Compendium of Abstracts

International Conference

on

“Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning”

November 13-14, 2025

Biswa Bangla Convention Centre, New Town, Kolkata

Organized by

Department of Animal Genetics & Breeding
West Bengal University of Animal and Fishery Sciences
37 & 68, K.B. Sarani, Kolkata-700 037 INDIA

Under the Aegis of

Indian Society of Animal Genetics and Breeding (ISAGB)

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- **Livestock & Aquaculture** – Improving productivity, animal health, and nutrition through better genetics, vaccines, and market access.
- **Agriculture Delivery Systems** – Strengthening soil, seed, extension, and market systems to ensure farmers have access to quality inputs and services.
- **Adaptive & Equitable Food Systems** – Promoting gender equity, climate adaptation, and nutrition through inclusive programs.

Contact: www.gatesfoundation.org
Agricultural Development | Gates Foundation

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Cover & back page designed by Intech Printers & Publishers
Printed by: AVA Enterprise & Associates

सत्यमेव जयते

राज्यपाल, पश्चिम बंगाल
Governor of West Bengal
রাজ্যপাল, পশ্চিমবঙ্গ

MESSAGE

It is heartening to know that an International Conference ISAGBCON-2025 on "Precision Animal Breeding through Artificial Intelligence and Machine Learning" and XIX Annual Convention of the Indian Society of Animal Genetics and Breeding (ISAGB) is being organised by the West Bengal University of Animal and Fishery sciences in collaboration with Indian Society of Animal Genetics and Breeding (ISAGB) in Kolkata during November 13-14, 2025.

The livestock sector is a crucial component in India's agrarian economy and rural livelihoods. Through the National Livestock Mission, the Government of India has given immense boost to the livestock sector across the country. The Mission focuses on generating employment, promoting entrepreneurship opportunities in the livestock, poultry, sheep, goat, and piggery sectors, and increasing per-animal productivity through breed development, and feed and fodder development. Other key initiatives include the Rashtriya Gokul Mission for indigenous bovine breeds and the Animal Husbandry Infrastructure Development Fund for large-scale infrastructure projects and support investment in infrastructure for dairy and meat processing, animal feed plants, breed improvement, and waste management.

I am confident that the stakeholders of the livestock sector will make the most of these initiatives and schemes of the Government.

While the Government has created a support and infrastructure base the educational and research institutions must come forward and contribute their part in 'Lab to Field' initiative. In this direction, the integration of Artificial Intelligence and Machine Learning into animal breeding that has the potential to revolutionize traditional livestock management by enabling data-driven decision-making, enhancing genetic selection and promoting sustainable production systems must be encouraged.

राज्यपाल, पश्चिम बंगाल
Governor of West Bengal
রাজ্যপাল, পশ্চিমবঙ্গ

It is befitting and also heartening to note that the Conference is being held in West Bengal, that has been in the vanguard of scientific and intellectual advancements. I am sure the experts assembled here will deliberate and exchange notes on the latest cutting-edge technologies and techniques in this very crucial sector. I am confident that at the end of the day meaningful collaborations and innovative solutions will emerge that will give further impetus and direction in the advancement of precision animal breeding in India and overseas.

I extend my best wishes to the organisers, participants and delegates for the successful conduct of the conference and hope that it will generate impactful outcomes for the livestock sector and rural development.

Dr. C. V. Ananda Bose

09.11.2025

শ্রী স্বপন দেবনাথ
ভারপ্রাপ্ত মন্ত্রী
প্রাণী সম্পদ বিকাশ বিভাগ
পশ্চিমবঙ্গ সরকার

Sri Swapan Debnath
Minister-in-Charge
Animal Resources Development Department
Government of West Bengal

No. 489/MIC/ARD/25

Dated 29th October, 2025.

MESSAGE

I am delighted to know that Department of Animal Genetics & Breeding, WBUA&FS is going to organize the XIX Annual Convention of ISAGB and International Conference on "Precision Animal Breeding through Genomics, Artificial Intelligence, and Machine Learning" in collaboration with the Indian Society of Animal Genetics & Breeding (ISAGB) on and from 13th to 14th November 2025, at the Biswa Bangla Convention Centre, Kolkata.

Livestock farming has always been an integral part of rural livelihood and nutritional security in India, particularly in West Bengal, where smallholders and marginal farmers form the backbone of animal husbandry activities. The emergence of Artificial Intelligence (AI) and Machine Learning ((ML) offers unprecedented opportunities to revolutionize traditional breeding and management systems through data-driven decision-making, genomic prediction, and precision farming approaches.

The theme of this conference is highly relevant and timely, as it aligns with our collective goal of achieving sustainable livestock development through scientific innovation and technological integration.

My heartfelt greetings to the organizers and wish a grand success of the XIX Annual Convention of ISAGB & the Conference.

(Swapan Debnath)

Sri Swapan Debnath
Minister-in-Charge
Animal Resources Development Department
Government of West Bengal

Dr. Tirtha Kumar Datta
Vice Chancellor
WBUA&FS

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প্রদীপ কুমার মজুমদার
ভারপ্রাপ্ত মন্ত্রী
পঞ্চায়েত ও গ্রামোন্নয়ন দপ্তর এবং
সমবায় দপ্তর
পশ্চিমবঙ্গ সরকার

Pradip K Mazumdar
MINISTER-IN-CHARGE
Department of Panchayats &
Rural Development and
Department of Co-operation
Govt. of West Bengal

06/11/2025

MESSAGE

I am pleased to convey my warm greetings and best wishes to all participants, organizers, and distinguished guests attending the XIX Annual Convention of the Indian Society of Animal Genetics and Breeding (ISAGB) and the International Conference ISAGBCON-2025 on "Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning," being hosted by the West Bengal University of Animal and Fishery Sciences in Kolkata on 13th and 14th November, 2025.

Livestock rearing forms a crucial component of the rural economy, contributing significantly to income generation, employment, and nutritional security of millions of households across India. In West Bengal, where the Panchayats and Rural Development Department work closely with local self-governments to uplift rural communities, the adoption of scientific tools such as Genomics, Artificial Intelligence (AI) and Machine Learning (ML) can bring about a paradigm shift in productivity and profitability.

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These technologies can help optimize:

- Improved prediction of breeding outcomes.
- Shorter breeding cycles through early selection.
- Genomic insights into disease resistance and stress tolerance.
- Optimized resource use and reduced environmental footprint.
- Better productivity and reduced losses from disease or inefficiency.

Thus, these can improve the entire breeding programs, improve animal health and management, and thereby strengthen the rural economy. However, the use of these technologies be fraught with challenges, viz.

- Need for large, standardized datasets.
- High investment in genomic testing and computing.
- Need for interdisciplinary expertise combining genetics, data science, and animal husbandry.

The Panchayats and Rural Development Department recognize the importance of such innovations in strengthening grassroots institutions and ensuring inclusive growth.

The conference theme is both timely and forward-looking, underscoring the need to integrate digital innovations with traditional livestock practices to promote sustainable rural development.

I am confident that the deliberations during this international event will lead to actionable strategies that empower farmers, enhance capacity building, and foster inclusive growth in the livestock sector.

I congratulate the organizers for their commendable initiative in bringing together scientists, policymakers, and stakeholders on a global platform and extend my best wishes for the success of the conference and its lasting contribution to rural prosperity through precision animal breeding.

Pk Mazumdar
Pradip K Mazumdar

Shri Tirtha Kumar Datta
Vice Chancellor
West Bengal University of Animal & Fishery Sciences
68, Kshudiram Bose Sarani,
Kolkata - 700037

कृषि वैज्ञानिक चयन मंडल
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डॉ. संजय कुमार एफ एन ए, एफ एन ए एस सी, एफ एन ए ए एस सी, एफ सी आई एस आई
अध्यक्ष

Dr. Sanjay Kumar FNA, FNASc, FNAASc, FCISI
Chairman

Date: 28/10/2025

MESSAGE

I am pleased to learn that the Indian Society of Animal Genetics and Breeding (ISAGB), in collaboration with the West Bengal University of Animal and Fishery Sciences, is organizing the XIX Annual Convention of ISAGB and the International Conference ISAGBCON-2025 on "Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning," to be held on November 13-14, 2025, in Kolkata.

The theme of this conference aligns with India's national vision of developing resilient, productive, and sustainable livestock and poultry systems that support rural livelihoods and nutritional security. With one of the world's largest livestock populations and a rapidly expanding poultry sector, the need for scientific innovation in breeding is both timely and crucial.

Precision breeding, powered by genomics, AI, and machine learning, offers immense potential to enhance genetic gains, improve disease resistance, and boost production efficiency. As the apex body for recruiting and nurturing agricultural scientists, the ASRB recognizes the importance of such interdisciplinary efforts that blend technology, innovation, and national priorities.

I am confident that ISAGBCON-2025 will stimulate valuable dialogue, collaboration, and innovation, strengthening India's animal breeding research and its contribution to sustainable agriculture. My best wishes to the organizers for the grand success of this important conference.

(Sanjay Kumar)

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डा. राघवेंद्र भट्टा
उप महानिदेशक (पशु विज्ञान)
Dr. Raghavendra Bhatta
Deputy Director General (Animal Science)
M. V. Sc. Ph.D., Postdoctorate (Japan, USA)

No. AS/PS/DDG(AS)/Message/2025
Dated 6th November, 2025

MESSAGE

I am delighted to learn that the International Conference on 'Precision Animal Breeding through Genomics, Artificial Intelligence, and Machine Learning' is being organized by the West Bengal University of Animal and Fishery Sciences, in collaboration with the Indian Society of Animal Genetics and Breeding (ISAGB), in Kolkata during November 13–14, 2025.

India's livestock and poultry sectors form a vital pillar of the nation's agricultural economy, contributing significantly to food security, rural livelihoods, and income generation. With one of the world's largest livestock populations and a rapidly expanding poultry industry, our country stands at the crossroads of immense opportunity and multifaceted challenges. To meet the growing demand for animal protein and ensure sustainable growth, it is essential to embrace cutting-edge breeding technologies that enhance genetic potential, improve disease resistance, and optimize production efficiency.

The Indian Council of Agricultural Research (ICAR) remains steadfast in its commitment to fostering innovation, capacity building, and interdisciplinary collaboration across the animal sciences. This conference represents a timely and visionary initiative that brings together leading experts in animal genetics, data analytics, and biotechnology to explore the transformative potential of precision breeding. The integration of genomics with artificial intelligence and machine learning is revolutionizing livestock and poultry development—enabling targeted genetic selection, accelerating breeding cycles, and promoting climate-resilient production systems.

I sincerely commend the organizers for their dedication and efforts in convening this international event. May this conference serve as a catalyst for transformative research, knowledge exchange, and global cooperation in the field of precision animal breeding.

I extend my best wishes for a highly successful and impactful conference.

(Raghavendra Bhatta)

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Dr. Tirtha Kumar Datta
Vice Chancellor

No. : VCS/WBUAFS/ M-5/1266
Date 4th November, 2025

Message

It is with immense pride and pleasure that I welcome all distinguished delegates, scientists, academicians, and industry professionals to the XIX Annual Convention of the Indian Society of Animal Genetics and Breeding (ISAGB) and the International Conference ISAGBCON-2025 on "Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning," being organized by the West Bengal University of Animal and Fishery Sciences on 13th and 14th November, 2025 in Kolkata.

This conference marks a significant milestone in our collective pursuit of excellence in animal science and offers a timely opportunity to spotlight the evolving landscape of animal husbandry in West Bengal. The state has long been recognized for its rich diversity in livestock and poultry resources, and its deep-rooted contributions to rural livelihoods, nutritional security, and agricultural sustainability. With growing demand for high-quality animal protein and increasing challenges posed by climate change and disease, West Bengal's animal husbandry sector stands at the cusp of transformation.

The convergence of genomics, artificial intelligence, and machine learning is redefining livestock breeding ushering in an era of precision, efficiency, and resilience. These technologies offer transformative solutions to enhance genetic gain, improve productivity, and support sustainable development across species and production systems. For West Bengal, this means unlocking new potential in indigenous breeds, strengthening disease resistance, and empowering farmers with data-driven tools for better decision-making.

As a leading institution committed to advancing veterinary and animal sciences, our university is honoured to host this prestigious international event. We believe that fostering interdisciplinary collaboration and global dialogue is essential to drive innovation and translate research into real-world impact. The ISAGBCON-2025 provides a vital platform for sharing knowledge, forging partnerships, and inspiring the next generation of scientists and practitioners.

I extend my heartfelt appreciation to the Indian Society of Animal Genetics and Breeding for their continued leadership and to all contributors for making this event possible. May the deliberations and outcomes of this conference pave the way for a smarter, more resilient animal husbandry sector in West Bengal and across the nation.

With best wishes for a successful and enriching convention.

(Tirtha Kumar Datta)

Indian Society of Animal Genetics and Breeding
M 31, First Floor, Sector-41, South City-1, Gurugram-122001 (Haryana)

Dr. B.P. Mishra
President

Date: 3110-29-025

MESSAGE

It is with great pleasure and pride that I extend my warm greetings to all deleg researchers, academicians, and industry professionals participating in the Annual Convention of the Indian Society for Animal Genetics and Breed (ISAGB) and the International Conference ISAGBCON 2025 on —Precision Anir Breeding through Genomics, Artificial Intelligence and Machine Learning,□ be hosted by the West Bengal University of Animal and Fishery Sciences in Kolkat 13th–14th November, 2025.

This conference marks a significant milestone in our collective pursuit of excelle in animal genetics and breeding. The convergence of genomics with artif intelligence and machine learning is revolutionizing the way we understand improve livestock populations. These technologies offer unprecedented precisior genetic evaluation, selection, and management—ushering in a new era of data driven, sustainable animal agriculture.

The society has always championed innovation, collaboration, and scientific ri Through this international platform, we aim to foster dialogue among global exp share cutting edge research, and inspire actionable strategies that can trar breeding programs across species and geographies. The insights generated he not only advance academic knowledge but also empower practitioners policymakers to address the pressing challenges of food security, climate resili and animal welfare.

I congratulate the organizing committee for their tireless efforts in curating timely and impactful event. I am confident that this ISAGBCON 2025 will serve a catalyst for future ready breeding systems and strengthen our commitmer scientific progress and societal benefit.

President

WEST BENGAL UNIVERSITY OF ANIMAL AND FISHERY SCIENCES

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Prof. Partha Das, Ph.D.
Registrar (Actg.)

No. WBUAFS/Edn./M-5/765/2025 **Date: 31.10.2025**

MESSAGE

It is with great pleasure that I extend my warm greetings to all delegates, researchers, academicians, and professionals participating in the XIX Annual Convention of the Indian Society for Animal Genetics and Breeding (ISAGB) and the International Conference ISAGBCON 2025 on "Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning," being hosted by the West Bengal University of Animal and Fishery Sciences on 13th and 14th November, 2025 in Kolkata.

This prestigious event reflects the university's commitment to advancing scientific inquiry and fostering innovation in the field of animal breeding. The integration of genomics with artificial intelligence and machine learning is revolutionizing livestock research and development—offering new dimensions of precision, efficiency, and sustainability. These technologies hold immense promise for enhancing genetic potential, improving productivity, and addressing the evolving challenges of food security and climate resilience.

As Registrar, I am proud to witness our institution serve as a platform for global collaboration and knowledge exchange. The presence of eminent scientists, thought leaders, and young researchers at this ISAGBCON 2025 will undoubtedly enrich the academic discourse and inspire future-ready solutions for the livestock sector.

I congratulate the Indian Society for Animal Genetics and Breeding and the organizing committee for their tireless efforts in bringing this international conference to fruition. I wish all participants a fruitful and intellectually stimulating experience.

(PARTHA DAS)

To
The Organising Secretary
ISAGBCON 2025,
Department of Animal Genetics and Breeding
Faculty of Veterinary and Animal Sciences,
West Bengal University of Animal & Fishery Sciences,

Directorate of Research, Extension and Farms
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Prof. Subhasis Batabyal,
Director of Research, Extension & Farms (Actg.)

Ref. No.: WBUAFS /DREF / _______/2025 Date: 31.10.2025

Message

*It gives me immense pleasure to welcome all delegates and participants to the **XIX Annual Convention of the Indian Society for Animal Genetics and Breeding (ISAGB)** and the International Conference, ISAGBCON 2025, on **"Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning."***

This conference reflects a shared vision to harness science, technology, and innovation for the betterment of society. The fusion of knowledge and digital intelligence is opening new horizons in livestock development, empowering farmers and researchers alike to shape a sustainable and resilient future.

As Director of Research, Extension & Farms, I take pride in our University's role in fostering collaboration, creativity, and global partnership. I congratulate the ISAGB and the Organizing Committee for their dedicated efforts.

May ISAGBCON 2025 ignite ideas that inspire lasting progress in animal science and human welfare.

Batabyal.

(Prof. Subhasis Batabyal)
Director of Research, Extension & Farms
West Bengal University of Animal and Fishery Sciences

West Bengal University of Animal & Fishery Sciences

FACULTY OF VETERINARY & ANIMAL SCIENCES

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Prof. (Dr.) Nilotpal Ghosh
Ph.D., FNAVS(I), FNAPM, FNAVNAW, FAAAS
DEAN

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Memo No: WBUAFS/VAS/2025/ M-1212 **Dated: 31.10.2025**

Message

It is a matter of great pleasure to welcome all distinguished delegates, scientists, academicians, industry professionals, and young researchers to the **XIX Annual Convention of the Indian Society of Animal Genetics and Breeding (ISAGB) and the International Conference on "Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning",** being organized by the Department of Animal Genetics and Breeding, Faculty of Veterinary & Animal Sciences under the West Bengal University of Animal and Fishery Sciences at Biswa Bangla Convention Centre, Newtown, Kolkata.

The Faculty of Veterinary and Animal Sciences at WBUAFS carries forward the glorious legacy of over a century of veterinary education and research in this historic city. With a steadfast commitment to excellence, the faculty continues to nurture innovation and scientific inquiry that contribute to the sustainable growth of the livestock sector and the well-being of our farming community.

In today's dynamic era, the convergence of genomics, artificial intelligence, and machine learning offers unprecedented opportunities to revolutionize animal breeding practices. This conference provides an excellent platform for scientists, academicians, and professionals from India and abroad to deliberate on recent advances, exchange ideas, and foster collaborations aimed at achieving precision and sustainability in animal production systems.

I convey my sincere appreciation to the esteemed leadership of the Indian Society of Animal Genetics and Breeding for entrusting us with the privilege of hosting this prestigious convention and international conference at our university. I also extend my heartfelt wishes to the organizing committee and all participants for a highly engaging and productive deliberation that will lead to meaningful outcomes and strengthen our collective efforts toward advancing the field of animal genetics and breeding.

Best wishes for the grand success of the conference.

(Prof. Nilotpal Ghosh)
Dean

Department of Animal Genetics & Breeding
Faculty of Veterinary and Animal Sciences
WEST BENGAL UNIVERSITY OF ANIMAL AND FISHERY SCIENCES
37, Kshudiram Bose Sarani, Belgachia, Kolkata -700037, West Bengal

Dr. Uttam Sarkar
Assistant Professor & Organizing Secretary, ISAGBCON -2025

MESSAGE

It is with immense pleasure and a deep sense of responsibility that I welcome all esteemed delegates, researchers, academicians, and industry professionals to the XIX Annual Convention of the Indian Society of Animal Genetics and Breeding (ISAGB) and the International Conference ISAGBCON-2025 on “Precision Animal Breeding through Genomics, Artificial Intelligence and Machine Learning,” being hosted by the West Bengal University of Animal and Fishery Sciences on 13th and 14th November, 2025 in Kolkata.

This conference is a testament to our collective commitment to advancing the frontiers of animal science through the integration of cutting-edge technologies. The convergence of genomics, artificial intelligence, and machine learning is reshaping the landscape of animal breeding—offering transformative solutions for genetic improvement, disease resistance, and sustainable livestock production. The ISAGBCON-2025 aims to provide a vibrant platform for scientific exchange, interdisciplinary collaboration, and the dissemination of innovative research that can drive real-world impact.

As Organizing Secretary, I am honoured to be part of this landmark event and grateful for the enthusiastic participation of experts from across the country and around the world. I extend my sincere thanks to the Indian Society of Animal Genetics and Breeding, our university leadership, and the dedicated organizing team for their unwavering support and tireless efforts in making this conference a reality.

I am confident that the deliberations and interactions during this ISAGBCON-2025 will inspire new ideas, forge lasting partnerships, and contribute meaningfully to the development of precision breeding strategies that benefit both science and society.

Wishing everyone a successful, enriching, and memorable conference experience.

Uttam Sarkar

[Dr. Uttam Sarkar]

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With best compliments from:

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Ministry of Agriculture and Farmers Welfare

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Programme Schedule

ISAGBCON-2025 WBUAFS, Kolkata

13-14 November, 2025

Biswa Bangla Convention Centre (BBCC), New Town, Kolkata-700 156

Day 0: 12-11-2025 (Wednesday)	
13:30-14:00 PM	**Registration**
14:00-17:00PM	**Pre-Conference Workshop** & High Tea
Day 1: 13-11-2025 (Thursday)	
9:00-10:00 AM	**Registration** **Venue:** BBCC, Main Entry Gate Level 2 (second floor)
10:00 AM-12:00 Noon	**Inaugural Session** followed by Keynote Addresses **Venue:** Auditorium Hall No. 7 Level 1 (first floor)
12:00-12:10 Noon	High Tea Break **Venue:** Food Area Hall No. 2 Level 2 (second floor)
12:10-1:00 PM (13-11-2025)	**Plenary Session I** **Venue:** BBCC, Auditorium Hall No. 7 Level 1 (first floor)
	1. Speaker: Dr. Subir S. Majumder, Director General, Gujarat Biotechnology University, & Former Director, NIAB, Hyderabad ▪ Lecture: Generation of a High Density SNP Chip using Indigenous Cattle, the First Step for Genomic Selection Chairpersons: 1. Prof. Purnendu Biswas, Former Vice Chancellor, WBUAFS, Kolkata 2. Dr. Mihir Sarkar, Director, ICAR-NRCY, Dirang, Arunachal Pradesh Rapporteur: 1. Dr. Santanu Banik, Head, ICAR-NDRI (ERS), Kalyani, WB
1:00-2:00 PM	Lunch Break **Venue:** Food Area Hall No. 2 Level 2 (second floor)
2:00-3:30 PM (13-11-2025)	**Technical Session I**: Next Generation Breeding: Integrating Genomics & Phenomics **Venue:** BBCC, Auditorium Hall No. 7 Level 1 (first floor)

	Chairpersons: 1. Dr. B. P. Mishra, Former Director, ICAR -NBAGR, Karnal, Haryana 2. Dr. U. Rajkumar, PS, ICAR-DPR, Hyderabad 3. Dr. Subodh Kumar, PS & Head, DAG, ICAR-IVRI, Izatnagar Rapporteurs: 1. Dr. Arnab Sen, PS & Station In-Charge, ICAR-IVRI-ERS, Kolkata 2. Dr. Ayan Mukherjee, Asst. Prof., Animal Biotech., WBUAFS
	Lead Papers
	1. Speaker: Dr. Mintu Nath, Senior Lecturer, University of Aberden, U.K. ▪ Lecture: From Association to Causation: Integrating Mendelian Randomisation Tool for Enhanced Genomic Prediction in Livestock 2. Speaker: Dr. Alfred De Vries, SPO, Bill & Melinda Gates Foundation, USA ▪ Lecture: Optimized Breeding Tools for Herd Productivity Gains under Challenging Conditions 3. Speaker: Dr. Gopal Gowane, PS, ICAR-NDRI, Karnal ▪ Lecture: Future-Ready Genomic Evaluation Strategies for Indigenous and Crossbred Cattle in Smallholder Systems 4. Speaker: Dr. Nilesh Nayee, DGM, Animal Breeding - Field Projects, NDDB ▪ Lecture: Fast Tracking Genetic Progress in Bovines using Genomics and ARTs
	Best Abstracts
	1. Speaker: Dr. Rani Alex, PS, AGB, ICAR-NDRI, Karnal ▪ Lecture: Implementation of Genomic Selection in Indigenous Sahiwal Cattle at ICAR-NDRI 2. Speaker: Prof. Ashis Kumar Ghosh, AGB, GBPUA&T, Pantnagar ▪ Lecture: Expression Profile of Bola DRB 3.2 Gene in Crossbred Cattle
2:00-3:30 PM (13-11-2025)	**Poster Session I**: Genetic Architecture and Quantitative Foundations of Animal Breeding Venue: BBCC, Auditorium Pre-Conference Area-G Level 2 (2nd floor)
	Chairpersons: 1. Prof. P. K. Senapati, Former Dean, F/o-VAS, WBUAFS 2. Dr. T. K. Ghosal, Head, ICAR-CIFE, Kolkata 3. Dr. Ajoy Mandal, PS, AGB, ICAR-NDRI (ERS), Kalyani, WB

3:30-5:00 PM (13-11-2025)	**Technical Session II** : Tools for Accelerated Genetic Improvement: Applications in Plants, Animals and Aquatic systems Venue: BBCC, Auditorium Hall No. 7 Level 1 (first floor)
	Chairpersons: 1. Dr. Vineet Bhasin, Former PS (AG&B), ICAR Head Qtrs., New Delhi 2. Dr. Tarun Kumar Bhattacharya, Director, ICAR -NRCE, Hisar 3. Dr. Pushpendra Kumar, PS, DAG, ICAR-IVRI, Izatnagar 4. Dr. Vikas Vohra, PS & Head, AGB, ICAR-NDRI, Karnal Rapporteurs: 1. Dr. Amit Kumar, PS, DAG, ICAR-IVRI, Izatnagar 2. Dr. Aruna Pal, Assoc. Prof., LFC, WBUAFS
	Lead Papers
	1. Speaker: Dr. Srinivas Jahageerdar, PS, Fish Genetics and Biotechnology, ICAR - CIFE, Mumbai ▪ Lecture: From Fish to Farm: Genetic Tools in Aquaculture and Their Relevance to Livestock and Plant Breeding 2. Speaker: Dr. Kutubuddin Ali Molla ▪ Lecture: Precision Genome Editing at Scale: Next Generation Tools for Accelerated Improvement in Crops, Livestock, and Aquaculture 3. Speaker: Dr. Mahesh R. Neupane, Animal Scientist, Animal Genomics and Improvement Laboratory, USDA ▪ Lecture: A Case Study on Digital Transformation in Conventional Cattle Breeding 4. Speaker: Dr. Periasamy Kathiravan, PS, ICAR-NRCM, Medziphema & Former Livestock Geneticist, IAEA, Vienna ▪ Lecture: From Ear Tags to Genomics: ICT Innovation for Accelerated Livestock Improvement in Developing Countries.
	Best Abstracts
	1. Speaker: Dr. Ravi Kr Gandham, Head, Animal Biotech., ICAR-NBAGR, Karnal ▪ Lecture: Cattle Genome : Insights into Indian Zebu 2. Speaker: Dr. Asit Jain, Associate Professor, AGB, NDVSU, Jabalpur ▪ Lecture: Cathepsins Inhibition by E-64 during Oocyte Maturation Enhances Developmental Competence of Buffalo Embryos via Apoptosis Suppression

3:30-5:00 PM (13-11-2025)	**Poster Session II** : Next Generation Breeding: Integrating Genomics & Phenomics Venue: BBCC, Pre-Conference Area-G Level 2 (2nd floor)
	Chairpersons: 1. Dr. A. K. Pandey, PS, DAG, ICAR-IVRI, Izatnagar 2. Dr. Monika Sodhi, PS, Animal Biotech., ICAR-NBAGR, Karnal 3. Dr. Jamuna Valsalan, Asst. Commissioner, MFAHD, GoI, New Delhi
6:30-8:30 PM	Cultural Programme & Dinner
Day 2: 14-11-2025 (Friday)	
8:00-9:00 AM	Breakfast **Venue:** Food Area Hall No. 2 Level 2 (second floor)
9:00-10:00 AM (14-11-2025)	**Plenary Session II** Venue: BBCC, Auditorium Hall No. 7 Level 1 (first floor)
	1. Speaker: Dr. Mehar Singh Khatkar, Senior Researcher, School of Animal and Veterinary Science, Adelaide University, Adelaide, Australia ▪ Lecture: Beyond Genomics: Phenomics and Artificial Intelligence to Transform Economic Trait Evaluation in Livestock
	Chairpersons: 1. Dr. S. M. Deb. Former Director, NRCY, ICAR-Emeritus Professor, WBUAFS 2. Dr. Yash Pal, Director, ICAR-CIRB, Hisar 3. Dr. Manish Kumar Chatli, Director, ICAR-CIRG, Makhdoom Rapporteurs: 1. Dr. K. N. Raja, SS, AGB, ICAR-NBAGR, Karnal 2. Dr. Asit Jain, Associate Professor, AGB, NDVSU, Jabalpur
10:00 AM-12:00 Noon (14-11-2025)	**Technical Session III**: Exploring IoT and Artificial Intelligence in Animal Food System Venue: BBCC, Auditorium Hall No. 7 Level 1 (first floor)
	Chairpersons: 1. Dr. N. H. Mohan, Director, ICAR-NBAGR, Karnal 2. Dr. P. K. Rout, PS (AG&B), ICAR Head Qtrs., New Delhi 3. Dr. S. K. Chaturvedi, Former PS, ICAR-CIRC, Meerut Rapporteurs: 1. Dr. S. K. Niranjan, PS, AGB, ICAR-NBAGR, Karnal 2. Dr. Tapas Biswas, SS, IVRI-ERS, Kolkata

	Lead Papers
	1. Speaker: Dr. Suresh Raja Neethirajan, Professor & University Research Chair, Dalhousie University, Canada ▪ Lecture: Welfare by Design: Harnessing AI and IoT for Compassionate and Climate-Ready Livestock Systems 2. Speaker: Dr. T. K. Mohanty, PS, LPM, ICAR -NDRI, Karnal ▪ Lecture: Precision Livestock Farming using Sensors and Artificial Intelligence: Optimizing Resources and Productivity 3. Speaker: Dr. Soumen Mandal, PS, Human Centered Robotics and Cybernetics Group, CSIR-CMERI, Durgapur ▪ Lecture: Leveraging AI-IoT Powered Wearables for Small Cattle Holder Systems. 4. Speaker: Dr. Srinivas Kiran Ambatipudi, Professor, Dept. of Biosciences and Bioengineering, IIT Roorkee ▪ Lecture: Smart Wearabe Sensor System for Monitoring Buffaloe Health.
	Best Abstracts
	1. Dr. Vikas Diwakar, AGB, NDRI, Karnal ▪ Lecture: Comparative Analysis of Artificial Intelligence Based Prediction Algorithms for Breeding Value Estimate in Murrah Buffalo 2. Dr. B. N. Shahi, Professor, AGB, GBUA&T, Pantnagar ▪ Lecture: Comparative Evaluation of Machine Learning Models for Prediction of First Lactation 305-Day Milk Yield in Crossbred Cattle
10:00 AM-12:00 Noon (14-11-2025)	**Poster Session III** : Biological Systems, Reproductive and adaptive genomics Venue: BBCC, Pre-Conference Area-G Level 2 (2nd floor)
	Chairpersons: 1. Dr. Sujoy Dhara, Head, ICAR-CIRB, Hisar 2. Dr. Soumen Naskar, PS, AGB, ICAR -IIAB, Garkhatanga, Ranchi 3. Dr. Indrajit Ganguly, PS, AGB, ICAR-NBAGR, Karnal
12:00 Noon-1:00 PM (14-11-2025)	**Technical Session IV** : ISAGB Young Scientist Presentation Award Venue: BBCC, Auditorium Hall No. 7 Level 1 (first floor)
	Chairpersons: 1. Dr. Bhushan Tyagi , Joint Commissioner (RGM), Dept. of AHD, New Delhi 2. Dr. Sanjeev Kumar, Former Director (A) & PS, AGB, CARI, Izatnagar 3. Dr. Umesh Singh, PS, ICAR-CIRC, Meerut

	Rapporteurs: 1. Dr. C. S. Mukhopadyaya, PS, CoAB, GADVASU, Ludhiana 2. Dr. Ananta Kumar Das, Professor & Head, AGB, WBUAFS	
1:00-2:00 PM (14-11-2025)	**Round Table Meet of stakeholders on Industry-Academician Interface** Venue: BBCC, Auditorium Hall No. 7 Level 1 (first floor)	**General Body Meeting** of the ISAGB Venue: BBCC, Glassroom Level 0
Industry Meet	Coordinator: Dr. Partha Sengupta, Asst. Director, PBGSBS Chairpersons: 1. Dr. V. K. Saxena, Former ADG (AP&B), ICAR, New Delhi 2. Dr. A. K. Thiruvenkadan, Professor, TANUVAS, Chennai 3. Dr. G. S. Konar, CEO, PBGSBS Rapporteurs: 1. Dr. H. K. Narula, Former PS, ICAR Head Qtrs. 2. Dr. Manik Pakhira, Professor, Avian Sci, WBUAFS	
2:00-3:00 PM	Lunch Break **Venue:** Food Area Hall No. 2 Level 2 (second floor)	
3:00-4:00 PM	Award Ceremony **Venue:** BBCC, Auditorium Hall No. 7 Level 1 (first floor)	
4:00-5:00 PM	Valedictory Session **Venue:** BBCC, Auditorium Hall No. 7 Level 1 (first floor)	
5:00-6:00 PM	High Tea **Venue:** Food Area Hall No. 2 Level 2 (second floor)	

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OS-01

IMPLEMENTATION OF GENOMIC SELECTION IN INDIGENOUS SAHIWAL CATTLE AT ICAR-NDRI

Vikas Vohra*, Parth Gaur, Akshata Patil, Rani Alex, Gopal Gowane, and TV Raja
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ICAR-National Dairy Research Institute, Karnal -132001, Haryana, India

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ABSTRACT

Pioneering studies were conducted to implement genomic selection at ICAR-NDRI herd through evaluation and selection of indigenous Sahiwal bulls based on their genomic estimated breeding values (GEBVs) for the 305 days' milk yield. Genomic selection was implemented using single-step Genomic Best Linear Unbiased Prediction (ssGBLUP) method, and a genomic evaluation pipeline for dairy animals was established using ssGBLUP. First lactation milk records and pedigree data of 1435 animals spanning over the period of 1957 to 2024 from the Sahiwal herd of ICAR-NDRI, Karnal, were used. Genotype of 503 Sahiwal animals was generated using BovineSNP50 v3 BeadChip (Illumina). Out of the total SNPs genotyped from the chip only 41.37% SNPs were used to estimate the genetic parameters. Genotypic call rates less than 90%, animals with a call rate lower than 0.90, minor allele frequency, MAF (< 5%) was taken to avoid uninformative SNPs. GEBVs were estimated for 45 pedigreed Sahiwal Bulls and the top 3 breeding bulls had percentage superiority (GEBVs) of 21% to 22% over the rest of bulls. It was realized that the ssGBLUP methodology integrates pedigree, genomic, and phenotypic information into a unified genetic evaluation framework, effectively addressing inconsistencies in recorded pedigree data, including errors or cases of misidentified parentage. Thus, for a typical animal breeding program, with resource constraints and incomplete pedigree, the use of the ssGBLUP model is recommended for routine genomic evaluation and selection of potential candidates for successful implementation of a genomic selection program.

Keywords: GEBVs, genomic evaluation, heritability, ssGBLUP.

OS-02

EXPRESSION PROFILE OF BOLA DRB 3.2 GENE IN CROSSBRED CATTLE

Ashis Kumar Ghosh
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ABSTRACT

The bovine leukocyte antigen (BoLA-DRB3) gene encodes cell surface glycoprotein that initiates immune response by presenting processed antigenic peptides to CD4 T helper cells. DRB3 is the most polymorphic bovine MHC class II gene which encodes the peptide-binding groove. DRB3 gene has been extensively evaluated as a candidate marker for association with various bovine diseases and immunological traits. The present study was undertaken on 200 crossbred cattle maintained at Instructional Dairy Farm (IDF), G.B.P.U.A. & T., Pantnagar, Uttarakhand to investigate the expression profile of BoLA DRB 3.2 gene. Six alleles were identified and ammino acid sequences were obtained. Comparing variability of different amino acid sequences, it was observed that the functional mutation in allele E was maximum followed by B, F, A, C and D allele. Proteins coded by B and F alleles were unstable. The functional domain was identified with the help of InterProScan a protein domain identifier. The domain ID of the identified protein was PD000328, which was a class II MHC glycoprotein transmembrane class antigen precursor signal beta chain. Using Swiss Model Workspace, the modelling of identified hypothetical protein structures encoded by six different alleles was done and three-dimensional model of the proteins was visualized by Rasmol software. The physico-chemical properties of the proteins coded by DRB3.2 gene were accessed using ProtParam bioinformatics tools. Occurrence of glutamic acid was maximum in the amino acid composition of the protein irrespective of the alleles. MHC II binding prediction was done by taking human as a model for identification of epitope regions in protein coded by DRB3.2 alleles in crossbred cattle using IEDB analysis. The antigen binding sites for each allele were successfully identified. The higher consensus percentile rank indicated the better antigen binding site.

Keywords: Antigen binding, BoLA DRB3 gene, Crossbred cattle

OS-03

Ravi Kumar Gandham[12†§], Mahesh Neupane[3†], Sarwar Azam[1]†, Neelam Topno[1†], Manas Ranjan Praharaj[1], Kathiravan Periasamy[4], Subir Das[5], Pankaj Kumar[1], Himanshu Patil[1], Dhirendra Suthar[1], Neelima Hosamani[1], Sayta Pal Arya[1], Shakti Kumar[1], Vikas Vohra[6], Raju BMK[7], Avnish Kumar Bhatia[2], Manishi Mukesh[2], Amod Kumar[2], Mahesh Dige[2], Benjamin D Rosen[3], Curtis P Van Tassell[3]* and Subeer S Majumdar[1]‡*

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ABSTRACT

India's diverse zebu cattle exemplify adaptation and breed differentiation. We developed the 788K IndiGau SNP array on sequencing 40 breeds of Indigenous cattle. Genotyping 2,169 animals from 40 breeds was conducted to map genetic diversity (Fst, ROH, FROH), population structure (Phylogeny, admixture, and Ne), and key phenotypic traits (GWAS for milk - dual and draft; GWAS for height; GWAS for adaptation - coat colour, climatic zone comparison, comparison of breeds of extreme climates and Conserved regions of low diversity (CRsLD)). The array exhibited a minor allele frequency (MAF) of 0.27 in Indian cattle, compared to 0.17 for the BovineHD 770K chip, demonstrating its superior informativeness for indigenous populations.The genomic data revealed a strong north-south ancestry split and a recent decline in effective population size. Breeds such as Vechur, Siri, and Umblachery showed breed-specific signatures of positive selection, while other breeds exhibited CRsLD regions harbouring genes linked to characteristic phenotypes. A concentrated selective sweep on chromosome 6 was identified in dairy breeds, encompassing LEF1, OSTC, COL25A1, and ETNPPL. Dwarf stature was associated with loci on chromosomes 19 (ALOX12, MINK1) and 13, whereas climate-related signals involved stress-response and pigmentation genes on chromosomes 13, 18, and 22.Positive selection was inferred using iHS scores, their empirical distributions, haplogroup frequency patterns, and Tajima’s D. By integrating PCA-assisted XGBoost, we achieved highly accurate breed classification on an independent cohort. This study represents the first comprehensive genomic comparison of 40 Indian Zebu breeds, utilizing the world’s largest SNP chip - IndiGau.

Keywords: IndiGau, High density, Adaptability, Machine learning

OS-04

CATHEPSINS INHIBITION BY E-64 DURING OOCYTE MATURATION ENHANCES DEVELOPMENTAL COMPETENCE OF BUFFALO EMBRYOS VIA APOPTOSIS SUPPRESSION

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ABSTRACT

Cumulus cells (CCs) are essential for follicular growth, influencing both oocyte quality and embryo developmental competence. This study investigated whether inhibiting CC apoptosis could improve buffalo embryo development. The expression profiles of cathepsins (Cath B, K, S, Z) and apoptosis-related genes, pro-apoptotic (BID, BAX, CYC-C, Caspase-3) and anti-apoptotic (BCL2, XIAP), were quantified by qRT-PCR in in-vitro–produced embryos (2-cell to expanded blastocyst) derived from superior (A-grade) and inferior (B-grade) cumulus-oocyte complexes (COCs), with or without cysteine protease inhibitor E-64 supplementation during in vitro maturation (IVM). Cath B protein localization was assessed via immunocytochemistry, and DNA fragmentation by TUNEL assay. After 24 hours IVM and 14 hours IVF, embryos were cultured for seven days. In both A- and B-grade embryos, cathepsins and pro-apoptotic transcripts remained stable at the 2–4 cell stages but raise sharply at the 8-cell stage, coinciding with a reduction in anti-apoptotic gene expression. E-64 supplementation significantly down regulated Cath B, Z, BID, BAX, CYC-C, and Caspase-3 expression, particularly before major embryonic genome activation ($\leq$8-cell stage), while modestly increasing BCL2 and XIAP transcripts. Cath B protein intensity was higher ($P<0.05$) in embryos from B-grade oocytes, with E-64 treatment reducing levels consistent with mRNA data. TUNEL assays showed a higher incidence of apoptosis in embryos from inferior COCs, whereas E-64 reduced TUNEL-positive cells across developmental stages. Supplementation with 10 µM E-64 increased blastocyst yield from superior-quality oocytes and improved blastocyst quality from both grades. In conclusion, E-64-mediated cathepsins inhibition during IVM reduces mitochondria-dependent apoptosis, thereby enhancing developmental competence in buffalo embryos. Targeted regulation of proteolytic and apoptotic pathways during oocyte maturation may improve embryo survival and quality, offering potential advantages for assisted reproductive technologies in buffalo.

Keywords: Cathepsin B; E-64; Apoptosis; Buffalo, Embryo

OS-05

COMPARATIVE ANALYSIS OF ARTIFICIAL INTELLIGENCE BASED PREDICTION ALGORITHMS FOR BREEDING VALUE ESTIMATE IN MURRAH BUFFALO

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ABSTRACT

Accurate estimation of breeding values is a critical criterion for selecting superior animals, leading to improved productivity and profitability. With the growing volume of data generated on farms, evaluating the potential of Machine learning (ML) for early genetic predictions becomes increasingly important. ML, a branch of AI, focuses on non-parametric methods for making precise and reliable predictions. Considering this, the study was undertaken to evaluate algorithms, namely, Random Forest (RF), Extreme Grading-Boosting (XGB), and Artificial Neural Network (ANN). Forty-two (42) years of milk yield records of Murrah buffalo herd from NDRI, Karnal were used for estimation of breeding values using Best Linear Unbiased Prediction (BLUP). These BLUP estimated breeding values were further used to train the ML algorithms including in 90:10. Also, the ML algorithms were also trained on monthly milk yield of each animal up to 5 months. The ML algorithms were then evaluated for their ability to predict breeding values based on cumulative monthly milk yield up to 5 months and for 305 days' milk yield records. The correlation coefficients between true and predicted breeding values up to 5 months' monthly milk yield varied from 60 to 75%. Similarly, the coefficient of determination (R^2) varied from 35 to 55%. XG-Boost exhibited superior predictive performance and adaptability under real-time data simulation conditions, indicating its potential for early and dynamic estimation of breeding values in Murrah Buffalo for developing a support system for making breeding decisions.

