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ICAR NIVEDI

Transforming Animal Health

वार्षिक प्रतिवेदन Annual Report

2025

NERVE CENTRE OF ANIMAL DISEASE INTELLIGENCE FOR A HEALTHY INDIA

- DIAGNOSTICS & REFERENCE SERVICES
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भाकृअनुप-राष्ट्रीय पशुरोग जानपदिक एवं सूचना विज्ञान संस्थान

ICAR-National Institute of Veterinary Epidemiology and Disease Informatics


राष्ट्रीय पशुरोग जानपदिक एवं सूचना विज्ञान संस्थान
NATIONAL INSTITUTE OF VETERINARY EPIDEMIOLOGY AND DISEASE INFORMA

वार्षिक प्रतिवेदन
2025

ANNUAL REPORT
2025

ICAR-National Institute of Veterinary Epidemiology and Disease Informatics

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Front cover page: Administrative cum Laboratory Building of ICAR-NIVEDI

Back cover page : Honorable Agriculture Minister Addressing Staff and Farmers at ICAR-NIVEDI & National Award for e-Governance 2025 (Gold) for NADRES-v2.0

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Director's Foreword

It is my privilege to present the Annual Report of ICAR-NIVEDI for the year 2025, highlighting the institute's continued leadership and key scientific contributions in veterinary epidemiology, disease informatics, and livestock health management. During the year, ICAR-NIVEDI strengthened national livestock disease surveillance, diagnostics, and forecasting through multidisciplinary research, One Health approaches, and data-driven innovations.

A major achievement was the conferment of the National Award for e-Governance 2025 (Gold) for NADRES-v2, an AI- and GIS-enabled disease forecasting platform providing district-level predictions for 15 major livestock diseases along with timely advisories to stakeholders. The institute also expanded its research portfolio with 15 new externally funded projects, bringing the total to 51 ongoing projects.

Significant research advancements were made in understanding major bovine, small ruminant, and swine diseases through integrated epidemiological, molecular, and genomic approaches. Studies on haemoprotozoan infections, Lumpy Skin Disease, brucellosis, leptospirosis, and antimicrobial resistance generated critical insights for disease control and managements. Development of advanced diagnostics, including ELISA and multiplex PCR assays, and contributions to vaccine research further strengthened disease detection and prevention strategies. Large-scale serosurveillance under national programmes demonstrated improved population immunity against priority diseases such as PPR and Classical Swine Fever.

The institute also made notable progress in disease informatics and modelling. NADRES-v2.0 enabled early warning by predicting high-risk disease events, while climate-driven and spatial analyses supported hotspot identification and preparedness planning. Socio-economic studies highlighted the impact of diseases such as African Swine Fever and emphasized the benefits of improved biosecurity and farmer-centric interventions.

ICAR-NIVEDI strengthened collaborations through MoUs with leading institutions and continued capacity building through training programmes and outreach activities. The institute produced 78 research publications and 23 technical outputs, while advancing innovation through copyrights and patent applications.

I sincerely acknowledge the continued guidance and support of ICAR Headquarter, the Department of Animal Husbandry and Dairying (DAHD), Government of India, State Animal Husbandry Departments, collaborating institutions, and all stakeholders. I also commend the dedicated efforts of the scientists, staff, and partners of ICAR-NIVEDI.

I sincerely acknowledge the continued guidance and support of the Secretary, DARE & Director General, ICAR, Dr. M. L. Jat, the Deputy Director General (Animal Science), Dr. Raghavendra Bhatta; and the Assistant Director General (Animal Health), Dr. Divakar Hemadri. I also thank all NADEN Investigators, collaborating centers and my colleagues at ICAR-NIVEDI for their dedicated efforts.

I look forward to continued collaboration and valuable feedback from stakeholders and the scientific community to further strengthen our collective efforts in livestock disease surveillance, health management, and public health protection.

(Baldev Raj Gulati)

Kisan Diwas Celebration on 23rd December 2025

Executive Summary 1

During 2025, ICAR-NIVEDI carried out extensive multidisciplinary research to strengthen livestock disease surveillance, epidemiology, diagnostics, vaccine evaluation, and One Health–based disease control strategies in India. The institute addressed major diseases affecting bovines, swine, and small ruminants, alongside zoonotic infections and antimicrobial resistance (AMR). Advanced approaches such as molecular epidemiology, genomic analysis, disease informatics, spatial modelling, and environmental surveillance were integrated to better understand disease dynamics and transmission patterns. A total of 15 new externally funded projects (including three international projects) were initiated, increasing the total to 51 ongoing projects. A major institutional achievement was the National Award for e-Governance 2025 (Gold) for NADRES-v2, an AI and GIS enabled disease forecasting platform that predicts 15 livestock diseases at the district level and disseminates advisories to stakeholders. The institute also made strong contributions in research output and capacity building, including 78 research publications, 23 technical outputs, 28 training programmes, and multiple collaborations through MoUs. Revenue generation and intellectual property development further strengthened its national leadership in livestock health research.

Significant progress was made in understanding and controlling bovine diseases through integrated epidemiological, molecular, and One Health approaches. Surveillance studies in Karnataka and Chhattisgarh revealed widespread prevalence of haemoprotozoan infections such as *Theileria*, *Babesia*, *Anaplasma*, and *Trypanosoma*. Risk factors included tick infestation, grazing practices, and housing conditions. Molecular studies showed high genetic diversity in pathogens, emphasizing the need for continuous surveillance and vector management. Research on Lumpy Skin Disease virus (LSDV) confirmed its presence across 23 states, including buffalo populations. Genetic analysis of LSDV identified unique viral characteristics, suggesting regional evolution. Co-infections with haemoprotozoan parasites and vector transmission through biting flies were also documented. Diagnostic advancements included development of ELISA assays for blackleg disease, demonstrating high sensitivity and specificity. Immunological studies identified vaccine candidate proteins, enhancing prospects for subunit vaccine development. Under the national Brucellosis control programme, large-scale seromonitoring indicated a 71% seroconversion rate, with regional variations highlighting the need for improved vaccination strategies. One Health surveillance confirmed continued circulation of brucellosis and leptospirosis at the human–animal interface. Environmental studies showed contamination of soil and water with pathogenic *Leptospira*, while integrated interventions reduced human disease prevalence. Laboratory research also established a standardized infection Hamster model and developed rapid multiplex PCR diagnostics for Leptospirosis. AMR studies revealed the presence of resistant pathogens such as MRSA and ESBL-producing *E. coli* across animals, humans, and environments, emphasizing the importance of integrated surveillance. Additional findings included evidence of bovine tuberculosis (4.67% prevalence in Karnataka) and sentinel detection of PPR antibodies in cattle (6%). Overall, these efforts significantly enhanced national capacity for disease detection, monitoring, and control, contributing to improved livestock and public health.

Research on small ruminants involved extensive diagnostic, epidemiological, and

genomic investigations. Over 2,100 samples were processed, confirming diseases such as PPR, pasteurellosis, anthrax, brucellosis, and haemoprotozoan infections. Sixty outbreaks were investigated, with 44 confirmed through laboratory diagnosis. Field investigations highlighted the role of animal movement and tick exposure in disease outbreaks. A major haemoprotozoan outbreak in Karnataka demonstrated the importance of biosecurity and quarantine measures in organized farms. Under the PPR Eradication Programme, large-scale seromonitoring showed a significant increase in population immunity from 41% (2023) to nearly 75% (2025), with vaccine effectiveness around 72%. Many regions achieved over 70% herd immunity, indicating strong progress toward PPR eradication goals by 2030. Genomic studies confirmed the dominance of Lineage IV PPR virus strains across India, with close similarity to strains in neighbouring regions. Advanced diagnostics such as multiplex RT-PCR and recombinant antigen-based ELISAs for anthrax and enterotoxaemia were developed, improving disease detection and surveillance. Other findings included widespread bluetongue virus exposure, significant prevalence of contagious caprine pleuropneumonia, and detection of multiple *Mycoplasma* species in respiratory infections. Zoonotic surveillance identified exposure to Chandipura virus and highlighted risks from tick-borne diseases at the wildlife–livestock interface. Genomic analysis of *Bacillus anthracis* revealed significant diversity and dominant lineages, aiding epidemiological tracing. Overall, these studies strengthened surveillance systems, improved diagnostics, and supported national disease control programmes.

Swine disease research focused on surveillance, outbreak investigation, and vaccine evaluation. Under the Classical Swine Fever Control Programme, antibody prevalence increased from 30.1% to 77.7%, indicating successful vaccination efforts. Molecular studies showed no active CSF virus circulation in sampled populations. Notably, the first co-infection of Porcine Epidemic Diarrhoea Virus (PEDV) and African Swine Fever Virus (ASFV) was reported in India. Outbreak investigations identified biosecurity lapses and human-mediated transmission as key factors. Targeted interventions effectively controlled disease spread. Surveillance also confirmed circulation of Japanese Encephalitis Virus (JEV) in pigs, with 35.6% seropositivity and the first isolation of Genotype I in India. from pig. Diagnostic tools, including ELISA for ASF, were developed to strengthen monitoring.

In disease informatics, NADRES-v2.0 played a central role in forecasting disease risks using AI and machine learning. The system processed millions of data points monthly and predicted up to 1,200 high-risk events, enabling early warning through advisories and risk maps. Climate-driven epidemiological studies demonstrated the impact of environmental factors on disease dynamics. Spatial modelling techniques identified disease hotspots and supported predictive frameworks for 15 major diseases. Farmer surveys indicated increasing climate-related stress, and awareness programmes promoted adaptive practices. Large-scale serosurveillance under national programmes generated extensive datasets for diseases such as FMD, Brucellosis, CSF, and PPR, supporting real-time monitoring and decision-making. Risk mapping of LSD and modelling of Japanese Encephalitis further enhanced understanding of disease transmission. Socioeconomic studies revealed significant economic losses due to ASF outbreaks, with mortality accounting for nearly 78% of losses. Modelling showed that improved biosecurity could reduce mortality by 49% and outbreaks by 75%. Livelihood interventions improved income and resilience among farmers in multiple states.

ICAR–NIVEDI strengthened collaborations through seven MoUs with leading institutions. The institute made notable academic contributions with 78 research papers, and authored 23 book chapters/technical publications, technical bulletins and delivering invited lectures at national and international platforms. To further enhance expertise, scientists also actively participated in 18

conferences, 9 workshops and 6 trainings. It also advanced innovation by registering two copyrights and filing three patents. Capacity-building efforts included 28 training programmes, while revenue generation reached ₹51.33 lakh through diagnostics and technology transfer. Staff members received 9 awards and fellowships across scientific conferences and professional societies and the institute won 2 gold and 2 silver medals at the ICAR South Zone Sports Tournament. Overall, with strong institutional support and stakeholder collaboration, ICAR–NIVEDI reinforced its position as a national leader in livestock health research and innovation.

In conclusion, the integrated efforts of ICAR-NIVEDI in 2025 significantly strengthened India's capacity for livestock disease surveillance, diagnostics, modelling, and control. The adoption of advanced technologies such as AI, genomics, and spatial analytics, combined with One Health approaches, enabled improved disease preparedness and response. The institute's contributions not only enhanced livestock productivity and farmer livelihoods but also played a critical role in safeguarding public health and supporting national disease control programmes.

The institute gratefully acknowledges the continued guidance and support of ICAR Headquarters, the Department of Animal Husbandry and Dairying (DAHD), Government of India, State Animal Husbandry Departments, and collaborating institutions, as well as the cooperation of field veterinarians and stakeholders across the country.

कार्यकारी सारांश 1

वर्ष 2025 में भा.कृ.अनु.प.-निवेदी ने भारत में पशुधन रोग निगरानी, महामारी विज्ञान, निदान, टीके मूल्यांकन, और वन हेल्थ-आधारित रोग नियंत्रण रणनीतियों को सशक्त करने के लिए व्यापक बहु-विषयक अनुसंधान किया। संस्थान ने गोवंश, सूअर और भेड़-बकरी को प्रभावित करने वाले प्रमुख रोगों, जूनोटिक संक्रमणों और प्रतिजैविक प्रतिरोध (AMR) का समाधान किया। आणविक महामारी विज्ञान, जीनोमिक विश्लेषण, रोग सूचना विज्ञान, स्थानिक मॉडलिंग, और पर्यावरणीय निगरानी जैसे उन्नत दृष्टिकोणों को रोग गतिविज्ञान और संचरण पैटर्न को बेहतर ढंग से समझने के लिए एकीकृत किया गया।

इस अवधि में 15 नवीन बाह्य वित्तपोषित अनुसंधान परियोजनाओं (जिनमें 3 अंतरराष्ट्रीय परियोजनाएँ सम्मिलित हैं) का शुभारंभ किया गया, जिससे संस्थान में संचालित कुल परियोजनाओं की संख्या 51 हो गई। संस्थान की एक महत्वपूर्ण उपलब्धि राष्ट्रीय पशु रोग रिपोर्टिंग और प्रारंभिक चेतावनी प्रणाली – सं. 2 (NADRES-V2) के लिए वर्ष 2025 का राष्ट्रीय ई-गवर्नेंस पुरस्कार (स्वर्ण) प्राप्त करना रहा। यह कृत्रिम बुद्धिमत्ता (AI), मशीन लर्निंग एवं भौगोलिक सूचना प्रणाली (GIS) आधारित एक उन्नत रोग पूर्वानुमान प्रणाली है, जो जिला स्तर पर 15 पशुधन रोगों का पूर्वानुमान कर हितधारकों को समयबद्ध परामर्श उपलब्ध कराती है।

संस्थान द्वारा अनुसंधान प्रकाशनों, तकनीकी निष्पादनों एवं क्षमता निर्माण के क्षेत्र में भी उल्लेखनीय योगदान दिया गया। वर्ष के दौरान 78 शोध पत्र प्रकाशित किए गए, 23 तकनीकी बुलेटिन प्रकाशित किए गए तथा 28 प्रशिक्षण कार्यक्रम आयोजित किए गए। इसके अतिरिक्त, विभिन्न संस्थानों के साथ समझौता ज्ञापनों (MoUs) के माध्यम से सहयोगात्मक गतिविधियों को सुदृढ़ किया गया। राजस्व सृजन एवं बौद्धिक संपदा के विकास ने पशुधन स्वास्थ्य अनुसंधान के क्षेत्र में संस्थान की अग्रणी भूमिका को और सुदृढ़ किया।

गौवंशीय रोगों की समझ एवं नियंत्रण के क्षेत्र में महामारी विज्ञान, आणविक एवं 'वन हेल्थ' दृष्टिकोणों के माध्यम से महत्वपूर्ण प्रगति दर्ज की गई। कर्नाटक एवं छत्तीसगढ़ राज्यों में किए गए निगरानी अध्ययनों से *थीलिरिया, बेबेसिया, एनाप्लाज्मा* तथा *ट्रिपैनोसोमा* जैसे हीमोप्रोटोज़ोआ संक्रमणों का व्यापक प्रसार परिलक्षित हुआ। अध्ययनों में यह पाया गया कि टिक संक्रमण, चराई प्रथाएँ तथा आवासीय व्यवस्थाएँ प्रमुख जोखिम कारक हैं। आणविक विश्लेषण से रोगजनकों में उच्च आनुवंशिक विविधता का पता चला, जिससे सतत निगरानी एवं वेक्टर नियंत्रण की आवश्यकता स्पष्ट होती है।

लम्पी त्वचा रोग वायरस (LSDV) के व्यापक अनुसंधान से भारत के 23 राज्यों में इस विषाणु के सक्रिय संचरण की पुष्टि हुई, विशेषकर भैंस पशुधन में। वायरल जीनोम विश्लेषण से LSDV की क्षेत्र-विशिष्ट आनुवंशिक विविधता और स्थानीय विकासीय विशेषताएँ प्रकट हुईं। अध्ययन में लम्पी त्वचा रोग से ग्रस्त पशुओं में *Theileria*, *Babesia*, *Trypanosoma* और *Anaplasma* जैसे रक्त-परजीवियों का सह-संक्रमण भी पाया गया, जहाँ *Stomoxys* और *Tabanus* जैसी काटने वाली मक्खियाँ इन परजीवियों के जैविक वाहक के रूप में कार्य करती हैं।

निदान प्रौद्योगिकी के क्षेत्र में ब्लैक क्वार्टर (काला पैर) रोग के लिए ELISA-आधारित परीक्षण विकसित किए गए, जो अत्यधिक संवेदनशीलता (sensitivity) और रोग-विशिष्टता (specificity) प्रदर्शित करते हैं। समानांतर रूप से, प्रतिरक्षात्मक अध्ययनों द्वारा ब्लैक क्वार्टर रोग के कारक जीवाणु (*Clostridium chauvoei*) के प्रमुख रक्षा-प्रेरक प्रोटीन (immunogenic proteins) की पहचान की, जिससे आधुनिक पुनः-संयोजक-प्रोटीन-आधारित (subunit) टीके विकास की वैज्ञानिक नींव प्रशस्त हुई।

राष्ट्रीय ब्रुसेलोसिस नियंत्रण कार्यक्रम के अंतर्गत किए गए व्यापक सीरो-मॉनिटरिंग से 71 प्रतिशत सीरो-कन्वर्जन दर दर्ज की गई, जिसमें क्षेत्रीय भिन्नताएँ भी परिलक्षित हुईं, जो टीकाकरण रणनीतियों के सुदृढ़ीकरण की आवश्यकता को इंगित करती हैं। 'वन हेल्थ' निगरानी के अंतर्गत जहाँ मनुष्य और पशु एक-दूसरे के संपर्क में आते हैं, वहाँ ब्रुसेलोसिस एवं लेप्टोस्पायरोसिस के लगातार फैलने की पुष्टि हुई। पर्यावरणीय अध्ययनों से मिट्टी एवं जल में रोगजनक *लेप्टोस्पाइरा* की उपस्थिति पाई गई, जबकि एकीकृत हस्तक्षेपों से मानव संक्रमण में कमी देखी गई। प्रयोगात्मक मॉडल अध्ययन में लेप्टोस्पायरोसिस के लिए हैम्स्टर संक्रमण मॉडल विकसित किया गया और बहु-लक्ष्य PCR निदान तकनीकें विकसित की गईं।

