attainment of peak yield were 1,943.77 ± 84.56 kg, 2008.27 ± 82.15kg, 291.13 ± 9.23 days, 11.88 ± 1.36 kg and 25.40 ± 1.28 days, respectively. The parity did not reveal any significant effect on all production traits studied.Similarily,for calving interval, dry period, service period were 608.97 ± 29.52 days, 319.63 ± 56.90 days and 339.29 ± 31.37 days, respectively. The parity had a significant effect on calving interval, but not in dry period and service period.Hence,large population of buffaloes may be screened to elucidate the polymorphism in future due to conserved nature of gene.

TECHNICAL SESSION-III

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ABST-3-001

1D 1H NMR BASED METABOLOME CHARACTERIZATION OF COLOSTRUM, TRANSITION AND MATURE MILK OF MURRAH BUFFALOES (*BUBALUS BUBALIS*)

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Murrah buffaloes are considered as the finest dairy breed and has the highest milk yield capacity. The colostrum milk is known to be rich in antiviral and antimicrobial biomolecules which protect the young calf, especially in the first week after birth. Additionally, colostrum contains vitamins, bioactive substances, antibodies, minerals, and growth factors. It contains a crucial component for the development of novel pharmaceuticals and food derivatives. So far, no information is available on the metabolic profile ofcolostrum, transition and mature milk of Murrah buffaloes. In this study, a total of 60 milk samples collected at 0, 2-, 4-, 6-, 50 and 100-dayspost calving representing colostrum, early transition and mature milk of Murrah buffaloes were collected. The samples were freeze dried and subjected to 1D ^{1}H 800 MHz NMR spectrometer equipped with a Cryoprobe (at 300 K) for the metabolic profiling of colostrum, transition and mature milk. The NMR spectra were analysed using PROFILER -Module of CHENOMX and a total of 26 metabolites were identified. The metabolites such as lactose, guanidoacetate, glycerophosphocholine, glycine, betaine, choline, NAG, O-PCh, UDP-Galactose, UDP-Glucose, Myo-Inositol, UDP-NAG, creatine, carnitine, creatine phosphate, creatinine, O- acetylcarnitine, fucose, glutamate, threonine, lactate, lactulose, leucine, malonate and maltose *etc*. could be identified with varying concentration. Partial least square discriminate analysis (PLS-DA) showed distinct grouping of colostrum and mature milk samples. The ranking of metabolites responsible for distinct separation of three sample types (colostrum, transition and mature milk) from each other was done based on variable importance in projection (VIP) score. The hierarchal clustering demonstrates that the metabolome signature of colostrum samples (0 day) is distinctly different from that of the rest of the samples. The analysis revealed that branched chain amino acids leucine, isoleucine, and valine were significantly high in colostrum samples. Additionally, metabolic pathway analysis showed that the different metabolites were principally enriched in amino acid metabolism, citrate cycle (TCA cycle), aminoacyl-tRNA biosynthesis, valine, leucine and isoleucine biosynthesis. In summary, our study could successfully utilize nuclear magnetic resonance technique to establish the metabolome signature of colostrum and milk samples of Murrah buffaloes. Further, the study highlighted the higher abundance of metabolites in colostrum *vis a vis* mature milk sample. Such information could provide tangible information on type of metabolites available in colostrum and mature milk of Murrah buffaloes for further commercial application.

ABST-3-002

ANNOTATION OF COPY NUMBER VARIATIONS IN SWAMP AND RIVERINE BUFFALO

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Structural variations (SV) are variations involving DNA segments and copy number variation (CNV) is a kind of SV, which occurs due to deletion, duplication and insertional translocation accounting 50bp to several mega base pair length. CNVs are commonly accepted as a major source for heritable variation as it covers a larger genomic portion and can be considered to be promising causal genetic markers. Genome-wide identification of CNVs were executed in swamp (Manipuri) and riverine (Jaffrabadi) buffalo using Read Depth based approach with reference to Mediterranean riverine buffalo assembly (UOA_WB_1). The present study was conducted to annotate detected CNVs from both the buffaloes. The full gene set (GTF file) of UOA_WB_1 assembly was taken from NCBI and then structural annotation was performed by identifying a consensus list among CNVs and gene set using BEDtools. Further, CNVs were processed for functional enrichment analysis in terms of Gene Ontology (GO) terms and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway with

DAVID software. With reference to *Bos taurus* for functional annotation, GO terms and KEGG pathways were assessed with statistically significant p-value <0.05. Total 2061 and 1999 genes were obtained including 1149 and 1121 protein coding genesin swamp and riverine buffalo respectively. Significant GO terms (Biological Process, Cellular component and Molecular Function) were found to be 18in swamp and 16 in riverine buffalo. There were 6 and 3 significant KEGG pathways in swamp and riverine buffalo accordingly. These genes were found to be associated with production, reproduction,growth and immunity traits

ABST-3-003

SNP MARKERS ENABLED BREED TRACEABILITY OF INDIAN CATTLE USING MACHINE LEARNING ALGORITHMS

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Allocation or assignment tests use genetic information to determine an individual's population membership, providing the most direct methods for determining the population of origin of unknown individuals. SNP chip data has been used for the identification of several breeds/species in recent years, thanks to the rapid development of single nucleotide polymorphisms (SNPs) Bead Chips and the availability of public databases. In the current investigation, we used Bovine SNP 50K chip data to tailor breed-specific SNPs for the target population, i.e., Tharparkar cattle breed via machine learning models for the first time in an Indian animal genomics scenario. We used a total of eight populations in the study, involving several exotic cattle breeds as well. This was done to increase the robustness of the final SNP panel. Machine learning algorithms, a genome-wide association study (GWAS), linkage disequilibrium (LD) analysis, and principal component analysis (PCA) were used to distinguish a target (case) group for comparison with control chicken groups. A total of 216 individuals were available, including 72 of Tharparkar cattle breed after quality control comprising 8,765 SNPs in total. After applying more filter parameters, we had a total of 500 SNPs to work with machine learning models. Moreover, 23, and 48 SNPs were selected as the minimum numbers of markers by the AdaBoost, Bagging Tree, Gradient Boosting Machines, and Random Forest machine learning classification models, which had accuracy rates of 95.2%, 95.2%, 98.4%, and 98.4%, respectively for 23 SNPs panel. For 48 SNPs panel accuracies were as follow, 98.4%, 95.2%, 96.8%, and 98.4%, respectively in same order. The GWAS, PCA, and machine learning algorithms used in this study are efficient in determining the optimal marker combination with the fewest markers that can distinguish the target population from a large number of SNP markers.

ABST-3-004

THE APPLICATION OF ANCESTRAL RECOMBINATION GRAPHS FOR INFERRING EVENTS OF EVOLUTIONARY SIGNIFICANCE

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The ancestral recombination graph (ARG) is an intricate graph structure that gives a complete record of the evolutionary relationships among the sampled orthologous and collinear genomic sequences. Thus, the entire ARG may be viewed as an ordered collection of coalescence and recombination nodes. Coalescence events cause two lineages to merge backward in time, whereas recombination splits lineages into two, resulting in alterations in the genealogy from one genomic region to the next. The recombination process is a powerful

evolutionary force that shapes genes and genomes, leading to the genetic and phenotypic diversity that we see today. As a result, an understanding of recombination is essential for making inferences about the genome structure and phylogenetic processes.The ancestral recombination graphs have the following applications: 1. estimation of the time to the most recent common ancestor 2. assessment of allele age or mutation rate 3. demographic inference (effective population size, gene flow, divergence times) 4. determining local ancestry 5. detecting archaic introgression events 6. identification of sequences under selective sweeps.With the advancement of cost-effective next-generation sequencing (NGS) technologies coupled with information derived from whole-genome sequencing and genome-wide association studies, we now have access to an increasing number of genomes. There are various ancestral recombination graph simulation and inference tools available, including ARGweaver (the most widely used), the IRIS tool, Relate, tsinfer+tsdate, and others. An accurate estimation of the ancestral recombination graph can be valuable in addressing almost every query in population genetics, however, the process of inferring ARGs is a challenging task.