Keywords: Artificial Intelligence, ML algorithms, Murrah, XG-Boost

OS-06

COMPARATIVE EVALUATION OF MACHINE LEARNING MODELS FOR PREDICTION OF FIRST LACTATION 305-DAY MILK YIELD IN CROSSBRED CATTLE

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ABSTRACT

Accurate prediction of milk yield is critical for enhancing dairy herd management, breeding strategies, and overall farm profitability. The present study aimed to predict the first lactation 305-day milk yield (FL305DMY) of crossbred cattle using different machine learning algorithms. Data spanning over 29 years (1990–2019) were collected from 567 daughters of 57 sires maintained at the Instructional Dairy Farm, G.B. Pant University of Agriculture and Technology, Pantnagar. Traits considered included 30, 60, and 90 days milk yield, first lactation peak yield (FLPY), first calving interval (FCI), first service period (FSP), days to attend peak yield (DPY), first dry period (FDP), and age at first calving (AFC). Feature selection revealed that 30-days, 60-days, and 90 days milk yields along with FLPY, having correlation values above 0.5 with FL305DMY, were the most significant predictors. Five machine learning models Multiple Linear Regression (MLR), Random Forest (RF), Gradient Boosting Regression (GBR), Extreme Gradient Boosting (XGboost), and Light Gradient Boosting Machine (LightGBM) were used to evaluate the data. The dataset was partitioned into training (80%) and testing (20%) subsets, and model performance was assessed using coefficient of determination (R^2) and root mean square error (RMSE). Results indicated that MLR performed the weakest ($R^2 = 0.55$, RMSE = 478.82 for testing). In contrast, RF outperformed all models, achieving the highest predictive accuracy ($R^2 = 0.85$, RMSE = 267.13 for testing). LightGBM and GBR demonstrated satisfactory prediction ability, whereas XGboost showed moderate performance. Overall, the Random Forest model was identified as the most robust and reliable approach for predicting FL305DMY in crossbred cattle. The findings underscore the potential of advanced machine learning models in dairy herd improvement programs, enabling early selection and management decisions. Future research may improve prediction accuracy by incorporating additional correlated traits and expanding dataset size.

Keywords: Crossbred cattle, milk yield prediction, machine learning models

Poster Session-I

Genetic Architecture and Quantitative Foundations of Animal Breeding

P1-01

CHARACTERIZATION OF MAYURBHANJ GOATS OF ODISHA: A COMPARATIVE STUDY WITH THE GANJAM BREED

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ABSTRACT

The present study aimed to characterize the morphometric and qualitative traits of Mayurbhanj and Keonjhar goats and compare them with Ganjam goats to determine whether Mayurbhanj and Keonjhar goats represent a distinct genetic group. A total of 406 goats, comprising 196 Ganjam and 210 Mayurbhanj animals, were sampled from six locations—Karanjia, Raruan, Sukruli, and Bahalda (Mayurbhanj), and Banspal and Ghatagaon (Keonjhar)—covering both sexes. Data on body weight, body length, chest girth, wither height, and ear length were recorded at birth, 3 months, and 12 months, along with qualitative traits such as head profile, ear orientation, coat color, and horn characteristics. Reproductive parameters including age at sexual maturity, age at first kidding, and kidding interval were also documented. Statistical analyses using least squares models accounted for the effects of sex and location. Highly significant ($P < 0.05$) differences were observed between breeds for most morphometric traits. Ganjam goats were consistently larger at all ages, with mean body weights of 2.53 kg at birth and 18.94 kg at 12 months, compared with 1.70 kg and 12.34 kg in Mayurbhanj goats, respectively. Males were superior to females across both breeds, indicating marked sexual dimorphism. Correlation analysis showed strong positive relationships ($r > 0.80$) among body weight, length, height, and chest girth, particularly in Ganjam goats, while Mayurbhanj goats exhibited tighter inter-trait associations suggesting coordinated growth. Qualitative features revealed distinct phenotypic patterns. Mayurbhanj and Keonjhar goats typically had convex head profiles, medium horizontal ears, dark tan coats with black muzzles, and uniform horn shape, while Ganjam goats displayed more variation in head, ear, and horn types. Despite smaller body size, Mayurbhanj and Keonjhar goats exhibited early maturity, shorter kidding intervals, and good prolificacy, underscoring their adaptability and potential recognition as a distinct, locally adapted genetic resource.

Keywords: Mayurbhanj goats, morphometric characterization, comparative analysis

P1-02

MORPHOMETRIC VARIATION AND PRINCIPAL COMPONENT ANALYSIS OF LOCAL BUFFALOES IN THE SOUTHERN REGION OF CHHATTISGARH, INDIA

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ABSTRACT

Morphometric characterization is essential for understanding structural variability and guiding selective breeding in indigenous buffalo populations. This study analyzed eight morphometric traits—chest girth (CG), body length (BL), height at withers (HW), horn length (HL), face length (FL), tail length (TL), dorsal body height (DBH), and ear length (EL)—in 446 local buffaloes of the southern region of Chhattisgarh using principal component analysis (PCA). Descriptive statistics revealed moderate variation in TL (76.48 ± 9.51 cm), CG (177.23 ± 20.34 cm), BL (132.90 ± 8.97 cm), HW (120.26 ± 6.98 cm), HL (39.95 ± 12.35 cm), FL (41.92 ± 6.06 cm), DBH (20.28 ± 3.04 cm), and EL (22.03 ± 3.87 cm), indicating substantial phenotypic diversity. The Kaiser-Meyer-Olkin measure (0.551) and Bartlett's test of sphericity ($\chi^2 = 757.69$, $p < 0.001$) confirmed the suitability of the dataset for PCA. Three principal components with eigenvalues >1 explained 63.43% of the total variance. Varimax rotation revealed Factor 1 representing body frame and thoracic robustness (TL, CG, HL), Factor 2 representing vertical growth and limb development (HW, DBH, FL), and Factor 3 representing cranial and body length proportions (BL, FL). Ear length contributed minimally to overall variation. The results indicate that structural robustness, vertical development, and body proportion are the primary axes of morphological variability in local buffaloes of the southern region of Chhattisgarh. These findings can inform selective breeding strategies, emphasizing animals with strong body frames, upright growth, and proportional cranial-trunk structures to enhance draft performance, grazing efficiency, and functional adaptability.

Keywords: Principle component analysis, local buffalo, breed characterization, selective breeding

P1-03

GENETIC STUDY ON MARATHA CAMP BUFFALOES IN SHIVAMOGGA DISTRICT OF KARNATAKA

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ABSTRACT

The present study entitled "Genetic study on Maratha Camp buffaloes in Shivamogga district of Karnataka" was undertaken during 2024–2025 to assess the population status, phenotypic traits, morphometry, milk production, and breeding management of this unique buffalo population. Survey across 16 villages in three talukas covered 193 households of predominantly Maratha (Gowli) community maintaining approximately 5,000 buffaloes, under traditional system with natural service. A total of 303 animals were evaluated for morphology and morphometry, and 150 milk samples were subjected to milk component analysis. The buffaloes showed medium body conformation resembling Surti and Nagpuri breeds. Coat colour was mainly black (68.00%), followed by brown (26.00%) and black–white spotted (6.00%). Distinct features included flat forehead (90%), sword-shaped horns (83%), horizontal ears (81.00%), black muzzle (64.00%), black hooves (76.00%), and black switch (64.00%). Udder traits were small (84.00%), bowl-shaped (51.00%), with cylindrical teats (53.00%). Morphometric values reflected adaptation to semi-intensive, low-input management: adult females recorded mean body length 118.31±0.38 cm, chest girth 170.78±0.36 cm, height at withers 117.27±0.23 cm, and body weight 320.90±5.33 kg, while adult males averaged 218.53±11.26 kg. Average milk yield was 1.92±0.07 litres/day, continuing until conception. Despite modest yield, milk quality was superior, with fat 6.61±0.18%, SNF 9.97±0.11%, protein 3.82±0.22%, and lactose 5.41±0.06%. Breeding relied mainly on natural service (97.77%), with limited AI (2.22%). Male selection was based on fitness and conformation, and females on milk yield and adaptability. The geographical isolation of a small immigrant population for about six to seven generations without intensive artificial selection has created a distinct buffalo population which is livelihood resource for this community.

Keywords: Maratha Camp buffaloes; Morphology; Morphometry; Milk quality traits

P1-04

ASSOCIATION OF LIVE BODY WEIGHT WITH MORPHOMETRIC TRAITS IN DIFFERENT POULTRY BREEDS

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ABSTRACT

The study was conducted on 300 birds; 100 each from Rhode Island Red (RIR), Kadaknath and Punjab Brown maintained at Poultry research farm under Directorate of Livestock Farms. The body weight and morphometric traits were measured bi-weekly from 12th to 26th week of age. Significantly ($p \leq 0.01$) higher correlation was observed between shank length (SL) and body length (BL) through most of the weeks. Keel length (KL) exhibits significantly ($p < 0.05$) higher correlations with BL, shank width (SW), and beak length (BKL) at the 12th and 14th weeks. BKL generally showed significantly ($p < 0.05$) higher correlations with wing length (WL), KL, and body girth (BG) across ages, except at the 14th, 22nd, and 26th weeks. Body Girth had significantly ($p \leq 0.01$) higher correlation with KL at most of the age groups. Body weight showed significantly ($p \leq 0.01$) higher correlation at all age groups in all genotypes with most of the morphometric traits except had weaker correlation with BG in RIR, with BKL and BG in Kadaknath and with BL in Punjab Brown poultry birds. Significant ($p \leq 0.01$) and positive regression coefficients of body weight on SL from 14 to 26 week of age were observed in RIR chicken. Significantly ($p \leq 0.01$) higher regression coefficients of body weight on CL were also found from 16 to 26th week of age. In Kadaknath poultry bird's, positive significant ($p \leq 0.01$) regression coefficients were observed of body weight on CL from 16 to 26 week of age and WL from 18 to 26th week of age. Moreover, in Punjab Brown poultry bird's, positive significantly ($p \leq 0.01$) regression coefficients of body weight was observed on CL from 14 to 26 week of age except 24th week of age, on KL from 16 to 26 week of age except 20th week of age and on WL from 14 to 20th week of age.

Keywords: RIR, Kadaknath, Punjab Brown, Body weight, Morphometric traits

P1-05

GENETIC VARIABILITY OF MILK PRODUCTION AND ITS EFFICIENCY TRAITS OF JERSEY CROSSBRED CATTLE

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ABSTRACT

The present study aimed to determine the genetic and non‒genetic factors influencing milk production and its efficiency traits in Jersey crossbred cattle maintained at ICAR–National Dairy Research Institute, Eastern Regional Station, Kalyani, West Bengal. Data comprising 1,854 lactation records from 581 animals and their pedigrees, collected between 1985 and 2024, were employed in the analysis. The evaluated traits included total milk yield (TMY), 305‒milk yield (305‒MY), and lactation length (LL) for production; calving interval (CI) and age at first calving (AFC) for reproduction; and milk yield per day of lactation length (MYLL), milk yield per day of calving interval (MYCI), and milk yield per day of age at second calving (MSC) for production efficiency. Genetic and non‒genetic factors influencing these traits were assessed using the MMLSML procedure in HARVEY, while variance components and genetic correlations were estimated using univariate and bi‒variate animal models through AIREML (WOMBAT) and Bayesian methods via Gibbs sampling (GIBBSF90+ and POSTGIBBSF90). Period of calving, parity, and genetic group significantly affected most traits, with animals having 50% Jersey and 50% Tharparkar inheritance showing the superior milk production and efficiency, reflecting the advantage of combining productivity and adaptability through crossbreeding. Heritability estimates from the AIREML approach for TMY, 305‒MY, LL, CI, and AFC were 0.23, 0.29, 0.04, 0.07, and 0.09, respectively, while Bayesian estimates were 0.19, 0.33, 0.05, 0.08, and 0.43, respectively. For production efficiency traits, heritability was moderate to high i.e., 0.30 (MYLL), 0.25 (MYCI), and 0.48 (MSC) in AIREML, and 0.31, 0.24, and 0.62, respectively, in Bayesian analysis. Most traits exhibited moderate to high repeatability. Genetic correlations were largely positive across all trait groups, with strong associations among production and production efficiency traits. Reproductive traits also exhibited positive relationships. Production and reproduction traits showed generally positive correlations, except antagonism between TMY and AFC, indicating complex genetic relationships between fertility and efficiency traits. These findings emphasize the potential of production efficiency traits as comprehensive selection indicators and reaffirm the role of advanced genetic evaluation tools in improving the overall productivity of Jersey crossbred cattle.

Keywords: AIREML, Bayesian, bi‒variate, Jersey crossbred, Variance components

P1-06

STANDARDIZATION AND VALIDATION OF TEST DAY MILK DATA FOR INDIGENOUS AND CROSSBRED DAIRY COWS USING R

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ABSTRACT

Ensuring the accuracy and reliability of milk yield data is a critical step toward robust genetic evaluation in dairy cattle improvement programs. This study describes a systematic data quality control (QC) process undertaken for indigenous and crossbred cows recorded under the BAIF Enhance Genetics Project (EGP). The initial dataset comprised raw test-day milk yield records from multiple states, covering 55,000 cows across different breeds and lactations. A comprehensive 23-step QC pipeline was developed in R software to standardize breed names, remove biologically implausible and inconsistent records, and ensure representativeness across seasons and centres. Reported crossbred breeds were harmonized to “HF X” and “JR X,” and rare indigenous breeds (with < 100 animals) were grouped as Other Indigenous. Cows were retained if their milk records were between 7 and 340 days post-calving, with 4 or more monthly records per lactation. Outlier removal was conducted using breed-specific thresholds animals with average yields exceeding 4 standard deviations or with lactation yield coefficients of variation (CV > 0.8) were excluded. After rigorous filtering, 30,662 crossbred cows (21,402 HF X and 9,260 JR X) with 575,501 test-day records and 12,448 indigenous cows with 166,509 test-day records were retained for downstream analyses. This corresponds to a data retention of 91.5% for animals and 89.3% for milk records after multi-stage cleaning. The resulting high-quality dataset ensures biological consistency and statistical robustness for subsequent analyses such as lactation curve modeling, genetic parameter estimation, and genomic evaluation. This standardized R-based QC workflow provides a reproducible framework for large-scale milk data validation in multi-breed dairy cattle improvement programs across India.

Keywords: Test-day milk yield, Data quality control, Crossbred and Indigenous cows, R programming

P1-07

FACTORS INFLUENCING TEST DAY MILK YIELD IN DAIRY CATTLE AND BUFFALOES UNDER FIELD CONDITIONS IN AJMER DISTRICT OF RAJASTHAN

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ABSTRACT

A field-based research project was conducted in Ajmer district of Rajasthan, India, to evaluate the influence of genetic and non-genetic factors on test day milk yield (TDMY) in dairy cattle and buffaloes. A total of 1,800 animals belonging to 515 farmers across 28 villages were monitored under a structured milk recording programme from 2019 to 2025. Analysis of variance (ANOVA) revealed that district, breed, season, and lactation phase significantly ($p < 0.001$) affected TDMY. Linear models fitted for Ajmer district further indicated highly significant ($p < 0.001$) effects of breed, year of calving, season of calving, and lactation stage on total milk yield. Breed showed the largest influence ($F = 359.265$), followed by year of calving ($F = 530.865$) and lactation stage ($F = 264.394$), while season of calving also had a smaller yet significant effect ($F = 10.507$; $p = 2.756e-05$). Breed-wise least square means (±SE) of total milk yield (litres/day) were: Holstein Friesian Crossbreed – 10.13 ± 0.13, Jersey Crossbreed – 8.73 ± 0.17, Indigenous Cattle – 8.27 ± 0.12, Non-Descript Cattle – 7.78 ± 0.19, Indigenous Buffalo – 7.87 ± 0.17, and Non-Descript Buffalo – 7.48 ± 0.14. The study highlights considerable variation in milk production due to breed composition and environmental conditions, emphasizing the need for systematic performance recording and breed improvement programs to enhance dairy productivity in arid and semi-arid regions of India.

Keywords: Test day milk yield, breed effect, lactation stage, crossbred cattle, buffalo

P1-08

IMPACT OF POSTBIOTIC PRODUCED FROM LACTOBACILLUS DH42 AS A REPLACEMENT FOR ANTIBIOTICS ON THE GROWTH PERFORMANCE, GUT HEALTH, AND IMMUNE RESPONSE IN BROILER CHICKENS

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ABSTRACT

This study aimed to evaluate the effects of dietary supplementation with a postbiotic (inactivated Lactobacillus DH42) on the growth performance, carcass traits, blood biochemical profile, gut microbiome, gut morphology, and immune response of broiler chickens. A total of 162 day-old mixed sex Ven Cobb 400 broiler chicks were randomly assigned to three dietary groups, each with six replicated pens (n = 6), containing nine broiler chickens: 1) basal diet without any growth promoter (CON), 2) basal diet with antibiotic (Bacitracin methylene disalicylate – BMD) at 500g/ton feed (AGP), and 3) basal diet with postbiotic (inactivated Lactobacillus DH42) at 1 ml/bird in drinking water (POS). Body weight, feed intake, and feed conversion ratios (FCR) were monitored weekly for 35 days. Blood biochemistry and immune response were evaluated at the day 28 and day 35 of the trial. Carcass traits, gut microbiome, and gut morphology were evaluated at the end of the trial. The results showed that postbiotic supplementation (POS) significantly increased final body weight, average daily gain and improved feed conversion ratio (FCR) compared to the control group ($P<0.05$). There were no significant differences in average daily feed intake (ADFI), antibody titres, carcass traits and most blood biochemistry parameters, except cholesterol concentration, which was significantly lower in the POS group compared to the AGP and CON groups. Both POS and AGP supplementation resulted in a significant decrease in caecal Escherichia coli counts and a significant increase in Lactobacillus counts compared to the CON group. Postbiotic supplementation also improved gut morphology compared to the AGP and CON groups. In conclusion, postbiotic supplementation shows promise as an alternative to antimicrobials in broiler production, with beneficial effects on broilers fed an antibiotic-free diet.

Keywords: Broiler chicken, Growth performance, Immune response, Postbiotic, Lactobacillus

P1-09

ESTIMATION OF GENETIC PARAMETERS ON PRE-HOUSING BODY WEIGHT IN RHODE ISLAND RED CHICKEN

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ABSRACT

In present investigation, 110 four-hatched RIR chicks that has undergone 31st generation of selection based on 40-week part-period egg production were evaluated for growth and production traits using least-squares analysis of variance. Overall, least-square means of body at 0,8,12,16 and 20 weeks of age were 34.1±1.0g, 532.3±15.5g, 953.3±35.1g, 1339.5±38.4g and 1601.8±41.7g, respectively. Least square means of age at sexual maturity (ASM) was136.7±1.7 days. The heritability estimates for BW0, BW8, BW12, BW16, and BW20 were 0.71±0.41, 0.37±0.31, 0.73±0.42, 0.42±0.34, and 0.49±0.36, respectively. Heritability estimates for growth traits were high and low for production trait (ASM). The genetic correlation of BW0 was moderately positive with ASM, BW20, low positive with BW12, and BW16 and moderately negative with BW8. The phenotypic correlations of ASM with all other traits were negative. The phenotypic correlation of BW0 and BW12 was positive with all traits except ASM. These findings suggest the usefulness of pre-housing body weight as selection criterion for growth performance in RIR chicken.

Keywords: Correlation, growth traits, Heritability, RIR Chicken

P1-10

COAT COLOUR IN BLACK BENGAL GOATS– A CHARISMATIC CHARACTERISTIC OR POTENTIALLY SIGNIFICANT ECHELON FOR ECONOMIC TRAITS?

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ABSTRACT

Black Bengal goat is the most important goat breed of Jharkhand. Irrefutably, it is an asset for India. Black Bengal goats have many coat colour variants in India as well as in Bangladesh, where it is abundantly found. Many genes control coat colour, although MC1R and ASIP are the most important amongst them. The genetic mechanism underlying coat colour inheritance and expression remains unexplored mainly due to the limited molecular-level research on coat colour mechanisms and their association with various economic traits in the Black Bengal goat. It is also because many genes than expected affect coat colour. Past studies clearly point towards the coat colour as an indicator of many important traits, as well as a probable model for the selection of superior Black Bengal goats amongst the population. The current study examines the effect of Coat colour on Body weight in Black Bengal Goats at different ages across four breeding clusters under the AICRP on Goat-Black Bengal Field Unit-BAU. Body weight is the most important economic trait in Black Bengal goats, as it is primarily a meat animal. So, the Black-Brown-White coloured variant of Black Bengal Goats has a mean body weight of 18.15±0.63. The weight is significantly higher than all other colours, a notable finding. At 3, 6 and 9 months of age, the mean body weight of Black-Brown-White coat coloured Black Bengal Goats was significantly higher than all other coat colour variants, and it was respectively 6.30 ±0.77 kg, 9.63±0.9 kg and 14.89±0.57 kg. Keywords–Transgenerational, melanogenesis, Melanocortin, syntenic gene.

Keywords: Transgenerational, melanogenesis, Melanocortin, syntenic gene.

P1-11

ESTIMATION OF MATERNAL AND ADDITIVE EFFECT FOR PRODUCTIVE TRAITS IN SAHIWAL (*BOS INDICUS*) CATTLE

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ABSTRACT

The present study aimed to assess production traits in Sahiwal cattle by analysing datafrom 130 animals born to 18 sires and 71 dams. The investigation focused on estimating (co)variance components and genetic parameters for productiontraits in Sahiwal cattle. Results from least–squares analysis indicated that there was highly significant effect ($p<0.01$) of the period of calving (POC) on key production traits viz., first lactationmilk yield (FLMY), 300–day milk yield (FLMY300), first peak yield (FPY) and significant effect ($p<0.05$) on first lactation length (FLL) in studied population. The least squares mean for these traitswere reported as:

FLMY (1969.23 ± 57.20 kg), FLMY300 (1921.23 ± 51.76 kg),FPY (9.49 ± 0.21 kg) and FLL (254.59 ± 5.17 days), respectively.Season of calving also revealed highly significant effect ($p<0.01$)on FLMY, FLMY300 and significant effect ($p<0.05$) on FLL. In the studied population, along with additive genetic variability maternal permanent environmental effect was also foundto be present for the trait FLL. Direct heritability estimates (h2) for FLMY,FLMY300, FLL, FPY, TLMY traits ranged from 0.21 to 0.31 in studied population. However, heritability for maternal permanent environmental effect was found to be 0.16 for trait FLL. These findings offer valuable insights into the genetic factors influencing production traits, contributing to the enhancement of breeding and management practices in Sahiwal cattle. KEY–WORDS: Sahiwal cattle, production traits, genetic parameters, heritability.

Key words: Sahiwal cattle, production traits, genetic parameters, heritability.

P1-12

ASSOCIATION OF LIVE BODY WEIGHT WITH MORPHOMETRIC TRAITS IN DIFFERENT POULTRY BREEDS

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ABSTRACT

The study was conducted on 300 birds; 100 each from Rhode Island Red (RIR), Kadaknath and Punjab Brown maintained at Poultry research farm under Directorate of Livestock Farms. The body weight and morphometric traits were measured bi-weekly from 12th to 26th week of age. Significantly ($p \leq 0.01$) higher correlation was observed between shank length (SL) and body length (BL) through most of the weeks. Keel length (KL) exhibits significantly ($p < 0.05$) higher correlations with BL, shank width (SW), and beak length (BKL) at the 12th and 14th weeks. BKL generally showed significantly ($p < 0.05$) higher correlations with wing length (WL), KL, and body girth (BG) across ages, except at the 14th, 22nd, and 26th weeks. Body Girth had significantly ($p \leq 0.01$) higher correlation with KL at most of the age groups. Body weight showed significantly ($p \leq 0.01$) higher correlation at all age groups in all genotypes with most of the morphometric traits except had weaker correlation with BG in RIR, with BKL and BG in Kadaknath and with BL in Punjab Brown poultry birds. Significant ($p \leq 0.01$) and positive regression coefficients of body weight on SL from 14 to 26 week of age were observed in RIR chicken. Significantly ($p \leq 0.01$) higher regression coefficients of body weight on CL were also found from 16 to 26th week of age. In Kadaknath poultry bird's, positive significant ($p \leq 0.01$) regression coefficients were observed of body weight on CL from 16 to 26 week of age and WL from 18 to 26th week of age. Moreover, in Punjab Brown poultry bird's, positive significantly ($p \leq 0.01$) regression coefficients of body weight was observed on CL from 14 to 26 week of age except 24th week of age, on KL from 16 to 26 week of age except 20th week of age and on WL from 14 to 20th week of age.

Keywords: RIR, Kadaknath, Punjab Brown, Body weight, Morphometric traits

P1-13

HERITABILITY OF MEAT QUALITY TRAITS IN SMALL RUMINANTS: A META-ANALYTICAL STUDY

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ABSTRACT

Meat quality in small ruminants, particularly sheep and goats are influenced by both genetic and environmental factors. This meta-analytical study aimed to estimate the heritability of major meat quality traits in these species. Small ruminants play a crucial role in global meat production, providing an affordable and acceptable source of protein and supporting the livelihoods of small and marginal farmers. A comprehensive review and synthesis of published studies were conducted to evaluate the heritability of key meat quality attributes, including ultimate pH, Meat color, tenderness, juiciness, and Marbling, Intermuscular fat, Water holding capacity (WHC) and Fatty acid profile. The pooled estimates revealed moderate to high heritability (0.2–0.5), suggesting a significant genetic component influencing these traits. The findings indicate that genetic selection and marker-assisted breeding can effectively enhance meat quality in small ruminants. This study provides a scientific basis for designing breeding programme aim to improve product quality and market competitiveness through targeted genetic improvement.

Keywords: Heritability, Meat quality, Small ruminants, Meta-analysis

P1-14

REPRODUCTIVE PERFORMANCE EVALUATION OF DIFFERENT GENETIC GROUPS IN LOOSE VS TIE HOUSING SYSTEM

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ABSTRACT

The aim of this study was to assess the effect of housing systems (loose vs tie stall) on the reproductive performance in three genetic groups of Sahiwal, Sahiwal crossbred and HF crossbred cows in Nagpur district of Maharashtra (India). A total number of 66 cows were assessed to study the effect of housing system on time required (days) for onset of estrus after parturition and conception rate following parturition. The Sahiwal group of cows consists of total 17animals comprising 8 in loose housing and 9 in tied housing, Sahiwal crossbred group consist total 17 animals 8 in loose housing and 9 in tied housing and the HF crossbred group consist of 17 animals in loose housing and 15 animals in tied housing system. The mean days required for first oestrous after parturition in Sahiwal genetic group in loose housing was 86.25 ± 6.11 days whereas 116 ± 7.46 days in tied housing system. In second genetic group of Sahiwal crossbred the mean values of first oestrous after parturition was 89.5 ± 5.2 and 105.22 ± 7.19 days in loose and tied housing while in third genetic group of HF crossbred cows the mean days required for first oestrous after parturition was 69.06 ± 2.64 and 84.87 ± 2.76 days. However the pooled mean for first oestrous after parturition in each genetic group were 102 ± 6.09, 97.82 ± 4.81 and 76.47 ± 2.35 days respectively in Sahiwal, Sahiwal crossbred and HF crossbred genetic groups. The conception rate (%) in loose housing was 50 % in first and second service, respectively and in tie housing system conception rate (%) were 33, 22 and 44 % in first, second and third service respectively in Sahiwal genetic group. Conception rate in Sahiwal crossbred genetic group in loose housing were 50, 12.5 and 37.5 % in first, second and third service while 11, 44 and 44 % in tie housing. In third genetic group of HF crossbred conception rate in loose housing were 58.8, 35 and 5.8 in first, second and third service respectively whereas 53, 20 and 26.6 % in tie housing. Comparison between genetic groups suggests that HF cross required less than 70 days for exhibiting the first post-partum oestrus and is most effective for early breeding and the first service conception rate is higher in cows reared in loose housing system as compared to tie system.

Keywords: Loose vs tie housing, Onset of estrus after parturition and Conception rate

P1-15

FACTORS AFFECTING QUANTITY AND QUALITY OF MILK IN BLACK BENGAL GOATS AND MILK YIELD PREDICTABILITY USING ARTIFICIAL NEURAL NETWORKS

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ABSTRACT

Less milk yield (MY) in Black Bengal goats (BBG) poses serious challenge for kid survivability and their future growth. The objective of this study is to evaluate managemental factors affecting MY and develop model(s)to predict MY. It might help compensating ration formulation for dams and kids. Thirty-fourBBG were hand-milked (3-times/day)at fortnight intervals and data analysed using GLM.The mean MY of BBG was 272.48±10.48 g/day. Age ($P<0.001$), kidding season ($P<0.01$) and lactation fortnight ($P<0.01$) significantly influenced MY/day. Age ($P<0.05$) affected morning, noon and afternoon MY, and kidding season affected ($P<0.001$) morning MY. Lactation fortnight influenced ($P<0.01$) noon and afternoon MY. Adults (>24month age) produced 54% more milk than youngers. Milk flow rate (MFR) was 11.11±0.41 (g)/hour; age, kidding season and lactation fortnight significantly affected MFR similar to MY.Parity and photoperiod did not significantly influence MY and MFR. Somatic cell counts significantly varied by age and lactation fortnight;twice in adult ($P<0.001$) than young. MY per-Kg $W^{0.75}$ significantly ($P<0.01$) varied by age, parity, kidding season and lactation fortnight, but not by photoperiods. Nulliparous does were more efficient milk-yielder /kg $W^{0.75}$as compared to multiparous.Overall persistency of MYwas 0.93±0.03, whichdidn't differ significantly by presently investigatedfactors.MY was predicted by a feed-forward backpropagation neural network with Levenberg-Marquardt training algorithm, using tan-sigmoidal (hidden) and Purelin (output) transfer functions. Increased neuron numbers (10 to 50) improved training and validation R^2, which ultimately reached 0.85 and 0.62, respectively after 1000 iterations. The difference in training and validation R^2 being >5% represents the possibility of overfitting, which might be reduced either by change of algorithm or increase in data point numbers. It was concluded that age, kidding season and lactation fortnightare important contributory factors that significantly influence quantity and quality of milk in BBG.

Key words: Black Bengal goat, Milk yield, Somatic cell count,Non-genetic factors

P1-16

STUDIES ON THE REPRODUCTIVE PERFORMANCE OF HD-K75 PIGS

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ABSTRACT

Data on reproductive performance of the progenies of 44 sires and 114 dams of HD–K75 pigs maintained over 6 years from 2012 to 2018 bred in the ICAR–AICRP on pigs located at CVSc, AAU, Khanapara, Guwahati were utilized through least squares analysis (LSA) to study various reproductive traits. The LSA of variance technique was carried out to study the effects of season of birth, sex, and parity on these traits. Duncan's Multiple Range Test (DMRT) was used to make all the pairwise comparisons among the means to test the significance of differences among the different subclasses for various traits. The overall least squares means (LSM) for age at sexual maturity, gestation length and farrowing interval were found to be 205.294±1.054, 113.70±0.119 and 216.781±2.565 days respectively. The overall LSM for litter size at birth, litter size at weaning, litter weight at birth and litter weight at weaning were found to be 7.747±0.088, 7.556±0.093 numbers and 7.804±0.084 and 74.644±0.0886 kg respectively. Effect of season of birth on age at sexual maturity, and season of birth and parity on gestation period was found to be non–significant. LSA of variance revealed significant difference between the various seasons in respect to farrowing interval. The effect of parity on farrowing interval was non–significant. Significant effect of season of birth on litter size at birth, litter size at weaning, litter weight at birth and litter weight at weaning was found. Parity had significant effect on litter size at birth, litter size at weaning, litter weight at birth and litter weight at weaning. The performance of HD–K75 pigs was found to be satisfactory under prevailing managemental conditions and are well adapted to the agro–climatic conditions of Assam. Hence, the popularization of this crossbreed pig variety would increase the production, livelihood, and income of the regional farmers.

Keywords: HD–K75 pigs, reproductive traits, least squares analysis

P1-17

GENETIC INSIGHTS ON TEST-DAY MILK COMPOSITIONAL TRAITS IN JERSEY CROSSBRED CATTLE

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ABSTRACT

The present study aimed to estimate the genetic parameters of test-day milk compositional traits–test day fat yield (TDFY), test day protein yield (TDPY), test day carrier yield (CY), and test day fat-to-protein ratio (FPR)—in Jersey crossbred cattle maintained at the Eastern Regional Station of the National Dairy Research Institute, Kalyani, West Bengal, India. A total of 5,187 test-day compositional records (2017–2023) were analysed. Genetic and non-genetic effects were evaluated using the MMLSML method in Harvey, while genetic parameters were estimated using repeatability animal model using both AIREML (Average Information Restricted Maximum Likelihood) and Bayesian approach in WOMBAT software. All traits under consideration were significantly ($P < 0.001$) affected by season of calving, year of calving and parity. Heritability estimates obtained by AIREML method for TDPY, TDFY, TDCY, and TDFPR were 0.18?±?0.03, 0.14?±?0.05, 0.11?±?0.05, 0.11?±?0.04 and 0.04?±?0.04 respectively, whereas the corresponding estimates were 0.19?±?0.03, 0.15?±?0.05, 0.12?±?0.05, 0.12?±?0.04 and 0.06?±?0.04 respectively in Bayesian approach. Repeatability estimates ranged from 0.23 to 0.29, reflecting moderate consistency across test day records and parities using both the methods. Genetic correlations revealed strong positive associations of TDFY with TDPY (0.90 to 0.97), whereas a moderate positive correlation was observed between TDFPR and TDFY. The low to moderate heritability in milk compositional traits indicates some scope for genetic improvement of these traits through selection and proper managemental practices and highlight the combined influence of genetic and environmental factors on milk compositional traits in Jersey crossbred cattle. Moreover, the positive genetic correlations suggest that selection on one trait can result in corresponding gains among the traits in study. Thus, the study suggest that multi-trait selection combined with optimal management practices could enhance both the quality and quantity of milk production.

Keywords: Test days, milk compositional traits, genetic parameters, Cattle

P1-18

GROWTH, PRODUCTION, REPRODUCTION, EGG & CARCASS CHARACTERS OF INDIGENOUS CHICKEN OF CHHATTISGARH PLAIN REGION

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ABSTRACT

The present study was undertaken to study the physical character, growth, productive and reproductive performance and carcass characteristics of the native chicken of Chhattisgarh plain. Parameters were considered as physical character, growth, productive and reproductive performance, biochemical and microelements status in blood serum and carcass characteristics. To produce pure native germplasm 1522 number of pure desi eggs were collected from different villages of Durg, Rajnandgaon and Khairagarh district. The most predominant plumage color observed in native chicken of Chhattisgarh was brownish black with birds with mostly single comb. Average weekly body weight 12th and 16th week of age were 103.52 ± 0.69, 246.65 ± 0.86, 453.09 ± 1.31, and 704.08 ± 2.93 g respectively. The average egg production per laying cycle was 12.69±0.54 eggs with average laying period of 19.34 days with average clutch size 3.06±0.11 and average clutch interval as 1.60±0.19 days. The average egg weight was 35.84 ± 0.20g. with average specific gravity, egg length, egg width and shape index as 1.065, 4.7 ± 0.21cm, 3.6 ± 0.13cm and 77.66 % respectively. The average albumin weight, percent albumin, yolk weight, percent yolk, albumin height, yolk height, albumin index, yolk index, haugh unit score, egg shell weight, percent shell and shell thickness obtained was 21.60±0.20g, 60.74%, 10.82±0.08g, 30.22%, 5.26±0.08mm, 14.75±0.13mm, 9.59%, 43.79%, 80.68, 3.25±0.05g, 9.09% and 0.30±0.002 mm respectively. At the time of slaughter average live weight of birds was 1176.77 ±43.02 g yielding the dressed weight as 850.78 g. The dressing percentage recorded as 72.79%. The meat composition analysis revealed that moisture content and dry matter content was 74.60±0.22% and was 25.39±0.22% respectively in which composition of crude protein, ether extract and total ash were 84.66 ± 0.02%, 3.35 ± 0.13% and 5.84 ±0.10%, respectively.

Keywords: Native chicken, Chhattisgarh, physical characteristics, reproductive, productive, egg quality traits, carcass traits

P1-19

EXTERNAL AND INTERNAL EGG QUALITY TRAITS OF NATIVE CHICKEN IN PLAIN REGION OF CHHATTISGARH

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ABSTRACT

The present study was conducted to evaluate the external and internal egg quality traits of native chickens in the Chhattisgarh plain region, specifically in Rajnandgaon and Mohla–Manpur–Ambagarh Chowki districts. A total of 100 eggs were randomly collected, dry cleaned, and subjected to quality analysis within 15 hours of collection. External traits measured included egg weight, length, width, shell weight, shell thickness, specific gravity, and shape index, while internal traits comprised albumen weight, albumen length, albumen height, albumen index, albumen ratio, yolk weight, yolk width, yolk height, yolk index, yolk ratio, and Haugh unit. The mean egg weight, length, width, shell weight, shell thickness, specific gravity, and shape index were 38.539 ± 0.56 g, 47.892 ± 0.42 mm, 38.96 ± 0.48 mm, 3.443 ± 0.05 g, 0.348 ± 0.006 mm, 1.046 ± 0.012, and 81.46 ± 0.77, respectively. Internal quality parameters recorded were albumen weight (22.972 ± 0.47 g), albumen index (10.403 ± 0.27), yolk weight (12.889 ± 0.23 g), yolk index (38.111 ± 0.67), yolk ratio (33.920 ± 0.67), and Haugh unit (83.15 ± 0.80). The results indicate that native chickens produce eggs with good shell quality and satisfactory internal quality.

Keywords: Native chicken, Egg quality traits, External quality, Internal quality,

P1-20

CHARACTERISATION OF INDIGENOUS GOAT POPULATION FOR ACCELERATED GENETIC IMPROVEMENT AND SUSTAINABLE PRODUCTION – AN INSIGHT FROM ASSAM

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ABSTRACT

In Assam, goat farming is a vital livelihood activity and rearing of indigenous goats contribute significantly to meat production, income and nutritional security of rural households. The present study documents the profile of local goat farmers and morphometric characteristics of these goats maintained under traditional management system. The study was conducted in Nalbari, Kamrup (Rural), Golaghat and Lakhimpur districts of Assam. The farmers typically maintained small flocks averaging 4.2 animals, composed of 41.5% does, 12.5% bucks, and 46.0% kids, under extensive conditions with natural grazing. The feeding relies mainly on native grasses and tree fodders such as jackfruit, subabool, dimaru, and kanchan, with negligible supplementation. The distinctive morphological features include a uniform black coat, convex head profile, horizontally erect ears, short tails, and well‑developed udder capable of supporting twin births. The males reach 14.55 ± 0.11 kg and females 12.40 ± 0.28 kg of body weight at 12 months of age. The buck and doe show proportional body conformation reflecting a compact but functional frame well‑suited for meat production in a resource‑limited environment. The age at first mating is 270 ± 33 days in males and 300 ± 22 in females with the age at first kidding as 488 ± 11 days. The litter size averages 1.48, and the lifetime number of kidding stands at 8.16. These findings highlight the importance of locally adapted indigenous goats to provide a readily accessible source of animal protein, micronutrients and income to resource poor households. Their traditional management by smallholder farmers highlights their role in dietary diversity and economic resilience of local food systems. The documented morphometric and performance traits may serve as a vital baseline for the application of genomic and selection tools aimed at accelerating genetic improvement and conservation of native goats of Assam.

Keywords: Indigenous goat, Assam, morphometric traits, genetic improvement

P1-21

ENHANCING THE FARMER'S INCOME BY ADAPTING THE NEW SYNTHETIC CATTLE BREED "FRIESWAL" IN TARAI REGION OF UTTARAKHAND

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ABSTRACT

The Field Progeny Testing (FPT) Programme was initiated by ICAR–Central Institute for Research on Cattle (CIRC), Meerut during the 8th Five Year Plan with the objective of improving the performance of crossbred cattle through the use of genetically superior bulls and adoption of scientific management practices under field conditions. The programme is currently being implemented at KVASU Manutny, BAIF Pune, GADVASU Ludhiana, and GB Pant University of Agriculture & Technology (GBPUAT), Pantnagar. At Pantnagar, the programme was launched in September 2009 to progeny test Frieswal bulls under field conditions and to enhance the genetic potential of crossbred cows in Udham Singh Nagar and Nainital districts of Uttarakhand. The programme presently covers 4,160 farmer beneficiaries across 235 villages, organized into eight clusters. To build capacity and improve field‑level participation, a range of extension activities were conducted, including 59 farmer training programmes (benefiting about 4,000 farmers), 10 heifer shows, 19 animal health camps, 4 refresher courses for inseminators‑cum‑data recorders, and 53 Kisan Chaupals. Up to August 2025, a total of 62,619 test inseminations were carried out, resulting in 34,417 confirmed pregnancies with a conception rate of 55%. A total of 26,735 calvings were recorded, which produced 12,134 female progenies. Of these, 2,517 progenies reached age at first calving (AFC) with an average of 36 months, and 2,131 completed first lactation with an average 305‑day milk yield of 3,325 kg at 3.5% fat. This reflects a 50% improvement in milk yield compared to the base population (2,214 kg), along with a reduction in Age at First Calving by 69 days over the past decade. Documented success stories of 24 progressive farmers to ICAR‑CIRC Meerut, confirmed that the programme significantly enhanced productivity and farmers' income, with beneficiaries reporting two‑to threefold increases, underscoring both genetic and socio‑economic gains.

Keywords: Frieswal bulls, crossbred cattle, milk yield, conception rate.

P1-22

INCREASED TREND OF IMPROVED PRODUCTION AND REPRODUCTIVE PERFORMANCE IN MURRAH BUFFALOES

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ABSTRACT

After induction of Network project on Buffalo Improvement for evaluation of progeny testing based on sire evaluation, there has been enhanced improvement recorded in production and reproductive traits as performance indicators in Murrah buffaloes maintained at ICAR-CIRB, Hisar. The initial pedigree selection of Murrah breeding bulls for test mating is done on the basis of 305 days or less lactation milk yield of elite dams (>3000 kg for second lactation and > 2500 kg for first lactation). The present study was undertaken to decipher the recent trends in productive and reproductive performance indicators during last ten years from 2015-16 to 2024-25. Data from nearly 250 breedable buffaloes during each year were mined for this study. During the last 10 years, total lactation milk yield (Kg), standard lactation milk yield (Kg), Average peak Yield (Kg), increased from 2483 to 3129, 2336 to 3004 and 11.17 to 15.49, respectively. The weight average (Kg) and herd average (Kg) also saw significant improvement from 8.04 and 5.21 in 2015-16 to 10.20 and 7.11 in 2023-24, respectively. During last 10 years from 2015-16 to 2024-25 average age of first calving (monthly), calving interval (days), dry period (days), service period (days), were significantly improved from 44.96, 449, 141 and 138 to 40.25, 434, 120 and 125, respectively. It may be concluded that there has been a significant improvement in productive and reproductive performance of the Murrah buffalo at ICAR-CIRB over the years and subsequently the institute has now become the potential source for production of high merit breedable bulls for semen dissemination throughout the country.

Keywords: Production, Reproductive performance, Murrah Buffaloes

P1-23

INHERITANCE OF GROWTH AND EARLY PRODUCTION TRAITS IN PD-1 LINE

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ABSRACT

The present study was undertaken to evaluate and improve the Vanaraja male line (PD-1) chicken through pedigree-based selection for higher body weight and shank length. For this purpose, a total of 50 sires and 250 dams were used in pedigreed mating, producing 3000–3500 chicks per generation over three generations. Selection was applied at six weeks of age based on a two-trait selection index considering body weight (BW6) and shank length (SL6). Pedigree hatchings were done; the fertility was 79.45 % and hatchability was 85.89 % on fertile egg set (FES) and 68.24% on total egg set (TES) respectively. The body weight and shank length at 4 and 6 weeks of age were 363.1±2.40 and 715.9±4.51 g and 61.87±0.17 and 80.42±0.22 mm, respectively. Least squares mean for BW6 and SL6 differed significantly ($P<0.05$) among generations, indicating genetic progress. The heritability estimate for body weight was 0.22±0.08, while estimate for shank length was 0.21±0.03. The 20-week body weight was 2182±4.94 g which was higher than the base generation. The ASM was 173.3±0.38 days. The egg weight at 28 and 32 weeks of age was 52.05±0.14 and 55.52±0.13 g, respectively. The part period egg production up to 28 and 32 weeks of age was 13.92±0.27 and 31.53±0.32 eggs, respectively. Selection differential and response values showed consistent improvement in six-week shank length and body weight across generations. Results demonstrate that the constructed selection index effectively enhanced the PD-1 line's juvenile growth traits, achieving steady genetic improvement while maintaining reproductive fitness. Index selection based on body weight and shank length is an ideal breeding strategy for the improvement of body weight and shank length in PD-1 chicken.