प्रतिजैविक प्रतिरोध (AMR) अध्ययन ने पशुओं, मनुष्यों और

पर्यावरण में MRSA और ESBL-उत्पादक ई. *कोलाई* जैसे प्रतिरोधी रोगजनकों की उपस्थिति का खुलासा किया, जिससे एकीकृत निगरानी के महत्व पर बल पड़ता है। अनुसंधान के अतिरिक्त महत्वपूर्ण निष्कर्षों में निम्नलिखित शामिल थे: (i) कर्नाटक प्रदेश में गोवंश में गोवंश तपेदिक (bovine tuberculosis) का सीरोलॉजिक प्रसार 4.67% पाया गया, जो राष्ट्रीय नियंत्रण कार्यक्रमों के लिए सार्थक निहितार्थ रखता है; (ii) कई राज्यों में सेंटिनल-सर्वेक्षण से गोवंश में Peste des Petits Ruminants (PPR) विषाणु के विरुद्ध विशिष्ट-प्रतिरोधक तत्वों (antibodies) का 6% प्रसार पाया गया, जो छोटे पशु-से-गोवंश प्रजातीय-सीमांत संचरण का सूचक है। कुल मिलाकर, इन प्रयासों ने रोग संसूचन, निगरानी और नियंत्रण के लिए राष्ट्रीय क्षमता में उल्लेखनीय सुधार किया, जो पशुधन और जनस्वास्थ्य में सुधार में योगदान दिया।

भेड़-बकरी पर अनुसंधान में व्यापक निदान, महामारी विज्ञान और जीनोमिक जाँचें शामिल थीं। 2,100 से अधिक पशुओं से नमूने एकत्र किए गए, जिससे PPR, पास्चुरेलोसिस, एंथ्रैक्स, ब्रुसेलोसिस और हीमोप्रोटोज़ोअन संक्रमण जैसे रोगों की पुष्टि की गई। 60 प्रकोपों की जाँच की गई, जिनमें से 44 प्रयोगशाला निदान के माध्यम से पुष्टि की गई। क्षेत्रीय अध्ययनों में पशु आवागमन एवं टिक संक्रमण को प्रमुख जोखिम कारक पाया गया। कर्नाटक में रक्त-परजीवी रोग के एक बड़े प्रकोप से पता चला कि संगठित पशु फार्मों में जैव-सुरक्षा और संगरोध कितने महत्वपूर्ण हैं।

PPR उन्मूलन कार्यक्रम के अंतर्गत व्यापक सीरो-मॉनिटरिंग से जनसंख्या प्रतिरक्षा 41 प्रतिशत (2023) से बढ़कर लगभग 75 प्रतिशत (2025) हो गई, जहाँ टीके की प्रभावकारिता लगभग 72% रही। कई क्षेत्रों में 70 प्रतिशत से अधिक सामूहिक प्रतिरक्षा प्राप्त हुई, जो वर्ष 2030 तक उन्मूलन लक्ष्य की दिशा में महत्वपूर्ण प्रगति का संकेत है। आनुवंशिक अनुक्रमण अध्ययन से पता चला कि भारत में PPR वायरस के लाइनेज IV उपभेद प्रमुख हैं, जो पड़ोसी देशों में पाए जाने वाले उपभेदों के समान हैं।

एंथ्रैक्स और एंटरोटॉक्सेमिया के लिए multiplex PCR परीक्षण तथा पुनर्संयोजक प्रतिजन (r-protein) आधारित ELISA निदान तकनीकें विकसित की गईं, जिससे रोग की शीघ्र पहचान में सुधार हुआ। अन्य निष्कर्षों में ब्लूटंग वायरस का व्यापक प्रसार, संक्रामक कैप्राइन प्ल्यूरोप्न्यूमोनिया की उच्च प्रचलन दर तथा श्वसन संक्रमणों में विभिन्न *माइकोप्लाज्मा* प्रजातियों की पहचान शामिल हैं।

जूनोटिक निगरानी से चंदीपुरा वायरस का संपर्क पता चला और दिखा कि वन्यजीवों और पशुओं के मिलने वाले क्षेत्रों में टिक के काटने से होने वाले रोग का खतरा कितना है। Bacillus anthracis के आनुवंशिक अध्ययन से इसकी विभिन्न किस्मों और प्रमुख प्रकारों की जानकारी मिली, जो रोग के फैलने का पता लगाने में मदद करती है। इन सभी अध्ययनों से निगरानी व्यवस्था बेहतर हुई, रोग की पहचान तेज़ हुई, और देश के रोग नियंत्रण कार्यक्रमों को सहायता मिली।

सूअर रोग अनुसंधान के अंतर्गत निगरानी, प्रकोप जांच एवं वैक्सीन मूल्यांकन पर विशेष ध्यान दिया गया। क्लासिकल स्वाइन फीवर नियंत्रण कार्यक्रम के अंतर्गत एंटीबॉडी प्रचलन 30.1 प्रतिशत से बढ़कर 77.7 प्रतिशत हो गया, जो टीकाकरण की सफलता को दर्शाता है। आणविक अध्ययनों में सक्रिय वायरस संचरण का अभाव पाया गया। उल्लेखनीय है कि भारत में सूअरों में PEDV और ASFV दोनों वायरस का एक साथ संक्रमण पहली बार रिपोर्ट किया गया। प्रकोप की जाँच से जैव-सुरक्षा में कमियों और मानव-माध्यम संचरण को रोग के मुख्य कारकों के रूप में चिन्हित किया गया, जिसके बाद लक्षित हस्तक्षेपों द्वारा रोग के प्रसार को प्रभावी रूप से नियंत्रित किया गया।

निगरानी अध्ययन से पता चला कि सूअरों में जापानी इन्सेफेलाइटिस वायरस (JEV) फैल रहा है, 35.6% सूअर संक्रमित पाए गए, और भारत में इस वायरस का एक नया प्रकार (जीनोटाइप I) मिला। अफ्रीकी सूअर बुखार से संक्रमित पशुओं के लिए ELISA परीक्षण विकसित किया गया, जिससे निगरानी बेहतर हुई।

रोग आसूचना प्रणाली में NADRES-v2 ने कृत्रिम बुद्धिमत्ता तथा मशीन लर्निंग तकनीकों का उपयोग करके रोग जोखिम पूर्वानुमान में मुख्य भूमिका निभाई। यह प्रणाली प्रतिमाह लाखों डेटा बिंदुओं को विश्लेषित करती है और लगभग 1,200 उच्च-जोखिम घटनाओं की भविष्यवाणी प्रदान करती है, जो सलाहों और जोखिम मानचित्रों के माध्यम से शीघ्र चेतावनी सुनिश्चित करती है। जलवायु और पर्यावरण संबंधी अध्ययन से पता चला कि मौसम और पर्यावरणीय बदलाव रोग के फैलाव को कैसे प्रभावित करते हैं। भूस्थानिक मॉडलिंग तकनीकों ने देशभर में रोग के केंद्रों (hotspots) की पहचान की और ब्रुसेलोसिस, FMD, CSF, PPR, ASF, लेप्टोस्पायरोसिस सहित 15 प्रमुख रोगों के लिए भविष्य-पूर्वानुमान मॉडल विकसित किए गए।

पशुपालकों के सर्वेक्षण से पता चला कि जलवायु बदलाव से उन्हें अधिक परेशानी हो रही है। जागरूकता कार्यक्रमों ने उन्हें नई और बेहतर खेती की विधियाँ सिखाईं।ष्ट्रीय निगरानी कार्यक्रमों के अंतर्गत व्यापक सीरोसर्वेक्षण से FMD, ब्रुसेलोसिस, CSF तथा PPR जैसे रोगों हेतु विशाल डेटासेट प्राप्त हुए, जो तात्कालिक निगरानी एवं प्रभावी निर्णय लेने में सहायक रहे।

लम्पी त्वचा रोग (LSD) का भौगोलिक जोखिम मानचित्रण तथा Japanese Encephalitis की गणितीय मॉडलिंग ने रोग संचरण के तंत्र की गहन समझ प्रदान की। सामाजिक-आर्थिक विश्लेषण से African Swine Fever (ASF) प्रकोपों से पशुपालकों को होने वाले गंभीर आर्थिक क्षति का आकलन किया गया, जिसमें पशु मृत्यु-हानि कुल नुकसान का 78% थी। महामारी-नियंत्रण मॉडलिंग ने प्रदर्शित किया कि उन्नत जैव-सुरक्षा उपायों से पशु मृत्यु-दर 49% तक घटाई जा सकती है तथा और रोग के प्रकोप 75% कम हो सकते हैं। किसान-केंद्रित आजीविका सहायता कार्यक्रमों ने कई राज्यों में ग्रामीण परिवारों की आय और संकट-सहनशीलता में उल्लेखनीय सुधार किया।

ा.कृ.अनु.प.-निवेदी ने अग्रणी संस्थानों के साथ सात समझौता ज्ञापनों (MoUs) के माध्यम से अंतर्संस्थागत सहयोग को सुदृढ़ किया। संस्थान के वैज्ञानिकों ने 78 शोध-पत्रों का प्रकाशन किया तथा 23 पुस्तक अध्याय, तकनीकी प्रकाशन एवं तकनीकी सूचना-पत्र (बुलेटिन) लेखन के माध्यम से ज्ञान-विस्तार किया, साथ ही राष्ट्रीय एवं अंतर्राष्ट्रीय विचार-मंचों पर आमंत्रित व्याख्यान प्रस्तुत किए।

संस्थान के द्वारा 28 कार्यशालाओं, प्रशिक्षण कार्यक्रमों और अन्य क्षमता-विकास गतिविधियों का आयोजन किया गया। वैज्ञानिक टीम के सदस्यों को राष्ट्रीय और अंतर्राष्ट्रीय वैज्ञानिक सम्मेलनों तथा व्यावसायिक संगठनों से 9 प्रतिष्ठित पुरस्कार और अनुसंधान फेलोशिप प्राप्त हुई। संस्थान के खेल दल ने ICAR दक्षिण क्षेत्रीय खेल प्रतियोगिता में 2 स्वर्ण और 2 रजत पदक की उल्लेखनीय उपलब्धि प्राप्त की। सारांश में, सशक्त संस्थागत प्रशासन, अंतर-क्षेत्रीय सहयोग और बहु-हितधारक भागीदारी के माध्यम से, भा.कृ.अनु.प.-निवेदी ने भारत में पशुधन स्वास्थ्य अनुसंधान, रोग सूचना विज्ञान और महामारी नियंत्रण के क्षेत्र में अग्रणी संस्थान के रूप में अपनी प्रतिष्ठा और नेतृत्व को पुनः प्रतिष्ठापित किया।

संक्षेप में, भा.कृ.अनु.प.-निवेदी के वर्ष 2025 में किए गए समन्वित प्रयासों ने पशुधन रोग सर्वेक्षण, आणविक निदान, भविष्य-पूर्वानुमान मॉडलिंग तथा महामारी नियंत्रण के क्षेत्र में भारतीय क्षमता को उल्लेखनीय रूप से सुदृढ़ किया। कृत्रिम बुद्धिमत्ता, संपूर्ण जीनोम विश्लेषण, भौगोलिक सूचना प्रणाली और स्थानिक विश्लेषण जैसी अत्याधुनिक तकनीकों को One Health समन्वित दृष्टिकोण के साथ संस्थागत किया गया, जिससे संक्रामक रोग जोखिम प्रशमन, शीघ्र चेतावनी और राष्ट्रीय तैयारी-प्रतिक्रिया क्षमता में वास्तविक सुधार सुनिश्चित हुआ। संस्थान के वैज्ञानिक-तकनीकी योगदान ने पशुधन उत्पादन, ग्रामीण आय-सुरक्षा और खाद्य सुरक्षा को सशक्त करने के साथ-साथ, जूनोटिक रोग निवारण, मानव-पशु-पर्यावरण जोखिम इंटरफेस प्रबंधन और भारतीय संक्रामक रोग नियंत्रण नीति-निर्माण में केंद्रीय भूमिका निभाई है।

संस्थान सचिव कृ.अ.श.वि. और महानिदेशक भा.कृ.अनु.प., डॉ. एम.एल. जाट, उप महानिदेशक (पशु विज्ञान), डॉ. राघवेंद्र भट्टा, सहायक महानिदेशक (पशु स्वास्थ्य), डॉ. दिवाकर हेमाद्री और ICAR के सभी अधिकारियों; पशुपालन और डेयरी विभाग, भारत सरकार सचिव, श्री नरेश पाल गंगवार, पशु पालन आयुक्त, डॉ. नवीना, राज्य पशुपालन विभागों के निदेशकों, सहयोगी संस्थानों, और देश भर के क्षेत्रीय पशुचिकित्सकों तथा हितधारकों के सहयोग के लिए कृतज्ञ है।

Introduction

2

The ICAR-National Institute of Veterinary Epidemiology and Disease Informatics (ICAR-NIVEDI), formerly known as the Project Directorate on Animal Disease Monitoring and Surveillance (PD-ADMAS), functions under the Indian Council of Agricultural Research (ICAR), Department of Agricultural Research and Education, Ministry of Agriculture and Farmers Welfare, Government of India. As a pioneering institute in the country, ICAR-NIVEDI is mandated to conduct research and development in veterinary epidemiology and disease informatics, with a focus on disease surveillance, monitoring, outbreak investigations and impact analysis of livestock diseases through a network of collaborative centers across various states. The Institute has a long successful history of delivering predicted informatics and epidemiological solutions for various animal diseases.

Established in Karnataka, the Institute began its journey in 1987 as the All India Coordinated Research Project (AICRP) on Animal Disease Monitoring and Surveillance, which was elevated to the status of Project Directorate (PD-ADMAS) in 2000 and subsequently re-designated as ICAR-NIVEDI in 2013. The coordinating network expanded from 4 centers in 1987 to 31 centers under AICRP-ADMAS by 2021 and since April 2021, has been reorganized as the National Animal Disease Epidemiology Network (NADEN), currently comprising 35 centers.

The role of ICAR-NIVEDI is significant in developing disease models, risk analysis, animal disease forecasting & forewarning. It is also working on the development of population assays and surveillance diagnostic kits for epidemiological serosurvey. ICAR-NIVEDI is also working on the development of spreadsheet modules for economic impact analysis of important endemic livestock diseases *viz*., FMD, PPR, BT, Brucellosis, HS and LSD in the country. The role of this institute in the eradication of Rinderpest from India and the development of the National Animal Disease Referral Expert System (NADRES), interactive software for animal disease forecasting is noteworthy.

The institute has seven patents granted to its credit and another three patents have been filed. With regard to copyright, twelve applications have been registered. The scientists of the institute have published more than 468 research papers in reputed national and international journals in the last six years. ICAR-NIVEDI also organizes

VISION

Achieving freedom from animal diseases, animal welfare, food and nutritional security through healthy foods of animal origin, poverty alleviation and economic growth of rural India.

MANDATE

- Epidemiology, informatics and economics of animal diseases including zoonosis
- Surveillance, forecasting and forewarning for management of animal diseases including Zoonosis
- Repository and Capacity Development

MISSION

Capacity building in frontier areas of Veterinary Epidemiology: dynamics of animal diseases including zoonosis and animal healthcare intelligence.

capacity-building programs for students, academicians, veterinarians and medical and para-medical professionals in the field of biosafety, animal health emergency, zoonotic disease diagnosis, descriptive epidemiology and disease modelling.

The Institute has national and international projects funded with various organizations and stakeholders, including DBT, ICMR, NCDC, NIE, NIMHANS, CDC, FAO, WHO, WOAH, ILRI, BBSRC, MRC-UK, UKCEH, DTRA, BMGF etc., for collaborative research, laboratory capacity building and human resource development. The institute has conducted more than 118 capacity-building training programmes on epidemiology, economic impact, sampling frame, GIS and RS and disease diagnosis including biosafety and biosecurity and farmers awareness on zoonoses and AMR. NaaVic, the Agribusiness incubation center, is a unique facility of NIVEDI, nurturing the startups/ entrepreneurs in the field of animal husbandry and veterinary services through identification, incubation, promotion and funding. This center has provided need based physical space for administrative and laboratory work, technical, business and networking support, facilities and services to test and validate their venture before the successful establishment of enterprises. Furthermore, during the year 2025 MoUs were signed with seven institutions, including Vellore Institute of Technology, India Meteorological Department and Bengaluru Science and Technology Cluster.

ICAR-NIVEDI is at the forefront of the societal development of scheduled caste and schedule tribe communities through DAPSC and TSP programs. Under these GoI initiatives, goats, chickens, feed, medicines and training programs have been provided to ensure economic and social upliftment and nutritional security for the children, rural women and youth.

In the pursuit of advancing education, ICAR-IVRI, Bengaluru has been designated as the educational hub and ICAR-NIVEDI was identified as integral component of this educational network with focus on two disciplines *viz*., Veterinary Public Health and Epidemiology and Veterinary Microbiology at ICAR-NIVEDI for teaching.

NIVEDI's active participation in the National Digital Livestock Mission (NDLM) of DAHD, Government of India and collaboration with other organizations focuses on disease modelling, surveillance, monitoring, forewarning, development of need-based diagnostics and population surveillance assay kits for field diagnosis. The Institute also undertakes capacity building, integrated One Health surveillance, outbreak investigations, forecasting of zoonoses and strengthening One Health support units. Estimation of economic losses from major livestock diseases, public health impacts, the economic burden of zoonotic infections and the influence of climate change on disease emergence and pathogen evolution through advanced modelling remain niche research areas for NIVEDI.

The future priority areas for ICAR-NIVEDI include strengthening the existing disease forecasting system by developing quality databases using village-and block-level livestock disease data, along with climatic and non-climatic risk factors. The Institute aims to advance research in animal disease simulation modelling for improved forecasting accuracy, model precision, validation and comprehensive risk assessment of endemic, emerging and re-emerging diseases. Development of risk maps will further enable optimal resource utilization and better disease management.

Through National Livestock Disease Epidemiology and Disease Modelling Program (INLEAD) funded by Gates Foundation, ICAR-NIVEDI will strive to transform and strengthen livestock disease epidemiology and disease modelling capacity in India to protect and promote livestock health.

Infrastructure Facilities

ICAR-NIVEDI houses state-of-the-art infrastructure to support advanced research in veterinary epidemiology, disease surveillance and diagnostics. The institute's unique Biosafety Level 2++ containment laboratory is among the few high-containment facilities in the country, enabling safe handling and investigation of high-risk pathogens. Notably, two laboratories-Peste des Petits Ruminants (PPR) and Leptospirosis-have been

designated as World Organisation for Animal Health (WOAH) Reference Laboratories, underscoring NIVEDI's global standing in livestock disease research.