ABST-3-005

DEEP LEARNING VIS-À-VIS GENOMICS AND LIVESTOCK

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Deep Learning is an old term, coined in 1940s but gained popularity in recent times. Thanks to the tremendous increase in the computational powers, the huge data sets being generated are now very well analysed. Here, deep learning plays an essential role and surpasses numerous machine learning approaches in both performance and accuracy. In fact, deep learning methods are a class of machine learning techniques that are capable of identifying hidden complex patterns in large datasets. Impressive advances in this field of analytics embrace their applications ranging from computer vision to natural language processing. A typical deep learning model consists of functional building block known as perceptron which mimics the brain neuron of higher organisms. A perceptron structure includes four parameters i.e., input values, weights and bias, net sum, and an activation function and it shoots the output only when the value of the outcome is greater than that of the threshold value. In a similar way, a group of perceptron's forms a neural network which consists of an input layer to which we have to feed the data, the output of the input layer is then utilized as input for hidden layers through networks and finally the analysis is transferred to the output layer. At the moment several neural networks are in usage such as Artificial Neural Network (ANN), Recurrent Neural Network (RNN), Long Short-Term Memory (LSTM), Generative Adversarial Network (GANs) and Autoencoders etc. ANN comprises of a set of fully connected nodes modelling the stimuli propagation of brain synapses-fire or not -across the neural network, while RNN constitutes connections between nodes form a directed graph along a temporal sequence. LSTM is a variation of the RNNs capable of learning long-term dependencies and actually are designed to avoid the long-term dependency problem. GANs and Autoencoders are more recent architectures that use two neural networks pitting one against the other and reduce the dimensionality of the data with low reconstruction loss. The ultimate goal in many deep learning tasks is to optimize model performance not on the available data (training performance) but instead on independent datasets (generalization performance). Application of deep learning in genomics include predicting sequence specificity of DNA and RNA binding proteins, predicting enhancers and regulating elements, identifying cis-regulatory regions and elements, quantifying methylation status, analysing gene expression and control of splicing. Development of transfer learning and deep generative models play an important in the future of genomic studies. Inpite of their applications, deep learning models face challenges in the field of genomics that include difficulty in interpretation of data, heterogeneity of data, imbalanced class and hyperparameter tuning.

ABST-3-006

STUDIES ON MINERAL MAPPING OF DIFFERENT AREAS OF RANCHI DISTRICT IN JHARKHAND

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The extent of nutritional expressions of qualitative traits depends on the environment of which feeding forms major portion. Availability of macro and microelements in the feed and fodder decide the quality of nutrition in the specific diet of the animals. It also affects the reproductive and eventually productive performance of the animals. Assessment of levels of major and micronutrients in soil which will reflect in feed and fodder resources based on the uptake of the said minerals. After consuming these diet components, animal will get those sources of the minerals by absorbing through blood stream. It becomes necessary to ensure their availability to animal for the balanced nutrition. Hence, it is important to make a mineral mapping to study the mineral contents in soil, feed, fodder and animal blood so that exact status of those minerals can be checked. For this, samples of soil, feed, fodder and blood were collected from 85 families distributed across five locations viz. Bandu, Chund, Itki, Khunti, Ormanji in Ranchi district of Jharkhand which were analyzed for assessing the status of micronutrients in the district. The analysis of soil samples for electrical conductivity, pH, nitrogen, phosphorous, potash, organic carbon indicated values 0.11±0.0098, 6.75±0.014, 255.06±3.20, 31.33±1.00, 149.43±2.00 and 0.50±0.019 respectively. The blood plasma levels of animals from all five centres of Ranchi were almost similar in all centers except iron which was more in Bandu as compared to other centers. All other elements were above the minimum normal range in soil, feed, fodder and animals. Rest of the trace elemental levels were within the normal range.

ABST-3-007

SELECTION OF SNP MARKERS FOR GENOMIC PREDICTION USING GENETIC ALGORITHM

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Genomic Selection (GS) is used to predict genomic estimated breeding values (GEBV) of candidate animals with known genotypes on the basis of a reference population with known genotypes as well as phenotypes. Accuracy of GS is affected by the number of markers, size and structure of reference population, and the prediction model. Genetic algorithms (GA) are computational procedures that start with a random string of variables and use genetic operators to progress towards optimum solution of a function over a number of generations. We used GA to find a subset of SNP markers to maximize the accuracy of genomic selection. The study utilized a public domain dataset on Pig consisting of 3534 animals, 52843 SNP markers and five masked traits - T1, T2, T3, T4, T5 with heritability values 0.07, 0.16, 0.38, 0.58, 0.62. Dataset on 10000 random markers was extracted from the original dataset. RR-BLUP was employed as the objective function of GA. Pearson correlation coefficient between observed phenotypic values and GEBV for a trait was used as a measure of prediction accuracy. Sixty percent of animals were used as training set, 20% as validation set and 20% as test set. Five experiments were conducted using GA and RR-BLUP. GA selected about half of all markers to provide average prediction accuracies (0.065 for T1, 0.46 for T5) that were comparable to the RR-BLUP using all the markers (0.067 for T1, 0.46 for T5). The prediction accuracies using RR-BLUP with 5000 randomly selected markers out of 10000 markers were lower (0.060 for T1, 0.45 for T5) compared to GA. Thus GA selected a subset of markers to provide better prediction accuracy compared to matching number of random markers.

ABST-3-008

IDENTIFICATION OF miRNAS IN THE MAGNUM TISSUE OF INDIGENOUS CHICKEN DURING EARLY LAYING PERIOD AND THEIR MODULATION DUE TO SE SUPPLEMENTATION

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The oviduct of chicken is responsible for the production of egg white and eggshell among the egg components. The magnum region of the oviduct is responsible for the egg white protein production. The present study was undertaken in the magnum tissue of the Aseel and Vanaraja chickens to identify the miRNA-mediated post-transcriptional regulation of mRNAs involved in the synthesis of various egg components during the early laying period (26 weeks) as well as to study the effect of additional 0.3mg of organic Se (Se enriched yeast). Custom miRNA sequencing of the magnum tissue of the oviduct was carried out in Aseel and Vanaraja chicken and a total of 127644010 reads were generated in 4 samples. The quality of raw reads sequenced was checked by using FASTQC and processed using TrimGalore (v: 0.5.0) and Cutadapt and a total of 90486476 reads were obtained. The clean reads were used with Gallus gallusdomesticus reference genome (GCF_000002315.3_Gallus_gallus-4.0_genomic.fna) and chromosomal coordinates of Gallus gallus microRNAs in mirBase (gga.gff3) to predict novel and known miRNA using the miRDeep2. Reads are mapped to the known mature and precursor miRNAs using miRDeep2 to predict the novel miRNAs. A total of 531 and 569 known miRNAs in control and treatment groups of Aseel were identified. Similarly, 566 and 349 known miRNAs respectively were identified in Vanaraja chicken. A total of 50 and 80 novel miRNAs in control and treatment groups of Aseel were identified. Similarly, 78 and 16 novel miRNAs respectively were identified in Vanaraja chicken. Number of miRNAs expressed in Vanaraja is less in the treated group compared to Aseel. The target genes regulated by downregulated miRNAs are more related to the reproduction function in Vanaraja, whereas in Aseel, the genes related to immune function, locomotion and metabolism are more. miRNAs related to growth and albumen production have also been identified in the control and treatment groups of Aseel and Vanaraja chickens.