Keywords: juvenile traits, shank length, PD-1 lines, genetic parameters

P1-24

GENETIC ANALYSIS OF BIRTH AND WEANING WEIGHT IN SALEM BLACK GOATS: DIRECT AND MATERNAL HERITABILITY

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ABSTRACT

This study aimed to estimate the direct and maternal genetic effects on growth traits in Salem Black goats. Data included records from 920 kids, progeny of 147 bucks and 804 does, collected between 2004 and 2019. The traits analyzed were birth weight (BW), weaning weight (WW), and average daily gain from birth to weaning (ADG). Three animal models were fitted using MTDFREML to estimate variance components: a basic model (Model 1), a model including permanent environmental effects (Model 2), and a full model (Model 3) that also included maternal genetic effects and the covariance between direct and maternal genetic effects. The least‐squares means for BW, WW, and ADG were 2.21 kg, 9.23 kg, and 78.27 g, respectively. Fixed effects (sex, season, year, and type of birth, parity) significantly influenced all traits. Estimates of direct heritability (h^2d) from the full model (Model 3) were 0.66 for BW, 0.30 for WW, and 0.11 for ADG. Maternal heritability (h^2m) estimates were 0.26 for BW, 0.07 for WW, and 0.01 for ADG. The results indicate that the maternal genetic effect is a substantial source of variation, particularly for birth weight. In conclusion, maternal genetic effects are crucial for pre‐weaning growth traits in Salem Black goats. Therefore, incorporating these effects into breeding programs is essential for the genetic improvement of early growth performance in this breed.

Keywords: Phenotypic Parameters, Genetic Parameters, Heritability, Direct Genetic Effect, Maternal Genetic Effect, Variance Components, Salem Black Goats

P1-25

PRINCIPAL COMPONENT ANALYSIS OF BREEDING VALUES BASED ON PRODUCTION AND REPRODUCTION TRAITS IN FRIESWAL CATTLE

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ABSTRACT

Breeding value is the estimation of an animal’s genetic merit for a trait based on its own and its relatives' performance. This estimation can be useful in selection programmes, helping a breeder identify genetically superior animals and increase production and reproduction traits in cattle. Principal component analysis applied to BVs has shown promise in addressing some of the challenges associated with sire evaluation. Principal component analysis (PCA) of production and reproduction traits in Frieswal cattle from breeding values estimated by AI‒REML was performed. A total of 1163 progeny records from 69 sires spanning over nine years were analyzed utilizing average information restricted maximum likelihood (AI‒REML) and principal component analysis (PCA). The traits included age at sexual maturity (ASM), age at first calving (AFC), gestation period (GP), first calving interval (FCI), number of services per conception (NSPC), first dry period (FDP), first service period (FSP), test day peak milk yield (TDPY), first lactation 305‒days milk yield (FL305‒DMY), fat percentage (FP) and first lactation length (FLL). PCA revealed four principal components, which explained 79.90% of the total variance. PC1 was related to FLL, FCI and FSP; PC2 exhibited high loadings for ASM and AFC; PC3 accounting for milk production (TDPY and FL305‒DMY); and PC4 for FP and FDP. The PCA identified four key components grouping related to production and reproduction traits in Frieswal cattle. This highlights the importance of multi‒trait selection for balanced genetic improvement in both production and reproduction efficiency.

Key words: AI‒REML, Breeding values, Frieswal, PCA

P1-26

PLUMAGE COLOUR AND PERFORMANCE TRAITS IN POULTRY: INSIGHTS FROM A MULTIVARIATE ANALYSIS USING A MACHINE LEARNING APPROACH

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ABSTRACT

Understanding the relationship between plumage colour and performance is essential for breed characterisation and selection in commercial broiler parent lines. This study utilised data from 362 PB1 females categorised into four plumage groups: Barred (BBD: 58), Brown (BR: 86), Brownish Grey (BG: 85), and Black (B: 143), maintained under the AICRP Poultry Breeding Project at the College of Veterinary Science, Ludhiana. Traits including BWT0, BWT5, BWT20, BWT40, BWT52, ASM, EWT36, ENO40, and ENO52 were documented as standard practices. Descriptive statistics revealed that BG birds exhibited the highest means for BWT0 (39.59g), BWT5 (1234.54g), and BWT40 (2926.41g). BR birds exhibited the highest ENO40 (59.29) and ENO52 (101.62) values. Birds with B plumage had the highest egg weight (52.82g). ANOVA revealed no significant effect of plumage on any trait, except for EWT36 ($p = 0.001$). Principal Component Analysis (PCA) of performance traits revealed that the first two components accounted for 44.40% of the variance, but did not demonstrate clear clustering by plumage colour. Dummy regression analysis further elucidated these relationships. Traits BWT5 and BWT40 demonstrated moderate positive coefficients for BG (21.10 and 36.17, respectively), whereas BBD and BR displayed weaker associations for BWT5 (6.21 and 11.19, respectively). R^2 values for all dummy regression models remained low (<0.040), signifying the restricted explanatory capacity of plumage colour. K-means unsupervised clustering was assessed through silhouette analysis, which indicated the optimal score at $k=2$. Cluster assignments exhibited weak alignment with plumage categories, corroborating the PCA findings. In conclusion, this study revealed that plumage colour did not significantly affect performance traits in the PB1 line. This is a favourable outcome, as it suggests that PB1, being a coloured broiler parent line, maintains stable performance irrespective of plumage variation. Such consistency is advantageous, where sub-group variation among parent lines could otherwise complicate selection strategies.

Keywords: Plumage colour, performance traits, Principal Component Analysis.

P1-27

MORPHOMETRIC CHARACTERIZATION OF THE INDIGENOUS GOATS OF ODISHA

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ABSTRACT

Goats contribute greater value to the rural economy. Phenotypic characterization is a first step to characterize the animals in a particular production environment. A multipurpose sampling of 248 goats (Black Bengal = 75, Ganjam = 70, Bolangir = 48, and Raighar = 55) was studied to characterize the unregistered (Raighar and Bolangir) goats of Odisha and registered (Black Bengal and Ganjam) goats of India. The univariate and multivariate statistical approaches and random forest analysis were used to differentiate the goat populations by their morphometric traits. The morphometric traits were significant for most of the traits between the goat populations. Raighar goats had consistently higher morphometric traits, such as wither height (62.54 cm), rump height (65.37 cm), heart girth (64.92 cm), paunch girth (69.77 cm), and leg length (43.68 cm), indicating the productive type of animals. Canonical discriminant analysis and random forest analysis revealed that body length, leg length, and height at the withers were good indicators to distinguish the goat population in the present study. The results of the present study suggest that random forest analysis can also be used to classify animal populations, provided it is validated by a large sample size. In conclusion, the present study highlighted the morphometric characterization of the indigenous goats of Odisha.

Key words: Canonical discriminant analysis, Goat, Random Forest analysis

P1-28

MODELLING KID SURVIVAL IN BLACK BENGAL GOATS THROUGH KAPLAN–MEIER CURVES AND COX PROPORTIONAL HAZARDS: A STUDY ACROSS AGRO-CLIMATIC CLUSTERS OF WEST BENGAL

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ABSTRACT

Kid mortality induced by various factors causes significant economic losses to the goat producers across India. In this study, the survivals from birth to 12 months of age of Black Bengal kids were investigated within framework of the survival analysis. The research work is the first ever report of critical analysis of survival potential with mean survival time, survival risk and cumulative hazard in Black Bengal goats. Records were accessed from 2010 to 2021, with 11996 animals reared under different agro-climatic clusters of West Bengal. The data was analyzed by using “survival” package of R. Kaplan Meier curve and Cox regression was fitted to the data after checking the assumptions of regression. The explanatory variables were cluster, year of birth, season of birth, type of birth, sex and parity of kidding. The kid mortality on the first day after birth was 0.14%, constituting 9.04% of overall mortality upto 3 months of age. The mortality until the end of 12 months was 14.45%. The p values are not significant ($P<0.05$) as revealed by the Likelihood ratio test, Wald test and Score (log rank) test and indicates a weak relationship between the different subclasses of each factor and increased risk of death of the kids. There is no significant ($p<0.05$) difference between the subclasses of each factor when the animal face death due to hazard. The Cox model assumes that the hazards are proportional (i.e. exp (coef) $\approx$1) for each factors. The results indicate that kids with the lowest birth weight have the highest survival risk and vice versa. Breeding for litter size reduces the likelihood of survival while increasing the number of kids born over time. Finally, manipulation of doe nutrition during pregnancy is required to increase the birth weight which in turn will improve kid survival.

Key words: Black Bengal goat, Kid survival, Cox regression, Kaplan Meier curve

P1-29

RANDOM REGRESSION ANALYSIS OF GENETIC PERSISTENCY IN MURRAH BUFFALOES USING WILMINKS' FUNCTION

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ABSTRACT

Data on performance traits across six lactations were collected from history sheets and daily milk recording registers maintained at Buffalo Farm, Department of Livestock Production Management, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, over a 12−year period (2010–2021). A single−trait linear mixed random regression test−day model based on Wilminks' function was applied to monthly test−day milk records of Murrah buffaloes. Genetic persistency was estimated as cumulative deviation of estimated breeding values from the day of peak yield to subsequent test days across different lactation stages and parities. Average test day (TD) milk yields (kg) in first lactation i.e. TD5, TD35, TD65, TD95, TD125, TD155, TD185, TD215, TD245, TD275 and TD305 were 3.33, 8.92, 9.57, 9.51, 8.96, 8.85, 8.14, 7.27, 6.68, 5.85, and 5.47 kg, respectively. The heritability for different test days in Murrah buffalo ranged from 0.269 (TD305) to 0.660 (TD5) in first, 0.124 (TD305) to 0.162 (TD5) in second, 0.122 (TD305) to 0.180 (TD5) in third, 0.025 (TD185 and TD215) to 0.033 (TD5) in fourth, 0.011 (TD215) to 0.229 (TD5) in fifth and 0.011 (TD95 to TD185) to 0.013 (TD305) in sixth parity, however, permanent environment effect varied from 0.054 (TD5) to 0.175 (TD305), 0.022 (TD5) to 0.038 (TD305), 0.492 (TD305) to 0.632 (TD5), 0.175 (TD5) to 0.232 (TD305), 0.002 (TD185) to 0.078 (TD5) and 0.034 (TD5 and TD35) to 0.044 (TD305) in corresponding parities. The mean genetic persistency across the six parities were −0.521, −0.278, −0.003, 0.004, 0.025 and 0.003, respectively. The overall trend in average persistency showed gradual increase across test days, from −0.03 (TD95) to −0.222 (TD305), with an overall average of −0.128. The results indicated that milk yield persistency was high during first three parities, followed by a marked decline from fourth lactation onward.

Keywords: Genetic persistency, Murrah, Random regression, Test day, Wilminks' function

P1-30

BENCHMARKING THE EFFICIENCY OF MACHINE LEARNING APPROACH TO PREDICT 305-DAYS MILK YIELD USING RANDOM TEST-DAY MILK YIELDS

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ABSTRACT

Large scale Milk Yield (MY) recording has remained a daunting challenge, particularly in developing nations majorly having small, scattered and un-organized farms. The challenges are lack of manpower and monitoring mechanism, marginal adaption of weaning at birth, and poor approachability to small and scattered farms. Adapting monthly standard test-day milk yield (STDMY) recording has drastically lessened the burden, but lacks flexibility in days of recording, and any deviation costs loss of accuracy in prediction of 305-days milk yield (305DMY). This problem could be addressed by fitting the traditional lactation curve model as well as by Machine Learning (ML). In recent years, the advent of ML algorithms has revolutionized the modelling and prediction of intricate datasets. Hence, this study aimed to assess the predictive prowess of five ML algorithms (ANN, RF, SMOreg, MLR, XGB) alongside two conventional lactation curve model (Wood's and PRF) for predicting 305DMY in two ways; firstly using standard monthly test-day milk yields (STDMY) and secondly using random test-day milk yields (RTDMY). A dataset comprising 940 lactations from Murrah buffaloes, Nili Ravi buffaloes and Crossbred cattle was utilized for developing models. MLR, RF, and XGB emerged as the most effective algorithms for predicting 305DMY. Further, RTDMY records resulted in comparable or better predictive performance compared to STDMY records. The estimated genetic parameters from ML predicted and actual 305DMY were close. Using MLR, RF, and XGB; the estimated breeding values (EBVs) for the predicted and actual 305DMY showed stronger positive correlations, outperforming lactation curve models. It was concluded that RTDMY can be as-effective-as STDMY with ML algorithms; and MLR, RF, and XGB are particularly promising for dairy breeding purposes. This study may pave the path for flexibility in milk recording for genetic evaluation while improving predictive accuracy for 305DMY by leveraging ML techniques.

Keywords: Random Test-day Milk Yields; 305DMY; Machine Learning; Genetic Evaluation;

P1-31

PANTING SCORE AS A HEAT STRESS ASSESSMENT TOOL IN SMALLHOLDER DAIRY FARMING SYSTEM IN EAST REGION OF INDIA

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ABSTRACT

The heat stress significantly impacts livestock productivity in terms of reduced production performance of animals and subsequent GHG emission. Out of many ways the panting score has been found to be a simple and non‑invasive method to determine the heat stress. The present study aimed at understanding and determining the and parameters that drives it in animals. The heat stress has been measured under EGP program through trained performance recorder by following the methodology designed by Mader et al., (2006). A total of 40,282 records pertaining to 7,032 crossbred animals were used for analysis. Additionally, we also captured weather data at each location and added composite weather parameters likes temperature humidity index and heat load Index. The data were subjected for the statistical analysis. Data visualization was done through line graphs by comparing weather parameters. The normality of panting scores was assessed using the Kolmogorov‑Smirnov test. The Kruskal–Wallis test was used to compare panting scores across states. A Duncan's post‑hoc test (with p‑value adjustment) was performed to identify statistically significant differences between groups, and the Bonferroni correction was applied to account for multiple comparisons and minimize false positives. The Principal Component Analysis (PCA) was performed to identify the primary contributors to heat stress by analyzing the relationships between climate variables and panting scores. All climate parameters and panting scores were standardized before analysis. The PCA biplots and loading plots were generated to visualize the contribution of each variable to heat stress. Statistical analyses were performed in R software (Version 4.4.2). Results showed Crossbred cattle experienced peak heat stress during summer (March–June), with a secondary increase observed in September–October. THI found to have primary influencer of heat stress from non–corrected data and correlation analysis. PCA confirmed that Temperature and THI were the primary determinants of heat stress. Production parameters can be linked with panting to deeper insights into adaptive mechanisms.

Keywords: Panting Score, GHG, EGP, THI

P1-32

GENETIC CHARACTERISTICS OF BIOFILM-FORMING ANTIMICROBIAL RESISTANT SALMONELLA ISOLATES FROM DUCKS AND THEIR ENVIRONMENT

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ABSTRACT

The study aimed to determine the genetic characteristics, viz. biofilm-forming ability, antimicrobial resistance and virulence of Salmonella spp. in healthy ducks from West Bengal, India. A total of 462 samples were collected from Indigenous, Khaki Campbell, and Pekin ducks and their associated environment. Salmonella isolates were screened for extended-spectrum β-lactamase (ESBL) genes (blaTEM, blaCTX-M, blaSHV, blaAmpC), biofilm genes (csgA, sdiA, rpoS, rcsA), and the virulence gene invA. Among the 436 isolates, 42.2% were ESBL producers, with notable occurrences of blaTEM (36.5%), blaCTX-M (20.6%), blaSHV (17.7%), and blaAmpC (32.6%). The nucleotide sequences were found similar with blaTEM-1, blaTEM-164, blaTEM-72, blaCTX-M-15, blaCTX-M-28, blaCTX-M-82, blaSHV-2, blaSHV-27, blaSHV-45, blaSHV-99, blaSHV-191, blaSHV-215, and blaSHV-249 in BLAST search. Concurrently, a diverse prevalence of biofilm-associated genes, including csgA (54.59%), sdiA (52.52%), rpoS (80.28%), and rcsA (63.76%), was observed. Furthermore, 141 (32.34%) Salmonella isolates possessed the invA gene. Of 26 selected strains, high multi-drug resistance was detected, mainly against tetracycline and cefixime. Phylogenetic analysis of ESBL gene sequences showed clustering across avian, animal, and clinical (human) Salmonella isolates, indicating potential interspecies transmission and evolutionary divergence. Significant positive correlations found in biofilm formation, resistance, and invA prevalence ($\tau = 0.656$, $\rho = 0.765$, $p<0.001$). Findings revealed, for the first time, that apparently healthy ducks may carry Salmonella with a triad of antimicrobial resistance, biofilm formation and virulence genes that has great impact on duck husbandry and One Health.

Keywords: Antibiotic resistance, Biofilm, Duck, Salmonella spp., Virulence

P1-33

PREVALENCE OF GASTROINTESTINAL NEMATODOSIS AS DETERMINED BY MORPHOLOGICAL IDENTIFICATION OF THIRD STAGE LARVAE (L3) OBTAINED BY COPROCULTURE IN GAROLE SHEEP OF SUNDARBAN DELTA, WEST BENGAL

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ABSTRACT

Gastro–intestinal parasitism in sheep comprises the nematode parasites as the common and major component and it is also quite prevalent in livestock of South 24 Parganas, the breeding tract of Garole sheep. The research work was conducted for the determination of the nematode species prevalent in the said areas by morphological characteristics of the third stage larvae (L3) by coproculture of the pooled faecal samples were collected from Garole sheep of 'Sunderban Delta' of South 24 Parganas is the home tract. The prevalence study was carried out for a complete annual cycle starting from August 2006 to July 2007. The entire work involved in the study was carried out in the laboratory of the Department of Veterinary Parasitology having the required facilities. The overall picture revealed Haemonchus as the predominant (70.17%) nematode species followed by in order of prevalence, Oesophagostomum sp. (15.08%), Trichostrongylus sp. (9.75%), Strongyloides sp. (7.5%) and hook worm (2.17%). The larval composition was compared between the seasons it was observed that the highest composition of Haemonchus sp. and Strongyloides were in monsoon (71.00% and 3.75%, respectively) and lowest in summer (69.50% and 2.00%, respectively), whereas Oesophagostomum sp had highest composition in winter (15.50%) and the lowest in monsoon (14.75%), the difference being statistically non– significant ($P > 0.05$). The composition of Trichostrongylus sp. and hook worm was highest in summer (10.25% and 3.00%, respectively) and the lowest in monsoon (9.00% and 1.50%, respectively). Although the seasonal variation in the composition of the nematode larvae was not statistically significant ($P < 0.05$) but the composition of hookworm was significantly higher in summer (3.00%) compared to monsoon (1.50%). The study reveals that like other sheep breeds Garole sheep also prone to G I nematodosis throughout the year.

Keywords: Garole sheep, Coproculture, GI nematodosis, Prevalence

P1-34

PERFORMANCE EVALUATION OF RED CORNISH × PLYMOUTH ROCK BLACK CROSSBRED CHICKENS ACROSS TWO GENERATIONS

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ABSTRACT

The study was conducted to assess fertility, hatchability, and growth performance in two successive generations (F_1 and F_2) produced from a cross between Red Cornish and Plymouth Rock Black chickens. The Red Cornish males were mated with Plymouth Rock Black females to produce the F_1generation, which was inter se-mated to obtain the F_2generation. Fertility in the F_1 generation was recorded at 88.85%, while a decline to 80.20% was observed in the F_2generation. Hatchability on fertile egg set (FES) and total egg set (TES) basis in the F_1generation was 85.64% and 76.10%, respectively. Corresponding hatchability in the F_2generation was 81.81% (FES) and 65.62% (TES), indicating a reduction in reproductive performance across generations. Growth performance, expressed as mean body weight (Mean ± SE), was higher in the F_1 than in the F_2 generation. The F_1chicks recorded body weights of 33.83 ± 0.14 g (day-old, n=500), 306.00 ± 2.94 g (4 weeks, n=497), 611.87 ± 7.06 g (8 weeks, n=475), 833.37 ± 9.14 g (12 weeks, n=426), 1031.83 ± 13.18 g (16 weeks, n=334), and 1181.00 ± 16.89 g (20 weeks, n=293). The corresponding values in the F_2 generation were 31.92 ± 0.15 g (day-old, n=250), 259.06 ± 2.43 g (4 weeks, n=250), 592.78 ± 2.79 g (8 weeks, n=207), and 802.15 ± 7.95 g (12 weeks, n=180). The findings indicate that crossbreeding between Red Cornish and Plymouth Rock Black resulted in satisfactory fertility and growth performance in the F_1generation, with a decline in these traits in the F_2generation. The results suggest the expression of heterosis in the F_1 generation and its possible reduction in later generations. **Keywords**: Red Cornish, Plymouth Rock Black, Fertility, Growth traits

P1-35

PHENOTYPIC AND SOCIO-ECONOMIC PROFILING OF NATIVE CHICKENS IN THE KISHANGANJ REGION OF BIHAR

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ABSTRACT

This comprehensive study was undertaken to systematically characterize the native chicken population, designated as the "Kishanganj Native Chicken," in the south-eastern districts of Bihar, namely Purnea, Katihar, Araria and Kishanganj. The primary objective was to document the unique attributes of this indigenous poultry genetic resource and evaluate its potential for sustainable and economically viable poultry farming in the region. A robust survey-based methodology was employed, covering 48 villages across 12 blocks within the four target districts. Data were collected from a randomly selected sample of over 3,000 chickens using a structured questionnaire, adapted from the National Bureau of Animal Genetic Resources (NBAGR) with minor modifications to suit the local context. This approach allowed for a detailed analysis of the intricate relationship between the farming community and their poultry. The family structure was predominantly nuclear, with Kishanganj recording 94.67% of families in this category. Educational levels varied, with Purnea having the highest illiteracy rate. Landholding, a key economic indicator, was largest in Araria and smallest in Katihar. The primary occupation for most farmers was as labourers or seasonal farmers, with 72.00% in Kishanganj relying on this, often involving migration. The average flock size was largest in Araria at 13.78 ± 1.03 birds per household, with a higher proportion of female birds (ranging from 37.96% to 48.72%) across the region. Regarding phenotypic characterization, five main colours were identified, with white, black and brown being the most dominant. Kishanganj district showed a higher prevalence of red and golden feathers. In terms of morphological traits, the single comb type was overwhelmingly predominant compared to the rose comb. White skin was more common than yellow skin, and white shanks were the most frequent compared to yellow, black, and slaty shanks. The red earlobe was also identified as a dominant feature, with Kishanganj recording 64.51%.

Keywords: Phenotypic Characterisation, Socio-Economic, Chicken, Native, Bihar

P1-36

AGRO-PASTORAL HARMONY: SEASONAL MIGRATION AND TRADITIONAL MANAGEMENT OF BANKA CATTLE IN BIHAR

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ABSTRACT

This study explores the unique adaptation, migratory tradition, and agro-pastoral symbiosis of Banka cattle; an indigenous population thriving in the semi-hilly and resource-constrained landscapes of southeastern Bihar, India. Banka cattle, shaped by generations of local herders in the Banka, Munger, and Jamui districts, demonstrate remarkable resilience, thriving on minimal resources by efficiently utilizing native forage, and showing strong thermotolerance and disease resistance. Each spring, herds of 400–500 cattle embark on a traditional seasonal migration from the uplands of Banka to the fertile Gangetic plains of Bhagalpur, responding to dwindling water and pasture availability. What sets these cattle apart is more than just their biology; it's their deep-rooted connection with the region's people and landscapes. Every spring, as water sources dry up, local herders begin an age-old journey with their herds marching together from the hills of Banka to the green, fertile Gangetic plains. This seasonal migration is not just for finding food and water; it's an annual ritual that brings together families, neighbours, and farming communities. Along the way, cattle graze and rest in farmer's fields, naturally enriching the soil with manure, while farmers provide herders with meals and water, a partnership that benefits all and keeps local traditions alive. The survival and productivity of these cattle are further shaped by the region's climate, with temperatures ranging from 10–40°C and annual rainfall of 1,000–1,200 mm. This system represents more than rural survival; it's a tapestry of shared ecological wisdom, social ties, and mutual respect between people, animals, and land. The Banka cattle's journey, shaped by generations of experience, has helped sustain both biodiversity and the rural way of life. By documenting these cattle and their unique migration, this work also celebrates the enduring bonds that keep Bihar's villages, ecosystems, and age-old knowledge vibrant and resilient in the face of change.

Keywords: Agro-pastoralism, Banka cattle, Bihar, migration pattern, traditional knowledge

P1-37

ANIMAL FEED BASED BIODIVERSITY RESOURCES MANAGEMENT IN MUSTANG DISTRICT OF NEPAL

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ABSTRACT

Mustang is the semi‒desert like, rain shadow northern district of Nepal, where Lord Muktinath temple is located for Hindu community. This district is socially, culturally and agro‒climatically different while compared to other districts of the country. Goat, sheep, Yak, Nak, and Chauries are the major livestock commodities in this districts which are contributing significantly in the livelihood of the households there. Horses, mules and donkeys are also used as means of transportation in this district where road network is very poor. Being behind Dhaulagiri and Annapurna Himalayas and in rain shadow area, green forage and pasture production is poor in this district. Cultivation of forage is only possible in limited irrigated areas while the rest of the areas are generally used as grazing lands and are dry throughout the year. Thus, one major problem related to livestock farming in this district is shortage of feed and fodder. This problem is more prominent in this district due to remoteness and environmental and geographical hardship of the area. Therefore, a study was accomplished by the technical specialists of Nepal Livestock Sector Innovation Project (NLSIP) supported by World Bank during April‒May, 2021 in Mustang district. From the study, the major livestock species Chyangra population per family was 184.26 and there was no relationship with number of family member of Chyngra farmers, take care by a haired herder. Chyangra are mainly kept in open land all most in the year, in winter months Chyngra are enclosed with 6‒7 feet height wall but no roof around the homestead of farmer. Major predators identified were big flying bird, jackal and snow leopard. Yakucha, Vhecha, Dhukcha, Krisikpa, Dhucha etc are major poisonous plant found in the grazing lands of Mustang district. Kote (Medicago falcata), Dhimchi, Ramcha, Buche grass and Marcha are the cultivated forage species while Talang, Chere (desert palnt), Pocha, Keryng, Phoko, Ramjang, Dubchiya etc. are natural grazing species in major grazing lands of Mustang district. Bains, Nahichimba and Bhote Pipal are using as fodder trees around the farmers cultivated fields for Chyngra goats. To promote livestock production there should be develop marketing facilities, irrigation, forage cultivation in large areas for winter feeding, collaboration with research institutes for genetic improvement and nutrition of Chyngra goats, Yak and Chauru* ries, promotion of pashmina industries, identification and nutritional evaluation of plants species for animal feeding etc are the recommended further research and development activities to uplift the economy of farmers in Mustang district of Nepal

Keywords: Animal feed, animal and plant biodiversity, Goat, sheep, Yak and Chauries

P1-38

ANALYSES OF CODON USAGE BIAS OF FOOT-AND-MOUTH DISEASE VIRUS (FMDV) SEROTYPE O GENOME VIS-A-VIS ADAPTATION TO THE HOSTS

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ABSTRACT

Foot-and-mouth disease (FMD) is a highly contagious viral disease that affects a wide range of cloven-hoofed animals, including cattle, pigs, sheep, and goats. FMD serotype O is one of the seven serotypes of the foot-and-mouth disease (FMD) virus, and it is the most prevalent serotype in India. Due to non-random use of synonymous codons, each organism shows preference for certain codons over others, a phenomenon termed codon usage bias. Codon usage patterns are essential information in revealing evolutionary relationships between species as well as host-pathogen coevolution and adaptation of pathogens to specific hosts. In this study whole genome sequence of 31 FMDV Serotype O isolates from India were downloaded from NCBI and analysed for two codon usage indices, Relative Codon Deoptimization Index (RCDI) and eRCDI. If codon usage by a pathogen and host is similar, then the RCDI value is close to one and indicative of a greater adaptation to the host. Additionally, the expected RCDI (eRCDI) was used as a threshold value to estimate whether the deviation is due to compositional biases or selection pressure. RCDI values of 11 genes of FMDV serotype O were calculated for 9 host species. RCDI and eRCDI analysis of all the genes of FMDV serotype O indicated that the host adaptability of the virus with the host in decreasing order is cattle, pig, goat, water buffalo, yak, sheep, camel, mithun, and african buffalo. Serotype O is most adapted to cattle and least adaptable to African buffalo. Since, RCDI < eRCDI it can be interpreted that the deviation is due to compositional biases rather than selection pressure.

Keywords: Foot and mouth disease virus, Codon usage bias, adaptation, RCDI

P1-39

MALRA GOAT AND MALLUK SHEEP: LADAKH’S NATIVE LIVESTOCK

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ABSTRACT

Ladakh’s native animal population/livestock heritage faces growing challenges from various forces like climate change, crossbreeding and habitat modification, with rising temperatures and reduced snow cover threatening generation of grazing lands and replenishing water resources. Crossbreeding with exotic breeds risks genetic dilution, endangering the resilience of indigenous breeds uniquely adapted to Ladakh’s extreme environment. To address these issues, ICAR‑NBAGR has started characterization of indigenous population under zero‑nondescript program, to identify and record local animal population. Further research efforts focus on identifying unique genetic traits and enhancing market opportunities for high‑value products. The preservation and registration of these unique animal genetic resources of Ladakh is very essential, not only for the livelihoods of local communities but also for the conservation of overall biodiversity and ecological niche of Himalayan region of Ladakh. The Malra goat, translates to “local goat;’ is a medium‑sized breed. Adapted to the cold, arid environment, produces modest amounts of fine cashmere fiber, ranging from 50 to 100 grams/animal annually. The Malluk sheep, derived from the Ladakhi words “mal” (local) and “luk” (sheep), is another key livestock breed. This breed is valued for producing quality wool, widely used in traditional Ladakhi culture such as carpet‑making and clothing. Both the Malra goat and Malluk sheep play a pivotal role in Ladakh’s organic farming systems. In a region where the use of chemical fertilizers is minimal, the manure from these animals acts as a natural fertilizer, rich in essential nutrients like nitrogen, phosphorus, and potassium. This manure enhances soil fertility, improves soil structure, and increases water retention, promoting sustainable farming practices.

Keywords: Indigenous, non‑descript,

P1-40

DEVELOPING BASELINE INFORMATION AND COMPOSITE SELECTION INDEX FOR COMMUNITY BREEDING OF NAGAMI MITHUN

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ABSTRACT

Mithun (*Bos frontalis*) is a free-ranging hill bovine species contributing significantly to cultural and economic needs of tribal communities in Northeast India. Till date, availability of comprehensive baseline information on specific breeds/populations of Mithun is very limited. The present study provides the first detailed report on qualitative and quantitative morphology, growth and production environment characteristics of Nagami Mithun. Data on 16 qualitative and 17 quantitative traits were recorded from 296 Mithun across six districts using the newly developed Mithun Bioprofiler and Sampling Toolkit. Additionally, 2,606 body weight records from 81 animals of different age groups were analyzed to model the growth curve. The results revealed Nagami Mithun is phenotypically defined by a predominant black coat (98.0% adults), black face (91.2% adults) and white leg socks (90.8% adults). Males typically displayed a distinct triangular or V-shaped skull, while both sexes showed a straight/shallow-dip forehead with a dorsal crest, features strongly defining breed identity. The quantitative morphometric analysis showed the mean body length, height at withers and heart girth to be 131.34±2.69cm, 136.79±1.73cm and 197.48±3.11cm in adult males, and 124.0±1.36cm, 133.39±0.89cm and 184.05±1.61cm in adult females respectively. The mean birth weight was 19.50±0.53kg and 18.92±0.44kg in males and females respectively. The growth rate and body weight gain in males was linear, reaching a mean weight of 421.0±16.36kg at 45 months of age after which it reached a plateau. Based on the baseline information generated, a community-based breeding scheme was formulated involving: (i) qualitative screening to ensure conformity with breed standards, (ii) pre-selection of young bulls, and (iii) selection of adult breeding bulls. A composite selection index was developed to evaluate bulls using weighted criteria for morphology, growth, adaptability, reproduction, temperament, and behaviour. The community-based breeding scheme offers a scientific and viable framework for sustainable improvement of Mithun in traditional production systems.

Keywords: Phenotypic characterization, sustainability, genetic evaluation

P1-41

EFFECTS OF BODY CONDITION SCORE ON FERTILITY PERFORMANCES IN SYNCHRONIZED JERSEY CROSSBRED COWS

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ABSTRACT

Body condition score (BCS) is a frequently overlooked factor that can significantly impact the success of artificial insemination (AI) in Jersey crossbred cows. This study aimed to investigate the influence of BCS on the AI success rate in Jersey crossbred cows on smallholder farms in Murshidabad district. Each cow received an intramuscular injection of 2 mL of PGF2α for estrus synchronization. Pregnancy confirmation was conducted through rectal palpation between days 35 - 40 post-AI. In this study randomized block design, three BCS category groups were used: low ($\leq$ 2.50), moderate, and high ($\geq$3.25), with thirty experimental units in each group. The results indicated that BCS had a significant impact ($p<0.05$) on AI success. The BCS group with a range of 2.75–3.00 showed the highest AI success rates, with values for Non–Return Rate–1 (NRR–1) at 63.33%, NRR–2 at 50.00%, Conception Rate (CR) at 50.00%, and Services per Conception (S/C) at 1.27. The BCS group $\geq$3.25 followed with NRR–1 at 46.67%, NRR–2 at 33.33%, CR at 33.33%, and S/C at 1.40. The BCS group $\leq$2.50 had the lowest AI success rates, with NRR–1 at 23.33%, NRR–2 at 16.67%, CR at 13.33%, and S/C at 2.33. The study highlights the impact of BCS condition on the effectiveness of AI in Jersey crossbred cows, with the optimal range for AI implementation identified as 2.75–3.00.

Keywords: body condition score, nonreturn rate, conception rate, service per conception, artificial insemination, Jersey crossbred cows

P2-03

WHOLE EXOME-BASED IDENTIFICATION OF COPY NUMBER VARIATION (CNVS) IN FOUR BUFFALO BREEDS OF INDIA

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ABSTRACT

Copy number variations (CNVs) are a large structural variant in the genome, which contributes to adaptation, genetic diversity and performance traits in animals. The present study aimed to identify the common and breed-specific copy number variation (CNVs) in 4 breeds of Indian buffaloes using exome sequencing. Read depth approach with a bin size of 100 was used in CNVnator software to call CNVs. Overlapped CNVs were concatenated into a copy number variation region (CNVR) to create a more reliable, manageable and interpretable map of genetic variation across a population. Further, genes in the common and specific CNVR were annotated using DAVID and literature was mined to associate genes and functional pathways with previous study. The maximum number of CNVs was identified in Murrah (74,848) and the minimum number of CNVs was identified in Gojri (38,763) breed, with deletions outnumbering duplications in all breeds. A total of 2,009 CNVR were identified, consisting of 1522 deletions, 482 mixed and 5 duplications. The common CNVR were numbered 596, breed-specific CNVR were 145, 191,129 and 301 identified in Chattisgarhi, Chilika, Gojri and Murrah breeds, respectively. It was calculated that CNVR region accounts for 1.91% of the buffalo genome. Annotation of common CNVR region found in four breeds revealed genes for oxytocin signaling pathway, CGMP-PKG signaling pathway, cAMP signaling pathway, calcium signaling pathway and insulin secretion, saliva producion and GnRH production.

Keywords: Copy number variation, Read depth, bin size, CNVR, Annotation

Poster
Session-II

Poster Session II: Next Generation Breeding: Integrating Genomics and Phenomics

P2-01

WHOLE MITOCHONDRIAL GENOME SEQUENCING REVEAL CERTAIN MUTATIONS IN CYTOCHROME B AND D LOOP ADVERSELY AFFECTING THE HEALTH OF SHEEP

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ABSTRACT

Mitochondria are more than just the powerhouse of the cell—they are dynamic, semi-autonomous organelles with critical roles in energy metabolism, calcium signaling, iron homeostasis, apoptosis, and innate immunity. While the mitochondrion contains 37 of its own genes, 13 were polypeptide coding genes, Cytochrome B has pivotal role for the electron transport chain and oxidative phosphorylation. D loop is equally important as control region, which is also the promoter for gene expression. The present study with whole mitochondrial genome sequencing, a NGS study reveal non-synonymous substitutions (F33L and D171N) and Indel mutations for Cytochrome B gene, even leading to a truncated protein. SNPs for D loop were also identified. Anemia, impaired function of major vital organs including the liver and kidneys, and altered mineral balance were observed in sheep carrying the mutation. Affected animals exhibited generalized debility, exercise intolerance, and, in severe cases, cardiomyopathy. These pathological findings were corroborated through integrated bioinformatics analyses, hematological and biochemical profiling, and evaluation of phenotypic and physiological parameters associated with vital organ function. Molecular characterization of the cytochrome B mutation revealed that the mutant variant disrupts the heme (iron-containing) and calcium-binding domains, both essential for the proper functioning of the mitochondrial electron transport chain. The amino acid substitution at position 33, located within transmembrane helix A in the hydrophobic Qi site near the heme-binding domain, is predicted to interfere with heme association and consequently impair electron transport activity. Computational analysis further indicated a reduction in the thermodynamic stability of the mutant protein. Considering the high genetic homology between ovine and human cytochrome B, the sheep model may serve as a valuable system for investigating human disorders associated with cytochrome B dysfunction. Future research directions include exploring therapeutic strategies such as recombinant protein replacement, gene therapy, and marker-assisted breeding for the selection of disease-resistant livestock.

Keywords: Mitochondrial genome, animal model, cytochrome B, D loop

P2-02

VARIATIONS OF Y-CHROMOSOMES IN KANGAYAM AND JERSEY CROSSED BULLS POPULATIONS

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ABSTRACT

In population genetic studies, paternally inherited Y chromosome markers are widely used to track down paternal lineages and examine variations in animal migration and population admixture. The identification of three haplogroups (Y1, Y2, and Y3) for modern bull comparisons was made possible by recent investigations of five polymorphism sites on the DDX3Y, UTY, and ZFY genes of bull MSY. Using optimized and validated allele-specific PCR (AS-PCR) protocols, five SNPs (ZFY9-120> C/T, ZFY10-655> C/T, DDX3Y1-425> C/T, DDX3Y7-123> C/T, and UTY19-423> C/A) of bull MSY were screened. These SNPs are helpful in effectively differentiating bull samples of Kangayam and Jersey crossbred cattle. The Y1, Y2, and Y3 haplogroups were screened in 50 bulls, 25 of which were Kangayam and 25 of which were Jersey crossbred bulls. With frequencies of 0.90 and 0.10, respectively, the study found that the Y1 and Y2 haplogroups were exclusive to Jersey crossbred individuals. The prevalence of the Y1 lineage mostly in Jersey bulls may be the cause of the high frequency of Y1 haplogroups. On the other hand, the Kangayam cattle breed lacks Y1 and Y2 and has clearly identifiable Y3 haplogroups. In addition to exotic and crossbred populations, the AS-PCR procedures may be helpful for accurate and dependable Y-SNP genotyping in a variety of native cow breeds.

Keywords: Diversity, Y-Haplotype, Y-SNPs

P2-03

WHOLE EXOME-BASED IDENTIFICATION OF COPY NUMBER VARIATION (CNVS) IN FOUR BUFFALO BREEDS OF INDIA

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ABSTRACT

Copy number variations (CNVs) are a large structural variant in the genome, which contributes to adaptation, genetic diversity and performance traits in animals. The present study aimed to identify the common and breed-specific copy number variation (CNVs) in 4 breeds of Indian buffaloes using exome sequencing. Read depth approach with a bin size of 100 was used in CNVnator software to call CNVs. Overlapped CNVs were concatenated into a copy number variation region (CNVR) to create a more reliable, manageable and interpretable map of genetic variation across a population. Further, genes in the common and specific CNVR were annotated using DAVID and literature was mined to associate genes and functional pathways with previous study. The maximum number of CNVs was identified in Murrah (74,848) and the minimum number of CNVs was identified in Gojri (38,763) breed, with deletions outnumbering duplications in all breeds. A total of 2,009 CNVR were identified, consisting of 1522 deletions, 482 mixed and 5 duplications. The common CNVR were numbered 596, breed-specific CNVR were 145, 191,129 and 301 identified in Chattisgarhi, Chilika, Gojri and Murrah breeds, respectively. It was calculated that CNVR region accounts for 1.91% of the buffalo genome. Annotation of common CNVR region found in four breeds revealed genes for oxytocin signaling pathway, CGMP-PKG signaling pathway, cAMP signaling pathway, calcium signaling pathway and insulin secretion, saliva producion and GnRH production.

Keywords: Copy number variation, Read depth, bin size, CNVR, Annotation

P2-04

MOLECULAR GENETIC ANALYSIS TO IDENTIFY THE CRYPTIC ALLELE FOR MERLE PATTERNING IN DOGS

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ABSTRACT

Merle patterning in dogs, caused by the insertion of a short interspersed element (SINE) in the genetic structure of SILV gene, is characterized by patches of diluted pigment intermingled with normal melanin. Sequencing analyses of SINE element localized in the canine SILV gene discovered a variability of the poly (A)-tail length which is responsible for the different expression of merle pattern. The SINE element with the length of poly(A)-tail between 91 to 101 nucleotides is responsible for the merle phenotype with all characters of merle pattern. On the contrary the dogs which have SINE element with the shorter length of poly(A) tail between 54 to 65 nucleotides are referred as cryptic merles without expresion of Merle pattern. The aim of this study was to improve molecular genetics method for the detection of cryptic allele for merle patterning in dogs. A total of 20 samples each from four dog breeds of Tamil Nadu viz., Rajapalayam, Combai, Kanni dog and Chippiparai were used in this study. Canine genomic DNA was isolated from samples of whole blood using commercial genomic isolation kit. Detection of merle (M), cryptic merle (Mc) and non-merle (m) alleles was done using M13-tailed primer protocol and two different allele-sizing methods for the verification of the electrophoresis result. In the analyzed population of dogs were detected 43 dogs with non-merle genotype mm, 17 dogs with merle genotype Mm, 12 dogs with double merle genotype MM and eight dog with merle phenotype but with the presence of cryptic merle allele Mc with the consequential genotype MMc.

Keywords: SILV gene, SINE element, Merle pattern, cryptic allele

P2-05

COMPARISON OF DDRAD DERIVED GENOME-WIDE SSR MARKERS IN OUTBRED AND INBRED SWISS ALBINO MICE

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ABSTRACT

Genetic monitoring of inbred laboratory animal populations developed at any laboratory is one of the key elements of quality control and mouse colony management. The present study aimed to mine microsatellite markers from ddRAD data of outbred foundation stock and F9 inbred generation of Swiss albino mice to assess homozygosity and heterozygosity for their comparative analysis. Genomic DNA (12 F0 outbred and 12 F9 inbred) was isolated from tail tissue samples of F0 outbred and F9 inbred Swiss albino mice and processed for genotyping by sequencing. Double digestion of DNA was done using EcoR1 and Mse1 enzymes, and ddRAD data was subsequently analysed to identify and characterize microsatellite markers at genome-wide level. The analysis involved three key steps: read pre-processing of reads, SSR mining, and primer designing using different software i.e., PEAR, stacks and QDD. A total of 508 SSR motifs were identified in the outbred group and 353 in the inbred group. Additionally, 828 primer sets were designed for the outbred group and 551 for the inbred group. Furthermore, SSR loci specific to the inbred and outbred groups were identified. Among these, eight SSR motifs (three specific to the outbred group, three to the inbred group, and two common to both) were validated using PCR and gel electrophoresis. The eight primer sets designed, successfully amplified respective DNA samples and produced reproducible bands on gel electrophoresis. The validated microsatellites were mapped to specific chromosomal locations using NCBI BLASTN with Mus musculus as the reference genome. In conclusion, the present study reports mining of SSR loci in outbred and inbred mice population. SSR loci were found to be more numerous and diverse in outbred population than the inbred population. The unique SSRs identified for outbred and inbred groups will be helpful in checking the strain purity, marker assisted selection, and breeding.