The institute maintains a well-equipped Spatial Epidemiology and GIS Laboratory, Disease Informatics Laboratory and a dedicated Disease Investigation Laboratory. A fully functional training hall with modern audio-visual facilities supports national capacity-building programs, along with a committee room for regular scientific meetings and a dedicated farmers' hostel to accommodate trainees during training programs. As a major national resource, NIVEDI hosts the National Livestock Serum Repository (NLSR), which currently holds over one lakh serum samples from various livestock species across multiple states and Union Territories, serving as a valuable archive for retrospective disease analysis and assay development.

To support its research ecosystem, the institute has established a 1000 Mbps high-speed WiFi campus ensuring robust IT connectivity. The institute also launched a toll-free Number (1800-599-4233) to facilitate enhanced disease reporting and advisory support for veterinarians and livestock owners. In addition, recreational facilities such as table tennis and carrom boards have been created for staff and students. As part of its eco-friendly initiatives, in addition to planting over 1,200 fruit trees (mango, jackfruit, avocado), more than 2,000 forest tree saplings were planted to enhance the green cover of the campus. Over 50 water percolation pits have been constructed for conservation and groundwater recharge.

FOCUS

- Improving disease monitoring and surveillance through the development of population assays and pen-side diagnostics
- Risk assessment of economically important animal diseases
- Adapting strategies to improve animal disease data quality
- Understanding the threat from animal diseases in the background of climate change and globalization
- Developing early warning system and disease modeling/forecasting
- Understanding the economic impacts of animal diseases
- Promoting innovations and improving human resource capacity
- Fostering linkages and collaborations with public and private, national and international organizations

THRUST AREAS

- Development of robust forecasting & forewarning models for important livestock diseases along with risk analysis
- Epidemiological investigation, surveillance and monitoring of endemic and re-emerging diseases of animals including zoonosis
- Development of diagnostics for population survey of economically important diseases including zoonosis
- Molecular epidemiology of pathogens, disease outbreaks and detection and control of infectious diseases
- Socio-economic impact and policy analysis of prioritized diseases

National Animal Disease Epidemiology Network (NADEN)

The National Animal Disease Epidemiology Network (NADEN) was established in 2021-22 after the closure of the AICRP on Animal Disease Monitoring and Surveillance (ADMAS). Coordinated by ICAR-NIVEDI, NADEN operates as a nationwide network of 35 centres across all states and Union Territories, including Regional Disease Diagnostic Laboratories (RDDLs), Animal Quarantine and Certification Services (AQCS) and additional centres from Ladakh, Uttar Pradesh and Rajasthan. The network plays a central role in

strengthening livestock disease surveillance and epidemiology to support timely, evidence-based disease control programs. By systematically collecting and integrating livestock disease data from all states, NADEN has enabled the development of AI and ML powered forecasting tools i.e. National Animal Disease Referral Expert System (NADRES v2.0). This platform generates monthly risk forecasts for 15 prioritized livestock diseases, facilitating early warnings and targeted interventions. Through outbreak investigations, sero-surveillance, risk mapping, pathogen monitoring and assessment of economic losses, NADEN continues to provide critical scientific inputs for national policy decisions, enhancing livestock health management and supporting farmer livelihoods across the country.

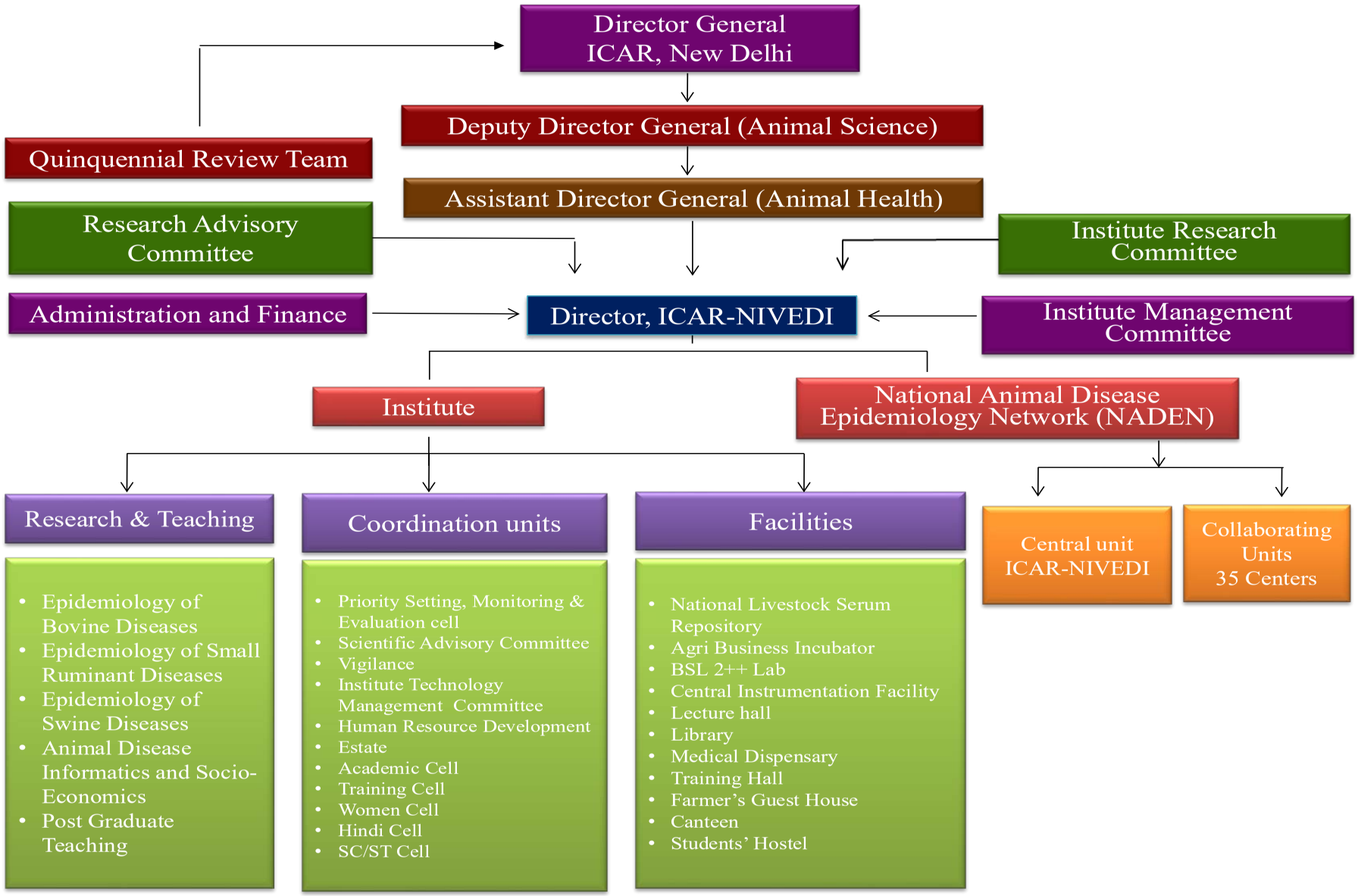
Summary of Expenditure (as on 31.03.2026)

Sl. No.	Head	Fund proposed as per RE (Rs. In Lakhs)	Expenditure made (Rs. In Lakhs)
1	Capital	117.73	117.73
2	Establishment expenses	1088.79	1088.79
3	Pension	74.33	74.33
4	General other than NEH, TSP and SCSP	987.27	987.27
5	NEH General	51.53	51.53
6	NEH Capital	0	0
7	TSP General	13.65	13.65
8	TSP Capital	0	0
9	SCSP General	26.22	26.22
10	SCSP Capital	0.75	0.75
	Total	**2360.27**	**2360.27**

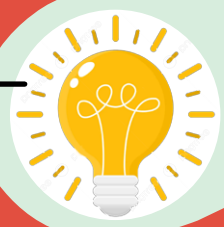
Revenue Receipts (as on 31.03.2026)

Sl. No	Particulars	Amount (In Rs.)
1	Sale of Kits	32,34,354.00
2	On-term term deposits (Interest accrued)	44,968.00
3	Licence Fees	11,37,860.00
4	Guest House Charges	6,76,379.00
5	Testing Charges	2,52,259.00
6	Other income	3,39,812.00
7	Training/Program Fee	19,75,107.00
	Total	**76,60,739.00**

Organogram


Director General
ICAR, New Delhi
Deputy Director General (Animal Science)
Assistant Director General (Animal Health)
Quinquennial Review Team
Research Advisory Committee
Institute Research Committee
Administration and Finance
Director, ICAR-NIVEDI
Institute Management Committee
Institute
National Animal Disease Epidemiology Network (NADEN)
Research & Teaching
Coordination units
Facilities
Central unit ICAR-NIVEDI
Collaborating Units 35 Centers
• Epidemiology of Bovine Diseases
• Epidemiology of Small Ruminant Diseases
• Epidemiology of Swine Diseases
• Animal Disease Informatics and Socio-Economics
• Post Graduate Teaching
• Priority Setting, Monitoring & Evaluation cell
• Scientific Advisory Committee
• Vigilance
• Institute Technology Management Committee
• Human Resource Development
• Estate
• Academic Cell
• Training Cell
• Women Cell
• Hindi Cell
• SC/ST Cell
• National Livestock Serum Repository
• Agri Business Incubator
• BSL 2++ Lab
• Central Instrumentation Facility
• Lecture hall
• Library
• Medical Dispensary
• Training Hall
• Farmer's Guest House
• Canteen
• Students' Hostel

1987-2000



- 1 July 1987: AICRP on animal disease monitoring and surveillance (AICRP-ADMAS) initiated
- The institute worked under National Project on Rinderpest Eradication (NPRE)
- Year 2000: Project Directorate on Animal Disease Monitoring and Surveillance (PD_ADMAS) established

2001-2010

- Institute awarded Sardar Patel Outstanding ICAR Institution Award in the year 2002
- ICAR Awards for Team Research for the Biennium 1999-2000 in the year 2002
- DBT Biotech Product Process Development and Commercialization Award for the development of veterinary ELISA diagnostic kits in the year 2002
- International OIE Meritorious Award in 2002 for RP eradication

2011-2015

- FAO Gold Medal, for outstanding contribution to global RP eradication programme in the year 2011
- Between 2012-2017, 17 additional collaborating units were added to AICRP-ADMAS
- Patent Granted on “A Kit for diagnosis of Brucellosis” on 20 January 2013
- Year 2013: PD-ADMAS promoted to National Institute of Veterinary Epidemiology and Disease Informatics (NIVEDI)
- ISO 9001:2008 certificate awarded in the year 2014
- Administrative Building, Utility Building and BSL-2 Inaugurated on 9 January 2015

LANDMARK ACHIEVEMENTS

2016-2020

- DBT Biotech Product Process Development and Commercialization Award for development of Brucellosis diagnostic kits in the year 2016
- Best Stall Award during National Sheep and Farmers Fair held at Avikanagar held during March 2016
- ISO 9001:2015 certificate awarded to ICAR-NIVEDI in the year 2017
- Training cum Farmers Hostel and Laboratory Block inaugurated on 30 June 2018
- Agribusiness Incubation Centre for Animal Husbandry and Veterinary Services (NaaViC) established in 2019
- Patent granted for:
  - Indirect ELISA kit for sero-diagnosis of brucellosis in livestock and humans on 20 April 2020
  - Diagnosis of human brucellosis by IgG and IgM based combo lateral flow assay on 30 December 2020

2021-2025

- Patent granted for:
  - Recombinant VSG and monoclonal antibody based competitive inhibition enzyme linked immunosorbent assay for the detection of antibodies against *Trypanosoma evansi* on 18 March 2021
  - Monoclonal Antibody based double antibody sandwich ELISA for the detection of *Trypanosoma evansi* antigen in animals on 21 June 2021
  - Recombinant non-structural proteins NS1 and NS3 as fusion protein (rNS1-NS3) based immuno-diagnostic assay for bluetongue on 27 January 2023
  - Recombinant chimeric protein for detection of anti-leptospiral antibodies and methods thereof on 18 September 2023
- Copyright registered: 12
- Release of Kits:
  - PPR Ab Check kit, Bovine Lepto LAT kit PPR Ag Check kit released on 26 March 2022
  - Lumpy Screen rELISA and LumpySure wELISA Kits were released on 8 July 2024
  - Capripox Detect (Sandwich ELISA for Sheep Pox, Goat Pox, and LSD), FLUKEVEY (Indirect ELISA for bovine fasciolosis) and CYSTISURE (Indirect ELISA for porcine cysticercosis) were released on 21 July 2025.
- International Recognition:
  - The Leptospirosis and PPR Laboratories have been recognized as reference laboratories by World Organization for Animal Health, Paris in the year 2024
- ICAR-NIVEDI was conferred with the prestigious National Award for e-Governance 2025 (Gold) by the Department of Administrative Reforms and Public Grievances, Government of India for the NADRES-V2.
- ICAR-NIVEDI received STQC Certification for the website (GIGW 3.0)

Inauguration of WOAH Reference Laboratory for Leptospirosis on 2nd January 2025

Research Achievements 3

Epidemiology of Bovine Diseases

Active Surveillance of Haemoprotozoan Parasites in Large Ruminants across Karnataka

Haemoprotozoan diseases represent a major yet under-recognised constraint to livestock productivity in India, causing substantial economic losses through high morbidity, reduced milk yield, and reproductive failure. An active surveillance-based cross-sectional study was conducted to characterise the epidemiology of major haemoprotozoan parasites in large ruminants across diverse agro-climatic zones of Karnataka. A two-stage random sampling design was employed to collect whole blood samples alongside epidemiological data. Samples were screened by PCR, confirmed by Sanger sequencing, and subjected to risk factor analysis using the Chi-square test.

Among the 227 bovine samples collected from seven districts of Karnataka, *Theileria orientalis* was the most prevalent pathogen, with positivity ranging from 27.8% (Udupi) to 93.3% (Bidar). *Anaplasma* spp. positivity was notable in Chitradurga (57.6%) and Bengaluru Rural (50.0%), while *Babesia* spp. were predominantly detected in Shivamogga (53.3%). *Theileria annulata* and *Trypanosoma evansi* showed lower and more sporadic occurrence across districts (Fig 1). The distribution pattern suggests significant agro-climatic and vector-driven heterogeneity in parasite prevalence across the state.

Risk factor analysis in Chhattisgarh identified tick infestation, insecticide use, proximity of grazing areas to forests, and housing characteristics as significant determinants of theileriosis occurrence ($p < 0.05$).

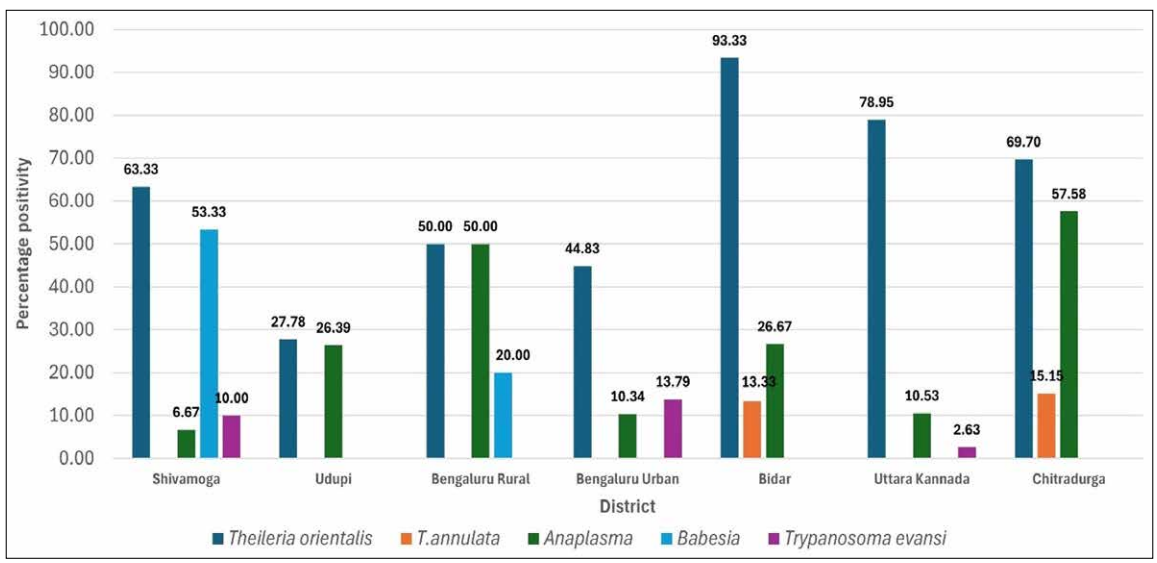


Fig 1: District-wise percentage positivity of different haemoprotozoan parasites.

(Sengupta PP, Siju SJ and Krishnamoorthy P)

Epidemiology of Lumpy Skin Disease Virus (LSDV) in Indian Buffaloes

Lumpy Skin Disease (LSD), caused by Lumpy Skin Disease Virus (LSDV)-a member of the genus *Capripoxvirus*-is a major transboundary viral disease of cattle and buffaloes that inflicts significant economic losses through reduced milk production, weight loss, hide damage, and trade restrictions. Although buffaloes have been considered more resistant to clinical LSD than cattle, their role as reservoir or amplifying hosts in LSDV transmission chains remains inadequately characterized. The present study investigated the molecular, sero-epidemiological, and histopathological aspects of LSDV infection in buffaloes across India.

For molecular characterization, 27 clinical samples (blood, scabs, and nasal swabs) collected from buffaloes of Karnataka, Telangana, Maharashtra, Kerala during 2022-2025 showing clinical signs consistent with LSD were analyzed using conventional and real-time PCR assays targeting the *P32*, *GPCR*, and *RPO30* genes. In parallel, a large-scale serological survey was conducted by screening 14,687 serum samples from apparently healthy buffaloes across 23 Indian states using an indirect ELISA; approximately 2% of samples from each state were additionally tested by Serum Neutralization Test (SNT) for confirmatory validation.

LSDV DNA was confirmed in 37.03% of clinical samples, with Ct values between 18 and 26, consistent with active, productive infection. Phylogenetic analysis placed the buffalo isolates clearly within the LSDV clade, distinct from sheeppox and goatpox viruses. Notably, isolates from Telangana harbored a unique 12-nucleotide in-frame deletion in the *GPCR* gene, a finding of epidemiological and potentially taxonomic significance, as the GPCR locus is a primary marker for capripoxvirus classification. The implications of this deletion for viral fitness or vaccine cross-protection warrant further investigation. Histopathological examination confirmed necrotic vasculitis and mononuclear cell infiltration with intracytoplasmic inclusion bodies in affected tissues, consistent with poxviral pathology.