ABST-3-009

MITOGENOME ANALYSIS OF CATTLE USING HIGH DENSITY SNP ARRAY

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Indicine cattle (*Bos indicus*) play a significant role in the economy of small and marginal farmers, as they are a potential source of milk, draft power and manure. Assessment of population structure and genetic diversity is a basic tool for genetic improvement. Current study was conducted to study genetic diversity and functionality of SNPs in mitogenome using 132 samples representing 7 Indian cattle breeds covering different geographical area and having different utilities *viz.,*milch (Gir, Sahiwal and Tharparkar), dual (Ongole and Hariana), draft (Kangayam) and miniature (Vechur) purposes. Analyses revealed 81 haplotypes with the haplotypic diversity ranging from 0.9333 ± 0.0477 to 0.9883 ± 0.0210 and higher diversity observed within breeds (~93 %). Nucleotide diversity ranged from 0 to 0.0862 ± 0.0446. AMOVA revealed that 2.61% of total variation was among the populations while 97.39% of the variation was found within the populations. F_{ST} values were significantly different for all pairwise combinations, representing ample amounts of genetic differentiation between populations. Multidimensional scaling revealed that the milch breeds belong to the same lineage as compared to clustering of dual- and draft- purpose breeds. Exploration of the functionality of mtDNA variants revealed *ND1, ND2, ND3, NDS, COXI, COX2, CYTB* and *ATP6* as the top genes annotated with mitogenome markers, which participate in biological process (cellular process, immune system, metabolic process), molecular function (catalytic activity, transport activity) and in myriad pathways (ATP synthesis, CCKR signaling, GnRH receptor, Inflammation mediation and Toll receptor signaling). In future, the identified functional variants can be studied further in large scale for efficient utilization in the breeding program.

ABST-3-010

SELECTION SIGNATURES FOR FIBER PRODUCTION ATTRIBUTES IN COMMERCIAL SPECIES

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Natural fibers derived from diverse animal species (sheep, goat, rabbit, yak, llama and alpaca) have gained increased attention in recent years due to their favorable environmental effects, long-term sustainability benefits, and remarkable physical and mechanical properties that make them valuable raw materials used for textile and non-textile production. Domestication and selective breeding for the economically significant fiber traits play an imperative role in shaping the genomes and thus, positively impact the overall productivity of the various fiber-producing species. These selection pressures leave unique footprints on the genome due to alteration in the allelic frequencies at specific loci, characterizing selective sweeps. Recent advances in genomics have enabled the discovery of selection signatures across the genome using a variety of methods. Fiber production has nearly doubled in the past 20 years, rising from 58 million metric tons in 2010 to 109 million metric tons in 2020, with plant fibers and animal fibers accounting for roughly 30% and 1.57 % of the global market share respectively (Textile exchange report, 2021). The increased demand for “green products” manufactured from natural fibers necessitates a detailed investigation of the genomes of the various fiber-producing plant and animal species to identify the candidate genes associated with important fiber attributes such as fiber diameter/fineness, color, length, and strength, among others. Detection of the selection signatures in the genome harboring candidate genes for fiber production and quality traits is achievable with the current technical advances, such as next-generation sequencing (NGS) technologies, high-density SNP arrays, and strong statistical and bioinformatics tools. Knowledge of the genomic regions subjected to selection can facilitate the adoption of optimal genomic selection and breeding programs for the genetic improvement of the targeted species.

ABST-3-011

DETECTION OF GENOME-WIDE COPY NUMBER VARIATION IN MURRAH BUFFALOES

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River buffalo are extremely important globally, especially Murrah breed. It is crucial because of its adaptation to harsh climate conditions and long productive lifespan, which allows it to farm across the countries and convert low-quality feed into valuable milk. In this study, based on the new high-quality buffalo reference genome UOA_WB_1, we firstly investigated the copy number variants in buffalo using Axiom® Buffalo Genotyping Array 90K (Affymetrix, Santa Clara, CA, USA) data, that were accessible for the Murrah breed. To the best of our knowledge of literature it’s the first ever CNV map reported for Murrah breed of buffaloes. A total of 7,937 CNV regions (CNVRs) were detected in 279 buffalo populations with a total length of 944,890,927 bp, with a mean length of 1, 18,636.1 bp. In addition, a total of 1,541 highly significant CNVRs covering 488 genes were detected in the Murrah buffalo population. We detected a set of CNVR-overlapping genes associated with conformation traits, immunity, nerve, milk trait, etc. according to the Animal Genome Cattle database. This study advances the understanding of genomic variation in Murrah buffaloes by constructing the first map of Murrah buffalo CNVs and providing insights into their recent selection and adaptation to the environment. The presence of a set of genes and QTL traits in the CNVRs could be linked to the Murrah buffalo's natural adaptive history as well as a recent selection for milk production.

ABST-3-012

IDENTIFYING AND ANNOTATING SIGNATURES OF SELECTION IN THE BOVINE GENOME FOR UNDERSTANDING ADAPTATION TO VARIOUS CLIMATES

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Selection and domestication have altered the genetic viewpoint of cattle breeds, resulting in a variety of commercially important features such as environmental adaption, appearance, and productivity attributes. In the current research, we have taken the genotyped data on 427 animals consisting of 15 cattle breeds. Therefore, in order to better understand how animals adapt to their environment, we have included indigenous, crossbred and native cattle. For this study, we included laboratory data that was already produced during earlier trials. Those are Frieswal (n = 14), Tharparkar (n = 72) and Vrindavani (n = 72). Additionally, data was also taken from an online data base which includes indigenous breeds like Sahiwal (n = 17); Red Sindhi (n = 10); Kankrej (n = 10); Ongole (n = 20); Hariana (n = 10); Nellore (n = 24); and taurine cattle breeds such as Holstein Friesian (n = 63); Jersey (n = 28); Ayrshire (n = 18); Guernsey (n = 21) and Brown Swiss (n = 24). We employed a total of nine summary statistics, including both intra-population statistics (Tajima's D, CLR, iHS, and ROH) and inter-population statistics (FST, FLK, XP-EHH, hapFLK, and Rsb). We have identified a few potential genes that are being selected to fight off unfavourable environmental conditions. Some of the genes include CLPB in the Frieswal and Ongole breeds, HSPB1 in the Brownswiss and also discovered in the Gir vs. Vrindavani analysis, HSPB2 and CRYAB in the Hariana, AARSD1 in the Guernsy breed, and ST13 in the Ongole breed, respectively. These are useful for binding chaperones, cellular heat response, and chaperone-dependent protein folding. Consequently, it aids in our understanding of how cow breeds are well adapted to our agroclimatic circumstances and rising temperature in the twenty-first century.