Keywords: ddRAD, Foundation Stock, Inbred, Outbred, Primer, SSR

P2-06

GROWTH IS UPREGULATED THROUGH CALCIUM UPTAKE- A MOLECULAR ANALYSIS FOR NUCLEAR- MITOCHONDRIAL CROSS TALK IN PIG MODEL

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ABSTRACT

Growth is a complex phenomenon involving varieties of metabolic processes including calcium metabolism. In this current study, we have explored certain nuclear and mitochondrial genes with definite role in calcium metabolism involved in better growth phenotype in pig model. We have grouped the Ghungroo pig population of similar age group in high growth and less growth based on body weight and daily body weight gain. Differential mRNA expression profiling revealed upregulation for certain mitochondrial genes, namely, ATP6, Cox1 and cytochrome B in the high growing pigs. Simultaneously, upregulation was also observed for nuclear gene MICU2 in better growing group, indicating a cross talk of mitochondrial and nuclear genes involved in calcium metabolism involving growth. 3D predicted in silico protein analysis revealed certain important domains for these genes involved in calcium binding and metabolism. In future these genes may be employed for genomic selection or may be exploited through gene editing for better growing pigs, yielding more pork, leading to economical and profitable pig industry. Considering pig as one of the best animal model to study in human, this study may be further employed for very commonly occurring calcium metabolism related disorders in human leading to osteoporosis and others.

Keywords: Nuclear-Mitochondrial genome cross talk, animal model, growth

P2-07

GENETIC POLYMORPHISM OF THE METHYLENETETRAHYDROFOLATE REDUCTASE (MTHFR) GENE AND ITS ASSOCIATION WITH MILK PRODUCTION TRAITS IN BARBARI GOATS

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ABSTRACT

The methylenetetrahydrofolate reductase (MTHFR) gene plays a crucial role in folate metabolism and DNA synthesis. Polymorphisms in this gene are linked to metabolic and reproductive traits affecting livestock performance. Mutations may alter enzyme activity and influence health and production. This study aimed to detect MTHFR genotypes through PCR-RFLP assay and assess their association with milk production traits in Barbari goats. The study was conducted on 100 adult female Barbari goats. Genomic DNA was extracted from blood using the Sambrook & Russell's method. The MTHFR gene, located on chromosome 16 with 15 exons, was analyzed for intron 1 variation. PCR revealed a 546 bp fragment, digested with BSaHI enzyme. Statistical analysis was then performed to determine frequencies and the association between MTHFR genotypes and studied milk traits. PCR-RFLP analysis showed distinct allelic patterns: the C allele was cleaved into 426 bp and 120 bp fragments, while the T allele remained uncut (546 bp). Instead of getting all the possible genotypes we only get the CC genotype, indicating monomorphism in Barbari goats. Further the presence of the restriction site for BsaHI in PCR products confirmed by sequencing. Hence, association analysis was not performed. Further studies with larger populations are needed to explore potential associations between MTHFR polymorphism and milk production traits.

Keywords: Barbari goat, Methylenetetrahydrofolate reductase, MTHFR gene, PCR-RFLP, Milk traits

P2-08

GENETIC POLYMORPHISM OF THE GROWTH HORMONE (GH) GENE AND ITS ASSOCIATION WITH MILK PRODUCTION TRAITS IN BARBARI GOATS

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ABSTRACT

The growth hormone (GH) gene, a key regulator of growth, metabolism, and lactation, is a strong candidate for marker-assisted selection to accelerate genetic improvement. The objective of this study was to investigate the genetic polymorphism of the GH gene, to determine genotypic and allelic frequencies and analyze its association with milk-related traits in Barbari goats. The PCR-RFLP was conducted on 100 adult female Barbari goats. Genomic DNA was extracted, and a region of chromosome 19, spanning exons 2 and 3 of the GH gene was amplified using PCR. The resulting 422 bp PCR products were subjected to HaeIII restriction enzyme. PCR-RFLP assay successfully identified polymorphisms within the GH gene of Barbari goats. Out of 100 screened samples, 02 animals were of BB (wild), remaining 86 and 12 animals were of AB and AA genotype, respectively. It revealed two alleles including the 'A' allele, which was cut into two bands (366bp and 56bp), and the 'B' allele, which remained uncut, with the allelic frequency 0.55 and 0.45 respectively. Further the presence of the restriction site for HaeIII in PCR products confirmed by DNA sequencing. However, no significant association was observed between these genetic variants and measured milk traits in Barbari goats. This highlights the complex, polygenic nature of milk production and underscores the need for further research in large population.

Keywords: Barbari goat, Growth Hormone gene, PCR-RFLP, Milk traits

P2-09

CATALOGUING OF POLYMORPHISMS IN CANDIDATE GENES RELATED TO REPRODUCTION IN HD-K75 PIGS

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ABSTRACT

HD-K75 pig is a crossbred variety of pig (75% Hampshire and 25% Desi) which has been developed by ICAR-All Indian Coordinated Research project (AICRP) on Pig, Assam Veterinary and Fishery University, Khanapara, Guwahati, Assam, India. These animals have proved to be well adapted to the climatic conditions of Assam and gaining much popularity. The nucleus herd maintained at AICRP on Pig, Khanapara is producing superior quality piglets for the benefit of rural pig farmers of Assam as well as nearby northeastern states. Reproduction is one of the major components which is directly associated with the profit of a farm and reproductive traits are used for selection of the superior animals to be used in breeding programs. There is a need of prioritization for precise and early selection of superior animals for maximum profitability. This can be achieved through molecular genetic technologies like marker assisted selection (MAS). Hence, a study was conducted to identify and catalogue polymorphism in genes related to reproduction. The genes considered for the study were RBP4 (Retinol Binding Protein 4) gene, ESR (Estrogen Receptor) gene, FSHβ (Follicle stimulating hormone β) gene and PRLR (Prolactin receptor) gene. A total of 50 blood samples were collected from HD-K75 pigs. PCR- Polymerase Chain Reaction–Restriction Fragment Length Polymorphism method was used to detect genetic polymorphism. RBP4 gene found to be polymorphic and rest genes were monomorphic. RBP4 gene showed polymorphism upon digestion by MspI restriction enzyme which yielded two types of fragment pattern, arbitrarily designated as AA and AB genotype, where AA genotype yielded three fragments (190bp, 136bp and 125bp) and AB genotype yielded four fragments (190bp, 154bp, 136bp and 125bp). The presence of polymorphism in RBP4 gene opens prospects for selective breeding programme based on MAS.

Keywords: Genetic polymorphism, reproductive traits, candidate gene, pigs

P2-10

VARIABILITY IN PROLACTIN AND FATTY ACID SYNTHASE GENES AND THEIR RELATION WITH MILK TRAITS IN GIR AND DANGI CATTLE

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ABSTRACT

Prolactin plays main role in synthesis of milk proteins, lactose, mammary gland development along with other major milk components and is required for initiating and maintaining lactation. FASN is a candidate gene for milk fatty acid composition and fat yield traits and its multifunctional protein aids in catalysis and de novo synthesis of fatty acids. The current research was planned to study polymorphisms in Prolactin and FASN genes and to study its relation with milk traits in Gir and Dangi cattle populations. The blood and test day milk samples were collected randomly from 103 adult milking Gir breed of cattle and 30 purebred Dangi breed of cattle from farmers's herd from Maharashtra state. Genomic DNA was extracted using DNA extraction kits. The PCR-RFLP, and direct DNA sequencing were used to identify variability within Prolactin and FASN genes. PRL-RsaI locus of exon3 region exhibited variability with 'A' allele frequency as 0.42 and B allele frequency as 0.58 in Gir cattle and for both A & B alleles as 0.5 in Dangi cattle. The association analysis at PRL-RsaI locus revealed significant differences for milk yield with 7.75±0.35*kg milk yield for AB genotype as compared to other AA (6.73±0.51) and BB genotypes (5.94±0.32) in 103 Gir cows; however no significant differences observed in Dangi cattle. Sequence alignment analysis found SNP T>A at 83rd position in exon5 region of Prolactin. The analysis at FASN-Ncil at Exon 34 region revealed monomorphic pattern with predominance of BB genotype in Gir cattle population. The identified polymorphism in exon3 region of Prolactin with association effect will aid in future selection with traditional methods for improvement of indigenous breeds for milk traits.

Keywords: Prolactin, FASN, PCR-RFLP, Sequencing, Milk Traits, Gir Cattle, Dangi Cattle

P2-11

EXPLORING THE POLYMORPHISM OF INSULIN-LIKE GROWTH FACTOR-1 GENE AND ITS ASSOCIATION WITH GROWTH TRAITS IN NATIVE GUREZ SHEEP OF JAMMU AND KASHMIR

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ABSTRACT

Growth is an essential quantitative trait of farm animals influenced by polygenic inheritance and the environment in which animals are raised. The present study was desined to investigate the polymorphism of the insulin-like growth factor-1 (IGF-1 gene) one of the crucial genes influencing growth and its association with growth traits, specifically birth weight (BW), weaning weight (WW), six-months body weight (6MW) and yearling body weight (12MW) in Gurez sheep breed, a vulnerable ovine genetic resource of Jammu and Kashmir maintained at Mountain research Centre Sheep Goat, Shuhama (SKUAST-K). Effect of animal's gender, birth type, dam's weight at parturition and season of birth were investigated to adjust the data for these variables. Data was analyzed with the mixed model least squares and maximum likelihood algorithms. The overall least square means of BW, WW, 6MW and 12MW were 2.75±0.06kg, 12.62±0.31kg, 17.73±0.36kg and 24.07 0.59kg respectively . The extracted DNA samples were subjected to Polymerase Chain reaction and restriction fragment length polymorphism .IGF-1 gene amplicons were restricted digested with Bfol enzyme. Three genotypes were identified designated as AA (294 bp), AB (294, 194, 100 bp), and BB (194, 100 bp) with frequencies 0.22, 0.32, and 0.46, respectively. The RFLP results were confirmed by DNA sequencing. The gene, genotype frequencies were not in alignment with Hardy-Weinberg equilibrium. The effect of birth type, dam's weight at parturition, and birth season on growth traits was significant (p0.05) on the analyzed growth traits. The Study needs validation with large population size and in other native breeds as well. The investigation unveiled polymorphism of Insulin Like growth factor -1 (IGF-1) gene suggesting genetic diversity within the examined population and indicating potential avenues for selection programs in this breed. Howver, it suggested tp analze large population for the validation purpose.

Keywords: insulin-like growth factor-Igene, Gurez sheep, growth traits, polymorphism.

P2-12

SCREENING OF POLYMORPHISMS IN MTNR1A AND VLDLR GENES USING AMPLICON SEQUENCING AND THEIR ASSOCIATION WITH EGG PRODUCTION IN ASWLH AND ABWLH CHICKEN

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ABSTRACT

A study on polymorphisms in MTNR1A and VLDLR genes and their association with egg production in Anand Synthetic White Leghorn (ASWLH) and Anand Bantamized White Leghorn (ABWLH) chicken was carried out with the objectives to identify single nucleotide polymorphisms (SNPs) in coding regions of these two genes and to assess their association with egg production up to 64 weeks of age (EN64). The Illumina custom amplicon panel for exon regions was designed using Design Studio. The sequencing run was performed for total 96 birds, viz., 48 birds each for ASWLH and ABWLH (24 birds each from high and low egg production groups) using Illumina Miseq platform. DNA sequence data were aligned against Galgal4 reference genome assembly using BWA v0.7.17. Variant calling was performed using SAM tools v1.12. The association analysis between identified SNPs and EN64 was done using PLINK v1.07. A total 31 SNPs were identified in different exon regions for these two genes. Out of total identified 31 SNPs, 25 SNPs were previously reported in dbSNP145 database whereas only 6 SNPs were found as novel SNPs. However, none of these SNPs were found to be significantly associated with EN64. There were non-significant associations between SNPs and EN64 may be due to limited sample size (48 birds for each population). Hence it needed to perform association study on a large chicken population of ASWLH and ABWLH.

Keywords: MTNR1A gene, VLDLR gene, Single nucleotide polymorphism (SNP), ABWLH, ASWLH, Egg Production, Amplicon Sequencing.

P2-13

SCREENING OF POLYMORPHISMS IN DRD1 AND PRLR GENES USING AMPLICON SEQUENCING AND THEIR ASSOCIATION WITH EGG PRODUCTION IN ASWLH AND ABWLH CHICKEN

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ABSTRACT

A study on polymorphisms in DRD1 and PRLR genes and their association with egg production in Anand Synthetic White Leghorn (ASWLH) and Anand Bantamized White Leghorn (ABWLH) chicken was carried out with the objectives to identify single nucleotide polymorphisms (SNPs) in coding regions of these two genes and to assess their association with egg production up to 64 weeks of age (EN64). The Illumina custom amplicon panel for exon regions was designed using Design Studio. The sequencing run was performed for total 96 birds, viz., 48 birds each for ASWLH and ABWLH (24 birds each from high and low egg production groups) using Illumina Miseq platform. DNA sequence data were aligned against Galgal4 reference genome assembly using BWA v0.7.17. Variant calling was performed using SAM tools v1.12. The association analysis between identified SNPs and EN64 was done using PLINK v1.07. A total 46 SNPs were identified in different exon regions of these two genes. Out of total identified 46 SNPs, 38 SNPs were previously reported in dbSNP145 database whereas 8 SNPs were found as novel SNPs. There were non-significant associations between SNPs and EN64 may be due to limited sample size, hence, it needed to perform association study on a large chicken population of ASWLH and ABWLH.

Keywords: DRD1 gene, PRLR gene, Single nucleotide polymorphism (SNP), ABWLH, ASWLH, Egg Production, Amplicon Sequencing.

P2-14

THE STRUCTURAL VARIATION OF THE BOVINE B-DEFENSIN 103 (BBD103) GENE AND ITS RELATIONSHIP TO IMPORTANT TRAITS OF BULL SEMEN

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ABSTRACT

The bovine β-defensin 103 (BBD103) gene, a member of the β-defensin family, plays a vital role in sperm function and fertility regulation. In the ARS-UCD1.2 genome assembly, BBD103 is annotated at three loci, producing three predicted proteins—BBD103A, BBD103A-like, and BBD103B—of which BBD103B shows the highest similarity to human β-defensin 103. The gene exhibits extensive copy number variation (CNV) across cattle breeds and is expressed in the cauda epididymis and testis. In this study, the BBD103B gene of Frieswal bulls was PCR amplified and sequenced using Sanger sequencing. Multiple sequence alignment of 18 bulls revealed 16 nucleotide variations. An independent samples t-test showed that superior bulls had significantly higher sperm motility ($p < 0.001$) but lower semen concentration ($p = 0.0018$) than inferior bulls. General Linear Model (GLM) analysis indicated that BBD103 nucleotide variations were not significantly associated with semen quality traits. Overall, while BBD103 displays structural diversity, its sequence variation alone does not strongly influence semen quality in Frieswal bulls.

Keywords: Structural Variation, Bovine β-Defensin, Frieswal Bull, Fertility, Semen, Sperm Function

P2-15

WHOLE-GENOME SEQUENCING OF NAGAMI MITHUN REVEALS GENETIC DIVERSITY AND SELECTION PATTERNS

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ABSTRACT

Nagami mithun (Bos frontalis), the state animal of Nagaland, is a culturally and economically significant bovine species of the Eastern Himalayan region. Despite its importance, the population has undergone a sharp decline and is increasingly threatened by reduced genetic diversity and inbreeding. To address these concerns, we performed whole-genome sequencing (WGS) of 12 Nagami mithun individuals, generating ~33.3 Gb of data per sample and profiling genomic diversity, inbreeding, and selection. Following stringent quality control, analyses were conducted on variants mapped to the Bos taurus reference genome. Genome-wide diversity was low ($H_o = 0.214 \pm 0.024$; $H_e = 0.301 \pm 0.127$; mean MAF ≈0.21; $\pi = 5.0 \times 10\square^{4}$), linkage disequilibrium decayed rapidly ($r^2 < 0.2$ within 50–100 kb), and historical effective population size (Ne) revealed a marked decline over the past ~20 generations. Runs of homozygosity (ROH) scans across three references (B. taurus, B. gaurus, B. frontalis) showed a predominance of short segments (≈0.1–1 Mb), consistent with ancient demographic bottlenecks, with longer tracts more evident under B. gaurus and B. frontalis. Genomic inbreeding estimates were moderate (FROH ≈ 0.10–0.20) but varied with the choice of reference genome, with consistently higher values observed under B. taurus. Genome-wide scans integrating ROH, $\theta\pi$, Tajima's D, and iHS identified overlapping candidate regions encompassing 23 key genes, including TNF, TLR4, MAPK1, MITF, ITGA2B, and VWF. Functional enrichment analyses highlighted pathways involved in vascular remodeling, immune response, muscle development, pigmentation, and hypoxia adaptation, with strong signals in MAPK, insulin, mTOR, and melanogenesis pathways. This study provides the first comprehensive genome-wide insights into the genetic diversity, inbreeding, and selection signatures of Nagami mithun. The findings offer valuable genomic resources for conservation, sustainable management, and future genetic improvement of this unique bovine population.

Keywords: Mithun (Bos frontalis), selection signature, genetic diversity, high-altitude adaptation, conservation genomics

P2-16

TRANSCONTINENTAL TRACING OF ANCESTRY AND SELECTIVE SWEEPS ENRICHMENT OF X-CHR IN INDICINE AND TAURINE CATTLE

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ABSTRACT

Analyses of genomic diversity across the X- chromosome (chr), and its comparison with autosomal diversity, offer valuable insights into the evolutionary dynamics shaping sex-linked genomic architecture. The X-chr, due to its unique mode of inheritance, exhibits distinct interactions between demographic processes and genetic variation. Consequently, investigating X-linked variation can uncover demographic and selective forces that are often undetectable using autosomal markers. So, the present study aimed to elucidate the population structure and genetic differentiation between indicine and taurine cattle at a resolution of X-chr using whole genome resequencing data from 50 individuals representing Indian indicine breeds (Ladakhi, Sahiwal, Kangayam, Nelore, and Gir), Chinese indicine breeds (Guangfeng and Wannan), and taurine breeds (Hereford, Simmental, and Hanwoo). Variant calling and quality filtering resulted in a total of 1,34,617 high-quality single nucleotide polymorphisms (SNPs). Principal Component Analysis (PCA), admixture modeling, and phylogenetic construction, revealed a clear genetic differentiation between indicine and taurine groups. Local ancestry inference on the X-chr of Ladakhi cattle revealed region-specific introgression and evidence of adaptive admixture from taurine-derived loci. Analyses of genetic diversity indices such as observed heterozygosity, nucleotide diversity (π), and linkage disequilibrium (LD) revealed lower diversity on the X-chr relative to autosomes, with pronounced reductions in heterozygosity and π values, particularly among taurine. Extended haplotype homozygosity based selection signatures (iHS and XP-EHH) on the X-chr of Indian indicine cattle in comparison with Chinese indicine and taurine , identified several significant SNPs (exceeding 3 standard deviations) located in the distal regions of the X-chr and these SNPs were associated with the genes involved in metabolism, reproduction, disease resistance, and immune response. Overall, this study is the first of its kind in cattle at large scale and provides a foundational framework for future research in X-chr specific evolutionary biology and functional genomics.

Keywords: X-chromosome, Cattle, SNPs, Diversity

P2-17

ELUCIDATING CONTRASTING GENETIC VARIANTS IN INBRED AND OUTBRED SWISS ALBINO MICE USING WHOLE GENOME SEQUENCING APPROACH

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ABSTRACT

Animal models are essential in biomedical research due to their physiological and genetic similarity to humans, with laboratory mice representing ~70% of experimental animals. Their small size, rapid reproduction, and well-characterized genome make them ideal for studying gene function, disease, and therapeutic responses. This study examined genomic variation between inbred (F20) and outbred (F0) Swiss albino mice using whole-genome sequencing (WGS). Twelve samples (six per group) generated ~1.32 billion reads, with ~99.9% mapping to the Mus musculus reference genome (GRCm39). Variant discovery identified 37.46 million variants in inbred and 41.30 million in outbred mice, with outbred showing higher SNP and INDEL frequencies. After filtering, 149,234 high-quality autosomal SNPs were used for population genetic analyses. Copy number variation (CNV) analysis showed similar CNV sizes (~2.4–2.6 Mb), with 87 unique CNVs in inbreds, 61 in outbred, and 98 shared. Genetic diversity measures revealed high homozygosity and positive inbreeding coefficients in inbreds, versus heterozygosity excess and negative coefficients in outbred. Linkage disequilibrium (LD) decay and runs of homozygosity (ROH) further distinguished the groups: inbreds exhibited persistent LD, longer haplotype blocks, and nearly double ROH coverage. Nucleotide diversity was lower in inbreds ($\pi = 4.80$) than outbred ($\pi = 10.17$), indicating genetic erosion. Genome-wide differentiation was moderate (FST ~0.04), but CNV-based Vst highlighted higher divergence on chromosomes 7, 10, and 12. Overall, WGS reveals that sustained inbreeding reduces heterozygosity and genomic diversity, whereas outbred mice maintain broader variation. Inbred mice provide genetic uniformity, enhancing reproducibility and statistical power, while outbred mice preserve variation, useful for complex trait studies. These findings underscore the complementary utility of both models and offer valuable guidance for biomedical research, genetic management, and optimal use of laboratory mouse resources.

Keywords: Swiss albino mice, Mus musculus, SNPs, INDELs, CNVs, Linkage Disequilibrium, ROH

P2-18

ASSOCIATION STUDY OF PROLACTIN GENE POLYMORPHISM WITH MILK TRAITS IN DANGI CATTLE

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ABSTRACT

The bovine Prolactin (PRL) gene is recognized for its significant association with milk yield, milk composition, and fertility traits. The prime objective of the present study was to identify polymorphisms within exon-3 and exon-4 of the bovine PRL gene and to know their association with important milk production traits of Dangi cattle. The RsaI/PCR-RFLP technique was employed to detect polymorphisms in the exon-3 and exon-4 regions of the PRL gene. A total of 66 blood and milk samples were collected from the Dangi cows reared at Cattle Breeding Farm and Dangi Cow Research Station, Igatpuri, as well as from farmers' herds in the Nashik district. Specific fragments of 156 bp (exon-3) and 294 bp (exon-4) were successfully amplified using annealing temperatures of 58?°C and 58.5?°C, respectively. RsaI-based PCR-RFLP analysis of the PRL gene exon-3 region revealed three distinct genotypes: AA (0.333), AB (0.303), and BB (0.364 with the presence of A (0.485) and B (0.515) alleles. Similarly, in PRL exon-4 region GG (0.469), GA (0.393) and AA (0.136) genotypes with the presence of G (0.629) and A (0.371) alleles were observed. The average estimated values for milk composition traits were fat – 5.155?±?1.718%, SNF – 8.511?±?1.183%, protein – 3.103?±?0.425%, and lactose – 4.651?±?0.637%. Statistical analysis revealed no significant association between these milk traits and the PRL gene exon-3 and exon-4 genotypes in the studied Dangi cow population. To validate and strengthen these findings, future studies involving a larger sample size may be beneficial in assessing the potential relationship between PRL gene polymorphisms and milk traits.

Keywords: Prolactin Gene Polymorphism, Association with Milk Traits, Dangi Cattle

P2-19

CHARACTERIZATION, PHYLOGENY AND DIVERSITY STUDY IN PIGS OF BASTAR REGION OF CHHATTISGARH STATE THROUGH MITOCHONDRIAL DNA D-LOOP NUCLEOTIDES SEQUENCE

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ABSTRACT

As there is no recognized breed of pig from Chhattisgarh state this study was aimed to characterize the pig in view of preserving rich indigenous genetic resources biodiversity and to investigate genetic diversity, relationship and matrilineal lineage of Bastar pigs. The data were recorded on about 1500 pigs (of different age groups) at random from homogenous population from different areas of Bastar region comprising Narayanpur, Bastar and Dantewada district on various parameters as per the standard guidelines and format of NBAGR Karnal for characterization of the pig breeds. For genetic/molecular characterization of the pigs, a total 60 blood samples were collected from different pockets of Bastar region. The Chhattigarhi pigs are of medium size, generally black in colour and their body is covered with medium sized bristles, have medium size horizontal ears with long straight snout and straight back. Principal Component Analysis extracted 5 components and first principal component comprising body measurements alone accounts 70% describing the general size & shape of the animals. The D loop region of different pig populations was sequenced and analyzed to identify distinct mtDNA haplotypes and it was found that non protein coding sequences of Bastar region pig samples had 06 polymorphic sites in a patch of 313 bp. The pig population under study had a total of 33 haplotypes with haplotype (gene) diversity of 0.275. Two of the Bastar region samples were identified as singletons in haplogroups 32 & 33. From the above study it may be concluded that the indigenous pigs of Chhattisgarh state have good performance and systematic breeding plan for their selection is needed. The multi variate approach has proven to be effective in differencing Bastar pigs from other indigenous breeds of India with clear morphometric differences that help in identifying the pure phenotype for future propagation.

Keywords: Indigenous pig, Bastar, Phenotypic traits, Descriptive traits, Carcass traits, Mitochondrial DNA, D-loop, phylogenetics, genetic diversity

P2-20

MITOCHONDRIAL COPY NUMBER VARIATIONS AFFECT GROWTH IN ASSOCIATION TO METICULOUS ROLE OF MITOCHONDRIAL PROTEINS IN SHEEP MODEL

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ABSTRACT

Mitochondria possess 37 genes of its own, out of which thirteen are polypeptide coding genes. In this current study, we have observed significant role for five mitochondrial protein coding genes, namely, ATP6, NAD1, Cox1, ND2 and ND6 in Garole sheep regulating growth quantified in terms of body weight at successive ages and daily body weight gain and grouped in high and low growing profiles. We predicted 3D protein model with the identification of important domains of functional importance. These mitochondrial proteins are directly involved in oxidative phosphorylation, TCA cycle and apoptosis. Differential mRNA expression profiling reveal more copy number of mitochondria in the sheep exhibiting better growth traits. The most important finding is that apart from energy metabolism, these mitochondrial proteins were directly involved with iron and calcium binding and metabolism, thereby affecting growth. Explored genes may be employed for genomic selection or gene editing for better growth of sheep yielding more mutton. Simultaneously, sheep may be employed as animal model to study human disorders involving calcium and iron metabolism.

Keywords: Mitochondrial genome, animal model, growth

P2-21

WHOLE-GENOME ANALYSIS AND DETECTION OF RUNS OF HOMOZYGOSITY IN THE INDIGENOUS GOLLA PIG POPULATION OF ODISHA, INDIA

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ABSTRACT

Indigenous pig populations, shaped by unique demographic histories involving isolation and genetic drift, represent valuable genomic resources for exploring selection signatures and local adaptation. The Golla, a medium-sized indigenous pig population native to Odisha, India, was characterized in this study through whole-genome sequencing (WGS) to assess its genetic diversity and potential selection footprints. A total of ten samples were collected from Ganjam and adjoining regions using random sampling. Following quality control, the raw FastQ reads were aligned to the Sscrofa11.1 reference genome using BWA-MEM2, and variant calling was performed with GATK Haplotype-Caller, yielding approximately 43 million variants, including 34.4 million high-confidence SNPs after stringent filtering. Further quality control using PLINK excluded variants and samples with >5% missing data, minor allele frequency (MAF) <0.05, or deviations from Hardy–Weinberg equi-librium ($p < 1\times10^{\square 6}$), resulting in a refined dataset of 23.2 million SNPs across nine samples. Runs of Homozygosity (ROH) analysis identified 3,064 homozygous segments, corresponding to 2,217 unique ROH hotspot regions, primarily located on chromosomes 1, 8, and 18, with mean lengths of 210–240 kb. Nineteen ROH hotspots shared by ≥5 individuals were detected, including a notable 1.2 Mb region on chromosome 15 overlapping genes such as PARD3B, NRP2, IGF1, SOX5, ZP4, and RORA. Functional annotation revealed significant enrichment in biological processes related to muscle hypertrophy, myoblast proliferation, skeletal muscle maintenance, and insulin-like growth factor (IGF) signaling pathways. These findings provide novel insights into the genomic architecture of the Golla pig population, highlighting potential regions under selection and contributing to a broader understanding of adaptive and productive traits in indigenous pig breeds.

Keywords: Golla, Runs of Homozygosity (ROH), ROH Hotspot, Indigenous Pig, Whole-Genome Sequencing, Selection Signature

P2-22

DNA METHYLATION DRIVEN TRANSCRIPTIONAL REPROGRAMMING OF MILK SOMATIC CELLS LINKS IMMUNE ACTIVATION WITH LACTATION SUPPRESSION IN SUBCLINICAL MASTITIS OF VRINDAVANI CATTLE

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ABSTRACT

Subclinical mastitis (SCM) is a major economic burden on the dairy industry, but its underlying molecular regulation is not fully understood, particularly in Indian crossbred cattle. This study presents the first integrative analysis of the DNA methylome and transcriptome in milk somatic cells to define the epigenetic and transcriptional changes associated with SCM in Vrindavani cattle. We utilized whole-genome bisulfite sequencing (WGBS) and RNA-sequencing on milk somatic cells isolated from healthy and SCM-positive cows. Our results reveal that SCM is characterized by a profound and targeted epigenetic reprogramming dominated by genome-wide DNA hypomethylation. We identified 62,940 differentially methylated cytosines (DMCs), with an overwhelming 93.8% being hypomethylated in the SCM group. These methylation changes were strategically concentrated in key regulatory regions, such as gene promoters and CpG island shores. Integrating these data with transcriptome profiles identified 1,407 unique differentially methylated and expressed genes (DMEGs), demonstrating a significant inverse relationship between promoter methylation and gene expression. These epigenetic modifications result in a coordinated redirection of transcriptional programs, effectively altering the cell's primary biological objectives. Promoter hypomethylation was tightly linked to the transcriptional activation of a robust, multi-layered immune response, including pathways for chemokine signaling, pathogen recognition (TLR4), antigen presentation, and immunometabolism. Conversely, promoter hypermethylation was associated with the coordinated silencing of genes essential for lactation (CSN3), hormone signaling, and core metabolic and homeostatic processes (OXCT1, PRKAR2B). Key gene expression changes were validated using qPCR, validating the regulatory link. This study establishes SCM as a state of targeted epigenetic reprogramming, where promoter hypomethylation activates sentinel immune pathways and promoter hypermethylation suppresses milk synthesis and hormone signaling. This study establishes a detailed mechanistic framework for SCM pathogenesis and provides a strong foundation for developing epigenetic biomarkers for early disease detection and genetic selection strategies to improve mastitis resilience.

Keywords: DNA methylation; Transcriptional regulation; Milk somatic cells; Subclinical mastitis

P2-23

COMPARATIVE TRANSCRIPTOMICS IN INDIGENOUS CATTLE REVEALS MOLECULAR REGULATORS OF MILK YIELD

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ABSTRACT

Milk yield is a key economic trait in dairy cattle, yet its genetic regulation in indigenous breeds such as Gir and Shweta Kapila remains underexplored. This study employed a transcriptomic approach to investigate the differential gene expression (DEG) in peripheral blood samples of high- and low-yielding animals within and between breeds of profiles Gir and Shweta Kapila cow. RNA sequencing followed by bioinformatic analyses identified 745 DEGs (309 upregulated, 436 downregulated) in high-yielding Gir vs. Shweta Kapila and 273 DEGs (136 upregulated, 137 downregulated) in low-yielding animals. Within-breed comparisons yielded 278 DEGs in Gir and 380 DEGs in Shweta Kapila. Gene Ontology (GO) enrichment indicated that DEGs were involved in immune regulation, metabolic processes, and signalling pathways relevant to lactation physiology. KEGG pathway analysis revealed breed-specific activation of MAPK, calcium, and PPAR signalling pathways, among others. Protein-protein interaction (PPI) networks identified key hub genes such as IFNG, THBS1, SDC1, and NKG7. Notably, C23H6orf132 was the only gene common across all comparisons, indicating its potential universal role in milk production. The comparison of transcriptomic profiles between high and low-yielding individuals highlighted key genes intricately linked to milk production, potentially serving as biomarkers for breeding programs and offer novel insights into the molecular mechanisms underlying milk yield differences in Indian cattle breeds. It may inform genetic selection and improvement programs aimed at enhancing dairy productivity in indigenous bovines.

Keywords: Indigenous cattle, Milk yield, Hub genes, Transcriptomics

P2-24

GENE EXPRESSION ANALYSIS OF CANDIDATE GENES ASSOCIATED WITH MILK SYNTHESIS IN SAHIWAL CATTLE

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ABSTRACT

Sahiwal cattle are among the most productive indigenous dairy breeds of India, widely appreciated for their milk yield and rich composition. On average, they produce 2,500–3,000 kg of milk per lactation with 4.5–5.5 percent fat, a level that often surpasses several exotic breeds. Since milk fat percentage largely determines its economic value, identifying genes influencing fat metabolism is crucial for enhancing the profitability of dairy animals. In this study, milk samples were collected from Sahiwal cows maintained at the Data Recording Unit of GBPUAT, Uttarakhand, under the All India Coordinated Research Project (AICRP) on Cattle, Meerut. Based on the 305-day lactation milk yield, animals were classified into two groups: high yield (2,400–4,000 lit) and low yield (500–1,500 lit), comprising six samples per group. RNA extraction was performed using the Trizol method, followed by cDNA synthesis using a reverse transcription kit (Thermo Scientific). The synthesized cDNA was used for real-time PCR, and expression levels were normalized using the housekeeping gene GAPDH. The SCD gene codes for an enzyme that catalyzes the conversion of saturated to monounsaturated fatty acids. The LPIN1 gene functions as a phosphatase that converts phosphatidic acid to diacylglycerol, facilitating lipogenic gene expression. The CDC42BP gene encodes a kinase that links prolactin signaling with cytoskeletal remodeling, influencing lipid droplet formation and secretion. The relative expression values (40–ΔCt) for Groups 1 and 2 were 35.90 and 37.25 (SCD), 30.99 and 33.41 (LPIN1), and 36.75 and 38.08 (CDC42BPA), respectively. These findings indicate elevated transcriptional activity related to fatty acid synthesis, elongation, and triglyceride formation pathways in the low-yield group. The integration of RT-PCR results with genomic markers in future studies could assist in identifying molecular indicators and refining breeding strategies to enhance milk fat content in indigenous dairy cattle such as Sahiwal.

Keywords: Sahiwal Cattle, Milk synthesis, Candidate genes, Expression analysis

P2-25

EXPLORING SYSTEMS BIOLOGY OF INDIGENOUS GOAT VIA DIFFERENTIAL MIRNOME PROFILING UNDER IN-VITRO EXPOSURE TO TLR3 LIGAND

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The present study aimed to explore whole microRNA (miRNA) expression in cultured peripheral blood mononuclear cells (PBMCs) of Beetal goats under in-vitro exposure to Poly I:C, a TLR3 ligand, to simulate viral infection. Data (2015-2023) on survival till one-year age was taken as indicator of fitness and was analyzed through logistic regression to assess effects of non-genetic factors: sex, season, and year of birth. The same dataset on Bayesian analysis in BLUPF90 suite of software provided a heritability estimate of 0.179±0.010 and breeding values for the animals. The Beetal goats were ranked by breeding value for fitness and grouped into high-fitness and low-fitness categories. PBMCs from two goats per group were isolated, cultured and exposed to Poly I:C. High-throughput sequencing for miRNA transcriptome of the treated PBMC culture alongwith control PBMC culture was performed and cleaned reads were processed for differential expression using established bioinformatics pipelines. This revealed distinct miRNA expression patterns between high-fitness and low-fitness animals and Poly I:C treated and control groups, reflecting functional role of miRNAs disease and defense. Enrichment analyses of DE miRNA target genes indicated involvement in immune-regulatory pathways. The miRNAs including miR-21, miR-155, and miR-146 were differentially modulated under simulated viral exposure and are key regulators of inflammatory signaling. The observed upregulation of immune-related miRNAs in high-fitness goats upon Poly I:C stimulation, as compared to their low fitness animals, suggests a stronger and more coordinated immune response. The target genes of the dysregulated miRNAs didn’t show significant dysregulation at transcription, emphasising existence of a post-transcriptional regulation possibly by miRNA. The discovery of miRNA signatures associated with immune competence can support the development of molecular diagnostics, early-warning systems, and precision breeding models. Such advancements align with the broader objectives of sustainable livestock farming, wherein genetic selection for disease resilience complements production and management interventions.

Keywords: Beetal Goats; Fitness; miRNome; TLR3; In-vitro Disease Simulation;

P2-26

GENOME-WIDE ASSOCIATION STUDY REVEALS SIGNIFICANT SNPS AND CANDIDATE GENES FOR HEIFER AND COW FERTILITY TRAITS IN SAHIWAL CATTLE

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ABSTRACT

Fertility traits are pivotal to the productivity and sustainability of dairy production systems; however, their genetic improvement remains constrained due to complex polygenic control and low heritability. Recent advances in genome-wide association studies (GWAS) have facilitated the identification of genomic regions influencing reproductive performance in cattle. This study aimed to identify single nucleotide polymorphisms (SNPs) associated with key fertility traits in Sahiwal heifers and cows. A total of 303 animals were genotyped using the Illumina BovineSNP50 BeadChip, and 28,286 high-quality SNPs were retained after quality control. Fertility traits were analyzed separately for heifers- age at first calving (AFC), interval to first/last insemination (IFL), and number of services per conception (NSPC) and cows, for which IFL, NSPC, service period (SP), interval from calving to first insemination (ICAI), and pregnancy rate (PR) were considered. Phenotypic values were adjusted for non-genetic factors including year of birth (YOB), season of birth (SOB), and AFC (excluded for the AFC trait itself), and population structure was accounted for using five principal components. GWAS was performed using the PLINK software, identifying 10 SNPs significantly associated with heifer fertility traits and 13 SNPs with cow traits. Gene annotation of significant loci revealed biologically relevant candidate genes, including IGFBP7, CNTN1, STUB1, PARVB, RHBDL1, and WFIKKN1 for heifers, and ABCC10, DLK2, TJAP1, LRRC73, YIPF3, POLR1C, XPO5, POLH, KLF12, PLA2G7, TDRD6, and TRPS1 for cows. Several of these genes have been previously implicated in reproductive processes such as steroidogenesis, follicular development, gametogenesis, and energy homeostasis. These findings contribute valuable insights into the genetic architecture of fertility in Sahiwal cattle. The identification of fertility-associated variants in a tropically adapted breed reinforces the relevance of tailored genetic improvement strategies for enhancing reproductive performance while maintaining production in the challenging climate.

Keywords: Sahiwal cattle, fertility traits, GWAS, SNPs

P2-27

COMPARATIVE GENOME-WIDE ASSOCIATION ANALYSES OF FERTILITY TRAITS REVEAL THE GREATER POWER OF MULTI-LOCUS OVER SINGLE-LOCUS METHODS

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ABSTRACT

Fertility is a critical determinant of reproductive efficiency and long-term productivity in dairy cattle; however, most fertility traits are complex and lowly heritable, being influenced by numerous genes with small additive effects. Traditional single-locus genome-wide association studies (GWAS) have been instrumental in identifying major quantitative trait loci (QTL), yet their ability to capture the polygenic architecture underlying reproductive traits remains limited. In recent years, multi-locus GWAS approaches have emerged as powerful alternatives that simultaneously account for multiple loci and gene–gene interactions, enhancing detection power and reducing false negatives. The present study compared single-locus and multi-locus GWAS to identify genomic regions associated with key fertility traits—Age at First Calving (AFC), Interval between First and Last Artificial Insemination (IFL), Interval between Calving and Artificial Insemination (ICAI), Service Period (SP), Number of Services per Conception (NSPC), and Daughter Pregnancy Rate (DPR) in Sahiwal cattle. Genotypic data generated using the Illumina BovineSNP50 BeadChip for 166 Sahiwal underwent stringent quality control in PLINK v1.9, applying thresholds for minor allele frequency (--maf 0.05), Hardy–Weinberg equilibrium (--hwe 0.00001), and genotype call rate (--geno 0.10), yielding 20,348 SNPs. Single-locus GWAS was conducted in PLINK v1.9 using a linear regression model, while multi-locus analyses employed six algorithms (mrMLM, FASTmrMLM, FASTmrEMMA, pLARmEB, pKWmEB, and ISIS EM-BLASSO) implemented in the mrMLM R package. A total of 42 SNPs in Sahiwal and 26 SNPs in Karan Fries showed significant associations with fertility traits across both analytical frameworks. Six SNPs in Sahiwal, annotated to TEAD4, FAM214A, LOC104973324, OR52J3, FBLN5, and TEKT5 were associated with multiple traits, indicating pleiotropic effects. Overall, the integration of multi-locus models substantially improved the detection of novel and biologically relevant candidate genes, demonstrating their superiority over traditional single-locus methods for unravelling the complex genetic basis of fertility in dairy cattle.

Keywords: Sahiwal cattle, fertility traits, GWAS, multi-locus

P2-28

GENOME-WIDE ASSESSMENT OF GENETIC DIVERSITY, POPULATION STRUCTURE AND SELECTION SIGNATURES IN RATHI CATTLE USING DDRAD SEQUENCING

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ABSTRACT

Rathi cattle, an indigenous Bos indicus breed of north-western India, represent an important genetic resource due to their adaptation to arid environments, resilience to heat stress and dairy potential. However, genomic information on this breed remains limited. In this research, 96 Rathi samples were genotyped with double-digest restriction-site associated DNA sequencing (ddRAD-seq) to produce high-resolution genome-wide SNP data. A significant proportion of reads (96.52%) were accurately aligned to the Bos taurus (ARS-UCD2.0) reference genome assembly, guaranteeing dependable variant identification. We got and annotated a total of 78,193 high-quality SNPs, which showed considerable nucleotide diversity ($\pi = 0.33 \pm 0.09$) and heterozygosity (Ho = 0.291 ± 0.084; He = 0.329 ± 0.104). Runs of homozygosity (ROH) made up 5.43% of the genome, and most of them were short segments (<2 Mb), which shows that there hasn't been much inbreeding lately (FROH = 0.0512). Effective population size (Ne) declined from 1454 (150 generations ago) to 94 at present, highlighting the impact of demographic bottlenecks and genetic drift. Population structure analyses (PCA, ADMIXTURE and STRUCTURE) revealed clear genetic distinctness of Rathi from other indigenous dairy breeds (Sahiwal, Tharparkar, Red Sindhi, Gir and Kankrej). Selection signature analyses (Tajima's D, CLR, ROH islands and iHS) identified candidate regions harboring genes linked to immunity (IL2RB, USP18), reproduction (INHBA, MEI4, HBA), lactation (LRRC8D, TRERF1, CCND3) and stress adaptation (CARHSP1, ITGAV). This study provides the first ddRAD-based genome-wide assessment of Rathi cattle using a large sample size, delivering valuable insights into their diversity, demographic history and adaptive potential and offering genomic resources for conservation, sustainable utilization and genetic improvement programs.