Seroprevalence in the large-scale survey varied markedly, ranging from 2.13% in Arunachal Pradesh to 81.39% in Uttarakhand — a gradient likely reflecting spatial variation in outbreak history, vector pressure, and vaccination coverage, with the exceptionally high values in Uttarakhand consistent with the extensive LSD outbreaks reported from the region in 2022–23 (Fig 2).

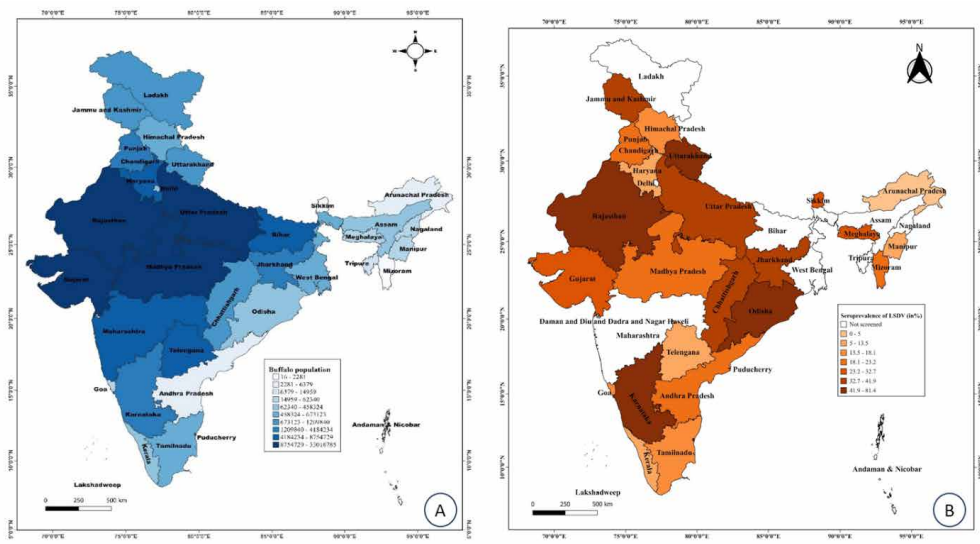


Fig 2: Spatial distribution and seroprevalence of LSD in Buffaloes across India.
A: Illustrates the state-wise buffalo population density across India. B: The seroprevalence of LSD in buffaloes varied from 2.13 to 81.3% with mostly correlating with buffalo population density.

These findings confirm that LSDV circulates actively in Indian buffalo populations and that buffaloes can sustain infection, supporting their potential role as epidemiological links in multi-host transmission networks. Strengthened molecular surveillance, targeted vaccination of buffalo populations, and integrated vector control are essential to reduce disease burden and transmission risk within India's livestock sector.

(Manjunatha Reddy GB, Chethan Kumar HB and Gulati BR)

Understanding the Evolutionary Journey of Indian Lumpy Skin Disease Virus

Lumpy Skin Disease Virus (LSDV), an emerging pathogen belonging to the genus *Capripoxvirus*, continues to pose a significant challenge to global livestock health due to its ongoing genetic evolution and transboundary spread. Through an extensive phylogenetic analysis of 15 partial and 3 whole genome sequences from cattle and Mithun from India, the Time to the Most Recent Common Ancestor (TMRCA) estimates of Indian strains suggest that the most recent common ancestor dates back to the last decade, indicating recent emergence and continued viral adaptation.

Maximum likelihood phylogenetic analysis based on the whole genome and *GPCR* gene sequences demonstrated clustering of global strains, highlighting the transboundary movement and genomic diversity of LSDV (Fig 3). A TCS haplotype network analysis further revealed distinct haplogroups across different geographic regions, including India, South Africa, China, and Russia. Several mutation events between haplogroups indicate ongoing genetic diversification of the virus, consistent with known patterns of geographic spread. Comparative analysis with studies on other *Capripoxviruses* and related viral pathogens suggests that LSDV shares similar evolutionary dynamics while also exhibiting unique genetic pathways that may contribute to its persistence and widespread distribution.

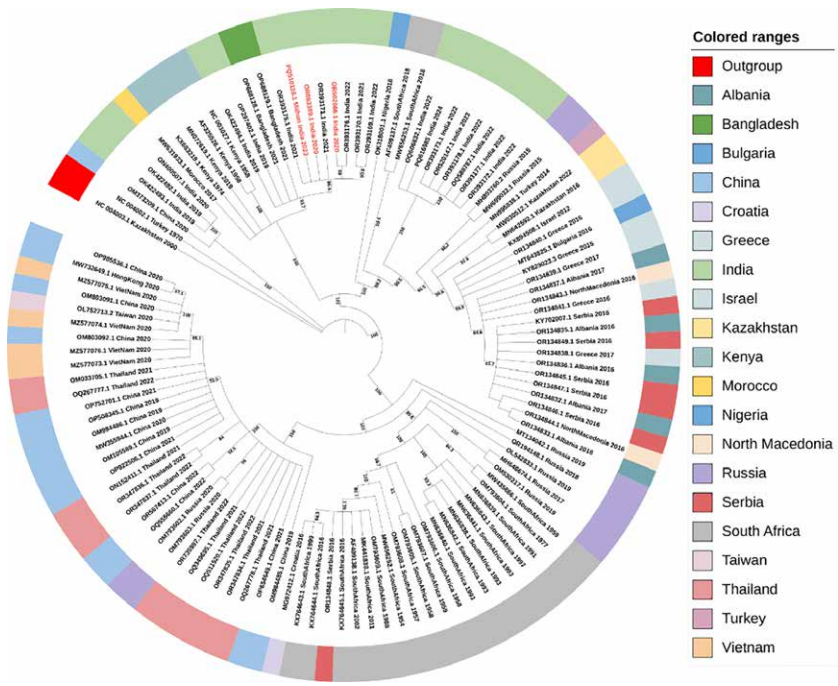


Fig 3: Phylogenetic analysis of the worldwide LSDV full genome sequences.

(Manjunatha Reddy GB, Chethan Kumar HB and Gulati BR)

Comorbidity Patterns and Transmission Risk Factors in Lumpy Skin Disease–Affected Cattle

Lumpy skin disease (LSD) is a re-emerging transboundary viral disease of cattle and buffaloes with significant socio-economic consequences. The virus is transmitted primarily by haematophagous arthropod vectors, including ticks and biting flies. Since ticks also serve as vectors and reservoir hosts for several haemoprotozoan parasites, LSD-affected animals in tick-endemic regions may be at heightened risk of concurrent parasitic infections. This study investigated comorbidity patterns and associated risk factors such as breed, sex, age, farm type, and vector presence in LSD-affected cattle using multiple diagnostic datasets.

A total of 300 samples from LSD-suspected cattle were screened for LSD, Infectious Bovine Rhinotracheitis (IBR), Malignant Catarrhal Fever (MCF), babesiosis, theileriosis (*Theileria annulata* and *T. orientalis*), and anaplasmosis. Of these, 176 animals (58.6%; 95% CI: 53.0–64.2%) were confirmed positive for LSD. A notable co-infection pattern was identified between LSD and *T. orientalis*, with 56.3% of LSD-positive animals concurrently infected with this parasite.

Transmission risk analysis identified haematophagous biting flies played major role (39%) in the joint transmission of LSD and *T. orientalis* than ticks, which is biologically consistent with the known epidemiology of *T. orientalis* as a fly-associated parasite. It should be noted, however, that *T. annulata*, which was also screened in this study, remains obligately dependent on *Hyalomma* tick vectors; thus, tick control remains an important component of the integrated management of theileriosis in these populations.

Multiple-pathogen co-infection burden was substantial: 51% of LSD-positive cattle harboured three or more concurrent infections, underscoring the clinical complexity that field practitioners encounter in LSD-endemic settings. Among the, LSD tested positive animals, a strong correlation was identified between LSD and oriental theileriosis caused by *Theileria orientalis*. Other significant associations were observed with IBR, Anaplasmosis, tropical theileriosis, Babesiosis, and MCF (Fig 4).

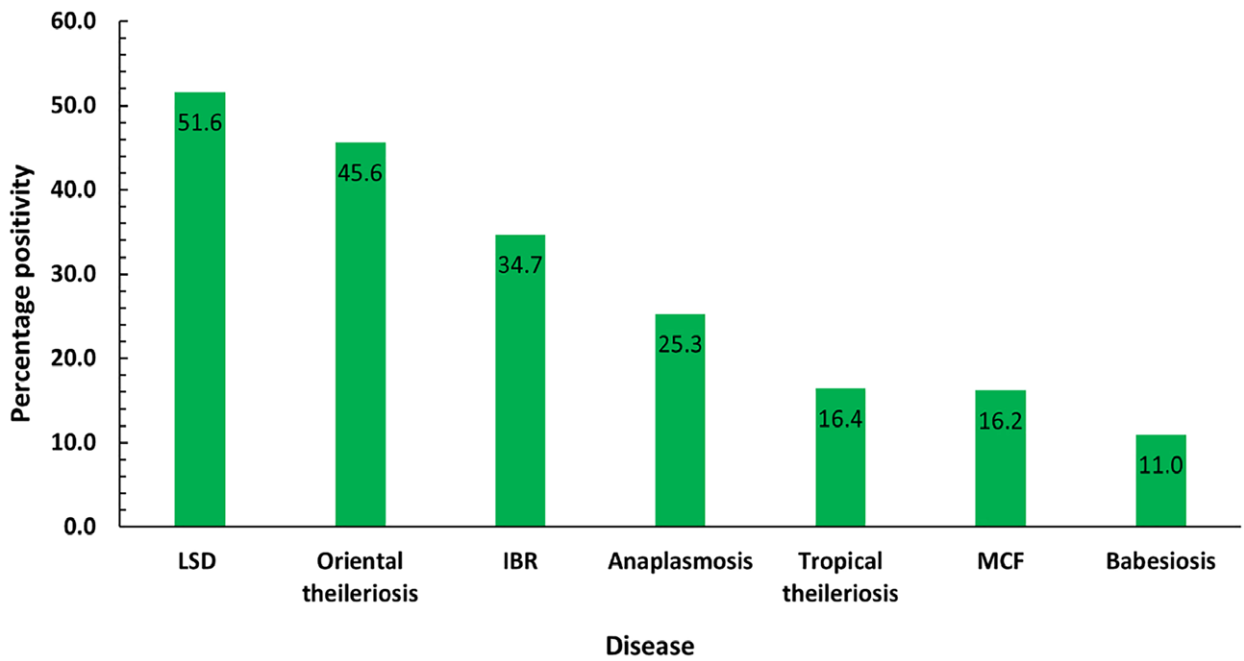


Fig 4: The bar diagram representing the percentage positivity of LSD, IBR, MCF, Babesiosis, Anaplasmosis, Oriental theileriosis and Tropical theileriosis.

Risk factor analysis indicated that male sex and indigenous breed were associated with comparatively lower disease occurrence, though this association requires careful interpretation — observed differences may reflect differential management, exposure levels, or herding practices rather than intrinsic biological resistance. This study demonstrates that LSD in field conditions is frequently complicated by concurrent haemoprotozoan infections, reinforcing the need for integrated diagnostic screening protocols that encompass multiple pathogens simultaneously.

(Manjunatha Reddy GB, Siju SJ, Chethan Kumar HB and Gulati BR)

Development of Native Antigen–Based Indirect ELISAs for Detection of Clostridium chauvoei–Specific Antibodies in Cattle

Blackleg, also known as black quarter, is an acute and often fatal myonecrotic infection of cattle caused by the anaerobic spore-forming bacterium *Clostridium chauvoei*. Although inactivated vaccines are available for disease control, assessing the antibody response following vaccination or natural infection in vaccinated and previously exposed animals is essential for evaluating vaccine efficacy and informing evidence-based immunization strategies in endemic regions. The present study aimed to develop and comparatively evaluate indirect ELISAs based on native whole-cell and flagellar antigens derived from *C. chauvoei* for the serological detection of blackleg-specific antibodies in cattle.

Both antigen types were extracted from *C. chauvoei* strain NIVEDIBQ1 and their immunoreactivity was confirmed using polyclonal antisera and convalescent cattle sera (Fig 5). The antigens were subsequently used to optimize two indirect ELISA formats, which were benchmarked against the indirect haemagglutination assay (IHA) as the comparator method. Optimal assay conditions, determined by checkerboard titration, included antigen coating concentrations of 250 ng (whole-cell) and 300 ng (flagellar), a serum dilution of 1:100, and anti-bovine HRPO conjugate dilution of 1:10,000.

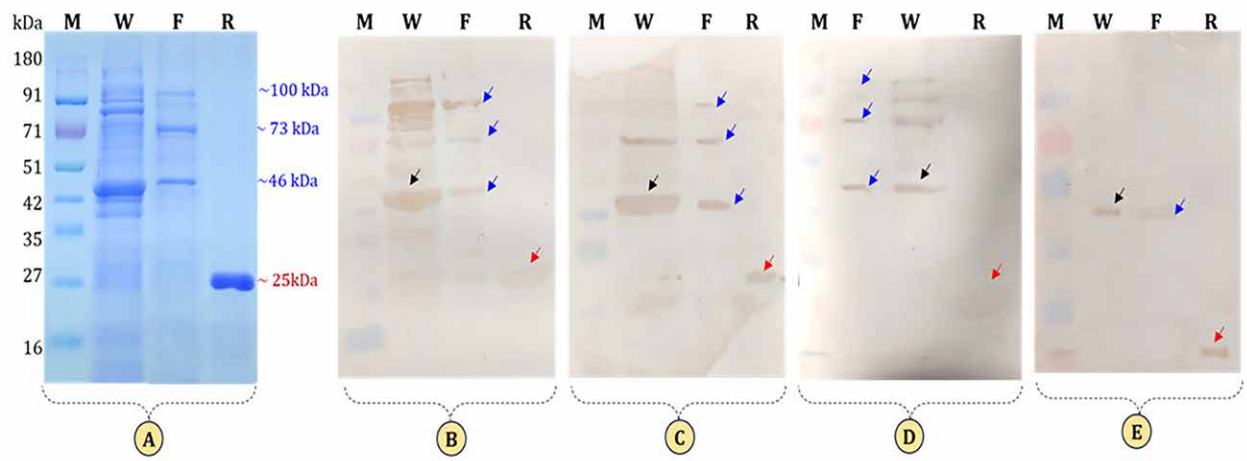


Fig 5: Immuno-reactivity of native (whole cell and flagellar) antigens. Panel A: SDS-PAGE of whole cell and flagellar antigens. Panel B Immunoblot of antigens using polyclonal sera of Rabbit, Panel C: Immunoblot of antigens using polyclonal sera of Guinea pig, Panel D: Immunoblot of antigens using convalescent sera of Cattle, Panel E: Immunoblot of antigens using polyclonal sera of Rabbit raised against recombinant flagellin (rFliC).

The optimized ELISAs detected *C. chauvoei*–specific antibodies at serum dilutions of up to 1:1600 (whole-cell) and 1:800 (flagellar antigen), without cross-reactivity against major bovine diseases (Anthrax, HS, FMD, Brucellosis, and LSD) specific sera. Cohen's kappa analysis of

agreement between each ELISA and the IHA indicated substantial agreement (κ = 0.725 for whole-cell and κ = 0.875 for flagellar ELISA).

ROC analysis, conducted on 200 samples, demonstrated strong discriminatory performance: the whole-cell antigen ELISA achieved a diagnostic sensitivity (DSe) of 96.0% and diagnostic specificity (DSp) of 95.0% at a percent positivity cut-off of >20.7632 [AUC was 0.991], while the flagellar antigen ELISA achieved a DSe of 95.0% and DSp of 97.0% at a cut-off of >18.579 [AUC was 0.996] (Fig 6).

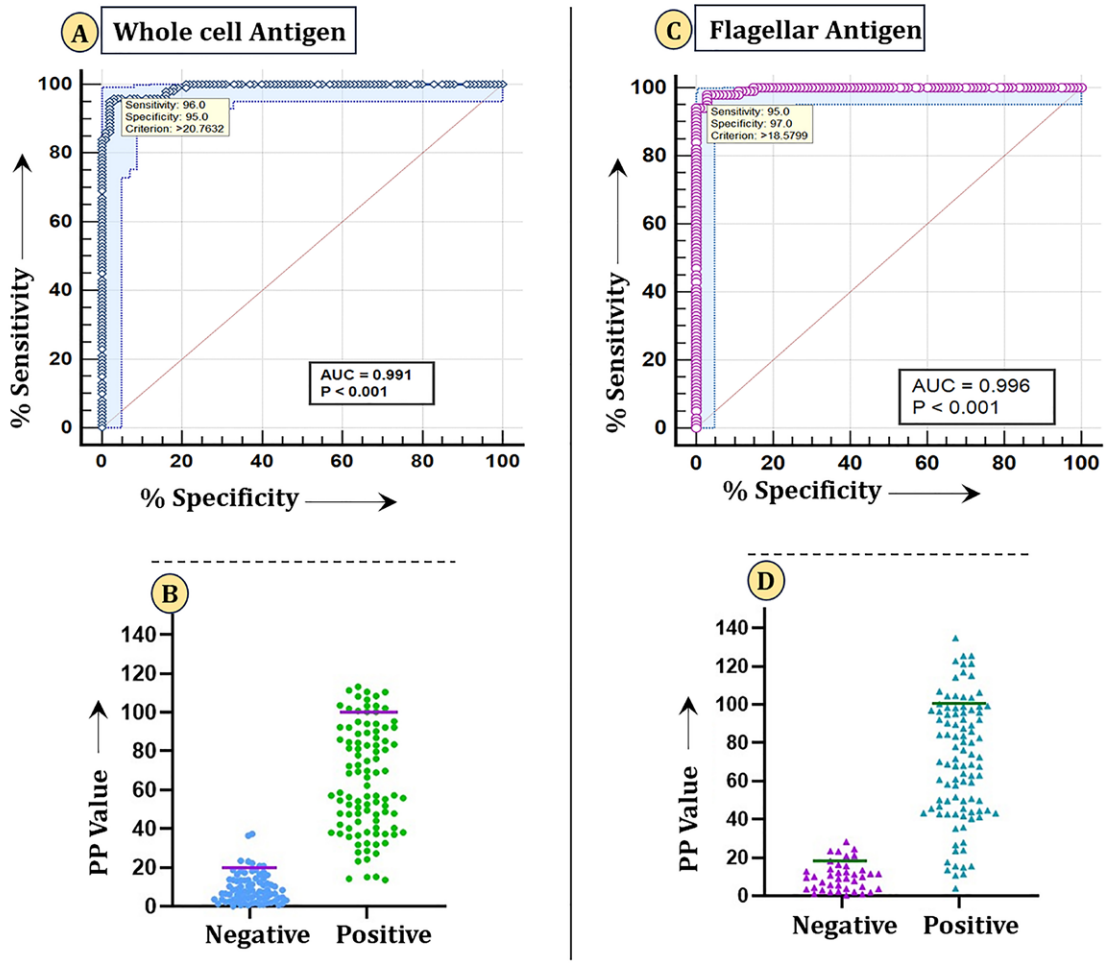


Fig 6: ROC analysis of indirect ELISAs. Whole cell antigen based indirect-ELISA; Panel A. ROC curve analysis, Panel B. Scatter diagram representing the range of known positives and negatives OD values; Flagellar antigen based indirect-ELISA; Panel C. ROC curve analysis, Panel D. Scatter diagram representing the range of known positives and negatives OD values.