ABST-3-013

WHOLE GENOME SNP MINING IN THE QTLS FOR FUNCTIONAL TRAITS IN SAHIWAL CATTLE

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Single Nucleotide Polymorphisms (SNPs), representing a single base change between two individuals at a defined genomic location are the most abundant source of genetic variation. The SNPs in candidate genes and QTL regions contributes to the variation in phenotypes of various quantitative traits. The present study was conducted to identify common variants in functional trait QTLs in cattle. The genomic DNA of 10 Sahiwal animals were sequenced using a reduced representation (ddRADseq) approach and raw sequence reads were obtained. The processed reads were aligned to *Bos taurus* genome and variants were identified. The filtered variants were mapped to the QTLs associated with various functional traits in cattle. The number of SNPS mapped to clinical mastitis QTLs were 1410 SNPs, while the somatic cell score QTLs were having 4355 SNPs. Among the udder and teat type QTLs, the udder cleft was having maximum SNPs in associated QTL regions followed by udder placement and udder attachment. With respect to disease resistance traits, a total of 5068 SNPs were mapped to bovine tuberculosis susceptibility QTLs, while 1345 SNPs were mapped to M. paratuberculosis susceptibility. Among the tropical adaptation traits, tick resistance QTLs were having 7689 SNPs while, QTLs for heat tolerance exhibited 2300 SNPs. The SNPs mapped to different QTLs may be further explored for studying the underlying genetic variation for functional traits associated with tropical adaptation traits in indigenous cattle breeds.

ABST-4-014

A COMPARATIVE APPROACH FOR IDENTIFYING SELECTION SIGNATURE USING NINE DIFFERENTSUMMARY STATISTICS

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This study provides the genomic selection imprints of a total of 427 animals from fifteen different breeds. In the current research, we have taken the genotyped data of fifteen different cattle breeds, including five taurine, two crossbreds, and eight indicine cattle breeds. It includes Tharparkar (n=72); Vrindavani (n=72); Frieswal (n=14); Gir (n = 24); Sahiwal (n = 17); Red Sindhi (n = 10); Kankrej (n = 10); Ongole (n = 20); Hariana (n = 10), Nellore (n = 24) and taurine cattle breeds like Holstein Friesian (n = 63); Jersey (n = 28); Ayrshire (n = 18); Guernsey (n = 21); Brown Swiss (n = 24). Our lab has generated data for Tharparkar, Vrindavani, and Frieswal. These three sets of data were produced from earlier research projects carried out in our lab over the past three to four years. Other data included in our study was taken from an online database. Several areas connected to milk production and adaptability were discovered by this investigation. The nine approaches we applied in this investigation were as follows 1. Integrated haplotype score (iHS), 2. Runs of homozygosity (ROH), 3. F_{ST} approach, 4. Tajima's D, 5. Composite likelihood ratio (CLR), 6. FLK, 7. hapFLK, 8. XP-EHH, 9. Rsb. We discovered 145 (Tajima's D), 208 (CLR), 180 (iHS), 224 (ROH), 128 (F_{ST}), 10 (FLK), 6 (hapFLK), 76 (Rsb), and 68 (XP-EHH) genes using the corresponding approaches, which may be the subject of a selective sweep. Some genes, including EPHA6, CTNNA2, NPFFR2, HS6ST3, NPR3, KCNIP4, LIPK, SDCBP, CYP7A1, NSMAF, UBXN2B, UGDH UBE2K, and DAB1, were shown to be shared by two or more different approaches. These genes are mostly linked to traits related to milk production and adaptability, providing evidence that these traits are the subject of intense positive selection.

ABST-3-015

GENOME-WIDE IDENTIFICATION OF COPY NUMBER VARIATION REGIONS IN INDIGENOUS CATTLE BREEDS OF TAMIL NADU

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Copy number variations (CNVs) are modifications in DNA structure comprising of deletions, duplications, insertions and complex multi-site variants. The read depth-based method implemented in CNVnator was used for calling copy number variant regions (CNVs) on sequenced data obtained from whole genome sequencing from 15 pooled samples belonging to five cattle breeds of Tamil Nadu. A total of 11,605 CNV regions (CNVRs) were identified covering a genome size of 18.63 per cent. Of these, 11,459 were restricted to autosomes. Among which, 11,013were deletions (losses), 353 were duplications (gains) and 93 were complex events. These CNVRs were annotated to 4,989 candidate genes. A total of 8,291 numbers of CNVRs were shared among all the five cattle breeds indicating high degree of admixture between them as also supported by PCA and STRUCTURE analysis. A sum of 1,172 CNVRs were exclusively reported in one or the other breeds that occupy 454 candidate genes. Annotation of candidate genes to QTL revealed many genes related to milk production (*BTN1A1, ABCA1, CTNNA2* and *LAP3*), disease resistance (*TLR4, LPP* and *DNAH8*), adaptability (*SOD1, ASL, CAST* and *SMARCAL1*), growth (*EGFR, NKAIN3*), reproduction (*BRWD1* and *PDE6D*), meat and carcass traits (*MAP3K5, FTO, BCL6, NCAM1* and *EPS15L1*) and exterior (*ATRN* and *MITF*) traits. Gene enrichment analysis based on the gene list retrieved from the CNVRs also disclosed over-represented terms ($p<0.01$) greatly associated with milk fat production. NETWORK analysis had identified 13 putative candidate genes involved in milk fat percentage (*ERBB2, PLCE1* and *PIK3C2G*), Milk fat yield (*PTPN1*), lactation persistency (*MAP3K5*), milk yield (*MAML2*), heat tolerance (*SOD1*), calving ease (*DOCK1, MAML3, PLCB1* and *ESR1*), growth (*EGFR*) and conformation traits (*GRB2*). Four out of five selected CNVRs were validated using real-time PCR.

ABST-3-016

NON-LINEAR MODELLING TO DESCRIBE LACTATION CURVE IN GIR COWS MAINTAINED UNDER SMALLHOLDER DAIRY SYSTEM IN GUJARAT STATE

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The main objective of the present study is to understand the effect of different factors affecting milk yield under the smallholder dairy farmer's production system and to develop lactation curves that will closely mimic the actual production potential of the breed. A total 6991 of test day milk records pertaining 392 Gir cows, collected by performance recorders from 4 different region namely Gir Somnath, Porbandar, Junagadh and Mehsana maintained by 160 smallholder dairy farmers. After thorough data cleaning process, a total of 5967 records related to 326 animals were available for the analysis. A mixed model was used to understand the effect of management and environment factors along with effect of animal. District, Lactation Number (1 to 5) and Lactation Stages (Early, Mid, Late) highly significant ($p<0.001$) for DMY.Also Record Month (Jan,Feb,Mar,Jun,July,Dec)and Record Year(2018 to 2022) not significant for DMY.After thorough literature review, eleven lactation curve models were selected to understand lactation pattern in Gir cows. The adjusted R^2 root mean square error RMSE, Bayesian information criteria (BIC) were used to evaluate the best fit model. After evaluation Ali and Schaeffer model (1987), Gamma Function (Wood 1967), Cubic Model (Dag 2005), Quadratic Cum log model (Khandekar 1956), Mixed log function (1995 a) provided best fit for lactation number 1 to 5. Hence it can be Ali and Schaeffer model function is the best model diagnostic criteria estimating the trend of milk production in Gir cattle.