Keywords: ddRAD sequencing, Genetic diversity, Population structure, Rathi Cattle, Selection Signature

P2-29

GENETIC DIVERSITY ANALYSES AND IDENTIFICATION OF BREED-SPECIFIC SNPS IN THARPARKAR CATTLE USING ddRAD SEQUENCING

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ABSTRACT

Tharparkar, an indigenous milch breed of India, is renowned for its ability to thrive in arid and desert environments while producing high-quality milk, thereby serving as a vital resource for the livelihood of rural communities. This study aimed to evaluate the genetic diversity of Tharparkar cattle using double digest Restriction site-Associated DNA (ddRAD) sequencing and to identify breed-specific single nucleotide polymorphisms (SNPs) for the development of an ultra-low-density SNP panel across five indigenous Indian breeds. We genotyped 48 Tharparkar animals maintained at the Livestock Research Station (LRS), Beechwal, RAJUVAS, Bikaner, Rajasthan. After stringent filtering, 121,554 high-quality biallelic SNPs were retained for downstream analysis. The population exhibited an average minor allele frequency (MAF) of 0.249 ± 0.117, with expected and observed heterozygosity values of 0.347 ± 0.103 and 0.291 ± 0.078, respectively. Genomic inbreeding coefficients calculated using different approaches (FHOM, Funi, Fgrm, and FROH) ranged from 0.106 to 0.125, reflecting a low to moderate degree of inbreeding. The predominance of short runs of homozygosity (0–2 Mb) indicated limited recent inbreeding, with homozygosity largely attributable to ancient common ancestry, genetic drift, or founder effects. The effective population size in recent generations was estimated at 82.6, which emphasizes the requirement for continued monitoring of genetic diversity. To identify informative markers, pre-selection statistics and the TRES (Toolbox for Ranking and Evaluation of SNPs) tool were applied, followed by the MAF-LD approach on a reference dataset comprising 260 individuals from five Indian breeds. This analysis yielded 309 informative SNPs, including 77 unique SNPs specific to Tharparkar, which could reliably distinguish this breed in both reference and validation datasets. Overall, our findings underscore the genetic uniqueness of Tharparkar cattle, highlight the effectiveness of ddRAD sequencing for detecting breed-specific SNPs, and stress the importance of targeted conservation strategies to safeguard this valuable indigenous genetic resource.

Keywords: Breed-specific markers, ddRAD sequencing, Genetic diversity, Informative markers, SNP, Tharparkar cattle

P2-30

WHOLE-GENOME RESEQUENCING REVEALS SELECTION SIGNALS FOR INTERMITTENT MILKING IN PANDHARPURI BUFFALO

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ABSTRACT

Pandharpuri buffalo, a distinctive indigenous breed of Maharashtra, India, has characteristic sword-shaped horns and intermittent milking capacity. However, the genetic basis underlying its ability to sustain milk production under intermittent milking remains poorly understood, limiting targeted improvement and conservation. To address this, whole-genome resequencing (WGS) was employed for its comprehensive capture of genomic variation, outperforming genotyping arrays and reduced-representation methods such as ddRAD sequencing. The majority of genomes exhibited coverage exceeding 30X, enhancing variant detection accuracy enabling robust population-level genomic inference. Within-breed selection signatures were detected using the De-Correlated Composite of Multiple Signals (DCMS), which integrates multiple tests while accounting for correlations to enhance power, accuracy, and robustness. In this study, intrapopulation selection signature statistical methods—Tajima's D, nucleotide diversity, integrated haplotype score, and number of segregating sites by length—were specifically combined within the DCMS framework to detect distinct selection signatures across the genome. The analysis identified 1,337 candidate genes associated with milk production, particularly intermittent milking. The identified selection signatures reveal the genomic basis of Pandharpuri buffalo's intermittent milking capacity and can inform genomic or marker-assisted selection strategies to drive genetic improvement, support conservation, and preserve this unique indigenous breed.

Keywords: Pandharpuri buffalo, Selection signatures, DCMS approach, Intermittent milking

P2-31

ELUCIDATING DIFFERENTIALLY METHYLATED REGIONS (DMRs) IN INBRED SWISS ALBINO MICE

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ABSTRACT

The present study aimed to identify and characterize genome-wide DMRs in inbred Swiss albino mice using whole-genome bisulfite sequencing (WGBS). Six tail tissue samples were collected, three each from outbred stock and inbred Swiss albino mice, and genomic DNA was extracted, subjected to bisulfite conversion, and sequenced with 20X coverage to generate paired end reads with 150 base pair read length. After pre-processing of raw reads, high-quality reads were aligned to the mouse reference genome (GRCm39 or mm39) using Bismark, followed by methylation calling and DMR detection using Bismark Methylation Extractor and MethylKit in R, respectively, with stringent thresholds for CpG coverage and statistical significance. A total of 80,979 significant differentially methylated cytosines (DMCs) were identified, comprising 5,024 hypermethylated and 75,955 hypomethylated sites. Genomic annotation revealed enrichment in promoters (50.8%), followed by exons (22.8%), introns (18.0%), intergenic regions (8.3%), and TSS (0.1%). Overall, 74,296 DMCs were located in genic regions, while 6,683 occurred intergenic. The average distance of DMCs from the transcription start site was 6,554 bp, with a median of 348 bp. A total of 26,253 significant DMRs were identified, including 1,024 hypermethylated and 25,229 hypomethylated regions. A total of 11,095 genes were identified as differentially methylated (1219 hypermethylated and 9876 hypomethylated), with a promoter-dominant distribution (5,560 genes), consistent with the patterns observed for DMCs and DMRs. Among these promoter-associated genes, 5,404 were hypomethylated and 156 were hypermethylated. Functional enrichment analysis revealed that these differentially methylated genes (DMGs) were significantly enriched in pathways related to growth and development, epigenetic regulation, immune regulation, and metabolic processes etc. In conclusion, this study revealed genome-wide hypomethylation with targeted hypermethylation in highly inbred mice, establishing the first methylation map of inbred Swiss albino mice and highlighting the role of DMRs in gene regulation and inbreeding effects on growth and fitness.

Keywords: DMRs, WGBS, DMCs, DMGs, Epigenetic regulation, Methylation map

P2-32

LANDSCAPE GENOMICS TO DECIPHER LOCAL ADAPTATION IN INDIAN LIVESTOCK

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ABSTRACT

India is a country of exceptional ecological as well as rich livestock diversity, which make it an ideal setting to study local adaptation at the genomic scale. Indigenous breeds of cattle, buffalo, sheep, goats, pigs, and poultry have evolved under diverse agro-climatic conditions ranging from arid deserts and humid tropics to high-altitude Himalayan landscapes. These populations carry genomic signatures shaped by natural and artificial selection for traits like thermotolerance, hypoxia adaptation, disease and parasite resistance, and metabolic efficiency. Landscape genomics, an emerging approach which integrates genomics, ecology, and spatial analysis, offers a powerful framework to directly link genetic variation with environmental gradients. Unlike traditional population genetic scans, it explicitly models genotype-environment associations, thereby identifying adaptive variants without the need for direct phenotypic measurements. Current landscape genomic methods broadly include (i) genotype-environment association (GEA) models such as redundancy analysis (RDA), latent factor mixed models (LFMM), and logistic regression approaches (e.g., SAMβADA); (ii) outlier detection methods (e.g., Fst, BayeScan, pcadapt) that identify loci under selection; and (iii) machine learning tools like Random Forests and gradient boosting, capable of capturing complex non-linear genotype-environment relationships. Together, these complementary approaches enhance robustness in detecting signals of adaptation. While global studies have demonstrated their application in various livestock species, the Indian livestock remain relatively unexplored. Yet, India now possesses vast genomic datasets from SNP chips and whole-genome sequencing, along with high-resolution climatic and spatial data from platforms such as India Meteorological Department (IMD) and WorldClim. Integrating these resources through landscape genomic frameworks can uncover adaptive alleles and pathways in native breeds, paving the way for climate-resilient breeding programmes, marker-assisted selection, and conservation of regionally adapted genetic resources. Harnessing landscape genomics for Indian livestock thus presents a timely opportunity to bridge knowledge gaps, support sustainable production systems, and strengthen food and livelihood security under changing climatic scenarios.

Keywords: Cattle, Buffalo, Landscape Genomics, WGS.

P2-33

HAPLOTYPE-BASED SELECTION SIGNATURE REVEALS GENOMIC EVIDENCE OF POSITIVE SELECTION FOR MILK PRODUCTION AND ADAPTIVE TRAITS IN SAHIWAL CATTLE

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ABSTRACT

Sahiwal cattle, renowned for their tropical resilience and dairy productivity, were investigated for selection signatures underlying key economic traits. This study utilized 51,278 SNPs from the BovineSNP50 BeadChip to genotype 192 animals, with 28,497 high-quality autosomal SNPs retained post-quality control. Three intra-population haplotype-based statistics (iHS, nSL, iHH12) were applied, revealing 816, 947, and 1,072 significant regions (score >2), respectively. Overlapping sweeps across methods revealed complementary detection strengths. Functional annotation emphasized genes linked to milk production and reproduction, with seven genes (CLSTN2, COX14, GPD1, SMARCD1, MCC, MACROD2, CTNNA3) consistently detected across all methods. Notably, CLSTN2 is associated with milk fat percentage, supporting milk quality traits, while GPD1 and SMARCD1 regulate lipid metabolism, crucial for milk synthesis and energy balance during lactation. MACROD2 and CTNNA3 are linked to fertility traits, enhancing reproductive efficiency. Functional annotation revealed strong enrichment for milk production traits (e.g., fat content, mammary gland development) and reproductive performance (e.g., embryo development, fertility pathways). QTL annotation showed 26-36% of regions tied to milk traits (yield, fat, protein) and 11-15% to reproduction (fertility, calving ease). These findings highlight the importance of selection on lactation and fertility genes in shaping the adaptive and productive traits of Sahiwal cattle. This genomic insight contributes to the strategic genomic selection and conservation of indigenous dairy breeds in challenging environments.

Keywords: Sahiwal cattle, selection signature, haplotype-based methods

P2-34

NON-REFERENCE SEQUENCES (NRSS) IN DIVERSE INDIAN BUFFALO BREEDS

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ABSTRACT

The Food and Agriculture Organisation (FAO) has considered the Buffalo (Bubalus bubalis) as a strategic asset that is undervalued. Buffaloes are known as "Black Gold" due to their contribution to global food security and economy. Reference genomes of higher quality serve as the keystone in the field of genomics to enhance animal productivity and wellness. To capture the population-specific variation, we need to construct a reference genome from many individuals from different breeds or species, which can represent their respective breeds/species. Reference genome from a large number of individuals comprehensively collects all the DNA sequences of a genus, species or population, and overcomes reference bias caused by a single (linear) reference genome during genomic analyses. The buffalo rank 2nd in milk production; it also plays a key role in the Indian agricultural economy. For genomic analysis in buffalo, as well as many other economically important species, like cattle, pigs, sheep, goats, and chickens, we are still reliant on a linear (single) reference genome. In this study, we identified the non-reference sequences by using short-read Illumina whole-genome sequencing data of 250 buffalo representing 10 different breeds of India. Procedure used in identification of non-reference sequences includes raw reads quality filtering, alignment to reference genome NDDB SH_1, generation of BAM file, extraction of unaligned reads, and de novo assembly of unaligned reads. As a result we have identified about 3 GB non-reference sequences from 250 buffalo's sample.

Keywords: non-reference sequences (NRSs), buffalo, WGS

P2-35

SNP HAPLOTYPE-BASED ANALYSIS OF MILK PERSISTENCY AND BREEDING EFFICIENCY IN SAHIWAL CATTLE

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ABSTRACT

Breeding efficiency and milk persistency are critical for the sustainability, profitability, and productivity of the dairy industry. Although phenotypic, genetic, and management approaches can be applied to improve them, but genetic methods provide permanent and cumulative gains in the herd. Haplotype-based GWAS (H-GWAS), which considers sets of closely linked SNPs in strong linkage disequilibrium, offers a more comprehensive representation of genomic variation than single-SNP GWAS. In this study, H-GWAS was conducted using sliding windows of 20 contiguous SNPs (step size 5) to generate haploblocks. A total of 4,359 haploblocks were formed for breeding efficiency and 4,370 for milk persistency. PCA of the genomic relationship matrix was incorporated to control for batch effects, followed by association analysis using a linear regression model in PLINK. In total, 75,253 and 71,008 haplotypes were identified for breeding efficiency and milk persistency, respectively, of which 18,123 and 20,568 had frequencies >5%. After Bonferroni correction, 5 significant haplotypes were attributed to breeding efficiency, and 3 haplotypes were specific for milk persistency. The biological roles of these genes were also studied which support their relevance for genetic selection, demonstrating that haplotype-based association with functional annotation can identify key determinants of complex traits and provide genomic resources to improve breeding efficiency and milk persistency in dairy cattle.

Keywords: Haplotype-based GWAS, Sahiwal, Milk persistency, Breeding efficiency, Candidate genes

P2-36

INTEGRATING AI, ML AND IOT WITH GENOMIC SELECTION FOR GENETIC IMPROVEMENT IN DISEASE-RESISTANCE AND RESILIENCE IN INDIGENOUS POULTRY

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ABSTRACT

Genetic improvement in livestock has progressed from traditional selection indices and mixed model equations to Best Linear Unbiased Prediction (BLUP) frameworks, enabling accurate estimation of breeding values. Yet, these linear models remain limited for complex traits such as disease resistance, characterized by low heritability, strong genotype–environment interactions, and polygenic control. Genomic selection methods such as genomic BLUP (gBLUP) and Bayesian approaches (Bayes-A, Bayes-Bπ, Bayes-Cπ) marked a breakthrough but often fail to capture non-additive effects, epistasis, and environmental dependencies in high-dimensional datasets. Recent advances in artificial intelligence (AI) and machine learning (ML) are transforming this landscape by enabling predictive modeling that integrates multilayered omics and environmental data. Algorithms such as Random Forests, Gradient Boosting, Support Vector Machines, and Deep Neural Networks can decode complex nonlinear relationships among immune-regulatory genes such as MHC-B, TLR, cytokine, and chemokine networks, and between genomic markers and immune traits, improving the accuracy of genomic estimated breeding values (GEBVs). Ensemble and graph-based neural networks enable high-resolution mapping of QTL and SNPs for immune-regulatory gene families, facilitating precise selection for humoral and cell-mediated immune responses. Simultaneously, Internet of Things (IoT)-enabled biosensors and smart farming systems continuously monitor environmental and physiological parameters–temperature, humidity, feed and water intake, behavioral activity, and thermoregulation–thereby refining phenotyping process and facilitating real-time assessment of disease susceptibility. AI-driven decision-support platforms integrate these multimodal data streams to derive adaptive, environment-specific selection indices. Furthermore, digital twin models and predictive epidemiological simulations replicate host-pathogen interactions under varying climatic and management conditions, supporting proactive selection for resilience.

The synergistic integration of AI, ML, IoT, and genomics establishes a next-generation framework for precision poultry breeding. This paradigm accelerates the identification and dissemination of disease-resistant genotypes in indigenous poultry such as *Haringhata Black* and native ecotypes of West Bengal, fostering climate resilience, genetic conservation, and sustainable rural livelihoods.

Keywords: Artificial intelligence, Machine learning, IoT, Genomic selection, Disease resistance, Indigenous poultry

P2-37

INTEGRATION OF ARTIFICIAL INTELLIGENCE TOOLS IN SEQUENCE BASED TYPING OF BOLA-CLASS II-DRB3 IN INDIAN CATTLE

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ABSTRACT

Introduction: BoLA- Class II- DRB3 gene, plays a central role in antigen presentation and immune regulation, influencing resistance to several diseases. Its exon 2 region is highly polymorphic and is commonly targeted for BoLA typing. While Sequence-Based Typing (SBT) is widely accepted for genotyping, existing workflow is manual, labor-intensive and slow. Present study combines molecular biology techniques with agentive-AI tools to automate allele identification to enhance the speed, scalability and reproducibility of BoLA-DRB3 typing in Indian cattle. Methodology: The study represents a systematic, optimized workflow for BoLA-DRB3 sequence based typing through Sanger sequencing across a cohort of 50 animals from 7 genetically distinct Indian cattle breeds (Red Sindhi, Jersey, Sahiwal, Nimari, Ongole, Deoni and Gir). We optimized amplification of DRB3 gene using reported primers and bidirectional sequencing was performed. We improved the sequence based typing with integration of Agentive-AI & Browser use automation to extract and identify alleles and similarity scores from .ab1 files. Results: An open source bioinformatics tool (Peak-Detect) was developed using browser-use, lovable.ai and custom prompts. The Peak-Detect system demonstrated fast, accurate operation, efficiently analyzing Sanger trace files with a mean processing latency of 4.82 seconds per query. The designed automated BLAST searches against IPD-MHC database, enabled batch processing with minimal manual input which reduced allele calling time by ~80% and improved consistency, speed, and scalability. Our analysis of 50 animals showed presence of 27 BoLA-DRB3 alleles with varied frequency distribution across the breeds. BoLA-DRB3*057:02 and BoLA-DRB3*012:01 emerged as the most prevalent in the sampled populations (~12% each). In conclusion, Peak-Detect can serve as a platform for real-time base calling, automated SNP scan and heterozygosity detection, peak quality controls and interactive chromatogram visualization with suitable backend integration. Integration of optimized wet-lab protocols with AI-powered data analysis can significantly enhance practical utility of BoLA-typing in livestock.

Keywords: BoLA-DRB3, Sequence based typing, AI Tools, Browser automation, Indian cattle

P2-38

A MULTI-APPROACH GENOMIC FRAMEWORK FOR TRAIT GENOMICS AND BREED-SPECIFIC CHARACTERISTICS IN SAHIWAL CATTLE

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ABSTRACT

Understanding the genetic basis of adaptive and economically important traits is crucial for the sustainable improvement and conservation of indigenous cattle breeds. In this study, we employed a comprehensive genomics framework combining selection signature analyses, genome-wide association studies (GWAS), and machine learning to investigate genomic regions underlying key traits in Sahiwal cattle. A Random Forest model was trained using multiple genomic summary statistics to classify selection sweeps with high accuracy (AUC $\approx$ 0.99), identifying 148 selective regions containing 284 genes. Notably, 26 genomic regions overlapped between selection signature analyses, machine learning predictions, and GWAS signals, highlighting loci of high biological relevance. Among the key genes, GHR, DGAT1, PTK2, IQSEC3, ABCG2, and IL2 emerged as central hubs in protein–protein interaction networks, reflecting their regulatory roles in production and adaptation. This integrative approach demonstrates the power of combining population genomics, machine learning, and GWAS to unravel the complex genomic architecture of indigenous breeds. The findings provide valuable insights for designing marker-assisted and genomic selection programs aimed at improving productivity while preserving the adaptive potential of Sahiwal cattle.

Keywords: GWAS, Machine learning, Random Forest, Sahiwal, Selection signature

P2-40

DEVELOPMENT OF A NOVEL HETEROLOGOUS SINGLE NUCLEOTIDE POLYMORPHIC (SNP) MARKER PANEL FOR PARENTAGE TESTING IN YAK

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ABSTRACT

Traditional parentage verification in yak (Bos grunniens) is challenging, particularly under the nomadic transhumance pastoral production system practiced in different parts of Asia. The present study reports the development of a novel heterologous single nucleotide polymorphic marker (SNP) panel for successful parentage testing under three different hypothetical scenarios: viz. conventional paternity testing (PE1), one parental genotype unavailable (PE2) and exclusion of both parents i.e. substituted offspring (PE3). Genome-wide SNP data derived from Axiom BovMDv3 cattle array on 340 yaks belonging to six populations located across different parts of Mongolia (Arkhangai, Khuvsgul, Khovd, Umnugobi, Uvurkhangai) and Pakistan (Gilgit Baltistan) were utilized. SNPs categorized as Poly High Resolution (showing all three genotypes) by Axiom Analysis Suite were filtered and assessed for minor allele frequency (MAF) and expected (He) heterozygosity using the following threshold: $MAF \geq 0.3$ and $0.3 \leq He \leq 0.6$. A set of 440 markers exhibiting high polymorphism and balanced heterozygosity was shortlisted for further breed wise evaluation. After evaluation in six different yak breeds, a final set of 142 SNP markers with highest exclusion powers for all the three hypothetical scenarios, PE1, PE2 and PE3 were selected. The cumulative PE values approached near-perfect accuracy exceeding 0.999999, which translates to an estimated error rate as low as 1 in 1,000,000. This extremely low error rate indicates a high degree of confidence in parent-offspring assignments and validates its superiority over bovine ISAG panel for parentage testing in yak breeding and conservation programs.

Keywords: exclusion power, paternity, bovine

P2-41

MACHINE LEARNING-AIDED INSIGHTS REVEAL LINKS BETWEEN Y-LINKED GENE CNVs AND SEMINAL TRAITS OF BULLS OF DIFFERENT GENETIC BACKGROUNDS

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ABSTRACT

The Y-chromosome possesses distinct features including holandric inheritance, absence of recombination, and lineage specific gene degeneration. The lineage specific transposition events have resulted in formation of Y-linked gene families in bovines like preferentially expressed antigen in melanoma, Y-linked, zinc finger protein 280A-like, Y-linked, and heat-shock transcription factor, Y-linked (PRAMEY, ZNF280BY, and ZNF280AY), with their copy number variations (CNVs) linked to male fertility. The present study examined the CNVs of three Y-linked genes (HSFY, ZNF280BY, and DDX3Y) in indicus (Bos indicus), taurus (Bos taurus) and crossbred bulls (Bos taurus x Bos indicus), along with their association with seminal traits. Semen samples from 60 superior service bulls across 14 breeds of three genetic backgrounds were evaluated for sperm motility characteristics (total motility, progressive motility, rapid motility, etc.) using Computer-Assisted Semen Analysis (CASA), while CNVs were measured through real time PCR (qPCR). Results revealed significant differences in seminal traits among genetic backgrounds, with taurus bulls exhibiting superior motility (total motility: 79.09±6.24%) compared to indicine (70.52±9.63%) and crossbred bulls (68.67±15.59%). Reduced sperm motility was noted in crossbred bulls, suggesting potential genetic dilution effects. Highest copy number (CN) for HSFY, ZNF280BY and DDX3Y genes were found in indicus bulls (LogCN: 4.80±0.10, 7.2±0.08, and 10.78±0.08, respectively) with breed-specific variations. Association analyses revealed positive relationships between HSFY gene CN and sperm motility traits in indicus bulls, while taurus bulls showed negative associations, indicating genetic background-specific gene effects. Machine learning models identified non-linear relationships, with optimal HSFY LogCN (4.8–5.2) and a threshold effect for ZNF280BY (7.5 LogCN) influencing seminal quality. This study underscores the impact of Y-linked gene CNVs on bull semen quality and emphasizes genetic background-specific variable influences on seminal traits. These findings provide important insights into genetic selection of bulls and breeding programmes aimed at increasing bull fertility.

Keywords: Copy number variation, bull fertility, HSFY, ZNF280BY, DDX3Y, genetic background, nonlinear relationship.

P2-42

VARIATION IN SPERM MITOCHONDRIAL DNA COPY NUMBER AND GENE EXPRESSION PROFILES: MACHINE LEARNING INSIGHTS INTO BULL FERTILITY

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ABSTRACT

Mitochondrial DNA copy number (mtDNAcn) in spermatozoa plays a critical role in cellular energy metabolism and has emerged as a promising indicator of sperm functionality and male fertility. Understanding its variation and association with seminal parameters is important for enhancing reproductive efficiency. The present study was conducted on superior service bulls (n=111) representing indicine, exotic, and crossbred genetic groups to investigate the variation in sperm mtDNAcn and its relationship with a comprehensive set of sperm motility and kinematic parameters. The expression levels of all 13 protein-coding mitochondrial genes and their association with mtDNAcn were also examined. Relative mtDNAcn was quantified using SYBR Green-based real-time PCR targeting mitochondrial (CYTB, ND1) and nuclear (β2M) genes. Statistical analysis, including correlation and regression, was complemented with machine learning models (Random Forest and Gradient Boosting) to reveal both linear and complex non-linear associations. Significant inter-group variation ($p < 0.001$) was observed, with indicine bulls showing the highest mtDNAcn (3.61 ± 0.32), exotics the lowest (1.63 ± 0.19), and crossbreds intermediate (2.43 ± 0.29). Among indicine breeds, Sahiwal bulls exhibited markedly higher mtDNAcn (5.14 ± 0.63) than Red Sindhi (2.33 ± 0.47) and Gir (2.55 ± 0.43). A similar trend was observed for mitochondrial gene expression, which showed strong correlation with mtDNAcn. Mitochondrial gene expression indices differed significantly among genetic groups ($p < 0.005$), and showed a positive correlation with mtDNAcn ($p < 0.05$). Traditional linear models identified negative associations of mtDNAcn with sperm viability, wobble, and linearity, whereas machine learning revealed non-linear relationships indicating increased total and progressive motility with higher mtDNAcn. Overall, mtDNAcn emerges as a meaningful indicator of sperm functional competence, with its effects operating through intricate, non-linear mechanisms that can be better elucidated through advanced machine learning approaches.

Keywords: mtDNAcn, mitochondrial gene expression, bull fertility, machine learning, non-linear relationship

P2-39

EXTERNAL EGG QUALITY ANALYSIS OF POULTRY EGGS USING ARTIFICIAL INTELLIGENCE

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ABSTRACT

In hatcheries, classification and grading eggs on the basis of various parameters is an important activity. One of the parameters includes egg dimensions. However manual methods are cumbersome, time consuming, prone to error and there is always risk of damaging the eggs during handling. Keeping this in view, the present research was undertaken to evaluate the potential of AI for predicting the egg dimensions automatically from images. For this purpose, egg image dataset was created, and computer vision was applied to them. Mean Absolute Errors (MAE) of the two final predictive models for egg size were found to be 0.28 for length and 0.19 for breadth, with Pearson Correlations of 0.81 for length and 0.85 for breadth for Model 1 and MAEs of 0.29 for length and 0.26 for breadth, with Pearson Correlations of 0.88 for length and 0.81 for breadth for Model 2.

Keywords: Artificial Intelligence, Egg, Morphometry, Poultry

P2-44

INTEGRATIVE TRANSCRIPTOMIC AND MACHINE LEARNING ANALYSIS REVEALS KEY HOST GENES AND PATHWAYS ASSOCIATED WITH BOVINE TUBERCULOSIS

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ABSTRACT

Bovine tuberculosis (bTB), caused by Mycobacterium bovis, remains a major infectious disease affecting cattle worldwide, leading to significant economic losses and posing a serious zoonotic threat to humans. Understanding the host genetic response to infection is crucial for improving disease resistance through genomic-assisted breeding. The present study aimed to identify key host genes and molecular pathways associated with tuberculosis infection in cattle using an integrative transcriptomic and machine learning framework. Publicly available RNA-seq data (GSE255724) were retrieved from the National Center for Biotechnology Information (NCBI) database and analyzed through differential expression analysis, Weighted Gene Co-expression Network Analysis (WGCNA) and SHapley Additive exPlanations (SHAP)-based machine learning models. A total of 3,434 differentially expressed genes (DEGs) were identified, including 2,021 upregulated and 1,413 downregulated genes in infected cattle compared to controls. WGCNA revealed several significant modules, turquoise, magenta, tan, blue and midnight blue, strongly correlated with tuberculosis infection. Six supervised machine learning models were developed and the Support Vector Classifier (SVC) achieved the highest predictive accuracy (0.72). Integration of DEGs, WGCNA and SHAP analyses identified the top 50 SHAP genes, which were significantly enriched in immune- and signaling-related pathways, including complement and coagulation cascades, neutrophil extracellular trap (NET) formation, TNF signaling, T cell receptor signaling, Wntsignaling and Hippo signaling pathways. Among these, SLC6A12, ADGRV1, CXCR4, SELE and RNF24 were identified as potential key regulators of the host immune response. This integrative approach provides genomic insights into host–pathogen interactions in bovine tuberculosis and identifies candidate genes that could support next-generation breeding strategies for disease resistance in cattle.

Keywords: Bovine tuberculosis; Transcriptomics; WGCNA; Machine learning

P2-45

POU1F1 GENE POLYMORPHISM AT EXON-2 AND EXON-3 REGION USING PCR-RFLP, SSCP AND DIRECT SEQUENCING IN GAOLAO CATTLE BREED POPULATION

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ABSTRACT

POU class 1 homeobox1 (POU1F1) is a member of the tissue-specific POU-containing transcription factor family and its expressions are required for the transcription of the genes involved in a signalling pathway important for milk protein expression, production, and secretion in mammals. The objectives of the present study were to study polymorphism at exon-2 and exon-3 region of the POU1F1 gene using PCR-RFLP, SSCP and Direct Sequencing in Gaolao cattle breed population. The blood was collected from 245 cows, and test-day milk traits were recorded. POU1F1 gene PCR-RFLP study at POU1F1G1-TaqI locus in iexon-2 region was polymorphic with the frequency of A, B, and C alleles as 0.52, 0.14 & 0.34 respectively. However; the studied population was not in equilibrium for the polymorphic locus. The POU1F1G1-TaqI polymorphism was not associated with milk traits. POU1F1 gene PCR-SSCP polymorphism analysis of 234 bp fragment (POU1F1G2) and 275 bp fragment (POU1F1G5*) of exon-3 region was monomorphic in 56 and 28 Gaolao cows respectively. Direct sequencing of POU1F1 gene fragment of exon 3 region (POU1F1G2) of 234 bp followed by SSCP revealed 01 computational transversion SNP. POU1F1G7-SSCP at exon-6 region was monomorphic in 28 samples of Gaolao cows. The above study shows existence of polymorphism in exon-3 and exon-6 regions of POU1F1 gene which is important candidate gene for milk production traits. The results will fill the information gap and it may be useful in future gene assisted selection and improvement strategies for milk traits.

Keywords: POU1F1 Gene, DNA Polymorphism, Milk traits, Gaolao cattle

P2-46

A PCR BASED APPROACH FOR SEX DETERMINATION OF CHICKEN EMBRYOS

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ABSTRACT

The chicken (Gallus gallus) plays a pivotal role in global food systems, contributing substantially to both meat and egg production. India, with an estimated poultry population of 851.81 million birds, ranks second in egg production and fifth in broiler meat output worldwide. Early and accurate sex determination in developing embryos is crucial for effective hatchery management, optimized resource utilization, and addressing ethical issues associated with post-hatch culling of unwanted male chicks. Traditional sexing techniques, developed before the advancement of molecular genetics, are often unreliable, labor-intensive, and require skilled expertise, limiting their large-scale application in the poultry industry. In avian species, the Chromodomain Helicase DNA-binding protein 1 (CHD1) gene, located on both the Z and W sex chromosomes, exhibits intron length polymorphism that enables accurate molecular sex identification through polymerase chain reaction (PCR) amplification. In the present study, genetic sex determination of chicken embryos was conducted by targeting the CHD1 gene. Liver tissues were collected from 17-day-old embryos, and genomic DNA was isolated using the phenol–chloroform extraction method. PCR amplification was performed using CHD1-specific primers, and the resulting amplicons were separated on a 2% agarose gel. Distinct electrophoretic banding patterns were observed under a UV transilluminator: a single 495 bp band confirmed male embryos (ZZ), while two distinct bands at 495 bp and 351 bp indicated female embryos (ZW). The findings of this study established that CHD1-based PCR is a reliable, rapid, and cost-effective molecular approach for early sex determination in chickens.

Keywords: CHD1 gene, Molecular sexing, PCR amplification, Chicken embryos, Sex determination

P2-43

TRANSCRIPTOMIC PROFILING OF HALLIKAR CATTLE AFFECTED WITH LUMPY SKIN DISEASE

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ABSTRACT

Lumpy skin disease (LSD) has emerged as a major transboundary disease affecting indigenous cattle populations, including the Hallikar breed of southern India. The present study was undertaken to study the Gene Expression Profiling in Hallikar cattle affected with Lumpy Skin Disease (LSD). Blood samples were collected from three PCR confirmed LSDV infected and three PCR negative LSDV uninfected Hallikar cattle, and RNA was extracted from peripheral blood mononuclear cells for transcriptome sequencing using the Illumina NovaSeq 6000 platform. Transcriptome sequencing generated high quality paired-end reads, which upon alignment to the Bos taurus reference genome revealed 18,994 expressed genes, including 3,128 significantly differentially expressed (2,635 upregulated and 493 downregulated) in LSD-affected animals. Functional enrichment analysis showed that differentially expressed genes were predominantly associated with cell cycle regulation, oxidative stress, DNA damage response and lipid peroxidation. KEGG pathway enrichment identified significant enrichment in Fanconi anemia, MAPK signaling, endocytosis, lysosome, autophagy and cellular senescence pathways. Network analysis highlighted six hub genes, namely TGFB1, FCN1, COL6A1, G3N0V0, G3MZE0 and G3N342, as key regulators of host response to LSDV infection. The findings provide valuable insights into the molecular mechanisms governing LSD pathogenesis and highlight potential genetic targets for future breeding strategies aimed at enhancing disease resilience in indigenous cattle.

Keywords: Cattle, LSD, RNA-Seq, DEG, Hub genes

P2-48

ASSOCIATION OF IGF1 POLYMORPHISM WITH REPRODUCTIVE PERFORMANCE IN ROHILKHANDI GOATS

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ABSTRACT

Reproductive performance is a key driver of productivity in goat husbandry, and understanding the genetic factors that underpin reproductive traits can accelerate targeted improvement of native breeds. The present study investigated the polymorphism in the IGF1 (Insulin-Like Growth Factor 1) gene and its association with reproductive traits in Rohilkhandi goats using PCR-RFLP analysis. Genetic variation was detected in the targeted fragment of the IGF1 gene. Reproductive traits evaluated included age at first kidding, average kidding interval, average litter size, kidding per year, kids per year, and body weight at first kidding, with mean estimates of 546.98 ± 10.52 days, 316.65 ± 6.21 days, 1.32 ± 0.05, 1.17 ± 0.02, 1.54 ± 0.06 and 16.09 ± 0.15 kg, respectively. Mixed-model analysis revealed that IGF1 genotypes had a significant effect ($p < 0.05$) on age at first kidding and body weight at first kidding, indicating that IGF1 polymorphism may influence reproductive performance in Rohilkhandi goats. This preliminary investigation provides a foundation for understanding the role of IGF1 gene variants in reproductive traits, and highlights the need for larger, multi-breed studies to validate these associations and identify reliable molecular markers for incorporation into marker-assisted breeding strategies aimed at improving reproductive efficiency in indigenous goats.

Keywords: Goat, IGF1, PCR-RFLP, Polymorphism, Reproductive traits

P2-49

ROLE OF ESR2 AND OTHER GENES REGULATING REPRODUCTION AND EGG PRODUCTION IN INDIGENOUS DUCK – A FUTURE POTENTIAL TO IMPROVE EGG PRODUCTION

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ABSTRACT

Anas platyrhynchos (domestic ducks) are primarily reared for egg production, as duck eggs are highly nutritious and fetch higher market value. However, duck meat is also rich in essential nutrients. Ducks possess unique traits such as resistance to several common avian diseases and may even remain asymptomatic carriers of avian influenza. Despite these advantages, indigenous duck populations exhibit certain production constraints, including lower average egg yield and a higher age at first egg (an indicator of delayed sexual maturity), when compared with exotic breeds. The present study aimed to elucidate the genetic basis underlying reproductive performance in ducks, particularly in relation to sexual maturity, egg production, and fertility. We performed a comparative genomic analysis between high egg–producing Bengal ducks and non-layer (infertile or sexually immature) ducks. Genes expressed in ovarian tissues of indigenous ducks were characterized, and key functional domains were identified for the first time. Differential mRNA expression profiling was conducted between layer and non-layer groups. Pronounced upregulated expression was observed for of ESR2, followed by DIAPH2, KMT2E, and ASCF2 in the high egg–producing Bengal ducks, whereas KSR1, A2M, BMPR1B, and ACVR1 were found to be downregulated. Further analysis suggested that these genes are significantly associated with egg production traits. Thus, Anas platyrhynchos may serve as a valuable model species for investigating the molecular mechanisms of reproduction. The upregulated genes may be potential targets for knock-in approaches, while downregulated genes could be manipulated through knockout or knockdown strategies using gene-editing technologies to enhance reproductive performance in ducks. Moreover, these genes could serve as molecular biomarkers for early selection of ducks with superior reproductive potential, potentially identifiable at hatch or even at the embryonic stage.

Keywords: ESR, duck, reproduction, egg production

P2-50

LINKING GENOMIC AND PHEROMONIC INTERVENTIONS FOR GENETIC GAIN AND LIVELIHOOD IMPROVEMENT IN SMALL RUMINANTS

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ABSTRACT

Advances in livestock breeding increasingly rely on the integration of genomic and phenomic information, forming the basis of generation breeding—a data-driven approach that accelerates genetic progress and enhances productivity. This study demonstrates how genomic and phenomic interventions, implemented under field conditions, can deliver tangible improvements in both biological and economic performance of small ruminants, particularly goats. A series of interventions combining genetic, nutritional, and health-based strategies were implemented among more than 17,000 smallholder farmers. The introduction of superior germplasm among 625 farmers produced the highest reproductive improvement, with kids per doe increasing from 2.06 ± 0.07 to 2.44 ± 0.10, reflecting a 15.57% rise. Nutritional interventions such as concentrate feed supplementation (9.65% increase) and mineral mixture supplementation (8.04% increase) significantly enhanced reproductive performance, while health-oriented measures like deworming and vaccination against PPR resulted in gains of 5.94% and 5.07%, respectively. Economic analysis revealed a parallel increase in farmer income, with superior germplasm adoption yielding a 23.96% rise (□2120 ± 230 to □2788 ± 265; $p < 0.001$). Nutritional and health interventions also contributed 16–18% income growth, all statistically significant ($p < 0.001$). These findings highlight the synergistic power of integrating genomic selection (genotype-based improvement) with phenomic evaluation (observable performance) in achieving rapid and sustainable genetic gains. The observed correlations between enhanced productivity and increased farmer income validate generation breeding as an effective model for precision livestock improvement. This genomics–phenomics convergence not only accelerates genetic progress but also strengthens livelihood resilience, ensuring sustainable growth of the small ruminant sector under diverse production systems.

Keywords: Generation breeding, Genomics, Goat, Productivity, Farmer income, Sustainability

P2-47

POLYMORPHIC MICROSATELLITE LOCI FROM DDRAD SEQUENCING DATA IN DIFFERENT INDIAN YAK POPULATIONS ADAPTED TO DIVERSE CLIMATIC CONDITIONS

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ABSTRACT

Microsatellites are highly polymorphic, codominant, and reproducible molecular markers that are fairly evenly distributed across the eukaryotic genomes. Although cattle-specific microsatellite markers have been employed in yak, no species-specific marker set has yet been established. The present study aimed to identify and validate polymorphic microsatellite markers in four distinct Indian yak cohorts, i.e., Arunachali, Ladakhi, Himachali, and Sikkimi using double-digest restriction-site associated DNA (ddRAD) sequencing data from 20 representative animals per cohort (n = 80). Approximately 260 million raw paired-end reads were retrieved and processed in the present study. Paired-end reads (n = 40 per cohort) were merged using PEAR, and the assembled reads were screened for RAD cut sites. Polymorphic microsatellite loci were elucidated and corresponding primer sets were designed using QDD program, utilizing only unique consensus sequences and singletons for primer designing. In-silico PCR amplification was performed using in_silico_PCR.pl, implemented in Perl v5.30.3 to validate primer specificity. A total of 32, 82, 149, and 31 polymorphic SSR loci were identified in Sikkimi, Himachali, Arunachali, and Ladakhi cohorts, respectively, of which 26, 72, 106, and 24 loci were successfully validated through in-silico amplification. A total of 32 microsatellites were common between the Himachali and Arunachali cohorts, while two loci were shared across all populations. On the other hand, 13, 39, 56, and eight loci were private to Sikkimi, Himachali, Arunachali, and Ladakhi yak, respectively. The in-silico validated polymorphic SSR markers provide a valuable genomic resource for assessing genetic diversity, population structure, and evolutionary adaptation in yak populations, and can be further evaluated and validated through wet-laboratory experimentation on larger cohorts.

Keywords: Consensus; Microsatellites; Polymorphism; Primer; QDD; SSR; Yak.

P2-52

GENETIC POLYMORPHISM, ASSOCIATION AND EXPRESSION STUDIES OF EGG PRODUCTION RELATED CANDIDATE GENES IN ASEEL

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ABSTRACT

The study aimed at genotyping and associating candidate genes i.e. cGH, MTNR1C and VIPR-1 with egg production traits in Aseel chicken. The relative mRNA expression of CRBP IV and cGH gene in liver, kidney and oviduct was also studied to find any significant association with egg production. The data on age at sexual maturity (ASM), body and egg weight at 20 and 40 weeks (BW20, BW40, EW28, EW40) and egg production up to 40 weeks (EP40) were recorded on 180 single-hatch pedigreed birds from 4th generation of Aseel undergoing selective breeding for higher BW20 maintained at Desi Fowl unit of ICAR-CARI, Izatnagar, Bareilly. Data were analysed by LS ANOVA using mixed model, sire as random effect and hatch as fixed effect. Average ASM and EP40 were 214.39±2.22 days, 40.88±2.70 eggs, respectively. Sire had significant effect ($P \leq 0.05$) on BW20 and EP40. BW and EW showed high heritability. EP40 showed medium heritability. The genetic and phenotypic correlation did not reveal any specific trend. cGH, MTNR1C and VIPR-1 RFLPs revealed polymorphism. Significant effect of cGH/ Sac I genotype on BW40 ($P \leq 0.10$) and EP40 ($P \leq 0.05$), MTNR1C/ Mbo I genotype on ASM and EP40 ($P \leq 0.05$), VIPR-1/ Hha I genotype on BW20 and BW40 ($P \leq 0.10$) were observed. Certain markers were identified: BB and AA genotype at cGH and MTNR1C locus respectively to improve EP40, AA genotype at cGH and VIPR-1 locus to improve BW40, AA genotype at MTNR1C and VIPR1 locus to improve ASM and BW20, respectively. Relative mRNA expression of CRBP IV and cGH gene in high and low egg production groups, differed significantly in liver ($P \leq 0.15$) and oviduct ($P \leq 0.001$) respectively. The study revealed significant findings on candidate genes and their potential application both in advanced marker assisted and in conventional full sib selection programs for genetic improvement of layer economic traits in Aseel.

Keywords: cGH, MTNR1C, VPR1, Expression study, Polymorphism, egg production

P2-53

UNRAVELLING CELLULAR HETEROGENEITY: AN INTRODUCTION TO SINGLE CELL TRANSCRIPTOMICS

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ABSTRACT

Single-cell transcriptomics (scRNA-seq) has emerged as a transformative technology for unravelling cellular heterogeneity, moving beyond the limitations of bulk RNA sequencing which averages gene expression. This approach enables the high-throughput profiling of the entire transcriptome at the resolution of individual cells, allowing for the identification of rare cell types, characterization of dynamic cellular states, and reconstruction of developmental trajectories, which are often obscured in bulk tissue analysis. The methodology typically involves tissue dissociation, single-cell isolation, barcoding with Unique Molecular Identifiers (UMIs), and next-generation sequencing. The resulting data demands sophisticated computational pipelines for preprocessing, quality control, normalization, and dimensionality reduction using tools like Seurat and Scanpy, followed by downstream analyses. The applications of scRNA-seq are vast and data rich, including cellular atlas construction, tumor heterogeneity analysis, lineage tracing in developmental biology, neuroscience, and immunological studies. The Tabula Sapiens Consortium, an NIH-initiated project, developed a multi-organ single-cell transcriptomic atlas of humans by profiling 500,000 cells from 24 tissues, identifying over 400 distinct cell types. It is also gaining traction in agriculture and Livestock research to enhance economic traits and disease resistance. Despite its vast potential, challenges persist in data standardization, managing high computational demands, and the complexity of integrating multi-omics and spatial data. Future perspectives point towards the standardization, enhanced clinical translation for personalized medicine, and the deeper integration of AI/ML to fully exploit the potential of single-cell biology and advancing towards promising transformative insights that will reshape our understanding of life's complexity and accelerate innovations across disciplines.