(Shivachandra SB and Chanda MM)

Seroprevalence of Anti-Clostridium chauvoei Antibodies in Cattle in Andhra Pradesh: A Cross-Sectional Survey

Andhra Pradesh is a recognized endemic region for black quarter (BQ) in India, yet systematic serological data on population-level immunity status in cattle remain limited. A retrospective cross-sectional serological survey was conducted using 810 archived cattle serum samples obtained from the National Livestock Serum Repository (NLSR), ICAR-NIVEDI, Bengaluru. Samples had been collected during 2017-18 from seven districts of Andhra Pradesh-Anakapalli, Chittoor, YSR Kadapa, Krishna, Kurnool, Nellore, and Vizianagaram-and were screened for anti-C. *chauvoei* antibodies using the native antigen-

based indirect ELISAs developed and validated in the preceding study.

Overall seropositivity was 57.0% (462/810) by the whole-cell antigen ELISA and 40.9% (332/810) by the flagellar antigen ELISA, reflecting substantial prior exposure or vaccination coverage in this population. District-wise seropositivity distribution is presented in Fig 7.

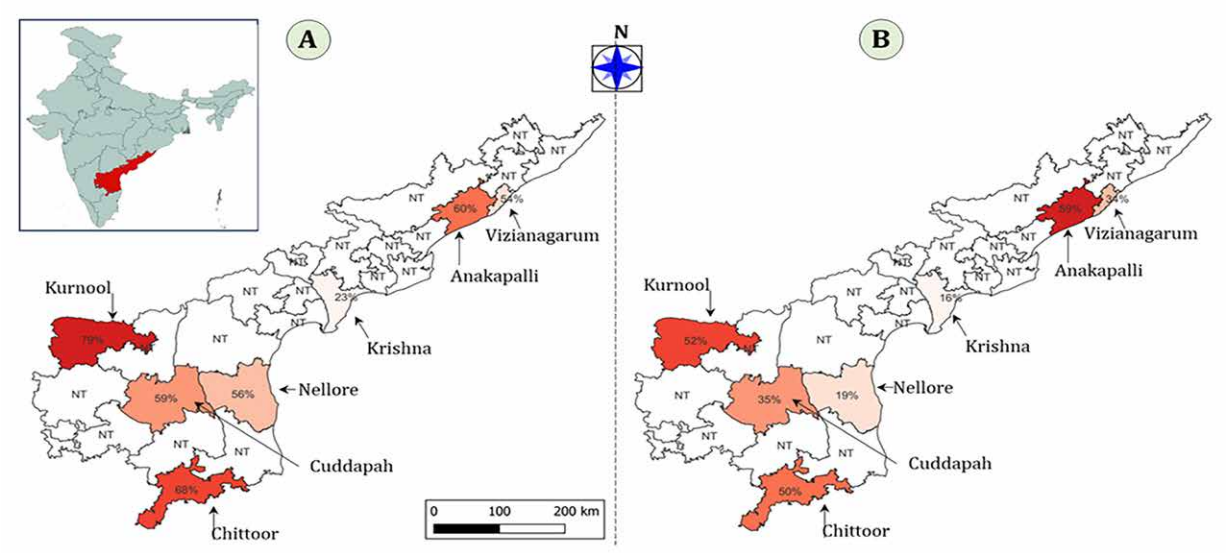


Fig 7: Percentage sero-positivity in different districts of Andhra Pradesh state, India. Panel A: with whole cell antigen based indirect-ELISA, Panel B: with flagellar antigen based indirect-ELISA.

Antibody levels among seropositive animals were further categorized by percentage positivity (PP) ranges. In the whole-cell ELISA, 29.6% of animals fell in the low-positive range (21–40 PP), 24.0% in the moderate range (40–80 PP), and 2.9% in the high range (>80 PP). In the flagellar ELISA, 26.7% were low-positive (21–40 PP), 12.3% moderate (40–80 PP), and 1.4% high (>80 PP).

Concordance analysis revealed that 295 samples (36.4%) were positive in both ELISAs, while 167 samples (20.6%) were positive exclusively in the whole-cell ELISA, and 37 samples (4.6%) exclusively in the flagellar ELISA. (the average CV was 1.77, which represents inter-assay CV for both ELISAs) The differential positivity pattern between assays suggests that the two antigens detect overlapping but distinct antibody populations. It is hypothesised that the higher positivity rate in the whole-cell ELISA reflects predominantly vaccine-induced responses-consistent with whole-cell antigens constituting the basis of most commercial clostridial vaccines-whereas the flagellar antigen ELISA, by targeting a surface-expressed motility antigen with distinct immunogenic properties, may preferentially detect antibodies arising from natural exposure or sub-clinical infection. This hypothesis, while biologically plausible, requires formal validation in controlled studies using sera from animals with well-defined vaccination and infection histories.

The majority of seropositive cattle exhibited low-to-moderate antibody levels, with high responders representing a small fraction, which may indicate waning immunity, incomplete vaccination coverage, or heterogeneity in immune responses attributable to breed composition-Andhra Pradesh cattle populations comprise both indigenous and crossbred animals. Although BQ vaccination is reportedly conducted by the Department of Animal Husbandry in endemic districts, district-wise vaccination coverage data were unavailable, precluding differentiation between vaccine-induced and naturally acquired seropositivity. This is an important limitation that constrains the epidemiological interpretation of these findings.

These results highlight the need for comprehensive BQ epidemiological assessments in Andhra Pradesh, integrating disease burden estimation, breed susceptibility evaluation, systematic vaccination coverage surveys, and longitudinal immunity monitoring to inform more targeted and effective prevention strategies.

(Shivachandra SB and Chanda MM)

Computational and Structural Analysis of Flagellin (FliC)–TLR5 Interactions in Cattle and Sheep: Implications for Subunit Vaccine Development Against Blackleg

Flagellin (FliC), the structural subunit of the bacterial flagellum of *Clostridium chauvoei*, functions both as a motility facilitator and as a pathogen-associated molecular pattern (PAMP) recognized by Toll-like receptor 5 (TLR5), a key innate immune sensor. Despite the established immunogenic properties of flagellin in gram-positive pathogens, the structural basis of FliC–TLR5 interaction in ruminant hosts and its implications for subunit vaccine design against blackleg remain unexplored. The present study addressed this gap through a comprehensive computational and immunoinformatic analysis of FliC across diverse *C. chauvoei* strains, with comparative evaluation of its interaction with TLR5 in *Bos taurus* and *Ovis aries*.

Multiple sequence alignment of FliC sequences from [n=9] *C. chauvoei* strains revealed the expected architecture of conserved N- and C-terminal domains (D0/D1) flanking a hypervariable central region (D2/D3)-a pattern consistent with the conserved TLR5-binding motif of bacterial flagellins. Immunoinformatic analysis predicted 13 potential B-cell epitopes; two highly conserved epitopes were prioritized as cross-protective vaccine candidates.

Three-dimensional structural models of FliC and TLR5 from both host species were generated and validated using standard structural quality metrics (Fig 8).

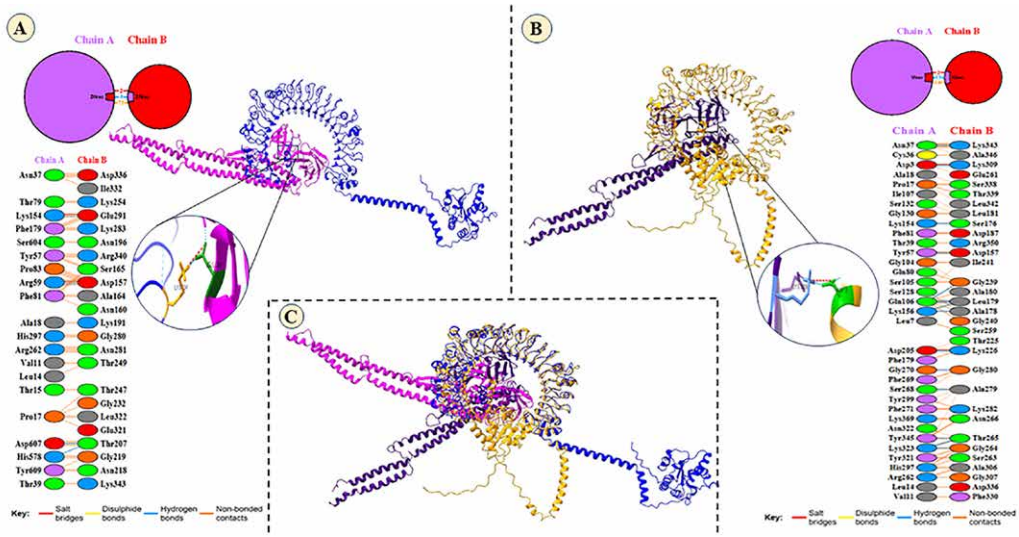


Fig 8: Structural representation of the interaction interfaces between FliC (Chain B) and Bos taurus TLR5 (Chain A). Panel A: FliC-TLR5 complex generated using AlphaFold predicted structures (FliC in magenta; TLR5 in blue). Panel B: FliC-TLR5 complex generated using SWISS-MODEL predicted structures (FliC in purple; TLR5 in golden yellow). Panel C: Superimposed structures of the FliC-TLR5 complexes generated from AlphaFold and SWISS-MODEL.

Molecular docking analysis identified significant FliC–TLR5 binding interactions mediated by ionic and hydrophobic contacts at the conserved D1 domain interface, with predicted

species-specific differences in interaction strength. The *Bos taurus* FliC–TLR5 complex exhibited stronger predicted binding, supported by a calculated binding free energy of −69.85 ± 3.70 kcal/mol; the corresponding value for *Ovis aries* TLR5 was -54.4 ± 1.70 kcal/mol, indicating comparatively weaker affinity in sheep.

Molecular docking analysis demonstrated strong FliC–TLR5 interactions mediated by robust ionic and hydrophobic interactions, indicating species-specific immune recognition. Further docking and molecular dynamics simulations revealed a stronger and more stable interaction between FliC and *Bos taurus* TLR5, supported by favourable binding energy (−69.85 ± 3.70 kcal/mol) (Fig 9).

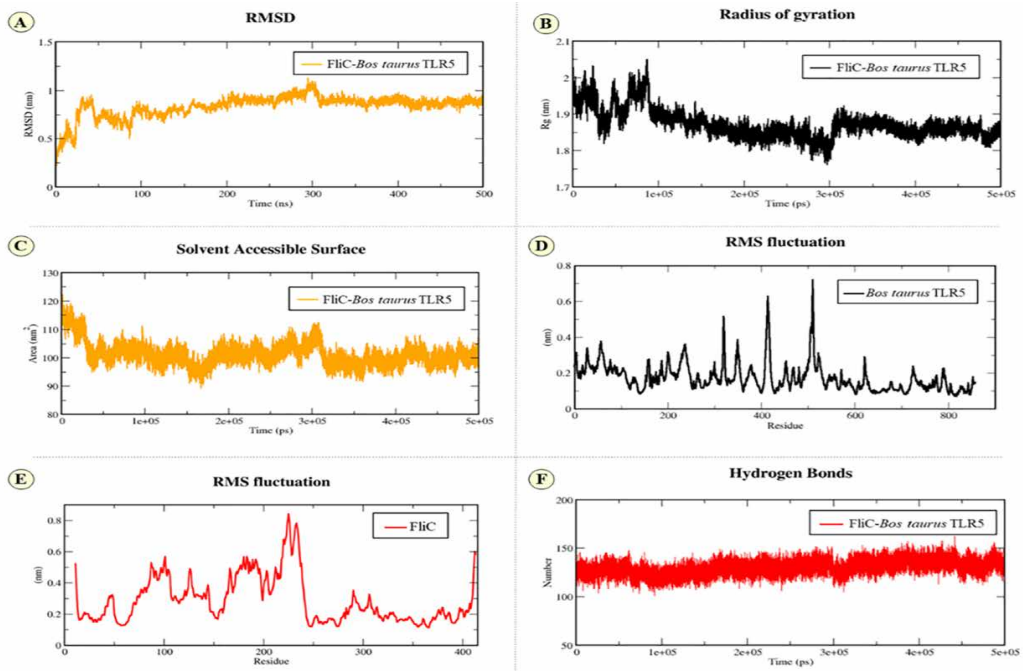


Fig 9: Molecular dynamics simulation of FliC-Bos taurus TLR5 complex. Panel A: RMSD analysis showing the stability of the complex over time; Panel B: Radius of Gyration (Rg) analysis; Panel C: Solvent Accessible Surface Area (SASA) analysis; Panel D: RMSF profile of Bos taurus TLR5; Panel E: RMSF profile of Clostridium chauvoei FliC protein; Panel F: Hydrogen bond analysis.

Molecular dynamics simulations further confirmed the stability of the TLR5–FliC complex, with key interacting residues localized within low-fluctuation regions, suggesting their critical role in maintaining structural stability. These findings support the potential of FliC as an effective PAMP capable of triggering a strong TLR5-mediated immune response in cattle. Overall, the study identifies FliC as a promising subunit vaccine candidate and provides insights into host-specific immune recognition mechanisms, contributing to the development of flagellin-based immunotherapeutics against *C. chauvoei*–induced blackleg disease in ruminants.

(Shivachandra SB and Chanda MM)

Sero-monitoring of Brucella abortus S19 Vaccination

Under the NADCP Brucellosis Control Programme (B-CP), a total of 12,771 serum samples received during the year 2025 for post-vaccination sero-monitoring were tested using an indirect ELISA to assess seroconversion. Although vaccination was implemented in 23 states as per Bharat Pashudhan portal, serum samples for post-vaccination sero-monitoring were received from only 11 states. The highest seropositivity was observed in the state of Haryana (87.28%) followed by Karnataka (82.24%) and Andhra

Pradesh (81.6%) (Table 1, Fig 10). These findings highlights the need for effective coordination among states to ensure enhanced vaccination coverage and for mandatory sharing of serum samples for monitoring seroconversion rates under the NADCP.

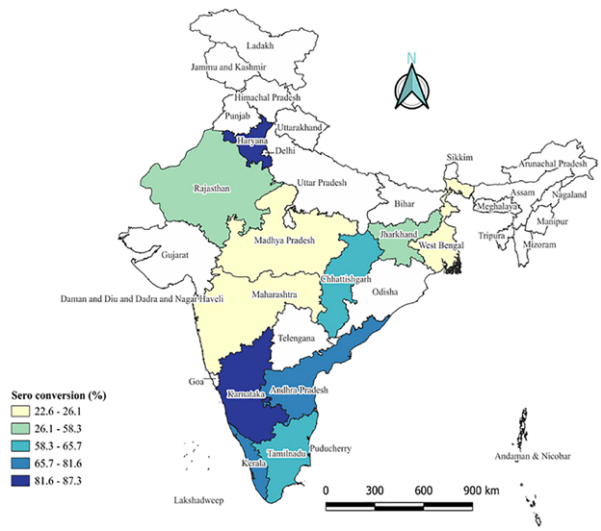


Fig 10: Map depicting state-level sero-conversion rates during the year 2025.

Overall, brucellosis vaccinations carried during 2025-26 were 2.92 million vaccinations and 1.35 million farmers were benefited as per Bharat Pashudhan in 23 states and 3 UT's and highest vaccination was in Bihar state. The data on calf population, vaccination coverage, and sero-conversion across selected states/UTs indicate notable variations in immunization performance and immune response. Out of a total calf population of 16.92 million, only 1.51 million calves were vaccinated, resulting in an overall vaccination coverage of 8.92%, which is considerably low. Among the states, Karnataka (32.69%), Andhra Pradesh (29.41%), and Haryana (25%) reported relatively higher vaccination coverage, which is also reflected in their higher sero-conversion rates of 82.24%, 81.6%, and 87.28%, respectively, indicating effective vaccine-induced immune responses. The findings highlight the need for strengthening vaccination programs, particularly in low-coverage states, improving data accuracy, and enhancing surveillance to better understand disease dynamics and immunity status across regions.

Table 1: State-level sample coverage and sero-conversion rates during the year of 2025.

S.No	State/UT	Total Calf population (in millions)	No. of vaccinations (in millions)	Percentage of vaccination (%)	No. of samples received	Sero-conversion rate (%)
1	Haryana	0.48	0.12	25	2076	87.28
2	Karnataka	1.56	0.51	32.69	2326	82.24
3	Andhra Pradesh	1.02	0.30	29.41	2060	81.6
4	Kerala	0.29	0.00	0	1020	69.02
5	Chhattisgarh	0.54	0.05	9.25	99	65.65
6	Tamil Nadu	2.27	0.41	18.06	507	64.29
7	Jharkhand	1.7	0.03	1.76	338	58.28
8	Rajasthan	3.24	0.01	30.77	1552	43.75
9	Maharashtra	1.14	0.00	0	1052	26.14
10	Madhya Pradesh	2.07	0.02	0.96	1533	24.91
11	West Bengal	2.61	0.06	2.29	208	22.59
Total		**16.92**	**1.51**	**8.92**	**12,771**	**63.27**

(Shome R and Nagalingam M)

Overall regional Brucellosis Seromonitoring Trends across Vaccination from 2021-2023

Nationwide analysis of brucellosis Seromonitoring in post-vaccinated bovine calves from 2021 to 2023 revealed distinct regional variations in seroconversion rates. Based on a combined datasets of 51,759 samples. The overall national seroconversion rate was 70.96% (36,730 positives), indicating widespread but regionally variable vaccine-induced antibody responses. Among the regions, the Southern region recorded a high proportion of seroconversion (75.10%), followed by the Union Territories (76.80%), North-Eastern (73.74%), and Western (72.98%) regions. Comparatively lower seroconversion rates were observed in the Northern (69.49%), Eastern (68.75%), and Central (61.46%) regions (Fig 11). Species-wise analysis further revealed a higher seroconversion rate in cattle calves (77.12%) compared to buffalo calves (67.34%). This highlights the disparity in vaccination coverage across the states and in cattle and buffaloes.