ABST-3-017

DUCK GENOME EVOLVED AS BETTER RESISTANT TO CHICKEN GENOME AGAINST AVIAN INFLUENZA - REVEALED THROUGH TRANSCRIPTOMICS

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The present study explored the host immune response against avian influenza or commonly known as Bird Flu, when indigenous ducks (Bengal duck) were observed to be better resistant against avian influenza (AI) virus in comparison to Haringhata black chicken and broiler chicken. The greatest concern for AI is that till date no satisfactory medicine or vaccines are available, leading to massive culling of poultry birds causing huge economic loss, and ban on export of chicken products, which emphasise the need develop alternative strategy for control of AI. We attempt to explore the genomics of duck and chicken initially through *in silico* approach of *molecular docking* of *haemagglutinin and neuraminidase surface protein* of AI virus for screening of certain genes, followed by differential mRNA expression profiling of innate immune response genes. In the next step, we attempt to explore the entire genome of both Bengal duck and Haringhata Black chicken and broiler chicken through RNA seq approach of transcriptomics. All the methodologies were followed in appropriate biosecurity measures in BSL3 and ABSL3 laboratories. Certain unique genes were explored when RIGI is expressed only in duck, but not expressed in chicken. Certain other sets of genes are overexpressed in duck, compared to chicken. Exploitation of these unique genes from duck through suitable gene editing technologies may lead to the development of *Bird flu resistant chicken*.

ABST-3-018

DEVELOPMENT OF KRISHNADHARA (NXG) AND TAMRAGIRI (NXF) BIO-FORTIFIED CHICKEN VARIETY ENRICHED WITH COPPER (CU) AND IRON (FE) IN EGGS

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Iron and Copper are the essential micronutrient for haemoglobin synthesis, tissue growth, energy metabolism and oxidative defense. Deficiency of iron, copper causes anaemia, osteoporosis, and low white blood cells count in human being. The optimum level of copper is required for absorption of iron from gastrointestinal tract (GIT). To prevent anaemia, exogenous iron and copper can be taken through diet. Organic iron and copper are the best source, which may be obtained through food such as egg. To enhance iron and copper content in eggs, one way is to develop biofortified chicken variety. In this regard, we adopted egg mineral mining and introgression approach to develop biofortified chicken variety. We assessed21 chicken populations for iron and copper content in egg. The egg iron and copper contents varied from 1.0 to 2.1 mg/100g and also 0.001 to 0.048 mg/100g across the lines, respectively. From these, lines, one male and one female parent line was selected based on their performance. For iron enrichment in eggs, weperformed three 3 crosses (NxF, GMLxIWFand PD4xIWF) were performed. For copper enrichment, five crosses (GhagusxGML, IWKxGML, IWFxGML, NxG&PD4xIWF) were performed using different selected breeds. Two varieties namely, Tamragiri (NxG) for copper (0.07±0.04) and Krishnadhara(NxF) for copper (0.07±0.01)and iron (2.52±0.18) present in eggs were the best crosses. We have also analysed the copper and iron contents in eggs of these two varieties under field conditions, where similar trends were observed. In this study, we succefully developed two potential varieties that can produce higher egg iron, copper content and good number of eggs.

ABST-3-019

A NON-LINEAR MODELING TO DETERMINE THE LACTATION CURVE FOR TEST DAY MILK YIELD, FAT YIELD AND FAT PERCENT IN CROSSBRED COWS REARED UNDER SMALLHOLDER DAIRY SYSTEM IN JHARKHAND STATE

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The objective of the study was to determine the factors influencing the production traits of crossbred cows in Jharkhand state and understand the lactation curve of test day milk yield, fat yield and fat percent for the crossbred cows in smallholder production system in Jharkhand state. The data of 131,751 milk records, and 31,667 fat percent pertaining to 4,119 and 2,117 crossbred cows, respectively were collected during October 2016 June 2022 from 4 distritcs Jharkhand state. The fat yield was calculated by multiplying the actual test day milk and fat percent. Cows with four or more monthly TD milk yield between 8 and 340 days after calving, in at least one lactation were retained while data quality control procedure remove cows with an average TD milk yield greater than 4 standard deviations (SD) above the population average. Lactation stage is divided into three categories 8 to 90 days (early), 91 to 180 days (mid) and 181 to 340 (late). Season was categorized into summer, Monsoon & Winter. A total of 13 lactation curve models were carried out to determine the best model fit for present data. The best model was chosen using goodness of fit criteria like higher adjusted R^2, low BIC and low root mean square error. The linear mix model was used for analysis of repeated records on same animals. The season was excluded from the analysis due to non-significant effect. District, lactation stage and parity were used as fixed effect, and found significantly affected all the traits. The Ali and Schaeffer model was found to be best suited for all three traits and could be used for prediction of missing records.

TECHNICAL SESSION-IV

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ABST-YS-001

GENETIC ANALYSIS OF GROWTH TRAITS IN SALEM BLACK GOAT UNDER FARM CONDITIONS

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Salem Black goats have considerable production potential under semi-arid, tropical conditions of north-western agro-climatic zone of Tamil Nadu. Evaluation of the growth performance of Salem Black goats at Mecheri Sheep Research Station, Pottaneri, Salem district, Tamil Nadu with data (n=1011) accrued over 19 years was carried out. The growth traits studied *viz*., birth weight and periodical body weights at weaning ,6-month ,9-month and 12-month as well as pre weaning (0-3) and post weaning average daily gain (ADG) (3-6, 6-9, 9-12, 3-12) were assessed in SPSS (v.26.0). Least squares mean for birth, weaning, 6-month, 9-month and 12-month weight were 1.952 ± 0.052, 8.252 ± 0.331, 11.901 ± 0.429, 15.450 ± 0.363, 20.669 ± 0.486 kg respectively. Pre weaning ADG (0-3) was 69.417 ± 3.604 g/day and post weaning ADG at 3-6, 6-9, 9-12, 3-12 were 36.745 ± 3.889, 25.943 ± 2.786, 52.641 ± 4.820, 40.586 ± 1.688 g/day respectively. The heritability estimates for birth, weaning, 6-month, 9-month and 12-month weight by REML using WOMBAT were 0.177 ± 0.066, 0.094 ± 0.055, 0.111 ± 0.068, 0.123 ± 0.082, 0.181 ± 0.122 respectively, indicating that growth traits were low to medium heritable in Salem Black goats.