Keywords: Barcoding, Differential expression, Gene Regulation, scRNA-seq

P2-54

DEEP PROTEOME PROFILING OF PASHMINA SKIN REVEALS THE BASIC DEVELOPMENTAL MECHANISM ASSOCIATED WITH FIBRE SYNTHESIS AND SHEDDING

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ABSTRACT

Pashmina, a speciality fibre, also known as Cashmere, is well known for its warmth, softness, fineness and aesthetic value. Pashmina fibre undergoes an annual cycle of growth and shedding via three phases: growth phase (Anagen), regression phase (Catagen) and resting phase (Telogen). To study the developmental mechanism of fibre synthesis, we employed LC-MS/MS based proteomics approach. We generated a comprehensive proteome map of pashmina goat skin using different Strategies. TMT based strategy resulted in a total of 754 DEPs in anagen vs catagen with 346 upregulated and 117 down regulated proteins. LFQ based strategy resulted in a total of 250 DEPs combinedly at all the five months of the annual cycle. A total of 179 (51 up- and 128 down-regulated), 202 (85 up- and 117 down-regulated), 140 (39 up- and 101 down-regulated) and 204 (29 up- and 175 down-regulated) DEPs were identified from middle anagen-late anagen, anagen-catagen, catagen-telogen and telogen-early anagen phases, respectively. The most essential signalling pathways involved in the Hair follicle (HF) growth and development were Wnt, Shh, Notch, PI3-AKT, Hippo and TGF-beta. Wnt pathway in the anagen stage promotes hair follicle regrowth. Apoptosis and TGF beta pathway were involved in hair follicle regression at the catagen stage. Some of the important proteins involved in the hair cycle, viz., CTNNB1, NES, POSTN, TRIM6 showed higher expression in anagen, followed by catagen and lowest expression in telogen phases. HSP70 and HSP27 were up regulated in anagen and serves as the negative inducers of the catagen phase. On the other hand, key proteins like TGFB1, LGALS7, SFN, PHB, Casp14, MECOM, PRDX5, PRDX6, S100A2 and those associated with apoptosis and cell cycle arrest showed higher expression in catagen. Our study revealed the kinetics of proteins that expressed at various stages of fibre development and shedding.

Keywords: Deep Proteome, Pashmina, Hair cycle

P2-51

APPLICATION OF CRISPR-CAS9 TECHNOLOGY IN ANIMAL PRODUCTION

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ABSTRACT

The growing global population is increasing the demand for animal protein, requiring innovative approaches in livestock production. CRISPR-Cas9, a genome editing tool derived from bacterial adaptive immunity, provides precise, efficient, and cost-effective means to improve animal health, welfare, and productivity. Guided by a single RNA molecule, Cas9 induces double-strand breaks at specific genomic loci, repaired via non-homologous end joining or homology-directed repair, enabling targeted gene disruption or insertion. Compared to Zinc Finger Nucleases and TALENs, CRISPR-Cas9 is simpler, programmable, and widely adaptable for both in vitro and in vivo applications.In livestock, CRISPR-Cas9 has produced disease-resistant animals, including pigs resistant to PRRSV and TGEV, cattle resistant to tuberculosis, and chickens resistant to Marek's disease and avian leukosis virus. It enhances production traits such as muscle growth via MSTN knockout, sex-determination in calves, and hypoallergenic milk and eggs, and corrects deleterious genetic mutations. The technology also enables surrogate sire strategies for rapid propagation of superior genetics. Beyond agriculture, CRISPR-Cas9 supports therapeutic applications for monogenic diseases, cancer, and zoonoses, pest control via gene drives, and de-extinction projects to restore biodiversity. CRISPR-Cas9–edited pigs lacking the CD163 gene showed 100% resistance to PRRS virus, preventing losses worth of US $664 million/year in the U.S. swine industry. In MSTN-knockout cattle, mutation efficiency reached up to 99.9%, producing a double-muscled phenotype. CRISPR editing in embryos achieved blastocyst formation rates of 13–26% and mutation rates up to 86% for target genes. CRISPR-Cas9 represents a transformative tool in animal biotechnology, offering precise genome manipulation to enhance livestock production, food quality, disease resistance, and therapeutic innovations, contributing to sustainable animal production and global food security.

Keywords: CRISPR-Cas9, Disease resistance, Genome editing, Livestock production, Production traits, Therapeutics

P2-55

GENOME-WIDE SSRs IDENTIFICATION AND DATABASE DEVELOPMENT IN JAPANESE QUAIL

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ABSTRACT

The Japanese quail (Coturnix coturnix japonica) presents unique challenges for genomic sequencing, that have historically complicated high-quality assembly generation. Recent advances have begun to address some of these limitations. Several higher-quality quail genome assemblies have become available. The Coturnix japonica 2.1 (GCF_001577835.2) assembly represents a significant improvement over earlier versions, with better contiguity metrics and more complete chromosome-level organization. From this genome, a total of 353,593 Simple Sequence Repeats (SSRs) were identified and categorized into perfect (275,457) and compound (78,136) types based on motif continuity. The database creation followed a three-tier architecture, consisting of a client tier, middleware, and database tier. The entire system, including both the user interface and database, has been developed on the OutSystems platform, which provides a low-code environment for building responsive web applications. Perfect SSRs are more prevalent, constituting about 66–85% of the total SSRs per chromosome, while compound SSRs account for 15–34%. Chromosome 1 contains the highest SSR count (80,700), though the relative proportions remain similar to other chromosomes. Replication slippage during DNA replication is the primary mechanism generating SSRs. Perfect SSRs may arise more easily via slippage when no interruptions exist within their motif. Over time, mutations, insertions, or deletions can disrupt these motifs, producing compound SSRs. Gene-rich and regulatory regions tend to conserve perfect SSRs due to selective pressure against disruptive mutations, whereas heterochromatic or high-recombination regions tolerate more sequence variations, increasing the proportion of compound SSRs. Regulatory elements and protein-coding regions favour stable perfect repeats, while high-recombination regions introduce interruptions that form compound SSRs. Whole-genome identification of SSRs in the Japanese quail has yielded a dense, uniformly distributed set of markers that underpin advances in population genetics, linkage and comparative mapping, quantitative trait loci (QTL) discovery, genetic diversity, conservation genetics, and marker-assisted breeding.

Keywords: Quail, simple sequence repeats, genome assembly, genetic diversity

Biological Systems, Reproductive and Adaptive Genomics

P3-01

GENETIC VARIABILITY AND ITS ASSOCIATION WITH REPRODUCTIVE EFFICIENCY TRAITS IN GOATS

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ABSTRACT

Small ruminants, especially goats, are highly valued for their meat, milk and fibre. The introduction of prolific breeds can boost productivity, offer farmers additional income and contribute to food security. This study aimed to examine the polymorphism of eight fragments of different genes related to reproductive efficiency in Rohilkhandi goats using PCR-RFLP and to analyse the association of these variants with various reproductive traits. The gene fragments analysed were FecB, FecXG, FecXI, FecXB, FecXH, GDF9, MSTN and IGF1. Genetic polymorphism was detected in the MSTN and IGF1 gene fragments out of the eight analysed. The reproductive traits evaluated included the age of the doe at 1st kidding, average kidding interval, average litter size, kidding per year, kids per year and weight of doe at 1st kidding etc., with a mean value of 546.98 ± 10.52 days, 316.65 ± 6.21 days, 1.32 ± 0.05, 1.17 ± 0.02, 1.54 ± 0.06 and 16.09 ± 0.15 kg, respectively. The least squares analysis of variance revealed a significant effect of MSTN genotypes ($p<0.05$) on the age and body weight of does at first, second and third kidding, as well as on kidding rate per year. Similarly, IGF1 genotypes showed significant effects ($p<0.05$) on body weight at first three kidding and on litter size at second kidding. Future studies involving larger sample sizes, additional breeds and a broader range of candidate genes will be necessary to obtain more accurate and reliable estimates of these associations.

Keywords: Goats, MSTN, PCR-RFLP, Polymorphism, Prolificacy, Reproductive traits.

P3-02

POLYMORPHISM ANALYSIS OF FECUNDITY GENES (FECB, FECXG, FECXI, FECXB, FECXH) IN ROHILKHANDI GOATS

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ABSTRACT

Goats are important small ruminants that contribute significantly to meat, milk, and fibre production. Enhancing reproductive efficiency through the use of prolific breeds can improve productivity, strengthen farmer livelihoods, and support food security. The present study examined polymorphisms in five fecundity-related genes—FecB, FecXG, FecXI, FecXB, and FecXH—in Rohilkhandi goats using the PCR-RFLP approach. Reproductive traits assessed included age at first kidding, kidding interval, litter size, kidding per year, kids per year, and body weight at first kidding, with mean values of 546.98 ± 10.52 days, 316.65 ± 6.21 days, 1.32 ± 0.05, 1.17 ± 0.02, 1.54 ± 0.06, and 16.09 ± 0.15 kg, respectively. No genetic polymorphism was detected in the analysed Fec gene fragments, indicating limited variability within this population. These findings provide baseline information on the genetic status of prolificacy-related loci in Rohilkhandi goats and emphasize the need for studies with larger populations, diverse breeds, and additional candidate genes to better evaluate their potential role in improving reproductive performance through molecular breeding.

Keywords: Rohilkhandi goats; Fec genes; reproductive traits; PCR-RFLP; prolificacy; genetic polymorphism

P3-03

AN INTEGRATIVE APPROACH COMBINING SELECTION SIGNATURES AND GWAS IDENTIFIES KEY GENES FOR ADAPTATION AND PRODUCTION IN RED SINDHI CATTLE

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ABSTRACT

The Red Sindhi cattle, one of India's leading dairy breeds, are highly valued for their superior milk production and adaptability to tropical climates. This study examined genetic diversity, selection signatures, and genome-wide association studies (GWAS) in Red Sindhi cattle using ddRAD sequencing data from 96 individuals. The results showed an average minor allele frequency of 0.149 ± 0.128, nucleotide diversity of 0.215 ± 0.114, and a polymorphic SNP proportion of 0.956. The effective population size decreased from 2387 to 264 over 13 generations, with the most recent at 125.9. We identified 490 genomic regions containing 1,282 genes under selective sweeps using Tajima's D, CLR, |iHS|, and ROH methods, overlapping with 574 quantitative trait loci (QTLs). Key genes such as MND1, RHOU, TRIM2, SRGAP2, FAM72A, RHEX, and AVPR1B showed strong positive selection, affecting reproduction, production, immune response, adaptation, and behavior. A notable sweep on chromosome 14 was linked to milk production traits. GWAS based on principal component scores identified important regions on BTA20 (55.88–56.38 Mb) and BTA21 (68.01–69.08 Mb) associated with reproductive and adaptation traits in Red Sindhi cattle. These regions, also found in selection signature analyses, include genes involved in crucial processes such as protein ubiquitination (BAG5), regulation of apoptosis (PPP1R13B), DNA repair (XRCC3), and mitochondrial ATP synthesis (ATP5MJ). Several MHC class II genes under selection pressure indicate strong immune competence, while stress-response genes support the Red Sindhi's remarkable heat tolerance.

Keywords: Cattle, ddRADseq, Evolution, GWAS, Red Sindhi, Selection signatures

P3-04

PRELIMINARY EVALUATION OF OVA PICK UP AND IN VITRO FERTILIZATION FOR EMBRYO PRODUCTION IN INDIGENOUS CATTLE BREEDS

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ABSTRACT

Reproductive biotechnologies such as artificial insemination (AI), multiple ovulation and embryo transfer (MOET), and in vitro fertilization (IVF) have shown tremendous potential to accelerate genetic improvement in livestock. Among these, IVF programs offer the highest scope for rapid genetic gain by reducing generation intervals. In developed countries such as the USA, Canada, and Brazil, IVF technology is already commercialized and widely applied. However, research on optimizing these techniques for indigenous cattle breeds remains limited. This preliminary study aimed to assess the efficiency of ova pick up (OPU) and IVF technology for embryo production in indigenous cattle breeds, including Gir, Sahiwal, Red Kandhari, Dangi, Deoni, and Gaolao. Donor animals were selected based on milk production and breed characteristics, maintained under farm conditions, and subjected to OPU using an intravaginal probe with a 20 G needle. Oocytes were collected in OPU medium, graded morphologically, matured in vitro, fertilized with quality semen of respective breeds, and cultured for seven days post-fertilization. A total of 1138 OPU sessions were conducted, yielding 8755 oocytes with an average recovery rate of 7.69 ± 0.40 oocytes per session (range: 1.0 ± 0.50 to 6.53 ± 0.93). The average blastocyst rate observed was 31.68 ± 2.38%. Breed-wise variations were noted in both oocyte recovery and blastocyst development rates. These findings highlight the potential of OPU-IVF as a promising reproductive technology for genetic improvement in indigenous cattle. Further optimization is required to enhance efficiency and establish standardized protocols suitable for local conditions.

Keywords: Ova Pick Up, IVF Technology, Indigenous Breeds, Embryo Production, Genetic Improvement

P3-05

A NOVEL HSP70 GENETIC VARIANT AND HEAT STRESS INDICATORS IDENTIFIED IN DEONI CATTLE (BOS INDICUS) USING THERMOGRAPHIC AND GENE EXPRESSION STUDIES

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ABSTRACT

This investigation was carried out on Deoni cattle, a dual-purpose indigenous breed in western India, evaluating their thermal comfort using infrared thermal imaging (IRTI) and genetic markers. A total of 15,500 thermal images from 950 animals across three phenotypic strains were analyzed. Thermal stress is crucial for assessing animal health, particularly in hot semi-arid climates. IRTI was used to measure surface temperatures at various body parts such as the muzzle, eye, ear, neck, dewlap, hump, thorax, and udder. The hump region showed stable temperatures (evening: 34.08±0.03°C; morning: 33.1±0.12°C), indicating its role in thermal regulation. A correlation of 0.41 was found between the hump temperature and the Temperature Humidity Index (THI). Body areas like the ear, eye, muzzle, and dewlap showed strong correlation (r = 0.7) with overall body temperature in the evening. Physiological parameters recorded were heart rate (53.5/min), respiration rate (20.4/min), and rectal temperature (36.93°C). Genetic analysis of the HSP70 gene revealed a single nucleotide polymorphism (A→G) resulting in an amino acid change. Although different genotypes showed slight differences in physiological responses, these were not statistically significant. A negative correlation was found between HSP70 gene expression and body temperature, suggesting its potential role in thermal stress response.

Key words: Deoni cattle, HSP70 gene, Infrared Thermal Imaging, Rectal Temperature

P3-06

REAL-TIME MONITORING OF BODY TEMPERATURE OF CATTLE USING NON-INVASIVE, SELF-POWERED, SENSOR BASED IOT DEVICE

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ABSTRACT

The primary objective of this study was to test the efficiency of IoT based instrument in monitoring real-time body temperature of cattle. The research work was carried out at Namkhana Block under South 24 Parganas district of West Bengal, India, which is located at an altitude of 4 meter (13ft) above sea level on 21.7699° N latitude and 88.2315°E longitude. The actual experiment was conducted during a period of three months, from1st September, 2020 to 30th November 2020. Ten lactating crossbred cattle were considered for this study. Three different temperature recording devices were used for this study viz., IoT (Internet of Things) based device, IR (Infrared) thermometer and clinical digital thermometer. Three experiments were conducted in crossbred cattle to validate body temperature recording from IoT device against the temperature recordings from IR thermometer and clinical thermometer. The cattle were exposed to three different managemental conditions like rest, feeding and exercise separately. The results of the first, second and third experiments provided a non-significant difference ($P>0.01$) between the body temperatures recorded by the IoT device and IR thermometer. Similarly, clinical thermometer showed significant difference ($P<0.01$) with IoT device and IR thermometer in rest, feeding and exercise condition. Secondly, IoT, IR and clinical thermometer captured the similar kind of increasing trend of body temperatures due to the effect of feeding and exercise in crossbred cattle. In conclusion, it can be said that the non-invasive, self-powered and sensor based IoT (Internet of Things) device emerged as an effective instrument for recording and monitoring real-time body temperature of crossbred cattle.

Keywords: IoT, IR (Infrared) thermometer, non-invasive, Sensor based

P3-07

BREED-SPECIFIC TRANSCRIPTOMIC SIGNATURES ASSOCIATED WITH ADAPTATION TO CHRONIC THERMAL STRESS IN INDIGENOUS AND CROSSBRED CATTLE

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ABSTRACT

Climate change and increasing environmental fluctuations have imposed significant thermal stress on livestock, directly affecting their health, productivity, and adaptability. Understanding breed-specific transcriptomic responses to thermal extremes is crucial for improving thermotolerance and sustainability in cattle production systems. This study presents a comprehensive transcriptomic analysis using RNA sequencing (RNA-Seq) to compare gene expression profiles between crossbred Karan Fries (KF) and indigenous cattle breeds (Sahiwal and Tharparkar) under conditions of chronic heat and cold stress. Blood samples were collected from heifers during spring, summer and winter seasons at the Livestock Research Centre, ICAR-NDRI, Karnal. PBMCs were isolated, and total RNA was extracted to construct cDNA libraries, followed by paired-end sequencing using the Illumina NovaSeq 6000 platform. Gene expression quantification and differential expression analysis were conducted, identifying p-value < 0.05. In winter, 74 genes were upregulated and 199 downregulated in KF compared to indigenous breeds, while in summer, 100 genes were upregulated and 128 downregulated. Further, analysis of unique and common differentially expressed genes among the three breeds relative to spring season identified 94 commonly upregulated and 1,055 commonly downregulated genes, in heat stress highlighting shared molecular responses to thermal stress across genetic backgrounds. Functional enrichment analysis using DAVID revealed upregulation of immune response and chemical stimulus pathways in KF during summer and winter, respectively. In contrast, indigenous breeds exhibited upregulation of antigen processing and presentation pathways in summer, and neural development-related pathways in winter. Protein–protein interaction network analysis using the STRING database identified key hub genes in in indigenous breeds including CXCL8, OLR1, and EGR1 (upregulated in summer), and, IFIT3, SOCS3, and DUSP1 (upregulated in winter). Overall, the findings highlight distinct transcriptomic signatures underlying breed-specific adaptation to chronic thermal stress.

Keywords: Transcriptome, heat stress, adaptation, breed specific

P3-08

RELATIVE EXPRESSION OF TH2 CYTOKINE GENES IN HAEMONCHUS CONTORTUS INFECTION: COMPARISON BETWEEN RESISTANT AND SUSCEPTIBLE GAROLE SHEEP

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ABSTRACT

Garole sheep of Sundarban delta of West Bengal has exhibited within breed resistance to gastrointestinal nematode infection as well as Haemonchus contortus. Resistant animals are generally identified phenotypically based on faecal egg count (FEC) and exploration of host's genetic resistance is an essential prerequisite for selective breeding programme. Resistant (n = 9) and susceptible (n = 9) Garole sheep selected on the basis of FEC record for one year were divided into three groups; infected resistant (n = 6), infected susceptible (n = 6) and healthy control (n = 6). Sheep of both the infected groups were orally challenged with H. contortus infective larvae and then FEC, PCV and relative expression of some Th2 cytokine (IL-4, IL-5, IL-6, IL-8, IL-10, IL-13) genes were measured from 0 days post infection (DPI) to 40 DPI at 10 days interval. Faecal egg count was significantly ($P<0.01$) lower in resistant sheep compared to susceptible sheep and spontaneous expulsion of H. contortus was observed from 30 DPI in resistant sheep. In resistant sheep PCV% was significantly ($P<0.05$) higher from 10 DPI than the susceptible sheep without any significant difference between the resistant and susceptible sheep. The relative expression of IL-4, IL-5, IL-8 and IL-13 genes increased significantly ($P<0.05$) from 10 DPI in resistant sheep compared to susceptible sheep. In resistant Garole sheep, the expression of IL-6, IL-10 and IL-25 genes upregulated significantly ($P<0.05$) on 30 and 40 DPI, on 20 DPI and from 20 to 40 DPI compared to susceptible sheep. The relative expression of different Th2 cytokine genes might have caused increased release of those cytokines in situ and thus might be responsible for active immunological response in resistant sheep resulting into elimination H. contortus from abomasum of infected sheep.

Keywords: Host resistance, Garole sheep, Haemonchus contortus, Th2 cytokine genes

P3-09

COMPREHENSIVE GUIDE TO GENES ASSOCIATED WITH NDV RESISTANCE IN POULTRY

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ABSTRACT

Newcastle Disease (ND) poses a severe global threat to poultry production, with conventional control methods like vaccination often failing to prevent viral shedding. This narrative review synthesizes decades of research establishing a robust genetic basis for inherent resistance to the Newcastle Disease Virus (NDV) in chickens, presenting it as a sustainable complementary strategy. Early studies, though sometimes confounded by factors like passive immunity, provided foundational evidence of breed-specific variations in susceptibility, from the initial work of Iyer and Dobson to the pivotal selection experiments by Cole and Hutt. These historical efforts confirmed that resistance is a polygenic trait, with modern estimates showing heritability for antibody response to vaccination can be as high as 0.60, underscoring its potential for genetic improvement. The genetic resistance to Newcastle Disease Virus (NDV) in poultry is a complex polygenic trait governed by a coordinated network of genes, beginning with innate immune sensors like TLR3, TLR7, and MDA5 that detect viral RNA and initiate a signaling cascade. This cascade involves key transcription factors such as IRF3 and IRF7, which drive the production of antiviral type I interferons (IFN-α/β) and subsequently stimulate the expression of powerful effector proteins like the Mx gene, which directly inhibits viral replication, and the OAS/OASL system, which activates RNAse L to degrade viral RNA. Furthermore, chemokines like CCL4 recruit immune cells to the infection site, while the eIF2 signaling pathway influences the host's cellular machinery to potentially restrict viral protein synthesis. Crucially, the Major Histocompatibility Complex (MHC), particularly haplotypes like B21 and B13, plays a pivotal role in antigen presentation and shaping a robust adaptive immune response, with genomic studies also identifying other significant players like ROBO1/2, TIRAP, and ETS1, collectively providing a comprehensive genetic roadmap for breeding NDV-resistant poultry through marker-assisted selection.

Keywords: Newcastle Disease, Genetic Resistance, Poultry, Heritability, Candidate Genes, QTL, Major Histocompatibility Complex, Genomic Selection, Breeding Programs

P3-10

GENOMIC BASIS OF HOST RESPONSE AGAINST NEWCASTLE DISEASE VIRUS IN ASEEL CHICKEN EMBRYO LUNGS

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ABSTRACT

In India, Ranikhet disease is the most prevalent and a challenging viral disease of chicken, and it caused by Newcastle Disease Virus (NDV), also known as Avian Paramyxovirus-1. Different chicken breeds exhibit varying responses to NDV infection, shows that breed specific host response, offer promising strategy to mitigate the limitations imposed by this disease. In this study, transcriptional profiling was compared between infected and healthy Aseel chicken embryo with an aim to assess the genetic basis of the host response to NDV. A total of 6 Aseel chicken 19th day old embryos were used for a viral challenge study, in that 3 Aseel embryos served as controls, while another three was inoculated with a lentogenic B1 strain of live NDV at a dosage of 50 percent embryo infective dose (106 EID50). Following inoculation, the embryos were incubated for 24 hours post infection then lung tissues were harvested. The mRNA was extracted from lung tissues and sequenced using Illumina sequencer. Our results revealed that NDV infection resulted in differential expression of 135 genes (DEGs) with p-values < 0.05. Significantly upregulated (logfc ≧2) 69 genes including APOA2, FGB, AHSG, HSPB9, HSP30C-like, HPD, APOB, TMEM158, PLG, and AvBD9, linked to immune signalling, inflammatory, and stress response. While downregulated genes 66 (logfc ≦2) genes such as KCNH5, CA13, SMAD7B, PCDH11X, CXCL14, GINS1, HBBH, EPB42, SLC41A3, CIMIP1 are involved in pro-inflammatory cytokine signaling, immune activation, and apoptotic pathways. Subsequent result revealed that NDV infection caused significant changes in four genes GO terms and 19 KEGG pathways. These findings underscore the altered molecular mechanisms caused by NDV infection during early developmental stages. This understanding underlines the virus's effect on host metabolism and immunological responses, which may help to control disease infection and improve poultry welfare and wellbeing through disease resistant breed genomic selection.

Keywords: Aseel, NDV Infection, Disease, Resilience, Transcriptomics

P3-11

MULTI-OMICS ANALYSIS FOR DELINEATING HOST IMMUNE RESPONSE GENES FOR SUB-CLINICAL MASTITIS IN MURRAH BUFFALOES

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ABSTRACT

Buffaloes (Bubalus bubalis) contribute nearly 45% of India's milk production, yet subclinical mastitis (SCM) remains a silent but major challenge, reducing yield, causing economic losses, and with its milk microbiota-immune response interactions still poorly understood. In this study, we conducted an integrated analysis of the milk microbiome and host mammary epithelial cell transcriptome to elucidate host-microbe interactions in Murrah buffaloes. Comparative transcriptome profiling revealed 4,046 significantly downregulated and 103 upregulated genes in SCM compared to healthy controls. Metagenomic analysis of milk samples identified 35 differentially abundant genera, highlighting microbial shifts associated with disease progression. Using Weighted Gene Co-Expression Network Analysis (WGCNA), we identified five gene modules, two of which were significantly correlated with the microbial taxa linked to mastitis. One module was enriched for immune-related pathways, reflecting immune dysregulation during SCM. From these modules, the top 10 hub genes were identified, with JPH4 selected as a key hub gene. Functional annotation suggested that JPH4 is involved in calcium ion transport, cell-cell signaling, and regulation of cytokine production, all of which are critical processes in mammary gland immunity. qPCR validation further confirmed that JPH4 (Junctophilin-4) was significantly downregulated in SCM samples, supporting its potential role as a candidate gene for disease susceptibility. Overall, this study provides novel insights into the host-microbiome interplay in Murrah buffalo subclinical mastitis, identifying immune-related pathways and hub genes associated with microbial taxa. Importantly, JPH4 emerges as a potential candidate gene for further investigation, with implications for developing molecular markers for disease resistance and selective breeding strategies in buffaloes. Using such marker-assisted selection (MAS) in breeding programs would reduce the need for antibiotics, lower treatment costs, and minimize milk loss due to disease.

Keywords: Subclinical Mastitis, Murrah Buffalo, Host-Microbiome Interaction, WGCNA, JPH4

P3-12

BOVINE MICRORNA SNIPPETS TARGETING PE/PPE GENE FAMILY IN *MYCOBACTERIUM TUBERCULOSIS* COMPLEX: CONSIDERING THE RNAI TO TURN OFF 'MOLECULAR SWITCH' OF VIRULENCE

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ABSTRACT

Bovine tuberculosis (bTB) is a chronic infectious disease of cattle caused mainly by several members of the Mycobacterium tuberculosis complex (MTBC). According to most recent report 44% of countries accounted occurrences of bTB, with about 50 million cattle estimated to be affected worldwide. In India TB prevalence among cattle and buffaloes is around 7.3% (95% CI: 5.6%, 9.5%), translating to an estimated 21.8 million infected cattle. The PE/PPE [Pro-Pro-Glu (PPE) motif] gene family in Mycobacterium is one of the largest and most distinctive groups of genes in the MTBC. Members of this gene family contribute to immune evasion by the pathogen, virulence and immunomodulation in host. Bovine microRNAs (miRNAs) are strongly implicated as regulators of gene expression and have been associated with a number of infectious and non-infectious diseases and intricate mechanism of host-pathogen interactions. In this study, we used the TargetScan bioinformatics tool, to predict the target of bovine miRNAs in MTBC PPE genes contributing to virulence. For cross-checking, we utilized additional prediction algorithms targeting relevant PPE genes. PPE family genes in MTBC were targeted by several bovine miRNAs. Significant targets were identified by GO terminologies and KEGG pathway-enrichment analysis (Log10 p-value >0.0001). We further validated the expression of selected miRNAs in bovine lung with tuberculous lesion. Insight into the biological role of bovine miRNAs in host-pathogen crosstalk will help to understand the regulatory patterns of these miRNAs. It is also noted that these miRNAs have deep impact on the immune response to tuberculosis infection. The research can help create novel host-derived diagnostic markers for accurate identification of bTB infected animals in the herd. Also, mimics of these miRNAs may have potential to be used as therapeutic to combat this zoonotic infection.

Keywords: bovine; tuberculosis, microRNA, bioinformatics

P3-13

EVALUATING THE THERAPEUTIC POTENTIAL OF QUERCETIN ON 4T1 INDUCED TUMORS IN MICE

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ABSTRACT

Breast cancer is a leading cause of cancer-related mortality worldwide, with triple-negative breast cancer (TNBC) presenting significant therapeutic challenges due to its aggressive subtype of breast cancer with limited treatment options and high metastatic potential. Conventional drugs like doxorubicin (DOX) are effective but cause severe side effects, including cardiotoxicity and chemoresistance. Natural compounds such as quercetin, a flavonoid with anticancer, antioxidant, and anti-inflammatory properties, have gained attention as potential alternatives or complementary therapies. This study evaluates therapeutic potential of quercetin in a 4T1 murine TNBC model. BALB/c mice were treated with quercetin, and outcomes such as tumor growth, survival, immune response, and organ health were assessed. Quercetin significantly reduced tumor volume, improved survival, and promoted apoptosis via the mitochondrial pathway, marked by increased Bax/Bcl-2 ratio, caspase-3 activation, and ROS modulation. It also protected against DOX-induced cardiac damage and muscle loss. Immunological analysis revealed quercetin improved markers like neutrophil-lymphocyte ratio (NLR) and total leukocyte count (TLC), suggesting enhanced anti-tumor immunity. Histopathology confirmed reduced tumor progression and protection of vital organs from TNBC-related damage. These findings suggest that quercetin holds significant promise as an adjuvant therapy for TNBC, offering a dual benefit of tumor suppression and systemic protection against chemotherapy-induced side effects. Further research is warranted to explore its potential for clinical applications, particularly in combination therapies for breast cancer treatment.

Keywords: Quercetin, TNBC, Mammary tumor, Apoptosis

P3-14

EFFECTS OF DIETARY BILE ACID ON THE EXPRESSION OF LIPID METABOLISM-RELATED GENES IN BROILER CHICKENS

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ABSTRACT

The present study was conducted to evaluate the effects of dietary bile acids (BAs) on the expression of lipid metabolism-related genes in broiler chickens. One hundred ninety-two (n=192) day-old mixed sex broiler chicks were randomly distributed into 3 experimental groups for a 35d feeding trial. Birds were fed a basal diet supplemented with 0 (control), 100 (BA 100) and 200 (BA 200) mg BAs/kg feed. The analysis of gene expression for sterol regulatory element-binding protein (Srebp1), adipose triglyceride lipase (Atgl), acetyl-CoA carboxylase (Acc), and fatty acid synthase (Fas) indicated notable differences in their regulation, implying varying effects of BA treatment on lipid metabolism. SREBP1, a crucial transcription factor in fatty acid synthesis, displayed a marked increase in BA 100 relative to the control group, but its expression decreased in BA 200. This trend implies that BA 100 promotes lipogenic activity, whereas BA 200 may impose regulatory limitations, possibly through negative feedback mechanisms. A similar trend was noted in Acc expression, which showed an increase with BA100 compared to the control, yet BA 200 caused a downregulation. ATGL maintained relatively stable expression across all conditions, with a minor rise in BA 100 in comparison to the control and BA 200. FAS showed moderate increases in both BA100 and BA 200 when compared to the control group, illustrating persistent lipogenic activity under the influence of BA. In summary, the overall expression trends of these genes indicate that while BA 100 boosts lipid biosynthesis, BA 200 may impose metabolic limitations that prevent excessive lipid buildup, likely via feedback inhibition mechanisms.

Key words: Bile acids, lipid metabolism, gene expression, broiler chickens

P3-15

EFFECT OF CURCUMA LONGA AND OCIMUM SANCTUM LINN. IN THE SEQUENTIAL PATHOLOGY OF INDUCED COLORECTAL CANCER IN MICE

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ABSTRACT

This study investigated the effects of Curcuma longa and Ocimum sanctum on Azoxymethane (AOM) and Dextran Sodium Sulphate (DSS)-induced colorectal cancer (CRC) in BALB/c mice. The study aimed to establish a rapid CRC induction model and assess the potential of these phytomolecules to modulate its pathology. Mice were randomly divided into four groups: negative control, positive control (AOM/DSS), Curcuma longa-treated, and Ocimum sanctum-treated. CRC was induced via intraperitoneal injection of AOM followed by oral administration of 1% DSS. Curcuma longa (30mg/kg) and Ocimum sanctum (50mg/kg) were administered orally. Cytological, histopathological, and immunohistochemical analyses were performed. Results showed successful CRC induction in the positive control group, characterized by cellular dysplasia, increased N:C ratio, disarranged cohesiveness, basophilia, and increased expression of Ki-67 and beta-catenin. Curcuma longa and Ocimum sanctum treatment groups exhibited decreased tumorogenesis characteristics compared to the positive control, evidenced by reduced cytological and histopathological alterations and diminished expression of Ki-67 and beta-catenin. This study demonstrates the successful establishment of a rapid CRC induction model in mice and suggests that both Curcuma longa and Ocimum sanctum possess significant anticancer activity against CRC.

Keywords: Curcuma longa, Mice, Ocimum sanctum, CRC, DSS, Pathology

P3-16

ROLE OF CURCUMINOID AND SESAMOID OIL IN COLON CANCER DEVELOPMENT AND PROGRESSION

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ABSTRACT

The words "colon" and "rectum" are combined to form the phrase "colorectal". The colon refers to the last six to eight feet of the intestine (also known as the large intestine) and the rectum refers to the final few inches of the large intestine. Healthy cells in the lining of the colon or rectum alter and grow uncontrollably to create a mass known as a tumor, which is how colorectal cancer develops. A tumor may be benign or malignant. Malignant refers to the ability of a cancerous tumor to develop and metastasize to other bodily regions. The study′s goal was to develop colorectal cancer in balb/c mice over a period of 70 days by using Azoxymethane (AOM) and Dextran sodium sulfate (DSS), as well as judging epithelial transformation of malignant cells and its pathology. The hypothesis for the development and modulation of its pathology by the application of Curcuma longa, Sesamum indicum, was met as a result of the experiment. Hematology, Serum Biochemistry, Cytology and Histopathology all revealed that the positive group had CRC generation. The cellular dysplasia, increased N:C ratio, and disarranged cohesiveness with basophilia could be observed in the cytological smear and histopathological section. Analysis of scores of different groups showed that the scores of the treatment groups were significantly lower than the positive control group. It’s suggested that the set of phytomolecules have efficacy against CRC.

Keywords: Colorectal cancer, Azoxymethane, Dextran Sodium Sulphate, Curcumalonga, Sesamum indicum, Cytology, Histopathology

P3-17

MICROBIOME PROFILING OF MASTITIC MURRAH BUFFALO MILK WITH A FOCUS ON ACINETOBACTER SPECIES

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ABSTRACT

Mastitis, an inflammatory disorder of the mammary gland, has been a major challenge in the dairy industry, incurring heavy losses to dairy farmers. Although targeted antibiotic regimes are successful for culturable microbes, the non-culturable and novel microbes are often overlooked. This limitation underscores the need for culture-independent techniques to explore the microbial composition and functional potential within the milk microbiome. Hence, the present study employed a whole-metagenome profiling to investigate and compare the microbial diversity among the milk samples of healthy and affected buffaloes. 16 Milk samples were collected from Murrah buffaloes and classified into three groups based on the California Mastitis Test score, i.e., Clinical (3), Sub-clinical (6), and Healthy (7). DNA extraction from milk was followed by Whole Metagenome Shotgun (WGS) sequencing to study microbial diversity. The genus Acinetobacter was most abundant in clinical cases (76%) and least in healthy animals (33%). Acinetobacter johnsonii was significantly associated (FDR = 0.0389) with clinical cases, which was nearly half of the Acinetobacter community. A greater Acinetobacter species richness was observed in SCM cases, which include A. baumannii (1.6%), A. haemolyticus (0.7%), A. indicus (0.6%) and many more. Conversely, Deinococcus was significantly abundant in healthy cases, highlighting its potential as a marker for healthy mammary microbiota. A total of 14,887 genes were assigned to Gene Ontology terms. KEGG analysis revealed enrichment in amino acid, carbohydrate, lipid, and energy metabolism pathways. Genes involved in peptidoglycan biosynthesis, such as murA, mraY, ftsI, murE, murF, and glmU, were enriched in mastitis samples dominated by Acinetobacter, indicating enhanced bacterial cell wall remodeling during infection. These findings could aid in reducing antibiotic resistance and treatment costs.

Keywords: Acinetobacter, Mastitis, Microbiome, Murrah, Whole metagenome

P3-18

INTERLEUKIN-6 AND BRAIN-DERIVED NEUROTROPHIC FACTOR GENOTYPES ARE POTENTIAL BIOMARKERS FOR EARLY RISK IDENTIFICATION OF ALZHEIMER’S DISEASE

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ABSTRACT

Alzheimer’s Disease (AD) is a progressive neurodegenerative disorder and the leading cause of dementia worldwide. Its multifactorial etiology involves complex genetic, biochemical, and environmental interactions. This study investigates the potential influence of Interleukin-6 (IL6) (-174G>C in the promoter region) rs1800797 and Brain-Derived Neurotrophic Factor (BDNF) (G196A; Val66Met) rs6265 polymorphisms on the pathogenesis of AD in an Eastern Indian population. A cross-sectional, hospital-based analytical study was conducted among 100 clinically diagnosed AD patients from a tertiary healthcare center in Eastern India (Bangur Institute of Neurosciences, Annex-1, IPGME&R). Comprehensive clinical, biochemical, and genotypic analyses were performed to explore associations between IL6 and BDNF variants with demographic and neuropsychological parameters. The BDNF Val/Val (GG) genotype was most prevalent (49%), followed by Val/Met (GA) at 37% and Met/Met (AA) at 14%. A significant correlation was observed between the Met/Met genotype and familial history of AD, suggesting a potential hereditary predisposition. Similarly, IL6 GG genotype, linked with elevated pro-inflammatory cytokine levels, was identified in 55% of cases, aligning with the inflammatory hypothesis of AD pathogenesis. Biochemical assessments revealed frequent Vitamin B12 deficiency and altered glucose profiles, both contributing to neuroinflammatory and metabolic stress. Neuropsychological evaluations demonstrated lower cognitive scores among patients carrying BDNF Met/Met and IL6 GG genotypes, indicating a gene–cognition association. The findings support the integrative role of genetic polymorphisms and biochemical factors in influencing AD susceptibility and progression. Despite the study’s limited sample size, the results highlight IL6 and BDNF genotypes as potential biomarkers for early risk identification and personalized intervention strategies in AD management. Future longitudinal studies are warranted to validate these associations and explore therapeutic applications targeting neurotrophic and inflammatory pathways.

Keywords: Alzheimer’s Disease, BDNF Val66Met, IL6 -174G>C, Neuroinflammation, Genetic Polymorphism

P3-19

SURVEY OF TICK SPECIES PARASITISING DOMESTIC GOATS IN FIVE DISTRICTS OF WEST BENGAL, INDIA

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ABSTRACT

Ticks are the most important ectoparasites that affect small ruminants. Ticks are also responsible for the transmission of various tick-borne diseases. Additionally, they can damage animal skin, cause anaemia, and induce tick paralysis. A research study was conducted to investigate and identify ticks infesting goats across five districts in West Bengal, India. Ticks were collected from the goat population in these districts. The predilection site of ticks was found to be that of goats′ ears. The two tick species collected were initially identified through morphological analysis using a stereomicroscope as Haemaphysalis bispinosa and Hyalomma kumari. Then the mitochondrial 16S rRNA sequences of these ticks were amplified using gene-specific primers in a PCR assay. The amplified 16S rRNA sequences of Ha. bispinosa and Hy. kumari ticks measured 456 bp and 457 bp, respectively. These fragments were sequenced and aligned with other sequences obtained by NCBI BLAST, which further validated the morphological analysis results, as the sequences perfectly matched the Ha. bispinosa and Ha. kumari gene sequences. Phylogenetic analysis of the gene sequences was conducted using MEGA XI. A logistic regression analysis was also performed on the collected data using Jamovi 2.5.3 to assess the impact of age (male and female), sex (male and female), and season (summer, rainy, and winter) on the prevalence of tick infestation in goats. The regression model yielded Deviance, AIC, and R^2McF values of 421, 431, and 0.0930, respectively. The predictive measures demonstrated accuracy and AUC values of 0.884 and 0.724, respectively. The R^2McF value and ROC suggest that the model possesses a certain degree of predictive capability regarding goat tick infestation. Chi-square test was also performed to see the effects of differences in sex, age and season. Both logistic regression and chi-square test revealed that the infestation was significantly influenced by differences in age and season only.

Keywords: Goat, logistic regression, mitochondrial 16S rRNA gene, phylogenetic analysis.

P3-20

CHARACTERIZATION AND DIFFERENTIATION OF MAJOR BACTERIAL PATHOGENS IN DUCKS IN WEST BENGAL

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ABSTRACT

Duck farming (Anas platyrhynchos domesticus) is gaining popularity in the coastal and northeastern regions of India. India holds the second-largest duck population globally, after China, with 23.54 million ducks as per the 19th Livestock Census (2012). Ducks are primarily reared in states like West Bengal, Assam, Tamil Nadu, and Kerala as a supplementary source of income and protein. Their hardiness, foraging ability, and disease resistance make them suitable for backyard farming by marginal farmers and self-help groups. Despite the potential, bacterial diseases pose a major challenge to duck productivity. Pathogens like Salmonella spp., Escherichia coli, and Riemerella anatipestifer are responsible for significant economic losses due to high morbidity and mortality, reduced growth, poor feed conversion, increased treatment costs, and decreased egg production. Salmonella causes acute and chronic infections, while E. coli affects both humans and animals worldwide. R. anatipestifer, once classified under Pasteurella, causes acute septicemia in young ducks and chronic lesions in adults. Clinical signs of these infections often overlap, leading to diagnostic confusion. This study aims to isolate and identify these bacterial pathogens from ducks in high-density duck-rearing districts of West Bengal. Prevalent serogroups of Salmonella spp. and E. coli will be determined. Major isolates will be characterized by PCR targeting virulence genes and their genetic relatedness assessed using RAPD-PCR. Pathogenicity will be evaluated by experimental infection in young ducks, both singly and in combination. Clinical samples (cloacal and nasal swabs) will be collected on the 5th day post-infection, and vital organs after death will undergo gross and histopathological examination. The findings will help in differential diagnosis, effective treatment, and control strategies, ultimately safeguarding duck health and improving the livelihood of rural farmers in disease-prone areas.

Keywords: Duck, Salmonella sp., Escherichia coli, Riemerella anatipesfer, PCR, RAPD-PCR, West Bengal

P3-21

IN-SILICO INSIGHTS OF ESBL VARIANTS AND TRACKING THE PROBABLE SOURCES OF ESBL-PRODUCING ESCHERICHIA COLI IN A SMALL-SCALE POULTRY FARM IN WEST BENGAL

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ABSTRACT

Poultry farms with compromised biosecurity face challenges of microbial infections, having negative impact on egg and meat production as well as public health. Microbial infections may be transmitted from poultry products to the human food chain including the antimicrobial resistant bacteria such as extended spectrum beta-lactamase (ESBL)-producing Escherichia coli. The study aimed to elucidate the transmission pathways of ESBL-E. coli in such settings, employing phylogenetic analysis and molecular docking simulations to explore the catalytic properties of β-lactamase variants. Sampling was conducted on a small-scale poultry farm in West Bengal, collecting 120 samples at three intervals during the broiler production cycle. E. coli isolates underwent resistance testing against eight antimicrobials, with confirmation of ESBL production. Genotypic analysis of ESBL genes and sequencing were performed, alongside molecular docking analyses and phylogenetic comparisons with publicly available sequences. Among 173 E. coli isolates, varying resistance profiles were observed, with complete resistance to cefixime and high resistance to amoxicillin and tetracycline. In the day-old sampling, 50.9 % (28/55) occurrence of ESBL-producing E. coli was detected. On the 20th day of production, there was a notable decline in occurrence. A significant shift occurred on the 40th day of production when the occurrence surged to 53.03 % (35/66) of the isolates. The primary rise in the occurrence of ESBL-producers raises the possibility of vertical transmission from grandparent to the offspring. Whereas occurrence of ESBL producers in the last phase of production cycle indicated about horizontal transmission and drinking water was identified as probable source. Phylogenetic analysis indicated partial clonal relationships with human clinical strains and other poultry strains from the Indian subcontinent. Molecular docking confirmed the catalytic efficiencies of these ESBL variants. Strict biosecurity measures could prevent the spread of antimicrobial-resistant bacteria in birds and their products in a small scale poultry farm.