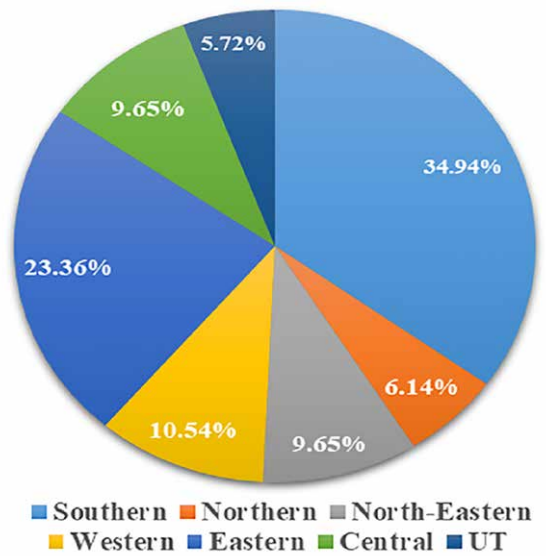


Fig 11: A multiregional epidemiological assessment of post-immunization seroconversion against brucellosis across India.

Across all regions, the 21–45 days post-vaccination (DPV) interval consistently showed peak seropositivity, highlighting this period as the optimal window for monitoring vaccine-induced antibody responses under diverse field conditions in India (Table 2).

Table 2: Overall day-wise trends in Brucella antibody kinetics in post-vaccinated bovine calves: Insights from 2021-2023.

S.No	Days Post Vaccination	Total samples tested	No. of Samples positive	Percent positivity (%)
1	DPV21-45	42993	31443	73.14
2	DPV46-60	3654	2474	67.71
3	DPV61-90	2898	1855	64.01
4	DPV91-120	2214	958	43.27
Total		51,759	36,730	70.96

(Shome R and Nagalingam M)

One Health–based Epidemiological Surveillance of Brucellosis and Leptospirosis at the Human–Animal Interface in Karnataka

Integrated surveillance for brucellosis and leptospirosis was conducted using a One Health framework in the districts of Chikkaballapura and Kolar, Karnataka. A stratified cross-sectional study design was implemented across six taluks and thirteen villages, covering 363 households. A total of 361 human samples and 772 cattle samples were collected following standardized One Health surveillance methodologies, institutional ethical clearance, and biosafety protocols.

Human samples were screened for brucellosis using the Rose Bengal Plate Test (RBPT), with confirmatory testing by the Serum Agglutination Test (SAT). Cattle samples were tested using RBPT and a Protein G–based indirect ELISA (iELISA). Leptospirosis surveillance in both humans and cattle was conducted using the Microscopic Agglutination Test (MAT) (Fig 12).

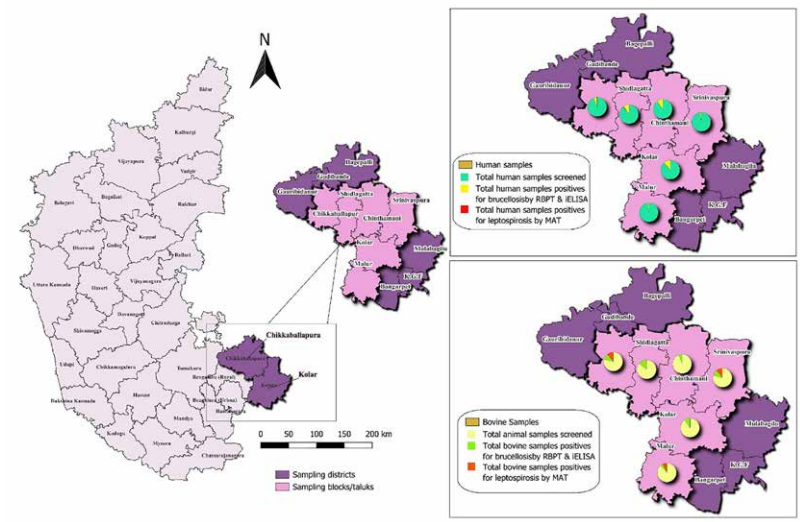


Fig 12: Taluk-wise seroprevalence of brucellosis and leptospirosis in humans and animals.

For brucellosis, 29 human samples were RBPT-positive (7.90%), of which 22 were confirmed by SAT (6.09%), indicating true serological exposure to *Brucella* spp., particularly among individuals with occupational livestock contact. The seven RBPT-positive but SAT-negative samples likely represent non-specific reactions, consistent with the known lower specificity of RBPT. Among cattle, 83 animals were RBPT-positive (10.75%), of which 70 were confirmed by iELISA (9.07%), demonstrating ongoing circulation of brucellosis in dairy cattle.

The difference in prevalence between cattle and humans (10.75% vs 7.90%) was statistically significant (χ^2 test, $p = 0.0137$), supporting a reservoir-driven transmission pattern. This association was further strengthened by a high odds ratio (OR = 8.15), indicating that the presence of infection in cattle significantly increases the risk of human exposure. Regression analysis confirmed animal infection as a significant predictor of human infection ($\beta = 0.377$; $p = 0.007$; $R^2 = 0.677$), demonstrating a strong epidemiological linkage between host populations.

Notably, 17 households (4.68%) showed concurrent brucellosis seropositivity in both humans and animals. This co-positivity was non-randomly distributed ($p < 0.01$), indicating clustered zoonotic spillover at the household level and reinforcing the role of shared exposure pathways within livestock-rearing systems. This represents the most epidemiologically significant finding of the study and warrants targeted follow-up investigations, including molecular strain typing (Fig 13).

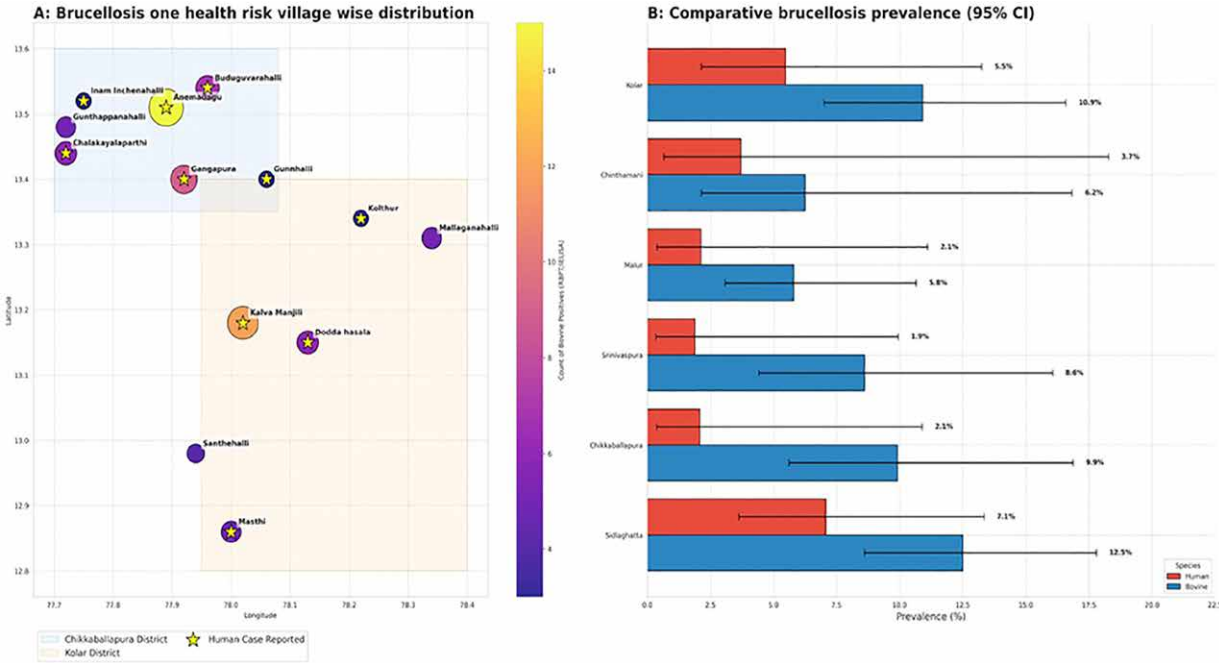


Fig 13: Panel A: Spatial distribution of brucellosis risk at the village level in Chikkaballapura and Kolar districts Panel B: Comparative prevalence of brucellosis in humans and bovines across study blocks with 95% confidence intervals.

For leptospirosis, only 1 out of 361 human samples (0.27%) and 45 out of 772 cattle samples (5.82%) were MAT-positive, indicating minimal human exposure but a comparatively higher burden in cattle (Fig 14). The >20-fold difference in prevalence suggests an environmentally driven transmission pattern. No households showed concurrent human–animal leptospirosis positivity (0%), and no statistically significant association was observed between human and animal infection (p = 0.229), supporting the absence of direct zoonotic linkage in the study population.

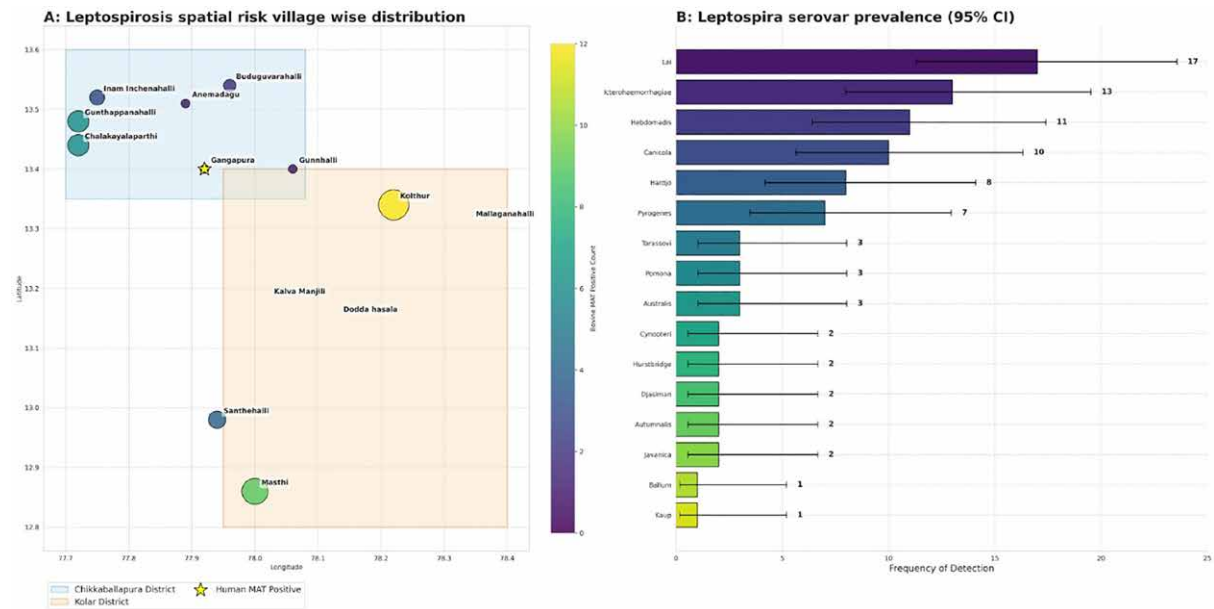


Fig 14: Panel A: Spatial distribution of leptospirosis risk at the village level in Chikkaballapura and Kolar districts. Panel B: Distribution and frequency of Leptospira serovars detected with 95% confidence intervals.

Spatial analysis revealed significant heterogeneity across districts, taluks, and villages. Chikkaballapur district exhibited higher brucellosis clustering, whereas Kolar showed relatively higher leptospirosis seroprevalence in cattle. Taluk-level variation was statistically significant ($p < 0.05$), with Sidlaghatta and Chikkaballapur taluks demonstrating clustered brucellosis transmission, while Malur and Srinivaspura taluks showed higher leptospirosis positivity.

At the taluk level, marked over dispersion and clustering were observed, with Chalakayalaparthi (24.24%) and Gunthappanahalli (18.18%) representing localized hotspots. In contrast, several villages showed negligible or zero co-positivity despite comparable sampling, indicating strong micro-level heterogeneity. The clustering pattern and variance suggest non-random disease distribution driven by localized ecological and management factors.

These findings demonstrate the value of integrated One Health surveillance in identifying concurrent zoonotic disease burden at the human–animal interface. The higher seroprevalence of brucellosis relative to leptospirosis likely reflects differences in pathogen ecology, transmission dynamics, and vaccination coverage rather than absence of risk. Overall, the results confirm a hierarchical pattern of spatial heterogeneity (village > taluk > district), emphasizing the need for risk-based, geographically targeted surveillance and intervention strategies.

(Shome R, Balamurugan V, Nagalingam M, Manjunatha Reddy GB and Chethan Kumar HB)

Development of a Multiplex Point-of-Care Diagnostic Assay for brucellosis, leptospirosis, scrub typhus

This study aims to develop a multiplex lateral flow assay (LFA) for simultaneous field detection of major zoonotic diseases — brucellosis, leptospirosis, scrub typhus — in both animal and human samples in north-eastern states.

Smooth lipopolysaccharide (sLPS) antigen was extracted and purified from *Brucella abortus* S99, a standard smooth reference strain, and its immunoreactivity confirmed in-house. The purified sLPS was subsequently provided to a commercial firm for LFA fabrication using recombinant Protein A/G conjugated with gold nanoparticles as the detection conjugate. This work represents the completed antigen development phase of the brucellosis LFA component, with strip fabrication and functional validation as the next planned steps.

Recombinant leptospiral outer membrane proteins LipL32, LipL21, Lsa27, and OmpL37 were revived from glycerol stocks, expressed in *E. coli*, and purified using His tag nickel affinity chromatography. Expression was confirmed by SDS PAGE at expected molecular weights (Fig 15). Functional screening by latex agglutination test using seropositive sera identified suitable antigens for lateral flow assay development.

Three partial fragments of the TSA56 Karp56 protein of *Orientia tsutsugamushi* were cloned into pET28a with an N terminal His tag, propagated in *E. coli* TOP10, expressed, and confirmed by SDS PAGE. Purification is complete, and western blot validation and functional evaluation are in progress.

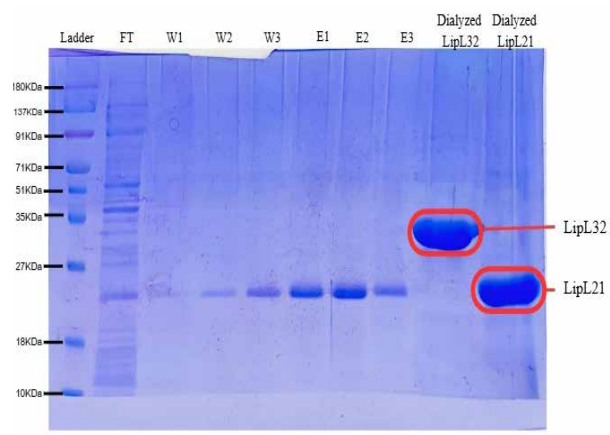


Fig 15: SDS-PAGE profile of purified and reconstituted recombinant LipL32 and LipL21 proteins.

As a component of human zoonotic disease burden assessment in North-East India, 68 human serum samples from clinically suspected scrub typhus cases were received from Guwahati Medical College, Assam, and screened using the Weil-Felix test (WFT). Two samples were seroreactive by OXK antigen, consistent with scrub typhus group rickettsial exposure; four samples were positive for OX19 antigen, indicating possible exposure to typhus group rickettsiae; and seven were positive for OX2 antigen, suggestive of spotted fever group (SFG) rickettsial exposure. It should be noted that WFT is a non-specific, cross-reactive assay of limited sensitivity and specificity by current diagnostic standards, and these results should be interpreted as presumptive serological signals rather than confirmed diagnoses.

(Shome R, Balamurugan V and Nagalingam M)

One Health Surveillance of Antimicrobial Resistance in Livestock, Animal Handlers, and the Environment (soil and water) in Karnataka

Antimicrobial resistance (AMR) in *Staphylococcus* spp and *Escherichia coli* was investigated across the interconnected domains of livestock, animal handlers, and the surrounding environment in Mandya and Ramnagar districts of Karnataka, India, reflecting a One Health perspective on the animal–human–environment continuum.

A total of 384 samples were collected during January to December 2025 using a multistage random sampling strategy. The samples comprised livestock (n = 240), animal handlers (n = 48), and environmental sources, including soil (n = 48) and water (n = 48), from eight villages each in Mandya and Ramanagara districts of Karnataka. Phenotypic antimicrobial susceptibility testing (AST), combined with genotypic confirmation, was performed. Multiplex PCR assays were used to detect key antimicrobial resistance genes (ARGs), including those associated with methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum β-lactamase (ESBL) production, enabling integrated interpretation of clinically relevant resistance across host species, animal handlers and environmental compartments.

Mandya district showed a higher burden of *Staphylococcus aureus* compared to Ramanagara. In Mandya, 32 isolates were obtained from livestock, along with three isolates each from animal handlers and environmental sources. Among these, two livestock isolates and one isolate from animal handlers were positive for the *mecA* gene, indicating MRSA, while no *mecA*-positive isolates were detected in environmental samples. In contrast, Ramanagara district yielded fewer isolates, with nine *S. aureus* isolates from livestock and one from environmental sources, and none from animal handlers. Only two livestock isolates were *mecA*-positive, and no *mecA* gene was detected in isolates from animal handlers or environmental sources.

Mandya and Ramanagara districts showed a broadly comparable distribution of coagulase-negative *Staphylococcus* (CoNS) isolates across livestock, animal handlers, and environmental sources, but differed in the pattern of *mecA* gene occurrence. In Mandya, a total of 35 CoNS isolates were recovered, including 24 from livestock, six from animal handlers, and five from environmental samples. The *mecA* gene was detected across all three compartments—two isolates from animal handlers, one from livestock, and one from the environment—indicating a wider dissemination of methicillin resistance within the One Health interface. In Ramanagara, 33 CoNS isolates were obtained, comprising 23 from livestock, four from animal handlers, and six from environmental sources. A slightly higher number of *mecA*-positive isolates (n = 4) was observed compared to Mandya, with three detected in livestock and one in environmental samples, while no *mecA* was reported in isolates from animal handlers.