ABST-YS-002

MELATONIN RECEPTOR (*MTNR*1*A*) GENE POLYMORPHISM AND THEIR ASSOCIATION WITH REPRODUCTIVE TRAITS OF BUFFALOES

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The Melatonin receptor (*MTNR*1*A*) is primarily related to reproduction function and predicted to be candidate genes for reproduction traits in buffaloes. A total of 204 buffalo blood samples from different genetic groups were collected along with data on age at first calving and calving intervals to investigate the genetic polymorphism of *MTNR*1*A* gene by PCR-RFLP method. At the *MTNR*1*A* / *Hpa*I locus, three genotypes viz., *CC*, *CT* and *TT* identified, had frequencies of 0.225, 0.505 and 0.270 respectively. The allele frequencies of *C* and *T* alleles were 0.478 and 0.522 respectively in the pooled population. The representative buffalo population existed in Hardy-Weinberg equilibrium. The distribution of *MTNR*1*A* / *Hpa*I genotypic frequencies revealed a heterozygosity value of 0.505, effective number of alleles (Ne) was 1.996, PIC value was 0.4990. The overall means of age at first calving and first to fourth calving intervals were 1385.76 ± 24.31, 587.76 ± 16.00, 586.66 ± 34.37, 520.44 ± 37.32 and 558.35 ± 40.39 days respectively. Association analysis of *MTNR*1*A* / *Hpa*I locus using General Linear Model revealed significant effect of location (P<0.05) on age at first calving, first calving interval and second calving interval. Individuals with the *CT* and *TT* genotypes (1356.78 ± 33.03 and 1378.38 ± 37.66 days) had shorter age at first calving than *CC* genotype and the differences were statistically significant (P<0.05). The buffaloes with *CC* genotype had shorter fourth calving interval (441.25 ± 62.16 days) than *CT* and *TT* genotypes. Individuals with the *CC* genotype had shorter age at first calving (P<0.05) and also shorter calving interval however, the difference was not statistically significant in buffaloes.

ABST-YS-003

GROWTH HORMONE GENE POLYMORPHISMS AS CANDIDATE MARKERS FOR CARCASS TRAITS IN KUTTANAD DUCKS OF KERALA

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A study was conducted to determine the genetic variability of the duck-growth hormone gene and its association if any, with carcass traits like pre-slaughter live weight and percentages of dressing weight, breast, leg and giblet yield in 30 Kuttanad dual-type native ducks of Kerala. The DNA pooling sequencing assay of exon 3 and partial intron 3 (227 bp) regionrevealed a novel SNP g.190 G>A(c.IVS3+19A>G or c.288+19A>G) and further genotyping of the SNP by HRM technique revealed three distinct melt curves corresponding to three genotypes *viz*., AA, AG and GG. The AA genotype had significantly higher ($p<0.05$) pre-slaughter body weight and dressed weight percentage than the other genotypes. PCR-SSCP and sequencing analysis of exon 5 and partial intron 4 (366 bp) region revealed one novel SNP g. 74 G>A (c.IVS4-24 G>A or c.451-24 G>A) with two alleles G and A, and two genotypes, GG and GA in the population. The GA heterozygotes were superior ($p<0.05$) in dressing and breast yield percentages while the GG homozygotes had a greater giblet yield percentage. Two SNPs *viz*., g. 31G>A (c.IVS3+67 G>A or c.288+67G>A) and g.59 C>T (c.IVS3+95 C>T or c.288+95 C>T) were revealed in intron 3 (355 bp) region yielding two diplotypes*viz*., GC/GC and AT/AT. Ducks with GC/GC diplotype had higher pre-slaughter body weight and breast yield than AT/AT diplotypes ($p<0.05$).It can be concluded that the four single nucleotide polymorphisms identified in duck-growth hormone gene under study can serve as a potential markers for the selection of Kuttanad ducks for carcass traits.

ABST-YS-004

TWAS REVEALED SIGNIFICANT CAUSAL LOCI FOR MILK PRODUCTION AND ITS COMPOSITION IN MURRAH BUFFALOES

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Milk is the most complex trait in dairy animals, and it's difficult to identify all causal variants contributing to it as their effect sizes are too small to be detected at current GWAS sample sizes.However, with the help of Transcriptome-wide association studies (TWAS) a fine map of eQTLs can be prepared. In an animal study, this is a maiden attempt to associate milk production in buffaloes using TWAS. Murrah buffaloes maintained at the institute herd were simultaneously studied through genomic profile (genotyped by sequencing) from blood and transcriptome profiling of a sub-sample from the secretory mRNA in the milk fat of buffaloes. These sub-samples, also genotyped for SNP markers, were treated as reference animals for the gene expression prediction in test animals. Gene expression prediction was performed using Elastic-Net and Dirichlet Process Regression (DPR) model with 5-fold cross validation and without any cross-validation. DPR model without cross-validation predicted higher number of genes. TWAS in test individuals based on predicted gene expression identified significant association of one unique gene for Fat%, and two unique genes for SNF% at Bonferroni corrected threshold. The false discovery rates (FDR) corrected *P*-values of top ten SNPs identified through GWAS was comparatively higher than TWAS. Gene ontology of TWAS identified genes was performed to understand the function of these genes, it was revealed that milk production and composition genes were mainly involved in Relaxin, AMPK, and JAK-STAT signaling pathway, along with CCRI, and other metabolic processes. The present study indicates that TWAS has better statistical power compared to GWAS in detecting key biological signals associated with milk production and its composition traits. Hence, it is concluded that TWAS can be effectively used to identify genes and cis-SNPs in a population which can be used for fabricating a low-density genomic chip for predicting milk production in Murrah buffaloes.

ABST-YS-005

SITE DIRECTED MUTAGENESIS OF PROLACTIN GENE IN CHICKEN THROUGH CRISPR/CAS9 MEDIATED GENE EDITING

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The key factor in regulating reproductive physiology in birds is the prolactin (PRL) hormone, which is released from the anterior pituitary gland, restricts egg production in chicken. Therefore, we hypothesised that reducing the expression of this gene might increase egg laying in chicken. The goal of the current study was to use CRISPR/Cas9 gene editing tools to edit the prolactin gene *in vitro* in pituitary primary cell culture. A complete construct of CRISPR/Cas9 linear vector was designed to target exon 2 and exon 4 of chicken PRL gene. The two constructs were were transfected in to established pituitary cell culture and subsequently, genomic DNA was extracted and amplified for exon 2and exon4 of PRL gene. The sequencing results revealed changes in nucleotide sequence as compared to the control group of the pituitary cells and the editing were observed at 46 (GGG>GAC), 48th (CTT>CCC), 49th (TTT>AAT) and 50th (GAT>GGG) codon of the edited group. Accordingly, the amino acid changes in the edited cells were observed as 46.G>D, 48. L>P, 49.F>N and 50.D>E. Similarly, in exon 4 alterations in the nucleotide were found at the 139th (CCA>CGC), 140th (GAT>CGC), 141st (ACC>ATA), 142nd (ATT>CCA), 143rd (CTC>TTC) and 144th (TGG>TCT) codons. The amino acid changes were observed at 139.P>R, 140.D>R, 141.T>I, 142.P>I, 143.L>F, 144.W>S and further, a stop codon was observed at the 147th codon position, due to frame shift mutation, which resulted in ceasation of translation. Further, PRL mRNA expression of control as well as PRL edited cells *in vitro* showed reduced expression of PRL gene in knockout chicken pituitary cells. Further, transcriptome profiling of PRL knockout cells in vitro showed a total of 75 differentially expressed genes (DEG) which were involved in PRL pathway and egg production associated processes.Finally, it is concluded that genome editing technology has the potential to edit gene for its further impact on regulating associated physiological processes.