Keywords: AMR, Biosecurity, ESBL, Poultry

P3-22

DIFFERENCES IN NUCLEOTIDE SEQUENCES OF lmo1030 GENE OF *Listeria monocytogenes* ISOLATES FROM MEAT AND FISH IN WEST BENGAL

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ABSTRACT

Listeria monocytogenes is Gram-positive, facultative anaerobic, foodborne zoonotic organism that affects both animals and human causing listeriosis. In the present study, analysis of lmo1030 gene (LacI family transcriptional regulator) PCR product was performed with isolates from meat and fish samples of retail markets in West Bengal. Purified lmo1030 gene PCR products from five isolates of *L. monocytogenes* were selected for custom sequencing and analysis. The partial sequences of *L. monocytogenes* strains of meat origin (FM6, FM13) and, Fish origin (FS217, FS218, FS219) were submitted to GenBank database with accession no. PP415239- PP415243. The isolates showed 99-100% similarity with the complete genome sequences of different isolates in world including two Indian sequences of human origin retrieved from NCBI GenBank. When compared with *L. monocytogenes* PNUSAL000019 serovar 4b, FM6 (from Quail meat) had six nucleotide mismatches and three changes in translated amino acid (aa) while FM13 (from Quail meat) had two mismatches and one change in aa sequence. FM6 and FM13 formed a different cluster from isolates of fish origin (FS217, FS218, and FS219) in phylogenetic analysis in MEGA 7 software. This study reveals minor variation in lmo1030 Gene of *L. monocytogenes* and highlights the need for monitoring L. monocytogenes strains.

Keywords: *Listeria monocytogenes*, lmo1030 gene, PCR, nucleotide, variation

P3-23

MOLECULAR DETECTION AND CHARACTERIZATION OF LISTERIA MONOCYTOGENES FROM FISH SKIN SAMPLES IN WEST BENGAL

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ABSTRACT

Listeria monocytogenes is a Gram-positive, highly adaptive, facultative anaerobic, ubiquitous foodborne zoonotic organism that affects both animals and humans, causing listeriosis. The present study was carried out to investigate the occurrence, virulence gene profile, biofilm-producing ability, and antimicrobial sensitivity pattern of Listeria monocytogenes strains isolated from fish samples from different districts of West Bengal. A total of 234 samples were collected from fresh fish skin (swab samples), primarily from rohu fish (Labeo rohita), covering two districts: Kolkata and South 24 Parganas in West Bengal. A total of 104 (44.44%) Listeria spp. isolates were obtained by cultural characteristics, biochemical tests, and later confirmed by Listeria genus-specific prs gene PCR (370bp). Among these Listeria positive isolates, 6 (2.56%) isolates were confirmed as L. monocytogenes by species-specific lmo1030 gene PCR (509 bp). PCR detection for the presence of virulence genes revealed all 6 isolates to be positive for hlyA (100%) gene, 5 (83.33%) were positive for iapA gene, 4 (66.67%) were having the plcA gene, and no positivity for the plcB gene. Again, 4 (66.67%) out of 6 isolates produced biofilm phenotypically (1 moderate and 3 weak biofilm producers) after 72 hours of incubation at 37^{0}. Molecular detection of the biofilm-associated genes, viz. luxS and flaA, revealed all the fish isolates to be positive for both genes. In-vitro antimicrobial sensitivity test of these 6 isolates showed 100% resistance to cefixime, followed by ceftriaxone/ tazobactam (83.33%), streptomycin, doxycycline, amoxicillin, and oxytetracycline (all 66.67%), and nitrofurazone (50%). The isolates were most sensitive to gentamicin (83.33%), followed by chloramphenicol, ciprofloxacin, enrofloxacin, and levofloxacin (all 67%). This study revealed a significant threat to public health, which requires regular monitoring and an appropriate disease control policy under the One Health concept.

Keywords: Listeria monocytogenes, Fish, Biofilm, Virulence, Antibiogram, West Bengal

P3-24

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF PREVALENT TICK SPECIES IN THE CATTLE POPULATION OF THE SOUTHERN DISTRICTS OF WEST BENGAL

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ABSTRACT

Ticks are the most common ectoparasite in cattle. The prevalence of ticks in a particular area is a matter of concern, as they act as vectors for transmitting haemoprotozoal, rickettsial, bacterial, and viral diseases in livestock, some of which are of zoonotic importance. A survey was conducted to identify the presence of specific ticks in the cattle population in the Birbhum, Purba Bardhaman, Paschim Bardhaman, Bankura, Nadia, North 24 Parganas and South 24 Parganas districts of West Bengal, India. The collection of ticks from cattle was carried out from January 2022 to December 2023. During this period, a total of 2057 cattle were randomly examined from different villages of the seven districts, and 516 cattle were found to be infested. The ticks from the cattle were collected in 70% and 95% ethanol. For morphological identification stereo-microscopy and scanning electron microscopy study was carried out, whereas for molecular identification, the mitochondrial 16S rRNA gene segment amplification was completed using PCR. The PCR product was sequenced, and the obtained data were subsequently used for phylogenetic analysis using NCBI-BLAST to download the related sequences, followed by the neighbour-joining method of MEGA-11 software to complete the analysis. Three tick species of Hyalomma anatolicum, Rhipicephalus microplus and Haemaphysalis bispinosa were identified. H. anatolicum is a primary vector for tropical theileriosis, whereas bovine babesiosis and anaplasmosis are caused by both R. microplus and H. bispinosa ticks. Climatic conditions of the southern districts remain hot and humid throughout the year, making it advantageous for the tick population growth and thus, heightening the chances of transmission of tick-borne diseases in cattle. Identification of ticks would provide a basis for evolving an effective control strategy for the management of tick-borne diseases in cattle. It indirectly accelerates the proper development and well-being of the cattle wealth of the state.

Keywords: Cattle, electron microscopy, mitochondrial 16S rRNA gene, tick identification.

P3-25

EVALUATING THE WELFARE OF DAIRY COWS ON SMALL AND MEDIUM-SIZED FARMS

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ABSTRACT

The purpose of the study was to evaluate and compare the welfare practices of dairy cattle on small and medium-sized farms and to offer appropriate suggestions for enhancing the animal welfare practices of these dairy farms in Uttar Pradesh. Data were gathered from 40 commercial dairy farms that used crossbred cattle and were divided into two categories based on the size of their adult herds: small (10–20) and medium (21–50). For small and medium dairy farms, the average welfare scores for component A were 14.65±0.70 and 15.70±0.69, respectively. At small and medium dairy farms, the average welfare scores for component B were 20.40±0.49 and 21.40±0.71, respectively. For medium-sized dairy farms, it was higher. At small and medium dairy farms, the average welfare score for component C was 23.85±0.67 and 23.95±0.70, respectively. The mean welfare score of 'Cow cleanliness score' and 'Abnormal behaviour' indicator was found to be very poor at all dairy farms. The overall mean welfare scores in all components out of a total score 100 by small, medium dairy farms were 58.67±1.19, 61.30±1.62, respectively with an overall mean of 59.98±1.31. The mean overall welfare score for medium dairy farms was higher. Overall, 52.50, 47.50 per cent of the total farms were ranked as in good, average welfare category, respectively. Thus, 52.50% of the total studied dairy farms had an acceptable welfare level. Seven PCs (Principal components) were identified using PCA (Principal component analysis) which were responsible for 73.98% of the total variance.

Key Words: Welfare, BCS, Lameness and Cow comfort

P3-26

ANALYZING TIME BUDGET AND SEASONAL BEHAVIORAL PATTERNS OF GAROLE SHEEP UNDER SEMI-INTENSIVE MANAGEMENT

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ABSTRACT

Understanding animal behaviour is crucial for improving management efficiency and productivity in livestock systems. This study investigated time budget activities and seasonal variations in Garole sheep with the objective of developing ethograms across physiological stages under semi-intensive management. Behavioural activities of lactating, pregnant, growing females, and adult breeding males were recorded continuously for 24-hour cycles over two years using IoT-enabled sensors and automated recording devices, ensuring minimal disturbance to routine practices. Data were analyzed using the GLM procedure in SAS 9.3 (2012). Results revealed significant seasonal influences on ingestive (fodder, concentrate intake, grazing), rumination (sitting, standing), maintenance (walking, roaming, drinking), eliminative (urination, defecation), resting (idling, sleeping), and locomotory behaviours. Fodder and concentrate intake were highest during the rainy season, while grazing activity peaked in winter. Walking was highest in summer, whereas roaming was more frequent in winter, particularly during daytime. Rumination was greater in summer, with sitting rumination predominant at night, except for specific deviations in breeding males. Pregnant and growing females exhibited higher eliminative activity in the rainy season, while lactating and breeding males differed seasonally in urination and defecation frequencies. Idle behaviour dominated the daily time budget, particularly at night, and was highest in winter while standing and in the rainy season while sitting. Sleeping was also greatest in winter, except for pregnant sheep, which slept more at night in summer. Ethograms generated through IoT-based monitoring identified idling as the most prominent activity, accounting for 42–46% of the daily budget across stages. Rumination, eating, and sleeping followed, with lactating ewes spending the most time ruminating (21.9%). Water intake, urination, and defecation frequencies remained comparable across groups. Furthermore, Garole sheep displayed colour discrimination ability (77.5%), indicating cognitive adaptability. These findings provide practical insights for optimizing feeding, resting, and space allocation, thereby improving welfare and productivity in semi-intensive systems.

Keywords: Animal behaviour; Ethogram; Garole sheep; Time budget

P3-27

IMAGE-BASED CATTLE IDENTIFICATION USING MACHINE AND DEEP LEARNING MODELS

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ABSTRACT

Livestock identification is essential for traceability, disease control, breeding and theft prevention in livestock management. Traditional methods like ear tagging, branding and RFID systems, while commonly used, suffer from issues like tampering, loss, and potential harm to animals. With the advancement of artificial intelligence, image-based cattle identification has emerged as a promising, non-invasive and reliable alternative. This study focuses on the development and evaluation of an image-based individual cattle identification system using machine learning, deep learning and pattern recognition techniques. High-resolution cattle images (face, side view of whole body) have been captured from 40 nos. of adult cattle at Haringhata farm, Mohanpur, Nadia, West Bengal using a Nikon-D5300 DSLR camera, then pre-processed to enhance clarity, reduce noise, and normalize lighting. The pre-process images are divided into training and test sets. The training set has been used to train the models and test has been used for validating the trained models using unknown sample images. The deep learning models like VGG19, InceptionV3, EfficientNetB0, EfficientNetV2B0, MobileNetV2, ResNet50, Xception, ZFNet, DenseNet121for facial images and machine learning models like Support Vector Machine, K- Nearest Neighbor, Decision Tree, Random Forest, Naïve Bayes, Artificial neural Network for body contour have been applied on training image set and accuracies, F1- scores, recalls, and confusion matrices have been generated from testing set. Finally, one model has been chosen which has given the best performance among the applied models in each case. The approach aims to achieve high accuracy and robustness under varying conditions, including different poses, illumination changes and partial occlusions. The maximum accuracy over 97% for facial images and 82.5% for body contour was achieved using different deep learning and machine learning models, respectively. The image-based cattle identification is scalable and non-invasive method having high accuracy, and can significantly contribute to the precision livestock farming.

Keywords: Cattle identification, Facial and body contour images, Deep learning, Machine Learning.

P3-28

GENERATION-WISE GROWTH AND REPRODUCTIVE PARAMETERS OF PROLIFIC AVISHAAN SHEEP IN SEMI-ARID RAJASTHAN

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ABSTRACT

Sheep farming in the country has shifted its focus from wool to mutton production due to rising meat demand and escalating prices. Flock productivity can be enhanced by increasing litter weight through the use of prolific sheep breeds. Avishaan sheep, developed by ICAR-Central Sheep and Wool Research Institute (CSWRI), Avikanagar, exhibits desirable traits such as high prolificacy, greater litter weight, higher milk yield to sustain multiple lambs, and resilience to harsh semi-arid climates. Avishaan was developed by crossbreeding three native breeds—Garole (12.5%), Malpura (37.5%), and Patanwadi (50%) with successful integration of the FecB mutation. Data on 2,511 lambs born to 1439 ewes were collected from the Avishaan flock maintained under semi-intensive management at ICAR-CSWRI, Avikanagar, over a 15-year period (2010–2025). The study included seven generations produced through inter-se mating of Avishaan sheep, with body weights recorded at different ages. Due to limited records, the growth and reproduction data of seventh generation were merged with sixth generation and considered for analysis. The reproduction data were analyzed using cross-tabulation and the chi-square test to assess statistical significance of generation and type of birth, while growth traits were analyzed using the General Linear Model (GLM) procedure in SPSS. The data were classified by generation (G1-G6), sex (male and female), type of birth (single, twin, and triplet), and period (P1-2010-13, 2014-17, 2018-21, 2022-25). The overall least squares means of body weights at birth, 3 month, 6 month and 12 month across six generations were 2.63±0.03, 13.00±0.37, 20.34±0.33 and 29.59±0.57 kg, respectively. All the included factors had significant effects ($P<0.01$) on different body weights, except generation, which had a non-significant effect on birth weight. Reproductive traits such as multiple births, prolificacy, and litter size showed an increasing trend across generations, ranging from 167.98 to 185.0%, 58.21 to 68.75%, and 1.67 to 1.85, respectively. These results indicate that the breeding strategies adopted for introgression of the FecB mutation have been effective and successfully implemented in the Avishaan flock.

Keywords: FecB, Mutation, generation, chi-square, Introgression

P3-29

EMPOWERING SMALLHOLDER DAIRY FARMERS VIA BAIF SAMVAAD: A DIGITAL FEEDBACK SYSTEM

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ABSTRACT

Effective communication between breeding programs and smallholder dairy farmers is essential for the successful implementation of genetic improvement initiatives. Farmers often lack access to clear, relative information on their animals' performance, which limits their ability to make informed breeding and management decisions. A simple animal ranking system was developed to explain phenotypic performance data into easy-to-understand feedback for dairy farmers. Individual animal lactation records were standardized and ranked against population averages for animals of the same breed and production environment. The feedback system includes performance certificates, disease diagnostic reports, the BAIF sire directory, farmer advisory messages, publications, and livestock management guidance, all circulated to farmers through the WhatsApp Chat Bot Service named "BAIF Samvaad." This automated interface transmits individual animal performance summaries and related information to each dairy farmer's registered WhatsApp-enabled mobile number. The ranking-based feedback system provided dairy farmers with clear, transparent, and comparative information on their animals' production performance. Automated data sharing improved the speed and reach of feedback delivery, while complementary incentives and technical support increased dairy farmer participation and trust in the phenotype performance recording. The distribution of animal performance information was systematically tracked, enabling monitoring of program reach and engagement. The combination of simple ranking tools and digital communication platforms strengthens dairy farmer engagement, promotes informed decision-making, and builds trust in breeding programs. This approach supports the scaling of performance-based and genomic selection initiatives in the smallholder dairy sector of India

Keywords: animal ranking, farmer engagement, digital communication, performance recording, genomic selection, and smallholder dairy

P3-30

LEVERAGING MACHINE LEARNING TO DECODE DRIVERS AND CONSTRAINTS IN INTEGRATED FARMING SYSTEMS: EVIDENCE FROM DIVERSE AGRO-CLIMATIC ZONES OF WEST BENGAL

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P3-31

COMMUNITY-BASED CONSERVATION OF BLACK BENGAL GOAT: A SUSTAINABLE APPROACH TO BREED PRESERVATION AND LIVELIHOOD ENHANCEMENT IN AJODHYA HILLS REGION OF PURULIA DISTRICT, WEST BENGAL

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ABSTRACT

The Black Bengal goat (*Capra hircus bengalensis*), an indigenous breed of West Bengal, is renowned for its superior meat quality, high reproductive efficiency (average kidding rate: 180–200%), and premium skin. Despite its economic and genetic significance, the breed has experienced a population decline of 25–30% over the past decade in the Ajodhya Hills region of Purulia district. This decline is primarily attributed to indiscriminate crossbreeding, poor health management, and limited institutional support. To address these challenges, a community-based conservation and livelihood development program was implemented across 80 goat-rearing households in six villages of Ajodhya Hills region of Purulia district of West Bengal during 2023-2024 to 2024-2025. Baseline assessments revealed an average flock size of 4.8 goats per household, contributing approximately ?12,500 annually to family income. The intervention focused on three core strategies: (i) selective breeding using superior Black Bengal bucks to maintain genetic purity, (ii) regular vaccination and deworming to improve herd health, and (iii) training programs to enhance goat management practices and promote value addition to goat-based products. After two years, the program demonstrated measurable success. Kid survival rates improved by 12%, average market weight of goats increased by 13%, and household income from goat rearing rose by 25%. These outcomes underscore the effectiveness of integrating breed conservation with livelihood enhancement strategies. The initiative not only preserved the genetic integrity of the Black Bengal goat but also strengthened the socio-economic resilience of smallholder farmers. This model offers a replicable framework for conserving indigenous livestock breeds while promoting sustainable rural development and biodiversity preservation in marginalized community

Keywords: Black Bengal, indigenous, selective breeding, community-based conservation, rural livelihood, socio-economic resilience.

P3-32

STUDY ON THE KNOWLEDGE LEVEL AND ADOPTION INDEX OF DAIRY FARMERS ABOUT IMPROVED DAIRY FARMING PRACTICES IN WEST BENGAL, INDIA

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ABSTRACT

India's rural economy depends heavily on dairy farming, especially for small and marginal farmers. This study evaluates the knowledge and adoption of improved dairy farming practices among dairy farmers in Murshidabad district, West Bengal. A total of 120 farmers from Burwan and Khargram blocks were selected through a random sampling method. Data were collected via structured interviews, and statistical analysis was conducted using SPSS 21.0. Findings revealed that farmers′ knowledge levels were significantly associated with factors such as income, herd size, material possession, and access to mass media. Additionally, adoption of improved dairy practices was strongly influenced by monthly dairy income and herd size. Socio-demographic factors—including landholding, education, gender, and age played a crucial role in shaping both knowledge levels and adoption behaviors. Notably, younger farmers, males, and those with higher education exhibited a greater inclination toward adopting modern dairy practices. The study highlights the necessity for well-structured extension programs aimed at bridging knowledge gaps and promoting the adoption of scientific dairy farming techniques. Enhancing infrastructure and strengthening extension services are vital for improving dairy productivity and economic returns in the region.

Keywords: Knowledge, Adoption index, Dairy, Farming, Farmers etc.

P3-33

EFFECTS OF ELEPHANT FOOT YAM (*AMORPHOPHALLUS PEONIIFOLIUS*) FLOUR ON QUALITY OF DUCK MEAT NUGGET UNDER REFRIGERATED STORAGE (4±1ºC)

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ABSTRACT

The present study was conducted with an objective to improve the quality of duct meat nugget incorporated with elephant foot yam (EFY) flour at 2.5% (T1) and 5.0% (T2)and the quality changes were studied as compared to control (without any EFY) under refrigerated storage condition(4±1ºC). The moisture and protein contentsof duck meat nuggets were significantly (P□0.01) different between the groups. The control product showed significantly (P□0.01) lowest and T2 showed highest protein content. The treated groups did not show any significant variation in fat and total ash contents of duck meat nuggets.Dietary fibre content of T2 was significantly ($P>0.05$) higheramong the treatment groups. Total phenolic values of T1 and T2were significantly ($P>0.05$) higher than control. There was a significant ($P<0.01$) effect of test ingredients on pH values of duck meat nuggetsand an increasing trend in pHwas observed during the progress of storage period. The TBARS value of T2 was significantly lower than T1 &control throughout the storage period.The treatment groups (T2 & T1) showed significantly ($p<0.01$) lower total plate counts (TPC) as compared to control although the TPC of all the experimental groups showed an increasing trend during the advancement of storage days. Except appearance, other sensory attributes were significantly higher (P□0.01) in EFY incorporated duck meat nuggets compared to control. T2 showed highest score of overall acceptability as compared to T1 & control. The results concluded that incorporation of 5.0% elephant foot yam flour improved the total protein content, dietary fibre content, physicochemical, microbiological and sensory attributes of duck meat nuggets.

Keywords: Elephant foot yam, duck meat nugget, meat quality & dietary fibre

P3-34

STANDARDIZATION OF CHICKEN PRIMORDIAL GERM CELLS IN FEEDER LAYER FREE CULTURE MEDIUM

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ABSTRACT

Chicken Primordial Germ cells (cPGCs) are the progenitor cells that give rise to germ cells, playing a vital role in transmitting genetic information across generations. They serve as a powerful model for genetic modification, conservation of avian species and production of transgenic chicken. The culture of cPGC under feeder layer–free conditions is a crucial advancement for avian biotechnology and genome editing applications. Feeder layer based PGC culture systems are adopted as they provide essential growth factors and cellular support, which often introduce variability and contamination risks. In this study, a defined, feeder-free culture medium was optimized to sustain long-term proliferation, viability, and germline competency of cPGCs. Key growth factors such as basic fibroblast growth factor (bFGF) and other factors were supplemented to mimic feeder-derived signals. Morphological assessment, proliferation kinetics, and expression of germ cell–specific markers (e.g., CXCR, BLIMP, NANOG, MYC, KLF, POUV, VASA and SOX2) confirmed the stability and identity of cultured PGCs. This standardized feeder-free system offers a reproducible and contamination-free platform for downstream applications, including CRISPR/Cas9-mediated genome editing and sex-specific breeding programs, thus contributing significantly to sustainable poultry research and production advancements.

Keywords: Avian Biotechnology, Chicken, Primordial Germ cells, Genome editing

P3-35

GENOME-WIDE ASSESSMENT OF POPULATION STRUCTURE, ADMIXTURE ANALYSIS AND PHYLOGENETIC ANALYSIS OF MALPURA AND PATANWADI SHEEP WITH WORLDWIDE SHEEP BREEDS

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ABSTRACT

This study examined the genome-wide population structure, admixture patterns, and phylogenetic relationships of two semi-arid Indian sheep breeds, Malpura and Patanwadi, and compared them with seven global sheep breeds from an online dataset. Principal Component Analysis (PCA) was performed in PLINK v1.9 to explore clustering patterns among breeds, with the resulting eigenvectors visualised in RStudio. ADMIXTURE analysis was conducted to evaluate ancestry proportions and genetic admixture across K values from 2 to 8. Phylogenetic reconstruction was carried out using RAxML (Randomised Axelerated Maximum Likelihood), and trees were visualised with iTOL v7. The PCA revealed a clear population structure, with PC1 explaining 55.78% of the total genetic variance. The analysis showed a distinct separation between European/Merino lineages and South Asian/Indian lineages, indicating major continental-level genetic differentiation. ADMIXTURE results indicated strong subdivision at low K values, reflecting the primary split between European and South Asian/Australian populations. At intermediate K values, finer subgroups emerged, corresponding to individual breed histories and selection patterns. Both Malpura and Patanwadi exhibited distinct population structures without signs of recent admixture, maintaining their genetic integrity as indigenous, semi-arid-adapted breeds. Phylogenetic analysis revealed shorter intrabreed branch lengths within the Indian clade than between continents, suggesting more recent divergence or ongoing gene flow among Indian breeds. Overall, despite geographic proximity and similar environmental adaptations, Malpura and Patanwadi retain distinct genetic identities while clustering within the broader South Asian sheep lineage. These findings offer valuable insights into the evolutionary history and genetic relationships of Indian semi-arid sheep breeds within the global sheep population, supporting their conservation as genetically unique resources.

Keywords: PCA, Admixture analysis, Phylogenetic tree

P3-36

INTEGRATIVE GENOMIC SIGNALS REVEAL ECOTYPE ADAPTATION IN SALEM BLACK GOATS FOR CLIMATE-SMART BREEDING

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ABSTRACT

This study investigates ecotype-specific adaptations in Salem Black goats, a resilient breed suited to small holder production systems in challenging environmental conditions. Data were collected from 11 unrelated Salem Black goats across four distinct locations in Tamil Nadu, India: Mecheri, Kolli Hills, Bargur, and the Livestock Farm Complex at Veterinary College and Research Institute, Namakkal. Employing a Decorrelated Composite of Multiple Signals (DCMS) framework—the first application of its kind to Salem goat populations—we integrated five complementary statistics (iHS, nSL, H12, ZHp, Tajima's D) across 500 kb genomic windows. This approach identified 11 selective sweep regions ($q < 0.05$), highlighting key adaptations: pigmentation (MCR1), environmental resilience (TRIM13, DNAJA3, CRY1), disease tolerance (NEK3, POLE2), and protein degradation (KLHDC2). Dominant regulatory elements, including Metazoa_SRP, 5S_rRNA, and U6, suggest enhancer-driven mechanisms underlying these adaptations. These findings elucidate the genetic basis of Salem Black goats' drought and heat tolerance, informing climate-smart breeding strategies to enhance resilience in livestock systems.

Key words: Salem Black goat, ecotype adaptation, selective sweeps, climate-smart breeding, DCMS, genomic resilience

P3-37

GENOMIC INBREEDING AND SELECTION SIGNATURES IN SALEM BLACK AND RED SOKOTO GOATS

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ABSTRACT

Goats are vital for socioeconomic stability in pastoral and agropastoral systems of India and Nigeria, where they face environmental stressors such as diseases, parasites, and extreme heat. However, the impact of genetic diversity and inbreeding on traits critical for resilience remains underexplored. This study investigates genomic adaptations and inbreeding effects in Nigerian Red Sokoto/Maradi (NG_RSK, n=21) and Indian Salem goats (n=11). Using the AdaptMap GoatSNP50 dataset aligned to the Capra hircus ARS1 assembly, we analyzed 46,213 SNPs for NG_RSK and 40,376 SNPs for Salem goats post-quality control to identify selection signatures using integrated haplotype scores and quantify genomic inbreeding (FROH). Key loci under selection in NG_RSK goats include ABCB5, CRY1, ITGB8, RFX4, and SAV1, associated with disease resistance and environmental adaptability. For Salem goats, significant loci include ATP7B, KCNJ11, SIGLEC1, TGFBR1, and ESRRG, linked to stress response and metabolic regulation. Genomic inbreeding was higher in NG_RSK (FROH: 3.67 ± 1.72) compared to Salem goats (FROH: 1.70 ± 0.37), indicating distinct inbreeding pressures. These findings highlight unique genomic adaptations enabling resilience in challenging environments and underscore the need to manage inbreeding to preserve adaptive genetic diversity. This study informs breeding programs aimed at enhancing goat resilience in diverse agroecological systems, supporting sustainable livestock production in India and Nigeria.

Keywords: Genomic inbreeding, selection signature, Salem black, Red sokoto goats

P3-38

INJECTABLE SILK-BASED HYDROGEL SYSTEM FOR TARGETED CHEMOTHERAPY IN MICE TUMOUR MODEL

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ABSTRACT

The research aimed to develop innovative biomaterials for cancer treatment and drug delivery applications. A silk fibroin (SF)--based hydrogel was developed from Bombyx mori (BMSF) and Antheraea assamensis (AASF) silk sources for controlled drug delivery applications. Doxorubicin (Dox) an anti-carcinoma drug was used as a drug of choice for targeted delivery. The hydrogels successfully encapsulated doxorubicin (Dox), showing sustained drug release over 60 days in the equal ration mixtures of silks. The in-vivo study was designed to develop a mammary carcinoma model in Balb/c mice and evaluate the tumour regression potential of a doxorubicin-loaded injectable hydrogel for cancer treatment. Mice were injected with varying concentrations of 4T1 cells, establishing a group injected with 1 x 106 cells as the most consistent model, with visible tumour formation by day 7. All the tumour-generated models were divided into three groups one with no treatment, one with Dox treatment and another with Dox-loaded hydrogel treatment. Histological and immunohistochemical analyses (H&E, CD31, Ki-67 staining) highlighted aggressive tumour characteristics, including high cellular density, angiogenesis, and proliferation. Untreated and saline-treated tumours showed robust vascular networks and high proliferation rates, indicating minimal therapeutic impact in the non-treated group. In contrast, free doxorubicin treatment resulted in significant tumour regression, characterized by adipose replacement and reduced angiogenesis. Doxorubicin-loaded hydrogel treatment further enhanced these effects, showing minimal tumour cell proliferation and substantial tumour cell elimination. These findings underscore the hydrogel's potential for controlled, sustained drug delivery in mammary carcinoma therapy.

Keywords: *NA*

P3-39

SELECTION SIGNATURE ANALYSIS IN INDIAN PIG BREEDS REVEALED GENES RESPONSIBLE FOR IMMUNE RESPONSE AND ADAPTABILITY

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ABSTRACT

Selection signatures represent distinct genomic patterns left by selection pressures, offering valuable insights into the evolutionary dynamics and genetic architecture of livestock populations. In the present study, we investigated genomic regions under selection in five indigenous Indian pig breeds, viz. Doom, Ghoongroo, Agonda Goan, Manipuri Black, and Mali to identify candidate genes associated with economically important traits. A total of 96 animals were genotyped using the Porcine 80K iScan array comprising 75,753 SNPs. Quality control of genotype data was performed in PLINK v1.9 by excluding unmapped SNPs, markers with a call rate below 90%, minor allele frequency less than 0.05, and loci showing significant deviation from Hardy–Weinberg equilibrium ($P < 0.00001$), resulting in a filtered dataset of 48,853 SNPs. Selection signatures were detected within each breed using the integrated haplotype score (iHS) approach implemented in the rehh R package, with a 100 kb scanning window and a threshold of $|iHS| > 3$ to identify candidate regions under selection. A total of 21, 8, 14, 49, and 34 genomic regions were detected in Doom, Ghoongroo, Agonda Goan, Mali, and Manipuri Black pigs, respectively. Genes located within these regions, including SLC10A1, ADGRG5, ANKRD44, CAMTA1, PTGER4, PSMD9, STIM1, STXBP3 (Doom); TMEM114, SPATA18, TBC1D2B, ADAMTS7 (Ghoongroo); TLR3, SLC25A4, WNT2, CFTR, IRF2, FGFR1 (Agonda Goan); KCNQ5, PLAC9, DAPP1, IL18BP, NUMA1, SLMAP, DNALI1, NR2F2, PBX1, RBMS3, LPB, ERBB4 (Mali); and SPTBN1, DLGAP1, CPOX, TRAM1, PDZRN4, SNX16, SLC10A5, IMPA1 (Manipuri Black), were associated with immune function, viral regulation, reproduction, disease resistance, growth, thermotolerance and adaptive traits. These findings provide novel insights into the genetic basis of adaptation and productivity in indigenous Indian pig breeds. Further validation using larger populations and high-density SNP arrays or whole-genome sequencing data is warranted to enhance the resolution and reliability of detected selection signatures.

Keywords: Selection signature, Pig genome, Adaptability, Diseases resistance

P3-40

GENOMIC EVALUATION OF CONFORMATION TRAIT - STATURE OF ADMIXED CROSSBRED COWS MAINTAINED AT SMALLHOLDER DAIRY FARMERS

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ABSTRACT

Crossbred cattle constitute a substantial proportion of the milch animal population in India. In addition to milk yield and reproductive performance, body conformation traits play a critical role in the selection of animals for sustainable productivity, improved health, and efficient management. Among these, Stature is one of the most widely studied linear type traits globally due to its strong association with body size, structural soundness, and overall performance. In the present study, Stature was evaluated as an important conformation trait in crossbred cattle recorded under the performance recording system of BAIF. A total of 5,582 animals were initially measured following the guidelines of the International Committee for Animal Recording (ICAR). Stature was measured in centimetres from the top of the spine between the hips to the ground. After rigorous data validation and cleaning, 5,392 animals were retained for analysis. Among these, genotype data from 2,306 animals were used to estimate genetic parameters. Genotyping was performed using the Gau SNP chip, and imputation was carried out to a high-density (HD) chip to enhance genomic coverage. Breed composition was estimated based on imputed genotype data. Genomic Best Linear Unbiased Prediction (GBLUP) was employed for genomic evaluation of Stature using a univariate animal model incorporating appropriate fixed and random effects, including herd as an additional random effect alongside the additive genetic component. The estimated heritability for Stature was moderate, indicating a substantial genetic contribution to phenotypic variation. This suggests that Stature can be effectively utilized as a selection criterion in breeding programs aimed at improving body conformation and overall productivity in crossbred cattle populations across India.

Keywords: Crossbreds, Stature, Genomic Evaluation, GBLUP, Gau SNP Chip, Heritability

P3-41

UNCOVERING SELECTION-DRIVEN GENOMIC LANDSCAPES OF REPRODUCTIVE TRAITS ON INDIAN CATTLE DIVERSITY

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ABSTRACT

This study investigates genome-wide selection signatures influencing reproductive traits across six cattle breeds using multiple statistical approaches. Reproductive efficiency is vital for livestock productivity, directly affecting the number of offspring and the overall sustainability of production systems. Early sexual maturity and higher fertility rates enhance selection intensity, leading to accelerated genetic gain and improved herd performance. To identify genomic regions associated with these traits, genotyping data from the Illumina BovineSNP50 BeadChip and GGP Bos indicus 70K array were analyzed. Four summary statistics were employed—two intra-population (Tajima′s D and iHS) and two inter-population (Rsb and XP-EHH). The regions under selection were subsequently annotated using the NCBI and Cattle QTL databases. In Gir cattle, several genes under positive selection were identified, including CACNA1H, KCNIP4, GDF9, SLC4A4, DHX57, EIF2AK3, and ME3, which are associated with traits such as age at puberty, sperm motility and count, sperm acrosome integrity, conception rate, and udder morphology. Two genes, ENTHD1 (chromosome 5) and PRDM16 (chromosome 16), were shared between Tharparkar and Gir and found to be under positive selection. ENTHD1 is linked to calving ease and stillbirth, whereas PRDM16 is associated with udder depth, height, and attachment. Additionally, several genes—RXFP2, FRY, ENTHD1, SREBF2, RNF10, NYAP2, VWF, PPP1R8, EYA3, BBX, and TRPM3—were consistently detected across multiple methods, suggesting strong selection pressure. These findings reveal the genomic regions and candidate genes underlying reproductive traits in Indian cattle. The results enhance understanding of the genetic mechanisms shaping fertility, adaptation, and domestication, and can inform genomic-based selection strategies to improve reproductive efficiency in indigenous and crossbred populations.

Keywords: adaptation, cattle, evolution, reproduction, selection signature

P3-42

COPY NUMBER VARIATIONS IN MITOCHONDRIAL GENOME HAVE A POTENT ROLE IN PARASITIC IMMUNITY AGAINST HAEMONCHUS CONTORTUS-A NOVEL REPORT

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ABSTRACT

Mitochondria is a cellular organelle responsible for a variety of function, apart from energy production through oxidative phosphorylation, TCA cycle, apoptosis, plays a major role in iron and calcium metabolism and immune functions against pathogens (bacterial, viral or parasitic). Unlike nucleus, mitochondria exist in multiple copies, with many copies of mitochondrial DNA. A metabolically active cell possess about 103 and 104 copies of the mitochondrial genome. Lowered mtDNA copy number leads to disorders or disease, in a similar way as mutation in mtDNA causes a wide range of disease or disorders. In this current article, we estimated mtDNA copy number through QPCR analysis of ATP6, NAD1, Cox1, ND2 and ND6 and revealed that healthy individuals have better mtDNA copy number compared to that of the infected ones under natural challenge in sheep model against the parasite Haemonchus contortus infection. We diagnosed the infected animals for H. contortus primarily with symptoms, followed by Faecal egg count and final confirmation through molecular diagnosis. We had characterized the mentioned mitochondrial genes gene from abomasum(stomach) of sheep, which is the site of predilection of this parasite. In our lab, earlier we have documented certain immune response nuclear genes to have antiparasitic role and cytochrome B as mitogenome. Quantitative expression profile for ATP6, NAD1, Cox1, ND2 and ND6 is an indication of the copy number of mitochondrial genes and we observed significantly better expression profile of mitogene in healthy sheep in comparison to infected animals. Thus, mitochondrial copy number is directly associated with antiparasitic immunity, first time reported.

Keywords: Mitochondrial genome, mitochondrial copy number, immune response, antiparasitic immunity, Haemonchus contortus,

P3-43

HIGH-THROUGHPUT PHENOTYPING (HTP) AS A TOOL TO ACCELERATE ANIMAL GENETIC IMPROVEMENT IN THE SUNDARBAN DELTA FOR CLIMATE RESILIENT FARMING

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ABSTRACT

Climate changes affect livestock directly (all the way through heat stress and increased morbidity and mortality) and indirectly (through quality and availability of feed, forage, and animal diseases). Small livestock farmers are the most exposed to climate change. In the Sundarban Delta, where livestock farming remains one of the major sources for livelihood, is the most vulnerable to the effects of climate changes. Therefore, it is need of the hour to elixir animal genetic resources of the region in terms of climate resilient livestock farming. The delta′s distinctive challenges like high salinity, extreme weather, and the threat of rising sea levels, makes High-throughput phenotyping (HTP), a valuable tool for breeding more climate resilient and productive livestock, in contrast to traditional selective breeding methods. In this context it is eminent that HTP techniques offer a new opportunity to enhance genomic improvement of livestock, especially for novel phenotypes; where generation interval remains lower. The use of sensors, big data, artificial intelligence, and machine learning can help animal farmers to explore more climate resilient animal genetic resources, whereas to lower production costs and increase effectiveness. One of the most relevant challenges in this context is the handling of large-scale data provided by automated processes such as image collection, continuous real-time sensor-based measurements, and spectroscopy reports, among others. Many studies have demonstrated that extraction of biologically relevant features from large datasets generated by automatic devices can be assessed further by using machine learning algorithms for the accurate prediction of valuable animal traits in respect of climate resilient livestock farming in the Sundarban Delta.

Keywords: High-throughput phenotyping (HTP), Breeding, Sundarban delta, Climate resilient farming

P3-44

FEATURE-DRIVEN MACHINE LEARNING APPROACH FOR GENE PREDICTION IN *STAPHYLOCOCCUS AUREUS*

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ABSTRACT

Accurate genome annotation is essential for understanding gene function and regulation in microorganisms. This study focuses on improving the annotation accuracy of *Staphylococcus aureus* by applying supervised machine learning (ML) models to precisely identify coding sequences (CDS) and explore potential novel genes. Conventional gene prediction tools often face challenges such as incomplete annotation, sequencing errors, and difficulty in recognizing non-canonical start sites. To address these limitations, data-driven ML approaches were employed to learn and generalize sequence patterns across multiple bacterial genomes. Two ML classifiers, Random Forest (RF) and Extreme Gradient Boosting (XGBoost), were trained using balanced datasets of experimentally validated CDS and long open reading frames (LORFs) from 60 diverse prokaryotic genomes. Sequence-derived features such as GC content, codon usage bias, ORF length, start codon patterns, and k-mer (2–6-mer) composition were extracted. The models were trained, cross-validated, optimized for hyperparameters, and subsequently applied to the S. aureus reference genome. Both RF and XGBoost achieved high predictive accuracy (0.94–0.97) with AUC values up to 0.988, demonstrating strong generalization across genomes. Application to S. aureus resulted in the prediction of 2,630–2,779 CDS, aligning closely with outputs from established tools including Prokka (2,630), DFAST (2,676), AUGUSTUS (2,677), RAST (2,684), and Helixer (2,779). Several unannotated CDS predicted by ML models showed significant BLAST hits to conserved bacterial proteins, indicating biologically relevant yet previously overlooked genes. No novel ncRNAs were detected, suggesting that S. aureus ncRNA annotation is largely complete. Overall, this ML-based framework offers a reliable, interpretable, and scalable approach for bacterial genome annotation, matching traditional pipelines in accuracy while uncovering additional conserved or uncharacterized genomic elements. It establishes a foundation for expanding ML-driven annotation to other microbial species and advancing large-scale functional genomics research.

Keywords: Staphylococcus aureus, machine learning, genome annotation, gene prediction, Random Forest, XGBoost

P3-45

COMPARATIVE TRANSCRIPTOMICS TO REVEAL MOLECULAR MECHANISMS OF FRESHWATER ADAPTATION AND METAMORPHOSIS IN MACROBRACHIUM ROSENBERGII LARVAE

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ABSTRACT

This study delves into the complex molecular mechanisms governing larval development and metamorphosis in the giant freshwater prawn, Macrobrachium rosenbergii, a species of significant aquaculture importance. While adult prawns are fully adapted to freshwater, their larvae require brackish water for successful development, a crucial period marked by a series of molts and a final metamorphosis into the post-larval stage. The objective of this research was to utilize a comparative transcriptomics approach to elucidate the key genetic pathways and differentially expressed genes (DEGs) influencing larval adaptation to freshwater. A comparative transcriptome analysis was performed on Macrobrachium rosenbergii zoea 1 larvae hatched in freshwater (0 ppt) and brackish water (10 ppt). Pooled libraries from triplicate samples were sequenced using Illumina Novaseq X Plus. High-quality (HQ) reads were mapped to the reference genome using STAR Aligner, and transcripts were assembled with StringTie, identifying 4,222 novel isoforms. The differential gene expression analysis identified 5,759 significant DEGs with 2,391 downregulated and 3,368 upregulated genes in the freshwater group. Functional enrichment analysis revealed significant enrichment of pathways such as Insect hormone Biosynthesis and Arachidonic acid metabolism. DEGs were associated with critical functions, including ion transport, osmoregulation, metabolism, and immune response. The key genes specifically involved in osmoregulation (e.g., Bumetanide-sensitive sodium-(potassium)-chloride cotransporter and Sodium/potassium-transporting ATPase) and molting (e.g., crustacyanin-like lipocalin, chitin-binding protein, and ecdysone receptor) were significantly altered. These findings highlight the molecular mechanism associated with physiological stress imposed by freshwater environment on M. rosenbergii larvae. The identified osmoregulation and molt related DEGs can serve as molecular markers which can be used in selective breeding programs to develop stocks of M. rosenbergii that are more robust and tolerant to lower salinities during the larval stage, potentially reducing the need for brackish water.

Keywords: Giant freshwater Prawn, transcriptomics, freshwater adaptation, DEGs

P3-46

STUDY ON PERCEIVED CONSTRAINTS & ITS ASSOCIATION WITH LIVELIHOOD EMPOWERMENT OF RURAL STAKEHOLDERS UNDER FARMERS FIRST PROJECT IN NADIA DISTRICT OF WEST BENGAL, INDIA

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ABSTRACT

The present study entitled “Study on Perceived Constraints and its Association with Livelihood Empowerment of Rural Stakeholders in Nadia District of West Bengal” was conducted under the Farmer FIRST Project of ICAR, Ministry of Agril. & FW, Government of India, by the Dept. of Veterinary and A.H. Extension Education, WBUAFS, Kolkata. The investigation aimed to assess the level of livelihood empowerment and identify the perceived constraints affecting farming communities in three adopted villages i.e. Ayeshpur, Baksha, and Dakshin Duttapara under Haringhata Block of Nadia District, West Bengal. A comprehensive baseline field survey was carried out during March 2025, covering 1001 respondents engaged in livestock–poultry, horticulture, and fishery-based livelihood enterprises in the functional area. Data were collected through a structured interview schedule, encompassing socio-economic attributes, livelihood capitals, empowerment indicators, and perceived constraints across production, resource, market, institutional, and infrastructural dimensions. Analytical tools such as descriptive statistics and chi-square tests were employed to examine the interrelationship between perceived constraints and livelihood empowerment indices. The findings revealed that economic and infrastructural barriers, limited institutional support and market access constraints significantly influenced the degree of livelihood empowerment among rural stakeholders. The study emphasizes the need for capacity-building interventions, technological backstopping, and inclusive policy measures to strengthen the livelihood capital base and ensure sustainable empowerment of farming communities in the region.

Keywords: Constraints, Livelihood, Empowerment, Stakeholders, Perceived etc.