In Mandya district, a total of 61 *Escherichia coli* isolates were recovered from livestock, along with four from animal handlers and 10 from environmental samples. Among these, eight isolates were ESBL-positive, including five from livestock, two from animal handlers, and one from the environment. In Ramanagara district, 66 *E. coli* isolates were obtained from livestock, five from animal handlers, and 13 from environmental sources. Of these, 19 isolates were ESBL-positive, comprising 15 from livestock, three from animal handlers, and one from the environment. Mandya and Ramanagara districts showed a similar overall recovery of *Escherichia coli* isolates, but differed markedly in ESBL positivity. Ramanagara showed higher ESBL burden driven mainly by livestock, whereas Mandya shows a lower pattern across the One Health sectors.

Both Mandya and Ramanagara districts exhibited a broadly similar antibiogram pattern for *Staphylococcus spp.* across livestock, animal handlers, and environmental samples. In both districts, isolates showed the highest resistance to cefoxitin and penicillin, while retaining good sensitivity to chloramphenicol and sulfamethoxazole–trimethoprim, indicating a consistent resistance profile across the One Health components. However, notable differences were observed in the antibiogram of *E. coli* between the two districts. In Mandya district, *E. coli* isolates from livestock demonstrated the highest resistance to tetracycline and ampicillin, while remaining sensitive to chloramphenicol and amoxicillin. Among animal handlers, the highest resistance was observed against tetracycline and sulfamethoxazole–trimethoprim. Environmental isolates showed a broader resistance pattern, particularly to tetracycline, ampicillin, and nalidixic acid (Fig 16).

In contrast, Ramanagara district showed a shift towards higher beta-lactam resistance. Livestock isolates of *E. coli* exhibited the highest resistance to ampicillin, cefoxitin, and amoxicillin, while remaining sensitive to chloramphenicol, amikacin, and aztreonam. Similarly, isolates from animal handlers also showed predominant resistance to ampicillin, cefoxitin, and amoxicillin. Environmental isolates in Ramanagara demonstrated resistance to ampicillin, cefoxitin, and tetracycline, but retained sensitivity to chloramphenicol. Overall, while Mandya district showed a predominance of tetracycline-associated resistance, Ramanagara district was characterized by higher resistance to beta-lactam antibiotics (ampicillin, amoxicillin, and cefoxitin). This suggests possible differences in antimicrobial usage patterns and selection pressure between the two districts,

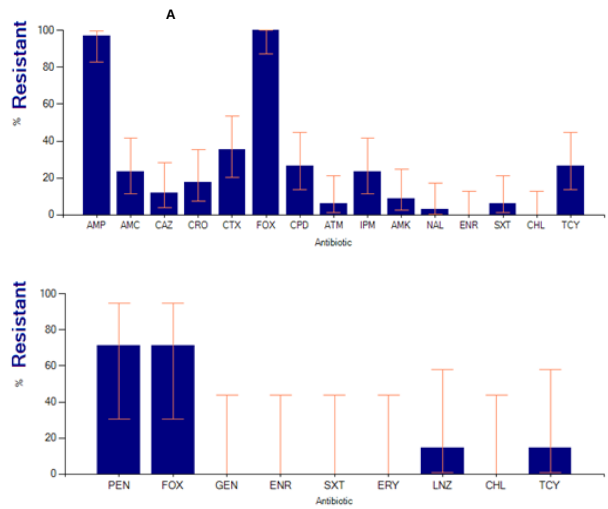


Fig 16: Antibiogram profile of ESBL E. coli. (Panel A) and Staphylococcus. (Panel B) in livestock in Mandya and Ramanagar Districts.

These findings highlight the widespread occurrence of antimicrobial resistance in food-producing animals, with potential spillover to humans and the environment through direct contact, shared microbial reservoirs, and contaminated waste streams. The study emphasizes the importance of a One Health approach for AMR surveillance and mitigation, recognizing that resistance determinants circulate across species boundaries and environmental compartments, posing a significant risk to animal health, food safety, and public health.

(Shivasharanappa N, Shome R, Krishnamoorthy P and Dubal ZB)

Antibiotic-Induced Phenotypic and Genotypic Adaptations in *Staphylococcus aureus* of Animal Origin under Vancomycin Stress

This study investigated antibiotic-induced phenotypic and genotypic adaptations in *Staphylococcus* spp. of animal origin under antimicrobial stress. As the *Staphylococcus* isolates were sensitive to the vancomycin (as tested by drug diffusion test and E test), the two sensitive isolates [V01 i.e. *Staphylococcus coagulans* (clinical isolate) & V02 (*Staphylococcus aureus*, NIVEDI isolate)] were selected for drug-induction studies using vancomycin exposure for 21 days at sub-MIC, Minimum Inhibitory Concentration (MIC) and supra-MIC concentrations, with phenotypic responses monitored daily through MIC determination, optical density (OD at 625 nm) and total viable counts (TVC). Prior to initiation of drug induction studies, the MIC of V01 & V02 was 8 µg/mL & 2 µg/mL, respectively. Briefly, the day of MIC determination by broth dilution was considered as day 0 of the induction study. After 24 hours incubation, MIC was recorded and the tube corresponding to ½ MIC was used as the inoculation source from day one (strong selection). An aliquot from this ½ MIC (4 µg/mL & 1 µg/mL) was taken in BHI and OD adjusted to 0.103 and 0.09 @ 625 nm showing TVC of 2.4 x 10^7 CFU/mL & 7.1 x 10^6 CFU/mL, respectively. The cultures were then subjected to two-step 10 fold serial dilutions in BHI broth assuming the final concentration would be 2.4 x 10^4 CFU/mL & 7.1 x 10^3 CFU/mL, respectively. From this, 1 mL inoculum was aseptically transferred into fresh broth containing the desired antibiotic concentration (at least 3 dilutions i.e. ½ MIC, MIC & 2MIC including control and blank) for day 1 of the induction experiment and incubated at 37°C for 18 hrs so that tube showing turbidity at highest concentration of antibiotic after 18 hrs was chosen as inoculum for the next day (Table 3, Fig 17). Antibiotic resistance profile by drug diffusion test, OD values and TVC was recorded daily for ½ MIC, MIC & 2MIC and control tubes.

Table 3: Scheme for the derivation of increasing concentration of vancomycin.

Vancomycin (µg/mL)	**Blank broth**	**Blank DW**	**Control**							
	0	0	0	0.125	0.25	0.5	1	2	4	8	16
BHI Broth (mL)	5	4	9	8.987	8.975	8.95	8.9	8.8	8.6	8.2	7.4
Antibiotic (µL)	0	0	0	12.5	25	50	100	200	400	800	1600
Inoculum (5 x 10^6 CFU/mL)	0	0	1	1	1	1	1	1	1	1	1
Total Volume			10 mL each								

Blank broth: Only broth, Blank DW: broth + sterile distilled water used for preparation of antibiotic working solution, Control: 9 mL broth + 1 mL inoculum

The minimum inhibitory concentration (MIC) of vancomycin against 5.1 × 10^6 CFU/mL was 4 µg/mL. At 8 µg/mL, despite initial bactericidal effect, subpopulations persisted and re-emerged later, showing altered MIC levels and suggesting stress-induced adaptation. During the induction experiment, a phenotypic change in colony morphology was also observed, with colonies shifting from golden yellow to white by day 16. The control tube did not receive any fresh antibiotic therefore consistently maintained high viable counts (13 to 17 log CFU/mL) throughout the study while culture exposed to 4 µg/mL showed an initial

decline in TVC during the first few days (until day 5), dropping from 12 log CFU/mL to 7 log CFU/mL, further dropped to zero by day 6, before peaking to 12 log CFU/mL on day 12, and maintaining until day 21.

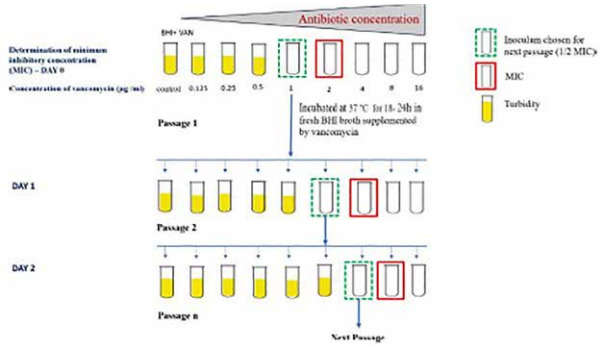


Fig 17: Schematic representation of multistep strong selection process.

The detail results of TVC, zone of inhibition (ZOI) at ½ MIC, MIC & 2MIC and control culture for V01 isolate are presented in Fig 18 & Fig 19 while for V02 isolate, it is presented in Fig 20 & Fig 21.

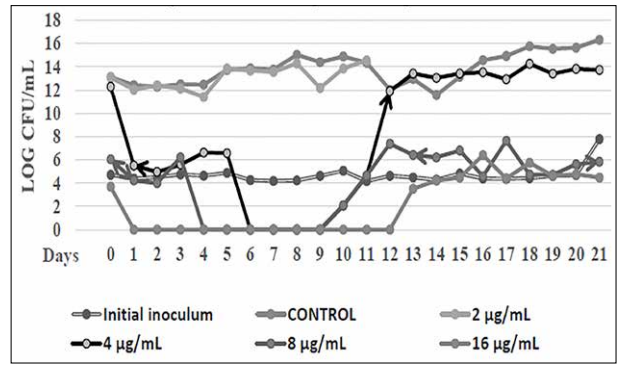


Fig 18: Total viable counts of S. coagulans (V01, clinical isolate) over 21 days at different concentrations of vancomycin.

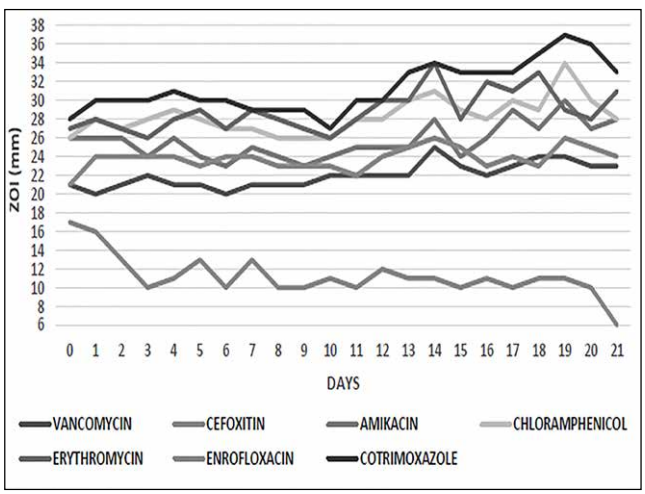


Fig 19a. ZOI for antibiotics not exposed to vancomycin

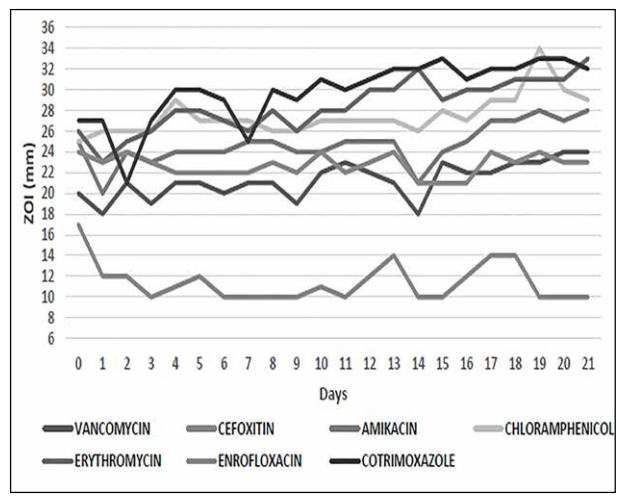


Fig 19b. ZOI for antimicrobials exposed to vancomycin at half MIC

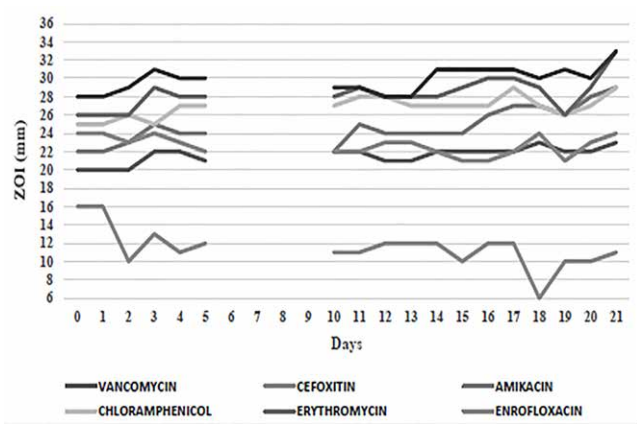


Fig 19c. Changes in ZOI of antibiotics exposed to vancomycin at MIC

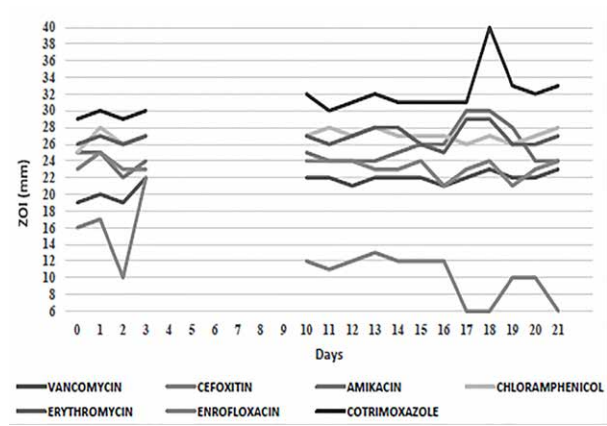


Fig 19d. Changes in ZOI of antibiotics exposed to vancomycin at twice the MIC

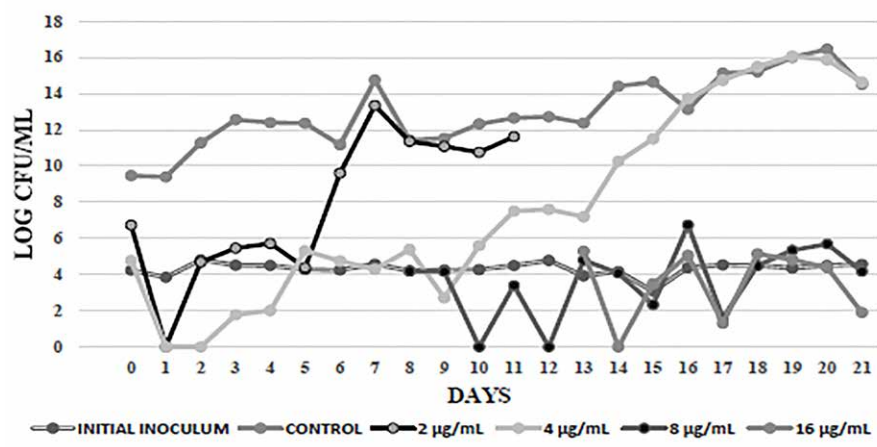


Fig 20: Total viable counts of S. aureus (V02, NIVEDI isolate) over 21 days at different concentrations of vancomycin

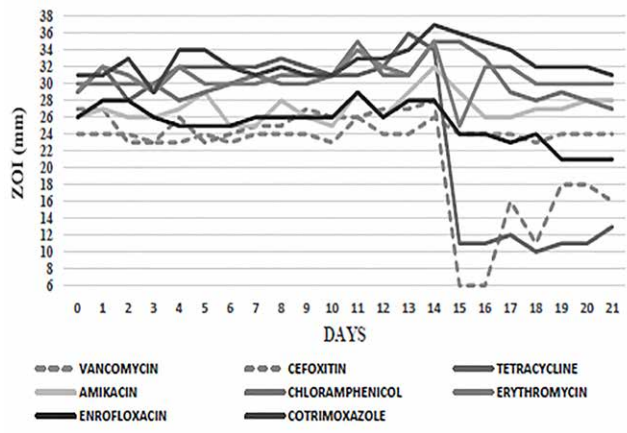


Fig 21a: ZOI for antibiotics not exposed to vancomycin.

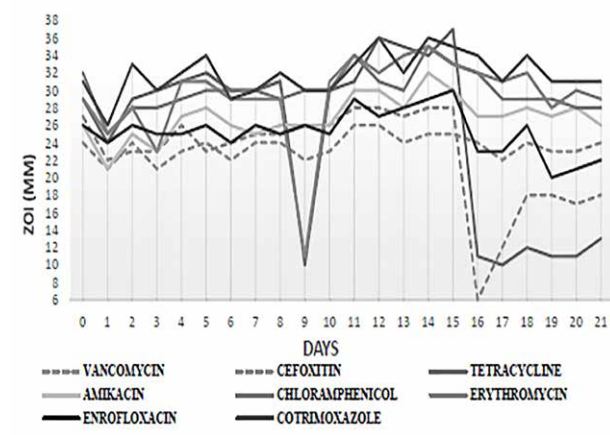


Fig 21b: ZOI for antimicrobials exposed to vancomycin at ½MIC

Fig 21: ZOI for antibiotics against S. aureus exposed to vancomycin at various MIC levels.

The isolates remained sensitive to vancomycin throughout the study period. A decline in cefoxitin susceptibility from day 16 indicated emergence of a methicillin-resistant phenotype under vancomycin-induced stress. Susceptibility to amikacin, erythromycin, cotrimoxazole, enrofloxacin, and chloramphenicol remained stable or showed collateral sensitivity, suggesting vancomycin adaptation may enhance susceptibility to certain antimicrobials. Exposure to MIC and supra-MIC concentrations of vancomycin induced cross-resistance to other antimicrobials, even those without previous exposure.

To investigate the genetic basis, genomic DNA from the isolates was extracted at different times and subjected to whole-genome sequencing. Genome data analysis is currently in progress to elucidate molecular mechanisms of antimicrobial stress adaptation. This study provides evidence of cross-resistance and collateral sensitivity, suggesting sub-MIC and prolonged antibiotic exposure may promote resistant subpopulation survival, which may complicate treatment outcomes. This reinforces the importance of judicious antimicrobial use in veterinary and clinical settings to prevent AMR acceleration.