ABST-YS-006

RNAi MEDIATED *IN VIVO* SILENCING OF TWO LIPOGENIC GENES FOR REDUCED SERUM AND EGG CHOLESTEROL IN CHICKEN

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In poultry, intensive genetic selection for rapid growth and egg production unintentionally selected for increased fat content in tissues. The study was aimed to knockdown the two important genes of *de novo* fatty acid biosynthesis viz. Acetyl Co-A Carboxylase A *(ACACA)* and sterol regulatory element-binding protein 1 *(SREBP1)* through shRNA mediated RNA interference (RNAi). It is a widely used post transcriptional silencing mechanism for suppressing expression of the target gene. Five shRNA molecules each were designed for each gene targeting the coding sequence of the respective genes and cloned in U6 promoter guided pENTR/ U6 vector (Invitrogen) to prepare RNAi cassette. Two best shRNA molecules were identified based on *invitro* study conducted under cell culture system for *ACACA* and *SREBP1* genes. Further, the recombinant DNA was transferred to the host genome through sperm mediated gene transfer and transgenic chicken were produced. The serum total cholesterol, triglycerides, HDL and LDL cholesterol in knock down birds was significantly lower by 23.8, 35.6, 26.6 and 20.9%, respectively in *SREBP1* knock down birds compared to the control birds. The egg total cholesterol and LDL cholesterol content was significantly lower in both *ACACA* and *SREBP1* transgenic birds by 14.3 ($P<0.05$) and 13.2% ($P<0.05$), and 10.4 and 13.7% ($P<0.05$), respectively compared to the control birds. In addition, we also observed that knockdown of lipogenic genes did not affect the level of steroid hormones in the knock down birds. Finally, it is concluded that the silencing of two lipogenic genes (*ACACA* and *SREBP1*) through RNAi reduced both serum and egg cholesterol content in knock down birds.

ABST-YS-007

EVALUATION OF MACHINE LEARNING ALGORITHMS FOR THE PREDICTION OF GENETIC MERIT

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ABSTRACT
As the amount of data on farms grows, it is important to evaluate the potential of artificial intelligence for making farming predictions. Considering all this, this study was undertaken to evaluate various machine learning (ML) algorithms using 52-year data for sheep. Data preparation was done before analysis. Breeding values were estimated using Best Linear Unbiased Prediction. 12 ML algorithms were evaluated for their ability to predict the breeding values. The variance inflation factor for all features selected through principal component analysis (PCA) was 1. The correlation coefficients between true and predicted values for artificial neural networks, Bayesian ridge regression, classification and regression trees, gradient boosting algorithm, K nearest neighbors, multivariate adaptive regression splines (MARS) algorithm, polynomial regression, principal component regression (PCR), random forests, support vector machines, XGBoost algorithm were 0.852, 0.742, 0.869, 0.915, 0.781, 0.746, 0.742, 0.746, 0.917, 0.777, 0.915 respectively for breeding value prediction. Random forests had the highest correlation coefficients. Among the prediction equations generated using OLS, the highest coefficient of determination was 0.569. A total of 12 machine learning models were developed from the prediction of breeding values in sheep in the present study. It may be said that machine learning techniques can perform predictions with reasonable accuracies and can thus be viable alternatives to conventional strategies for breeding value prediction.

ABST-YS-008

STATISTICAL MODELLING AND GENETIC EVALUATION OF GROWTH CURVE PARAMETERS IN BLACK BENGAL GOATS (*Capra hircus bengalensis*)

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The study was conducted on the available records of 10148 Black Bengal kids from the adopted villages under the project “AICRP on Goat Improvement, Black Bengal Field Unit, Kolkata during 2018-2019. The influence of genetic and non-genetic factors on the body weight from birth to 12 months of age was analysed by using Mixed Model Least-square and Maximum Likelihood Computer Program. The year of kidding, sex and type of birth had significant effect ($p<0.05$) on growth performance. But, the effect of season and parity were found to be non-significant over the body weights at 9 and 12 months. The estimated heritability of weight at birth, 3, 6, 9 and 12 months of age were 0.515 ± 0.507, 0.247 ± 0.169, 0.325 ± 0.548, 0.511 ± 0.322 and 0.311 ± 0.209, respectively. Positive genetic correlations among the periodical body weights revealed that mass selection of kids on the basis of weight upto 3 months can be a good criterion for achieving genetic gain in the future. Monomolecular, Three Parameter Logistic, Exponential, Gompertz and Richards models were used to compare the different growth curve parameters viz. asymptotic weight (a), scale parameter (b), maturity index (k) and point of inflexion (m). Based on the goodness of fit criteria, Richards model was considered as the best model to study growth curve parameters in Black Bengal kids since it had higher R^2 and lower RMSE and SSE values and can be used for formulating breeding and management for economic goat farming.

ABST-YS-009

GROWTH PERFORMANCE OF LOCAL GOAT IN SOUTHERN ODISHA

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There are around 64 lakh goat population in Odisha with Ganjam as the only registered breed having a population of 4 lakh. Others lesser known breeds include Malkangiri, Ghumusari and Narayanpatna and

other nondescript population. Many non-descript goat populations which is the result of thousand years of selection and development in the process of domestication suiting to local agro-climatic conditions have been contributing to the livelihood of the stakeholders since generations. All the goat breeds in southern Odisha are predominantly meat type and are medium in size. Ghumusari is black in colour whereas goats of Malkangiri and Narayanpatna breeds are mostly brown, however almost all coat colours ranging from shades of black & brown to white are seen. The flock size varies from 5 to 35 and survive on natural food resources. The females get sexually matured at 9 to 11 months of age and drop their first kid at maximum of 18 months. All three goat types give multiple births in which 60% takes place from second kidding onwards. The average body weight of Malkangiri males at 3,6,9 and 12 months of age are 8.12±0.23, 11.25±0.48, 13.87±0.85 and 16.82±0.37 kg respectively, whereas, for female the corresponding values are 7.74±0.24, 10.67±0.52, 12.88±0.67 and 16.12±0.44 kg, respectively. The average body weight of Ghumusari males at 3–6 months of age is 8.60 kg whereas at 7–12 months of age, it becomes 13.25 kg. Likewise, for their female counterparts the corresponding values are noted to be 8.15 and 12.07 kg, respectively. The adult female and male animals of Ghumusuri breed of more than 18 months of age weigh around 19.88 to 20.86 kg. Similarly corresponding values/estimates of adult Narayanpatna goats are estimated as 32.80±6.82 kg in males and 27.33±0.61 kg in females.

ABST-YS-010

POLYMORPHISM IN THE MINIMAL PROMOTER REGION OF ELONGATION OF VERY LONG CHAIN FATTY ACIDS PROTEIN 2 (*ELOVL2*) GENE AND ITS EFFECT ON SERUM TRIGLYCERIDES IN LAYER CHICKEN

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Poly unsaturated fatty acids (PUFAs) especially ω-3 and ω-6 are important components of cell membranes and are precursors to many other substances in the body such as those involved in regulating blood pressure and inflammatory responses. In mammals, fatty acids upto 16 carbons (palmitic acid) in length are synthesized by fatty acid synthase (FAS). A significant amount of the fatty acids (FAs) produced by FAS as well as fatty acids taken up from diet are further elongated into long chain fatty acids containing 18 carbon atoms or longer i.e., very long chain fatty acids (VLCFA). Formation of VLCFA is mainly performed in the endoplasmic reticulum (ER) by membrane-bound enzymes. All these enzymes are classified as belonging to a gene family (ELOVL) involved in the biosynthesis of very long chain fatty acids. The enzyme elongation of very long chain fatty acids protein 2 *(ELOVL2)* was found to be play a crucial role in the long-chain fatty acids elongation cycle. This investigation was carried out with the aim of elucidating the polymorphism in the minimal promoter region of *ELOVL2* gene and its relation with serum triglycerides in 150 control layer (CL) chicken (White Leg Horn breed random bred for 13 generations) at DPR, Hyderabad. A total of 8 haplotypes and 11 haplogroups were detected in promoter region of *ELOVL2* gene. Haplotype H5 was the predominant (0.348) and H3 was the least frequent (0.007). Association study revealed that the haplogroups had a significant association with serum triglycerides level. The birds containing H1H2 haplogroup had the highest (161.85±39.28 mg/dl) and H5H9 haplogroup had the lowest (111.77±5.82 mg/dl) triglycerides content in serum.In conclusion, the results in this study provided evidence that the polymorphism of *ELOVL2* gene had effect on serum triglycerides.