P3-47

NUCLEAR AND MITOCHONDRIAL DNA CROSSTALK REGULATES THE IMMUNE RESPONSE AGAINST DUCK PASTEURELLOSIS (BACTERIAL INFECTION) IN DUCK

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ABSTRACT

Mitochondria are not merely the "powerhouses" of the cell but are dynamic, semi-autonomous organelles that play pivotal roles in cellular energy metabolism, calcium homeostasis, iron regulation, apoptosis, and innate immunity. Although the mitochondrial genome encodes only thirty-seven genes, proper mitochondrial structure, enzymatic function, and dynamic behavior rely on the coordinated expression of more than two hundred nuclear-encoded genes. This intricate communication between mitochondrial DNA (mtDNA) and the nuclear genome establishes a tightly regulated genomic axis, the disruption of which is increasingly recognized as a contributing factor to diverse pathological conditions across species. In the present study, we investigated the mitochondrial–nuclear cross-talk regulating immune responses during Pasteurella-induced infection (duck pasteurellosis) in Anas platyrynchos as a model organism. Our in-depth analysis focused on mitochondrial genes—Cytochrome B and Cytochrome C—and their interaction with nuclear genes NLRP3, IL18, and STING, mediated through the NOD-like receptor signaling pathway, phagocytic pathway, and cytosolic DNA sensing pathway. Molecular docking revealed potential binding sites of IL18 with the bacterial pathogen, while histopathological and immunohistochemical findings further substantiated these molecular interactions. To our knowledge, this is the first report demonstrating such mitochondrial–nuclear cross-talk in an animal model, providing evidence of retrograde signaling from mitochondrial genes to nuclear immune regulators during bacterial infection.

Keywords: Nuclear DNA, mitochondrial DNA, nuclear-mitochondrial cross talk, Duck Pasteurellosis, duck, immunity

P3-48

INNATE IMMUNE RESPONSE GENES AS MX, TLR7, PKR AND OAS OF ANAS PLATYRYNCHOS AFFECT HOST RESISTANCE AGAINST DUCK PLAGUE INFECTION – A NOVEL REPORT

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ABSTRACT

Duck viral enteritis or Duck Plague is considered as one of the most important fatal diseases in water fowl. It is caused by Anatidalphavirus-1 from Herpesviridae family, which consists of double stranded DNA as genetic material. Hence, it is important to detect the host immunity of duck confering resistance to duck plague, for a sustainable development of duck industry. Innate immunity for the ducks are conferred by Pathogen associated molecular pattern (PAMP)s and Pathogen Recognition Receptor (PRR)s. In our earlier study, we could detect and reported promising innate immune response genes as RIGI, MDA5 and interferon alpha. In our current study, we could detect Mx, TLR7, PkR and OAS of Anas platyrynchos as immune response genes in gut associated lymphoid tissue (GALT) in kupfer cells of liver against Duck plague infection. Differential mRNA expression profiling was detected through real time PCR and later confirmed through protein profiling with western blotting.We studied histological section for liver, kupfer cells in both infected and healthy control. The detection and exploration of the genes will be helpful in future for development of resistant variety of duck against duck plague virus through genomic selection, or gene editing technologies. The current study may open up the newer avenues to study host immunity against herpes virus in animal model.

Keywords: Innate immune response genes, Mx, TLR7, PkR, OAS,, Anas platyrynchos, Duck plague

P3-49

EXPLORING THE EFFICACY OF AYAPANA TRIPLINERVIS AGAINST DRUG-RESISTANT AEROMONAS SPECIES IN FISH FARMING

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ABSTRACT

Motile Aeromonas Septicaemia (MAS), caused by pathogens like Aeromonas hydrophila and A. veronii, is a major threat to aquaculture, compounded by the rising incidence of multidrug-resistant (MDR) strains due to antibiotic misuse. This study aimed to characterize MDR Aeromonas isolates from diseased Labeo rohita in India and evaluate the in vitro antibacterial efficacy of Ayapana triplinervis leaf extract as an alternative therapy. Thirty bacterial isolates were obtained from fish showing clinical signs of infection. Biochemical identification confirmed the presence of A. hydrophila and A. veronii. Molecular identification of three major multidrug-resistant strains out of those thirty strains (NCBI Accession Nos. PV450193, PV450195, PV450197) confirmed one A. hydrophila and two A. veronii isolates. Pathogenicity was confirmed through experimental challenge, fulfilling Koch′s postulates, exhibiting high virulence (LD_{50}: 1.28×10^6–1×10^7 CFU/fish). Antibiotic susceptibility testing indicated mostly sensitivity to fluoroquinolones and chloramphenicol but resistance to clindamycin, cefepime, and vancomycin, suggesting emerging resistance trends. GC-MS analysis of the A. triplinervis ethanol extract identified β-selinene, Linolenic acid, Caryophyllene, n-Hexadecanoic acid and thymohydroquinone dimethyl ether as major bioactive compounds. The extract demonstrated potent bactericidal activity against the MDR Aeromonas strains, with low Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) values. The MIC values ranged from 1.0 to 4.0 µL/mL, and the MBC values from 4.0 to 16.0 µL/mL. The extract was most potent against the two Aeromonas veronii strains. These findings highlight the severe risk posed by MDR Aeromonas in aquaculture and position A. triplinervis as a promising, sustainable phytotherapeutic agent for controlling MAS, warranting further investigation into its in vivo application and safety.

Keywords: Multidrug-resistant Aeromonas., Motile Aeromonas Septicaemia (MAS), Ayapana triplinervis, Phytotherapy

P3-50

DEVELOPMENT OF A VIRUS-LIKE PARTICLE (VLP) VACCINE CANDIDATE FOR PORCINE CIRCOVIRUS TYPE 3

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ABSTRACT

Porcine circovirus type 3 (PCV3), a newly emerging porcine circovirus associated with porcine circovirus associated diseases (PCVAD) has caused substantial economic losses in the swine industry around the globe. However, currently available commercial vaccines based on PCV2a/2d whole virus or Capsid protein could not provide adequate protection against PCV3 infection. In this study, we have synthesized and expressed a full-length ORF2 sequence (645 bp) encoding Capsid protein of PCV3_Indian isolate in baculovirus-insect cell expression system. The codon-optimized ORF2 sequence was first cloned into pOPINE vector and then transfected with baculovirus DNA in Spodoptera frugiperda (Sf9) cells to generate recombinant baculovirus and express Capsid protein. The expression of ORF2 (approximately 28 kDa) was confirmed by Western blot and the assembly of Capsid proteins into VLPs was evaluated by Transmission electron microscopy. Further characterization and immunological assessment of PCV3 VLPs are underway.

Keywords: Virus Like Particle, Vaccine, PCV3

P3-51

IDENTIFICATION OF CANDIDATE GENES IN SELECTIVE SWEEPS ASSOCIATED WITH TROPICAL ADAPTATION AND DOMESTICATION IN SAHIWAL CATTLE USING DDRAD SEQUENCING

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ABSTRACT

Sahiwal, an indigenous zebu (*Bos indicus*) cattle breed of the Indian subcontinent, is renowned for its remarkable adaptation to tropical environments, disease tolerance, and superior milk production under heat stress. Understanding the genetic basis of these adaptive traits is essential for conservation and genetic improvement programs. The present study aimed to identify genomic regions and candidate genes under selection associated with tropical adaptation and domestication in Sahiwal cattle using double digest restriction-site associated DNA (ddRAD) sequencing. Genomic DNA from 26 unrelated Sahiwal cows was subjected to ddRAD sequencing, and the resulting SNP data were used to perform selective sweep analysis to detect regions of the genome under positive selection. Several genomic regions exhibiting strong selection signatures were identified, potentially linked to tropical adaptation and domestication. Genes associated with domestication traits such as coat colour and temperament—TYRP1, vWA3A, ZBTB20, NCKAP5, and DOCK1—were located within putative selective sweep regions. Candidate genes related to thermotolerance, including DNAJC3, DNAJC8, and PLCB1, were also detected among the selected regions, highlighting their role in maintaining cellular homeostasis under heat stress. Furthermore, genes implicated in gastrointestinal nematode resistance—CSMD2, RSAD2, ABCC2, HS6ST3, AADAC, PLB1, BST1, SLC6A20, RBP2, and ACAD11—were identified, underscoring the breed's adaptive immune competence. Collagen-related genes (COL11A1, COL19A1, COL23A1, COL25A1, COL26A1, COL4A3BP, COL4A4, COL5A1, COL8A1) and the keratin-associated gene KRT20 were also found to be under selection, reflecting structural adaptations that may contribute to skin integrity and tick resistance. This study provides novel insights into the genomic architecture of tropical adaptation and domestication in Sahiwal cattle. The identified candidate genes represent valuable targets for marker-assisted selection and genomic breeding strategies aimed at enhancing climate resilience and productivity in tropical dairy cattle.

Keywords: Sahiwal cattle, ddRAD sequencing, selective sweep, tropical adaptation, candidate genes, domestication.

P3-52

PROBLEMS FACED BY EXTENSION WORKERS AND DAIRY FARMERS IN UTILIZATION OF ICT TOOLS

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ABSTRACT

Information and Communication Technology (ICT) has emerged as a vital tool in modern agricultural extension and dairy development, enabling rapid access to knowledge, innovations, and services. However, the effective utilization of ICT tools among extension personnel and dairy farmers is often hindered by various constraints. The present study was undertaken to identify and analyse the problems faced by extension workers and dairy farmers in the use of ICT tools. The study was conducted among 20 extension workers and 80 dairy farmers of Ghaziabad and Meerut district of Western Uttar Pradesh. The data were collected using a structured interview schedule and analysed using frequency and percentage methods. The findings revealed that among the extension workers, the most prominent general problems were poor or slow internet connection (55.00%), lack of knowledge about the use of ICT tools and websites (45.00%), and inadequate computer facilities (40.00%). Physiological problems such as backache (30.00%) and headache (25.00%) were commonly reported, while social issues included were lack of time for visiting relatives (35.00%) and reduced real-life social interactions (25.00%). In the case of dairy farmers, the major general problems included lack of knowledge (47.50%), poor or slow internet connection (43.75%), and absence of DTH connection to televisions (40.00%). Physiological constraints such as backache (20.00%) and eye pain (17.50%) were reported among the dairy farmers with social concerns like reduced participation in social gatherings (20.00%) and limited time for friends and relatives. The findings indicate that both extension workers and dairy farmers face multiple technological, physiological, and social constraints in effectively utilizing ICT tools. The study highlights the need for improved internet connectivity, capacity-building programs, and ergonomic and social support measures to enhance ICT adoption and sustainable use in the dairy sector.

Keywords: ICT tools, constraints, internet connectivity, training needs.

P3-53

DIETARY SUPPLEMENTATION OF ZINC NANOPARTICLE CAN MODULATE THE EXPRESSION PROFILE OF ANTIOXIDANT AND ANTIVIRAL GENE IN CHANOS CHANOS

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ABSTRACT

Nanotechnology has become one of the most emerging topics now a days. Nano minerals already gained attention because bioavailability is now a very challenging issue. We have synthesized zinc nanoparticle and confirmed its size by microanalytical characterization. Then the experimental feed was fortified with inorganic, organic and synthesized nano-Zn separately. After completion of the feeding trial efficacy of different dietary Zn sources was analysed and compared in Chanos chanos. After a 120 days long in vivo trial, supplementation of nano-Zn proved to have a marked influence on growth performance and antiviral and antioxidant gene expression. The present study reveals the upregulation of Cu-Zn SOD, catalase and IRF3 gene expression among the fish body that were fed nano-Zn fortified diet. Highest mRNA expression of catalase and IRF3 gene was observed in the diet that was fortified with 40 ppm nano-Zn but highest Cu-Zn SOD expression was observed in the diet fortified with 20 ppm nano-Zn. IRF3 is very important part of antiviral signalling pathway. 3D structure of this protein revealed different Zn binding sites and interprets the possible activation due to high bioavailability of nano-Zn. Catalase is a heme containing enzyme and nano-Zn induce more heme group to bind with it and upregulate the expression of catalase. Now it can be said that nano-Zn has the potential to improve immunity and maintain antioxidant status of the body.

Keywords: Nano minerals, Gene expression, IRF3, Antioxidant, Bioavailability, Immunity

Abstracts under young Researchers' Presentation

ISAGB YOUNG SCIENTIST PRESENTATION

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TAIL-MOUNTED MULTI-SENSOR SYSTEM FOR ESTRUS DETECTION IN BUFFALOES

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ABSTRACT

Buffaloes are integral to the dairy industry, particularly in regions like South Asia, where they contribute significantly to milk production. However, reproductive management in buffaloes poses persistent challenges due to their silent and less overt estrus behavior compared to cattle. This subtle expression often leads to missed breeding opportunities, reduced conception rates, and overall lower productivity. Timely and accurate detection of estrus is therefore critical for improving reproductive efficiency and enhancing farm profitability. To address this issue, we have developed a tail-mounted, multi-sensor device specifically designed for continuous monitoring and prediction of estrus in buffaloes. The system integrates a tri-axial accelerometer, gyroscope, temperature sensor, and pulse sensor to capture both behavioral and physiological indicators associated with estrus. These sensors work in tandem to provide a comprehensive profile of the animal′s activity and health status. Data transmission is facilitated through the LoRa protocol, enabling low-power, long-range communication suitable for rural farm environments. WiFi connectivity allows for remote control of the device, including the ability to deactivate sensors during periods of inactivity to conserve battery life. A local storage module ensures uninterrupted data logging, even in the absence of network connectivity. The system′s gateway can support up to eight devices simultaneously, making it scalable for herd-level implementation. Complementing the hardware, a user-friendly mobile application provides real-time visualization of sensor data and actionable insights for farmers. This IoT-enabled solution not only enhances the accuracy of estrus detection but also supports early health monitoring and decision-making. By offering a cost-effective and scalable tool, our system bridges the technological gap in buffalo reproductive management and paves the way for smarter, data-driven livestock farming.

Key words: Buffalo, Estrus Detection, Sensors

YR-02/YRA/3

GENOME AND TRANSCRIPTOME LANDSCAPES OF ARUNACHALI YAK: A COMPREHENSIVE RESOURCE

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ABSTRACT

Arunachali yak (*Bos grunniens*), the first registered yak breed in India, is an important livestock species that plays a vital role in the Eastern Himalayan region by providing milk, meat, fiber and transport to the highlanders. However, limited genomic information has hindered comprehensive molecular studies in this breed. To address this, we report two complementary resources: a chromosome-scale reference genome and a full-length multi-tissue transcriptome atlas. The genome was assembled de novo using PacBio HiFi long reads, Bionano optical mapping and Hi-C scaffolding resulting in a 2.85 Gb assembly with a scaffold N50 of 102.9 Mb and 95.7% completeness based on BUSCO analysis. A k-mer based genome survey using GenomeScope 2.0 estimated the genome size to be approximately 2.3 Gb. Genome annotation identified 25,855 protein-coding genes, with over 80% functionally annotated. Repetitive elements made up 44.7% of the genome, with LINEs being the most abundant. To complement the genome, a transcriptome atlas was generated from 22 tissues using PacBio Iso-Seq, producing over 200,000 isoforms which included more than 10,000 novel transcripts and 4,319 high-confidence long non-coding RNAs. Functional annotation revealed broad representation of metabolic, endocrine and signalling pathways, contributing to improved gene models and isoform characterization. Together, these datasets provide the first comprehensive genomic and transcriptomic resources for the Arunachali yak, facilitating future studies in conservation genetics, evolutionary biology and molecular breeding.

Keywords: Arunachali yak, genome assembly, transcriptome atlas, conservation genetics

YR-03/YRA/6

COMPARATIVE TRANSCRIPTOMIC ANALYSIS OF SEMEN FROM HIGH AND LOW FERTILE FRIESWAL BULLS

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ABSTRACT

Fertility impairments and sperm abnormalities have been linked to specific RNA molecules present in bovine ejaculates. In spite of the widespread use of conventional semen-quality metrics, prediction of bull fertility remains unreliable. The limited prognostic value of standard diagnostic procedures motivates the exploration of sperm-derived transcriptomic signatures as fertility biomarkers. In the present study, we aimed to generate and compare the spermatozoal transcriptome profiles of high- and low-fertility Frieswal bulls, and to identify RNA expression correlates of fertility status. The work was performed at ICAR–Central Institute for Research on Cattle (CIRC), Meerut Cantt, Uttar Pradesh, India, under the aegis of the ICAR–AICRP on Cattle. Total RNA was isolated from categorized bull spermatozoa using TRIzol reagent (Invitrogen, USA), following the manufacturer's protocol with minor modifications. RNA integrity was evaluated with a Qubit 4.0 fluorometer, and RNA concentration and purity were determined spectrophotometrically with a Nanodrop 1000 by recording absorbance at 260 nm and 280 nm. Paired-end sequencing was conducted on sperm samples from twelve bulls using the NOVASeq 6000 platform (Neuberg Supratech Research Laboratories, Ahmedabad, Gujarat, India). Each sample yielded approximately 50 million 150-bp reads. Out of the 1,064 identified significant transcripts, 28 were found to be significantly upregulated, while 1,036 showed downregulation between the compared groups. Further validation of nine selected transcripts (N = 9) through RT-qPCR demonstrated a notable decrease in the expression levels of RACK1, ZNF706, PRM1, and CRISP2 genes in low-fertility bulls compared to high-fertility bulls. These findings suggest that these genes may serve as promising molecular markers for assessing fertility in crossbred bulls.

Key words: Transcripts, RNA, Biomarker, High fertile, Low fertile

YR-04/YRA/4

TRANSCRIPTOMIC PROFILING OF SPERMATOZOA IN INDIGENOUS TAMIL NADU GOAT BREEDS REVEALS KEY GENES INFLUENCING MALE FERTILITY

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ABSTRACT

The productive and reproductive efficiency of indigenous goat germplasm lags behind that of exotic breeds, primarily due to the absence of systematic selection in farmers′ flocks. Introduction of superior quality germplasm from established indigenous breeds, through artificial insemination (AI) offers a sustainable approach for genetic improvement. Since a single ejaculate of a buck could inseminate multiple does, a rigorous scrutiny of males becomes imperative before selection. Ascertaining a male to be fertile concentrating alone on the primary evaluation of routine seminal attributes could be fallacious as they do not weigh the intricate changes occurring in female reproductive tract before fertilization. Spermatozoal RNA (spRNAs) play a significant role in regulating the sperm function, fertilization and early embryo development. Profiling spRNAs could therefore provide critical insights into the molecular mechanisms underlying sperm quality and male fertility. Hence, the present study was carried out to unravel the differential gene expression between the high and low-quality semen producing bucks by RNA sequencing. Of the transcripts identified through sequencing, 1574 transcripts were differentially expressed between the high and low-quality groups and of which, 1083 were upregulated (> 0.5 log2fold change) and 358 genes were downregulated (< -0.5 log2fold change) in high quality group. The pathway analysis of the upregulated genes revealed their involvement in most of the important pathways like Calcium signalling pathway, axon guidance, WNT signalling pathway etc. among the 30 significant pathways, showing the vital role of the genes in regulating the sperm motility and fertility. The key genes associated with seminal attributes were further validated through qPCR assay. These findings provide valuable insights into the molecular determinants of sperm quality in indigenous goat breeds and offer a foundation for developing fertility biomarkers to enhance selection strategies in AI programs, ultimately promoting sustainable caprine production.

Keywords: Indigenous goats, Male fertility, RNA sequencing, Spermatozoa

YR-05/YRA/5

GENOME-WIDE ANALYSIS OF PROMOTER CPG ISLAND METHYLATION DYNAMICS IN KADAKNATH CHICKENS

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ABSTRACT

Epigenomics, an emerging field of genomics, investigates heritable changes in gene expression that occur without alterations in the DNA sequence, including those influenced by environmental stimuli and genomic imprinting. The present study aimed to compare the genome-wide methylation landscape of promoter-associated CpG islands (CGIs) in Kadaknath and commercial Layer chickens using whole-genome Nanopore sequencing. Global methylation profiling revealed a significantly lower mean CGI methylation level in Kadaknath (0.2758 ± 0.003) compared to Layers (0.3158 ± 0.003), indicating a more transcriptionally permissive epigenetic state in Kadaknath. Differential methylation analysis identified a total of 1,224 differentially methylated CGIs (DM-CGIs) between the two breeds (FDR < 0.001), of which 48.4% were hypermethylated and 51.6% were hypomethylated in Kadaknath. Gene feature–wise analysis revealed that approximately 11.9% of the DM-CGIs were associated with promoters, while nearly 49.9% were located within gene bodies, suggesting extensive regulatory impact. Among these, the promoters of FAHD2AL, SMTNL2, TADA2B, CORO1C, TDRKH, and UAP1 genes were found to be significantly hypermethylated and are involved in regulating metabolic processes, cytoskeletal dynamics, and reproductive functions. In contrast, GARNL3, Pou5f3, SASH3, PGF, TMEM238, and JAKMIP2 genes exhibited promoter hypomethylation, which is strongly associated with immune signaling and angiogenesis pathways, reflecting balanced metabolic adaptability in Kadaknath chickens. In conclusion, this study demonstrates a clear epigenetic divergence between Kadaknath and Layer chickens, with Kadaknath exhibiting unique gene-specific methylation patterns that may underpin its reproductive efficiency, adaptability, and resilience traits.

Key words: CpG Island, Epigenomic, Kadaknath, Promoter-Associated Methylation.

YR-06/YRA/8

PEDIGREE INBREEDING METRICS REVEAL INBREEDING DEPRESSION IN FERTILITY TRAITS AND SELECTION RESPONSE OF MURRAH BUFFALOES

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ABSTRACT

Understanding how inbreeding influences fertility and long-term selection efficiency is crucial for the sustainable genetic improvement of Indian dairy buffalo. The present study evaluated the impact of inbreeding on first-lactation reproductive performance in Murrah buffalo and its implications for selection response within the nucleus herd. Pedigree data of 6429 animals born between 1954 to 2018 at the ICAR–NDRI herd, Karnal, were analyzed to estimate inbreeding levels and their association with fertility-related traits and genetic gain. Individual inbreeding coefficients were computed from pedigree relationships using Wright′s formula implemented in ENDOG (version 4.8). Three major reproductive indicators—age at first calving (AFC), first service period (FSP), and first calving interval (FCI)—were analyzed through linear fixed-effect models, and the regression of these traits on inbreeding coefficients quantified the extent of inbreeding depression. Expected genetic gain for each trait was further estimated to assess how inbreeding affects the efficiency of selection. Buffaloes exhibiting inbreeding levels above 5% showed a significant reduction in reproductive efficiency. Genetic loss in AFC increased approximately fourfold, while both FSP and FCI nearly doubled compared with animals having 0.1–5% inbreeding, indicating that such levels are unsustainable for long-term improvement. The decline in expected genetic gain at higher inbreeding levels further demonstrated that excessive inbreeding reduces additive genetic variance and limits selection response. To ensure continuous genetic progress and reproductive stability, it is advisable to maintain inbreeding below 5%. The adoption of structured mating strategies such as rotational, minimum-coancestry, or genomic mating schemes can effectively control inbreeding accumulation while retaining selection intensity. Moreover, establishing a well-characterized, genotyped reference population will enhance the accuracy of genomic selection and promote balanced genetic improvement. Overall, the study emphasizes that maintaining genetic diversity is essential not only for conservation but also for achieving sustained productivity and long-term genetic advancement in Murrah buffalo breeding programs.

Key words: Murrah buffalo, inbreeding, reproductive traits, genetic gain, breeding strategy, genomic selection

YR-07/YRA/9

AI-DRIVEN CYTOLOGICAL DIAGNOSIS OF CANINE ROUND CELL TUMORS USING YOLOv8 AND DEEP LEARNING ARCHITECTURES FOR ENHANCED VETERINARY HEALTH MANAGEMENT

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ABSTRACT

Canine round cell tumors (RCTs) are diagnostically challenging neoplasms due to overlapping cytological features. This study proposes an AI-driven framework integrating object detection and deep learning-based classification for automated diagnosis of canine RCTs. In the first stage, the YOLOv8x (You Only Look Once, version 8) model was trained to localize tumor regions in cytology images and achieved precision of 0.85, recall of 0.88, and mean average precision at IoU 0.5 (mAP@0.5) of 0.93. In the second stage, five advanced architectures, EfficientNet-B2, ResNet50, DenseNet-121, Swin-Tiny Transformer, and ConvNeXt-Tiny, were fine-tuned and evaluated for multi-class tumor classification. On an independent unseen test dataset, ConvNeXt-Tiny achieved the highest accuracy (96.01%), followed by ResNet50 (94.56%), DenseNet-121 (94.56%), EfficientNet-B2 (93.11%), and Swin-Tiny Transformer (92.38%), highlighting ConvNeXt-Tiny as the top-performing model with strong generalization capability. The integrated YOLOv8 detection and deep learning classification pipeline demonstrated robust performance across RCT subtypes, indicating its potential to assist veterinary cytologists in rapid, objective, and accurate tumor diagnosis. This approach holds potential for supporting early tumor detection and enhancing veterinary oncology decision-making.

Key words: Canine round cell tumors, YOLOv8, ConvNeXt-Tiny, Deep learning, Convolutional Neural Network, Cytology

YR-08/YRA/11

GENETIC REGULATION OF GUT BARRIER PROTEIN ZO-1 BY THE ETHANOLAMINE/ARID3A/MIR-101A PATHWAY DRIVES LEAKINESS AND METABOLIC INFLAMMATION IN OBESITY/TYPE-2 DIABETES

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ABSTRACT

Obesity-associated dysbiosis is increasingly identified as a critical biological factor influencing gut health, epithelial integrity, and systemic inflammation in both human and animal populations. However, the molecular link through which altered microbial metabolism leads to barrier breakdown and metabolic dysfunction remains poorly defined. In this research, we characterize a metabolite-microRNA mechanism that connects dysbiotic microbiota to increased gut permeability and metabolic inflammation. Using a multi-system approach involving fecal microbiota transplantation (FMT), Caco-2 epithelial monolayers, murine intestinal organoids, and diet-induced obese mouse models, we observed that dysbiotic gut communities exhibit reduced capacity to utilize ethanolamine, a phospholipid-derived nutrient commonly consumed by commensal bacteria. This impairment leads to ethanolamine accumulation within the gut lumen. Elevated ethanolamine significantly reduced transepithelial electrical resistance, increased FITC-dextran leakage, activated TLR4-mediated inflammatory signaling, and suppressed tight-junction protein Zo-1, demonstrating its direct pathological role in epithelial barrier loss. Transcriptomic profiling revealed strong ethanolamine-induced upregulation of miR-101a-3p. Luciferase reporter assays confirmed that miR-101a targets conserved 3′UTR-binding sites in Zo-1 mRNA, thereby reducing post-transcriptional stability and tight-junction assembly. In vivo, miR-101a overexpression disrupted barrier integrity, whereas miR-101a knockout mice maintained Zo-1 expression, exhibited reduced endotoxemia, and showed improved glucose handling, confirming the requirement of this pathway for disease progression. Upstream regulatory analysis identified ARID3a as an ethanolamine-responsive transcription factor driving miR-101a expression. A translational intervention was tested using a human-origin ethanolamine-degrading probiotic (Lactobacillus rhamnosus HL-200). Supplementation depleted luminal ethanolamine, suppressed ARID3a/miR-101a signaling, restored intestinal junctional proteins, reduced inflammatory endotoxin translocation, and significantly improved metabolic parameters. Collectively, these findings define a novel microbiota/ethanolamine/miR-101a axis that regulates epithelial barrier function and metabolic inflammation. This work highlights ethanolamine-degrading probiotics as a promising precision-microbiome strategy with potential applications for improving gut health and metabolic resilience in both human and veterinary systems.

Key words: microRNA, Leaky gut, Endotoxemia, Obesity/Type-2 Diabetes, Probiotics

YR-09/YRA/7

AI-BASED GENETIC MERIT PREDICTION IN SHEEP

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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.

Key words: Breeding Value, Artificial Intelligence, Machine Learning, Artificial Neural Networks

YR-10/YRA/1

AUTOMATED DETECTION AND THRESHOLD-BASED ALERTING OF STRAY DOGS

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ABSTRACT

The free-roaming dog population of India poses a serious public safety, health, and animal welfare challenge. Approximately 20 million dog-bite cases and 20,000 rabies-related deaths occur each year in the country. Robust and widespread solutions are required for this problem, and monitoring stray animals using traditional methods could be challenging and inefficient. This study explores an AI-driven solution using advanced deep learning techniques for this problem. We developed a custom-trained YOLOv11s model using transfer learning based on a real-world dataset obtained from various locations of Srinagar and Ganderbal district of Jammu and Kashmir, India. This model detects and counts both dogs and humans in images taken from urban streets and campuses, with a particular focus on stray dog situations in Kashmir. Our system achieved precision rates of 0.995 for dogs and 0.991 for humans, with recall rates of 0.966 for dogs and 0.915 for humans. The mean average precision (mAP@0.5) was 0.973. This model was integrated into a user-friendly web application, enabling detection and the setting of configurable threshold-based alerts. This application characterizes the deployable use of YOLOv11s for urban stray dog surveillance in India. AI-based digital solutions provide scalable and minimally intrusive solutions for public safety and One Health.

Key words: Artificial Intelligence, Computer Vision, Management

YR-11/YRA/12

PHYLOGENY AND DIVERSITY STUDY IN PIGS OF BASTAR REGION OF CHHATTISGARH STATE THROUGH MITOCHONDRIAL DNA D-LOOP NUCLEOTIDES SEQUENCE

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ABSTRACT

As there is no recognized breed of pig from Chhattisgarh state this study was aimed to characterize the pig in view of preserving rich indigenous genetic resources biodiversity and to investigate genetic diversity, relationship and matrilineal lineage of Bastar pigs. The current study is the first of its sort to evaluate the mitochondrial DNA (mt DNA) control region i.e. 10 Displacement Loop (D-loop) in Chhatisgarhi pig of Bastar region. For genetic/molecular characterization of the pigs, a total 60 blood samples were collected from different pockets of Bastar region comprising Narayanpur, Bastar and Dantewada district. The DNA was extracted from blood samples using Non-enzymatic salting method and then (PCR) Polymerase Chain Reaction was performed for amplification of D-loop. The amplicons were purified and then sequenced using Sanger sequencing technique. The D loop region of different pig populations was sequenced and analyzed to identify distinct mtDNA haplotypes and it was found that non protein coding sequences of Bastar region pig sample had 06 polymorphic sites in a patch of 313 bp. The pig population under study had a total of 33 haplotypes with haplotype (gene) diversity of 0.275. Two of the Bastar region samples were identified as singletons in haplogroups 32 & 33. From the above study it may be concluded that the indigenous pigs of Chhattisgarh state have good performance and systematic breeding plan for their selection is needed. The findings of this study will be a baseline for effective breeding strategies and conservation management of this breed in future.

Key words: Indigenous pig, Bastar, Mitochondrial DNA, D-loop, phylogenetics, genetic diversity

YR-12/YRA/2

EVALUATION OF CHLOROCOCCUM SP. AS A FUNCTIONAL FEED ADDITIVE ON GROWTH PERFORMANCE, CARCASS CHARACTERISTICS AND HAEMATOLOGICAL PARAMETERS IN BROILER CHICKENS

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ABSTRACT

This study evaluated the effects of dietary Chlorococcum sp. supplementation on growth performance, carcass traits and haematological parameters in broilers. Sixty day-old Vencobb 400 chicks were randomly assigned to three groups: T0 (control), T1 (0.5% Chlorococcum sp.), and T2 (1% Chlorococcum sp.), and reared for 42 days on a standard corn-soya diet. Growth parameters such as body weight, weight gain, feed intake, and feed conversion ratio (FCR) were recorded weekly. Carcass traits and hematological parameters were evaluated to determine physiological and nutritional impacts of microalgae inclusion at trial completion. Birds of treatment T2 exhibited significantly higher ($p<0.05$) body weights during the 3rd and 5th weeks, indicating enhanced mid-phase growth. Feed intake was significantly higher ($p<0.05$) in T2 during weeks 1 and 4, though total feed intake remained statistically similar across treatments. FCR was numerically lowest in T2, with significant improvements ($p<0.05$) in weeks 1, 3, and 5, reflecting superior feed efficiency. Carcass traits, including dressing percentage and relative breast, thigh, and drumstick weights, were not significantly affected, indicating no adverse effect on meat yield. However, wing weight was significantly reduced in T1 and T2 ($p<0.05$). Among internal organs, gallbladder weight was significantly reduced in T2, and heart weight increased in T1 ($p<0.05$). Crop weight was significantly elevated in both algae-supplemented groups. Other visceral organs (liver, spleen, intestine, gizzard) remained unaffected, suggesting physiological safety. Haematological analysis indicated numerically improved values in red and white blood cell counts, haemoglobin concentration, and total protein levels in the supplemented groups, suggesting a positive effect on immune and metabolic health. Chlorococcum sp. at 1% dietary inclusion improved growth and feed efficiency without compromising carcass yield or organ integrity, supporting its potential as a sustainable, functional feed additive and alternative to synthetic growth promoters in broiler production.

Key words: Chlorococcum sp., Broiler, Feed conversion ratio (FCR), Carcass characteristics

YR-13

WHOLE-GENOME SEQUENCING REVEALS THE UNIQUE GENOMIC LANDSCAPE OF 33 CATTLE BREEDS ADAPTED TO CONTRASTING PRODUCTION SYSTEMS AND AGRO-CLIMATIC ZONES

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ABSTRACT

The present study was undertaken to elucidate the copy number variation map of 33 cattle breeds (364 genomes) with special reference to India, spanning different agro-climatic zones and rearing purposes i.e., hilly/cold-adapted, Indian plain milch, Indian draught, other indicine breeds and commercial transboundary breeds. Standardised procedures were used to achieve consistent base calling and sequencing for all samples in both trials. Using whole-genome sequencing (WGS) data, we processed the raw reads for quality control before aligning them to the ARS-UCD2.0 domestic cattle reference genome. The CNVnator program was used to detect CNVs, which were then clustered into 105,202 copy number variation regions (CNVRs). RIdeogram program was used to plot the distribution of CNVRs against gene density. BEDTools was used to determine the common (having the same chromosomal coordinates), overlapping (having at least one bp overlap), and unique CNVs and CNVRs based on the chromosomal coordinates of structural variants from various populations. Gene profiling of genomic regions found to harbour CNVs or selection signatures associated with stature in different populations was undertaken using GALLO package. The analysis revealed an average of 5,537 CNVRs per breed, with the highest number of duplications found in Gir cattle and the fewest in Holstein Friesian. This included an average of 1483.15 duplications, 3864.73 deletions, and 95.68 mixed CNVRs. Among hill/cold-adapted breeds, Ladakhi showed the most CNVRs. We identified and profiled CNVRs shared by specific populations, such as milch and hill/cold breeds, highlighting regions present in a high percentage of individuals (e.g., ≥90%). In milch populations (142 genomes), a total of 193460 regions were identified, among which 18314 were singletons, 50075 were present in ≥50% of individuals, 10595 in ≥70%, 2017 in ≥90% and 47 in 100% of animals. In hill/cold breeds (86), a total of 77073 regions were identified, among which 11847 were singletons, 10482 were present in ≥50% of individuals, 3634 in ≥70%, 734 in ≥90% and 17 in 100% of animals. These regions could represent genomic signatures of adaptation. The study establishes a comprehensive atlas of CNVs and CNVRs for Indian cattle breeds, providing valuable insights for future breed improvement programs.

Keywords: CNVR, Agro-climatic Zones; WGS; Atlas; Cattle.

YR-14

SIMULATION-BACKED SELECTIVE AND CROSSBREEDING STRATEGIES FOR GENETIC IMPROVEMENT OF INDIGENOUS CHICKENS UNDER LOW-INPUT MANAGEMENT

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ABSTRACT

Indigenous Jharkhand chicken populations maintained under low-input management system (tribal setup) represent invaluable reservoirs of genetic diversity but remain largely underutilized in systematic genetic improvement programs. In this study, we explored optimized strategies for their genetic enhancement through forward simulations, incorporating both genomic selection based on genomic estimated breeding values (GEBV) and crossbreeding approaches. Using ddRAD-seq, approximately 128,000 high-quality single nucleotide polymorphisms (SNPs) were identified and analyzed alongside 863 global chicken and wild junglefowl genomes. Population genomic analyses revealed that Jharkhand tribal chickens formed a distinct genetic cluster with minimal evidence of admixture, indicating relative isolation and preservation under traditional management practices. Selection scan analyses identified both population-specific and shared candidate genes associated with growth, skeletal development, lipid metabolism, and stress tolerance, highlighting ongoing adaptive evolution under local agro-climatic and management pressures. Landscape genomic analyses further identified genomic regions contributing to climatic adaptation. These climate correlated polymorphic regions and selection signatures were incorporated into a forward simulation study to evaluate selective breeding through different BLUP models. The simulated selection response over ten generations predicted modest genetic gains indicating limited improvement under selection schemes. Consequently, crossbreeding simulations were performed, revealing that a three-way cross involving (Cornish × White Leghorn) × Jharkhand indigenous chicken exhibited superior heterosis for key traits, including body weight, egg production and disease resistance. Additionally, gametic simulations under a no-recombination suggested that inbreeding coefficients could approach unity within 10–12 generations, thereby accelerating the development of inbred parental lines. Overall, our simulations provide theoretical insights into the optimal breeding schemes for genetic improvement of economically important traits of local chickens while preserving their adaptive genetic potential. Together, these findings demonstrate that while low-input (tribal) management has constrained productivity, it has been instrumental in conserving unique adaptive alleles and genomic integrity.

Keywords: Chicken, Genetic Improvement, Simulations, Low input management

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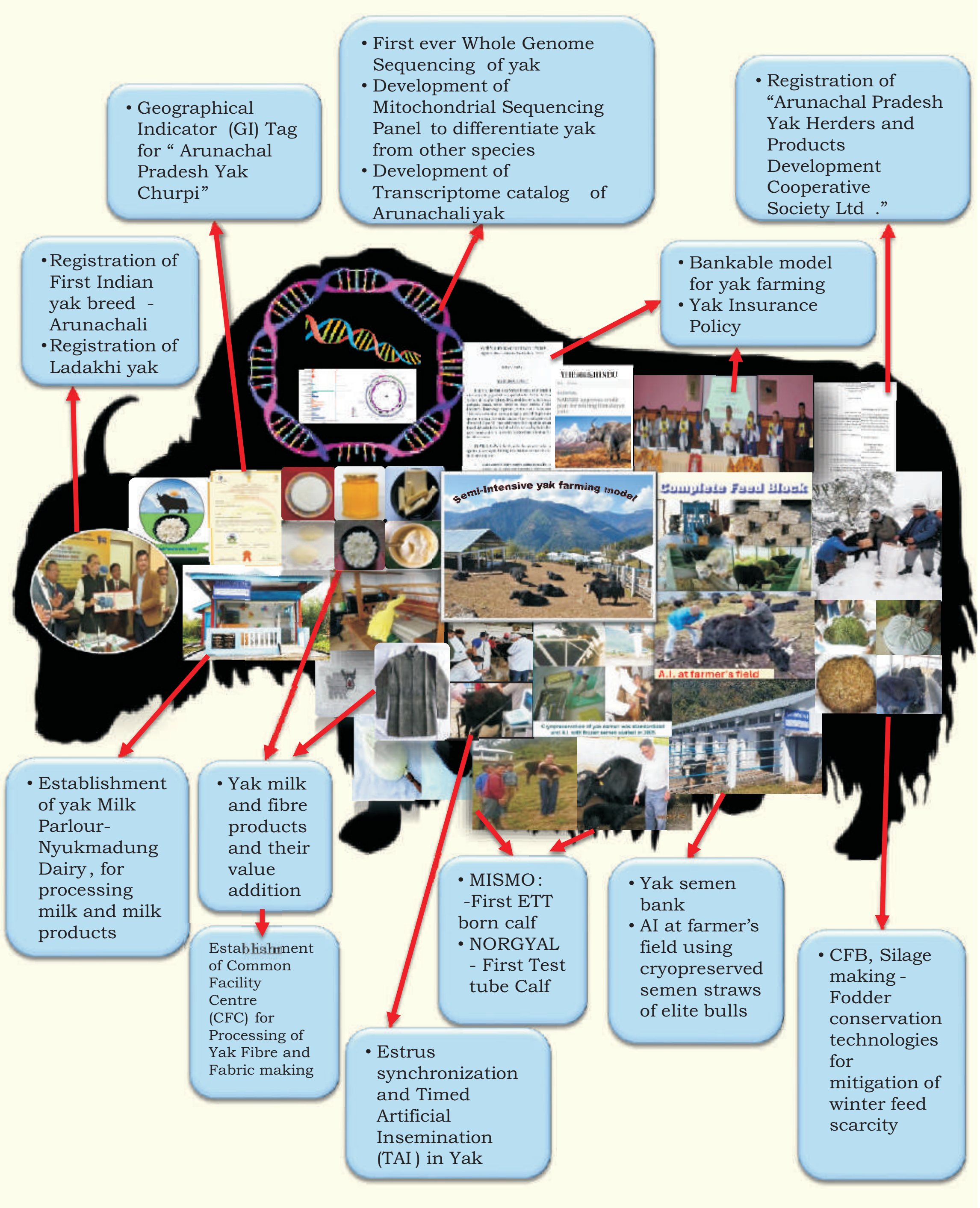

- Geographical Indicator (GI) Tag for " Arunachal Pradesh Yak Churpi"

- First ever Whole Genome Sequencing of yak
- Development of Mitochondrial Sequencing Panel to differentiate yak from other species
- Development of Transcriptome catalog of Arunachali yak

- Registration of "Arunachal Pradesh Yak Herders and Products Development Cooperative Society Ltd ."

- Registration of First Indian yak breed - Arunachali
- Registration of Ladakhi yak

- Bankable model for yak farming
- Yak Insurance Policy

- Establishment of yak Milk Parlour- Nyukmadung Dairy , for processing milk and milk products

- Yak milk and fibre products and their value addition

Establishment of Common Facility Centre (CFC) for Processing of Yak Fibre and Fabric making

- Estrus synchronization and Timed Artificial Insemination (TAI) in Yak

- MISMO : -First ETT born calf
- NORGYAL - First Test tube Calf

- Yak semen bank
- AI at farmer's field using cryopreserved semen straws of elite bulls

- CFB, Silage making - Fodder conservation technologies for mitigation of winter feed scarcity

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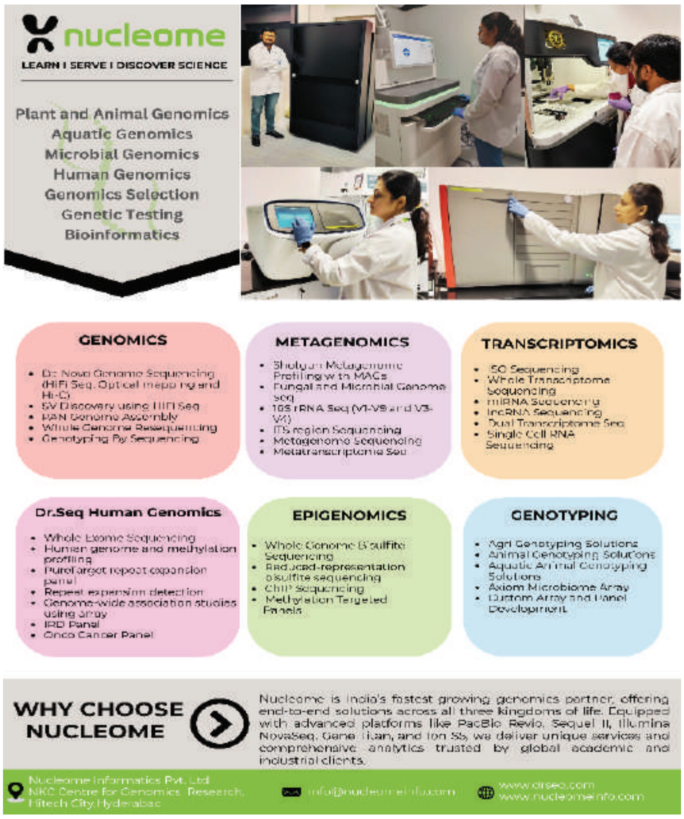

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- SV Discovery using HiFi Seq
- PAN Genome Assembly
- Whole Genome Resequencing
- Genotyping By Sequencing

METAGENOMICS

- Shotgun Metagenome Profiling with MAGs
- Fungal and Microbial Genome Seq
- 16S rRNA Seq (V1-V9 and V3-V4)
- ITS region Sequencing
- Metagenome Sequencing
- Metatranscriptome Seq

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