ABST-YS-011

DEVELOPMENT OF MODIFIED BrdU RESISTANT VERO CELL LINE

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Use of cell culture has been diversified in many fields like molecular biology studies, virus cultivation, antiviral,

cell biological, biochemical, toxicological and pluripotent stem cells as a therapy. Among the cell lines, Vero cells are most widely used, they are continuous, anchorage-dependent mammalian cells with a variety of uses in the molecular biology, and viral vaccines production. Thymidine kinase, a phosphotransferase enzyme, is essential for DNA synthesis and cell division. It is utilized in gene therapy as a suicide gene, as a tumour marker gene, for cell division detection, as an antiparasitic, as a selection marker in monoclonal antibodies production and in numerous antiviral medications. Using the Clustered Regularly Interspaced Palindromic Repeat/CRISPR-associated protein 9 techniques, the TK gene was knocked down in Vero cells to generate the TK-ve Vero cell line. Selection of the Vero TK-ve cell line using 5'-bromo-2'-deoxyuridine (BrdU) assay was optimized. All wild type Vero cells died within 15 days in the presence of the appropriate BrdU concentration, generating only Vero TK-ve cells. Sequencing confirmation of the single clone from the mixed TK-ve population of cells revealed that asingle bp insertion in the exon, led to the frame-shift inactivation of the TK gene. These Vero TK-ve cells can be used to select and propagate any recombinant viruses that have been modified to function in Vero cells.

ABST-YS-012

ASSESSMENT OF LINKAGE DISEQUILIBRIUM AND HAPLOTYPE BLOCK STRUCTURE IN INDIGENOUSCATTLE BREEDS OF TAMIL NADU USING WHOLE GENOME SEQUENCE DATA

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Future progress in animal genomics will enable genome-wide searches for polymorphisms linked to both qualitative and quantitative traits of Indigenous cattle breeds. This study would help to identify the genetic markers that tag the actual causal variants in the population by using results of linkage disequilibrium (LD) and haplotypes analysis useful to known the nucleotide sequences along the chromosome that are either preserved intact or separated by recombination over time in an evolution of these breeds and to aid investigators in localizing disease-resistant genes in the indigenous cattle population. A total of 79 animals grouped into 15 pooled samples were utilized in this investigation and were subjected to whole genome sequencing using Illumina NovaSeq TM 6000 and Illumina HiSeq 2500. The LD and haplotype block structure in native cattle breeds ofTamil Nadu were analysed both genome-wide as well as chromosome-by-chromosome.For a total of 62,095,778 pair-wise single nucleotide polymorphisms (SNPs), the overall mean linkage disequilibrium (LD) measured by r^2 was 0.484 ± 0.246, and the median r^2 was 0.493.A total of 4,13,277 haplotype blocks which covered 2.34 per cent of the autosomal genome were identified. There was a total of 15,89,118 SNPs distributed within the haplotype blocks covering a total length of 53.62 Mb.In overall, these results would support genome-wide association studies, genomic selection, organisation, and implementation of initiatives for indigenous cattle breed development and conservation in Tamil Nadu

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7	143	137	139	17	119	119	0.9	0.75
14	325	286	306	28	196	315	1.0	1.00
21	585	520	553	55	385	700	1.3	1.25
28	910	780	845	85	595	1295	1.5	1.30
35	1300	1105	1203	110	770	2065	1.7	1.35
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49	2340	2015	2178	155	1085	4060	1.9	1.70

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	Weight			Feed Bird		Cumulative		
wks	Males	Females	Average	Per Day	Week	Feed	Fcr	Mortality %
1	110	105	107	15	105	105	0.98	0.75
2	250	220	235	25	175	280	1.19	1
3	450	400	425	50	350	630	1.48	1.25
4	700	600	650	75	525	1155	1.78	1.3
5	1000	850	925	100	700	1855	2.01	1.35
6	1450	1150	1300	125	875	2730	2.1	1.5
7	1800	1550	1675	150	1050	3780	2.26	1.7
8	2200	1900	2750	160	1120	4900	2.28	1.9

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Age at Maturity	140days
Age at 50% Production	154days
Age at Peak Production	190days
Peak Production	93%
Hen Housed eggs to 80weeks	345eggs
Color of Eggs	Dark Brown
Average Egg weight	60gms.
Body weight at maturity	1650gms
Body weight at end	2.2kgs
Feed to 20weeks	7kg
Feed consumption during Lay	120gms/day.

INDBRO ASSEEL

AGE DAYS	MALES	FEMALES	AVERAGE	FEED/D	FEED/WK	CUM FEED	FCR	MORTALITY
7	69	51	60	10	70	70	1.167	0.75
14	92	68	80	15	105	175	2.188	1
21	161	119	140	25	175	350	2.500	1.3
28	265	196	230	30	210	560	2.435	1.4
35	345	255	300	40	280	840	2.800	1.5
42	495	366	430	50	350	1190	2.767	1.6
49	745	495	620	60	420	1610	2.597	1.7
56	923	697	810	65	455	2065	2.549	1.8
63	1081	849	965	75	525	2590	2.684	1.9
70	1219	901	1060	85	595	3185	3.005	2
80	1357	1003	1180	95	665	3850	3.263	2.1
90	1495	1105	1300	105	735	4585	3.527	2.2
100	1668	1233	1450	110	770	5355	3.693	2.3

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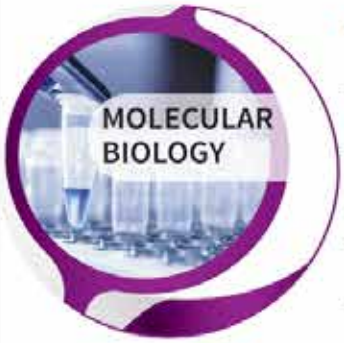

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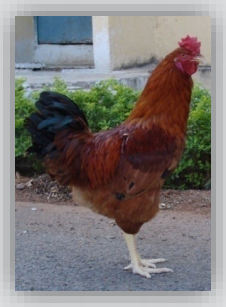

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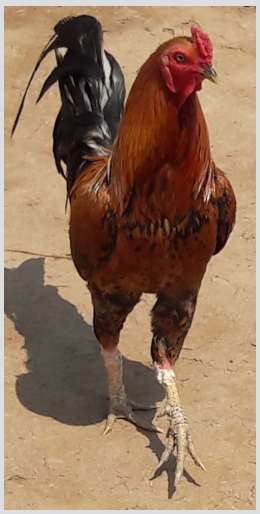
- Produce 140-150 eggs
- Presence of native inheritance



AICRP varieties
- Pratapdhan
- Kamrupa
- Narmadanidhi
- Jharsim
- Himsamridhi

भाकृअनुप
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