(Dubal ZB and Shivasharanappa N)

Genomic Diversity of ESBL-Producing Escherichia coli in Migratory sheep and their environments in southern Karnataka: A One Health Study

The occurrence and genomic characteristics of extended-spectrum β-lactamase (ESBL)–producing *Escherichia coli* remain poorly documented in India, particularly in migratory sheep flocks and their associated environments. To address this knowledge gap, the present study investigated the antimicrobial resistance profiles and genomic characteristics of ESBL-producing *E. coli* isolated during 2023-2025 from migratory sheep flocks and their associated farm environments in Chitradurga and Tumkur districts of southern Karnataka, India.

A total of 702 samples (sheep rectal swabs-565; Environmental samples: 137 including soil (n = 69), water (n = 26), and feed (n = 42)) were collected from Chitradurga and Tumakuru districts of Karnataka during 2023-2025. A total of 418 (59.63%) *E.coli* isolates (sheep-342; environmental samples-76) were identified based on culture, phenotypic and multiplex PCR. Among these *E.coli* isolates, a total of 98 isolates were identified as ESBL producers based on phenotypic standard disc diffusion, combined disc diffusion methods and multiplex PCR for *CTXM, SHV, TEM*, and *AmpC* genes. Seventy Nine ESBL-*E. coli* isolates were confirmed from sheep and 19 from environmental sources. Overall occurrence of ESBL-*E.coli* was 13.98% in sheep and 13.97% in environmental farm setting. 72 Samples were used for further downstream analysis for phenotypic and genotypic AMR pattern determination. Whole-genome sequencing and comparative genomic analysis of 72 ESBL-producing *E. coli* isolates (54 from sheep and 18 from environmental sources) revealed a diverse repertoire of antimicrobial resistance genes (ARGs). Predominant resistance determinants included genes encoding resistance-nodulation-cell division (RND) family antibiotic efflux pumps, mutations in the 23S rRNA associated with resistance to lincosamide antibiotics, penicillin-binding protein alterations conferring resistance to β-lactam antibiotics, and multiple β-lactamase genes, including *CTX-M, TEM, DHA, AmpC,* and *SHV* types. Antibiotic target alteration was the most prevalent resistance mechanism, accounting for 48.51% of resistance-associated reads, followed by antibiotic efflux mechanisms (39.31%). Plasmid analysis identified a total of 45 distinct plasmid replicon types, of which 21 were shared between sheep and environmental isolates, indicating extensive plasmid-mediated gene exchange. The most frequently detected plasmids across all isolates were IncFIB (AP001918) and Col (pHAD28).

Multilocus sequence typing (Achtman 7-gene MLST) and whole-genome MLST (wgMLST) analyses revealed that the predominant sequence types among sheep isolates were ST155, ST8492, ST8650, ST162, and ST602 (Fig 22). Notably, ST602 and ST8492 were detected in both sheep and environmental isolates, suggesting their widespread distribution and association with multidrug resistance (MDR). The presence of these sequence types across animal and environmental compartments underscores their significance as globally disseminated MDR clones and highlights an important One Health concern.

Overall, this study provides important genomic insights into ESBL-producing *E. coli* in a previously underexplored setting and emphasizes the need for integrated surveillance strategies under the One Health framework to mitigate the spread of antimicrobial resistance across animal, environmental, and human interfaces.

Figure 9: Achtman 7 gene MLST

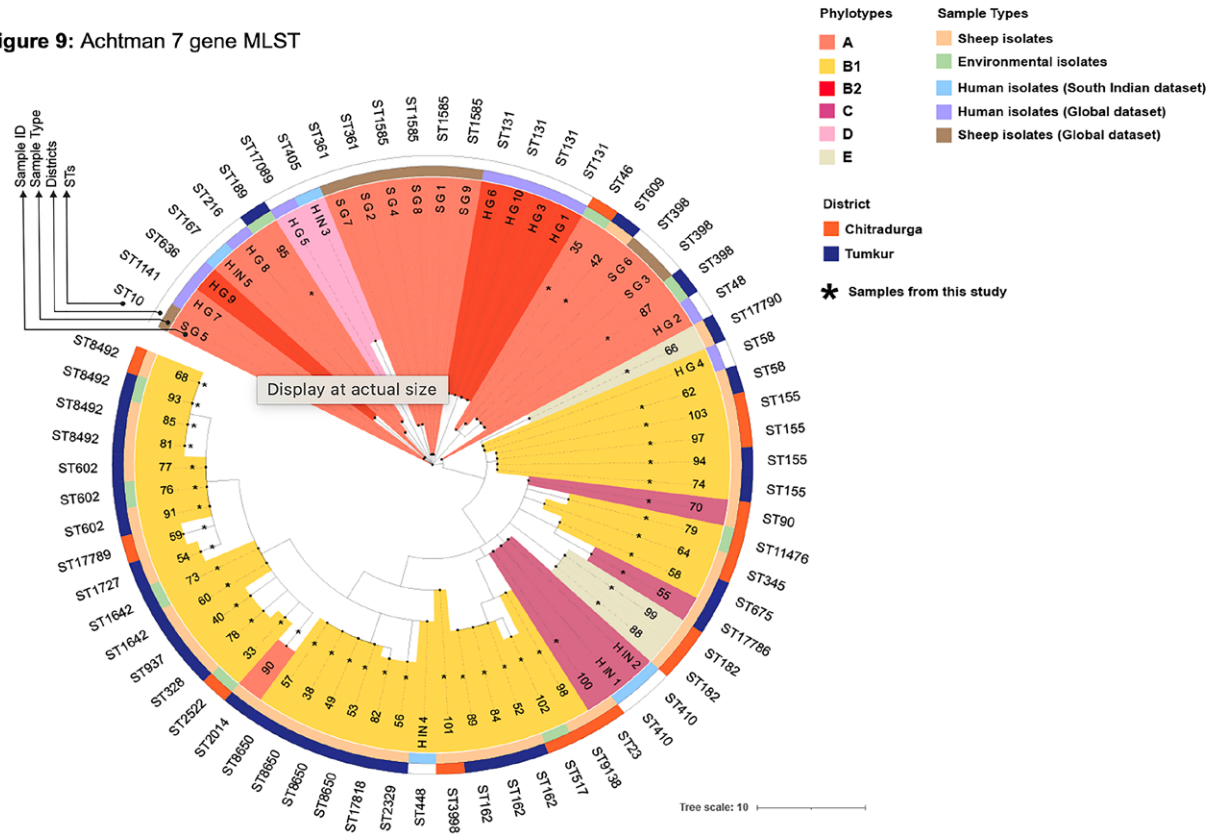


Fig 22: Circos plot showing Achtman 7 gene MLSTs and phylogroups with predominant Sequence Types (STs) in sheep and environmental isolates.

(Shivasharanappa N, Shome R, Patil SS, Krishnamoorthy P, Narayanan G and Chethan Kumar HB)

Genetic Diversity of Theileria orientalis in Cattle from Kerala, India

Theileria orientalis, an emerging haemoprotozoan parasite of cattle and buffaloes, has a global distribution and poses a significant economic constraint to the livestock industry. This study investigated the genetic diversity of *T. orientalis* across fourteen districts of Kerala, India during December 2024 to March 2025.

Molecular characterization based on the major piroplasm surface protein (mpsp) gene revealed the presence of multiple genotypes, namely genotype 3, 5, 7, N2, and N5, indicating considerable genetic variation within parasite populations in the region (Fig 23). Among the 102 mpsp sequences analysed, 65 isolates clustered within genotype 7, 33 isolates within genotype 5, two isolates within genotype N2, one isolate within genotype 3, and one isolate within genotype N5. The highest genetic diversity was observed in Kottayam district, where genotypes 5, 7, N2, and N5 were detected. Haplotype network analysis revealed the presence of 86 haplotypes with a high haplotype diversity of 0.97. A negative Tajima's D value (−0.775) suggested recent population expansion of *T. orientalis* in the region. Screening for other haemoprotozoan parasites also revealed mixed infections under field conditions, including *Theileria annulata*, *Babesia spp. Anaplasma* spp. and *Trypanosoma evansi*.

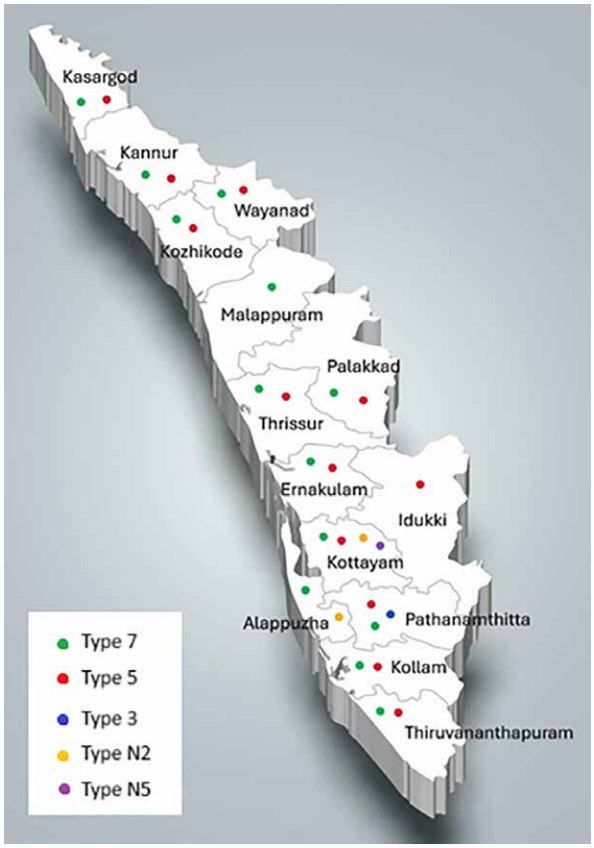


Fig 23: Distribution of T. orientalis genotypes across districts of Kerala. Genotypes are indicated by colored circles: Red (Type 7), Green (Type 5), Blue (Type 3), Yellow (Type N2) and purple (Type N5).

Further analysis identified single nucleotide polymorphisms (SNPs) in the cytochrome *b* gene of *T. orientalis*, which were compared with those of *T. annulata*. Although genetic variability was observed in the *cytochrome b* gene of *T. orientalis*, resistance-associated mutations commonly reported in *T. annulata* were not detected, suggesting possible differences in the molecular mechanisms underlying buparvaquone resistance. The predicted amino acid sequences of the 56 *T. orientalis* isolates analysed in this study showed 97–100% identity among themselves. In contrast, comparison of the *cytochrome b* protein sequences of *T. orientalis* and *T. annulata* revealed only about 50% identity. This observation raises questions regarding the efficacy and specificity of buparvaquone as a treatment for oriental theileriosis.

These findings highlight the need for in-depth investigations on drug efficacy and the development of alternative therapeutic strategies. Further studies on the genetic variability of *T. orientalis* and its potential impact on treatment outcomes are essential for improving disease management strategies.

(Siju SJ, Sengupta PP and Patil SS)

Sentinel Surveillance Reveals Low-Level Persistence of PPR Virus in Cattle and Buffaloes in India

Peste des Petits Ruminants (PPR) is a major viral disease of small ruminants, and ongoing control efforts in India have substantially increased population immunity in sheep and goat through widespread mass vaccination. In such settings, overt outbreaks may decline; however, low-level or subclinical circulation of PPR virus (PPRV) can persist undetected, especially in atypical hosts. Cattle and buffaloes, though not primary hosts can provide niche for virus survival under immune pressure and hence serve as useful sentinel species for identifying such silent transmission.

To assess ongoing PPRV circulation in bovines, a large-scale serological investigation was conducted in 2025 using serum samples from young bovines (cattle and buffalo calves under one year of age), selected to capture recent exposure. Sentinel surveillance was carried out across multiple states representing varying levels of small ruminant immunity and diverse epidemiological settings. A total of 3,341 samples were tested using a competitive ELISA (c-ELISA), with a percent inhibition cutoff of ≥50% for detection of PPRV-specific antibodies.

An overall seropositivity of 6.5% was observed, indicating continued low-level virus circulation. This represents a marked decline compared to previously reported levels (~20%) in pre-PPR-EP studies conducted across different regions of the country. State-wise seroprevalence, along with sample size, reported outbreaks, and corresponding small ruminant immunity levels, is presented in Table 4.

Table 4: Seroprevalence of PPRV-specific antibodies in sentinel hosts (cattle and buffalo calves) across Indian states.

State	No. of Samples Screened	% Positivity in PPR c-ELISA	Passive PPR Outbreaks Reported in 2025	% Population immunity against PPR after second round of vaccination
Telangana	669	9.8%	01	85.4%
Tamil Nadu	783	6.4%	01	80.7%
Chhattisgarh	434	2.9%	01	75%
Andhra Pradesh	560	6.4%	-	79.5%
Karnataka	472	9.1%	04	76.7%
Madhya Pradesh	423	4.2%	02	48.7%
Total	**3341**	**6.5%**		

These findings demonstrate that sentinel surveillance in young bovines is a sensitive approach for detecting subclinical PPRV circulation in highly vaccinated regions. Sustained monitoring in atypical hosts over successive years can provide early warning signals, guide targeted interventions, and support India's progress toward the global goal of PPR eradication by 2030.

(Balamurugan V and Manoranjan Rout)

Unraveling Leptospira Transmission Dynamics in Dakshina Kannada, India through a One Health Framework

Leptospirosis is a globally important zoonotic disease caused by pathogenic *Leptospira* species, manifesting as acute febrile illness and, in severe cases, progressing to multi-organ dysfunction. It remains endemic in tropical regions, including Dakshina Kannada (DK), Karnataka, where heavy rainfall, flooding, and favorable environmental conditions sustain transmission. The infection persists through complex interactions among animal reservoirs, environmental sources, and human populations, underscoring the need for an integrated One Health approach. This investigation integrates pathogen isolation, experimental infection, environmental surveillance, molecular epidemiology, and field-based interventions to elucidate leptospirosis dynamics in DK, Karnataka.

A virulent strain of *Leptospira interrogans* was isolated from a Greater Bandicoot rat near a human case in Hosabettu, Mangalore. After culturing and serial passage in golden Syrian hamsters, the strain regained virulence by the third passage, causing severe disease and death. Genome sequencing confirmed it as serogroup Autumnalis, with identical rat and hamster isolates (Fig 24). The strain showed high virulence (LD_{50} ≈ 177.83 cells/mL). Infected hamsters developed liver, kidney, and lung damage, with the kidney as the primary site of early infection. This low-passage strain now serves as a useful model for studying leptospirosis and developing diagnostics and vaccines. Ongoing transcriptomic studies aim to identify early diagnostic and immunogenic biomarkers.

Environmental surveillance in soil and water conducted in spatially identified hotspot villages revealed widespread contamination with *Leptospira*. Of the 33 environmental samples analysed, 73.5% (25/33) tested positive for the pathogenic *LipL32* gene, while 79.4% (27/33) were positive for the Leptospira genus-specific 16S rRNA gene (Table 5).

Table 5. Village-wise Detection, Isolation and Confirmation of Pathogenic Leptospira from Environmental (Water and Soil) Samples Using Molecular and Culture-Based Methods

Sl. No.	Village/Town	Total screened	Pathogenic (LipL32) PCR	16S rRNA (Lep1&2) PCR	Culture	Pathogenic (LipL32) PCR - Culture
1	Arekere byle	7	6	6	6	5
2	Baganbilla	8	4	4	1	0
3	Bander	2	2	2	2	1
4	Hossabettu	4	4	4	3	1
5	Karnadu	7	6	7	3	1
6	Thokur	5	3	4	0	0
	Grand Total	**33**	**25**	**27**	**15**	**8**

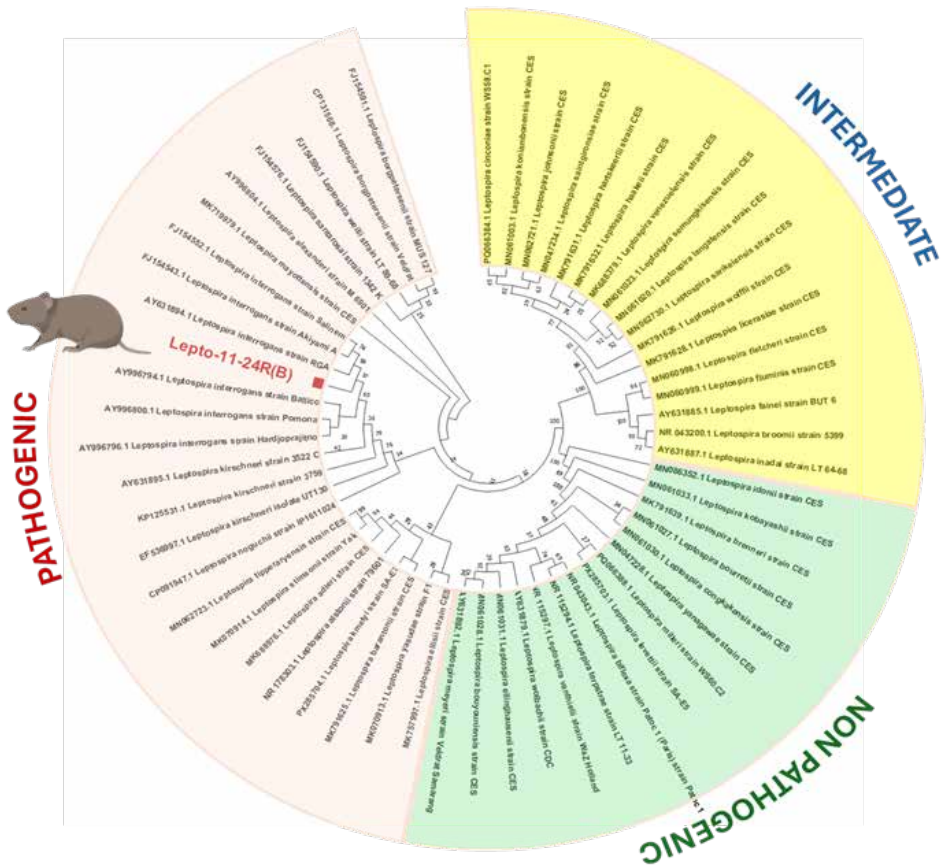


Fig 24: Phylogenetic tree of Leptospira spp. showing three clades: pathogenic (red), intermediate (yellow), and non-pathogenic (green). The study strain (Lepto-11-24R(B)) clusters within the pathogenic group, indicating close relatedness to pathogenic Leptospira interrogans strains.

Culture-based isolation yielded 15 viable *Leptospira* isolates, of which 9 (60%) were confirmed as pathogenic by *LipL32* PCR. Contamination was most pronounced in drainage water, wells, stagnant water bodies, and rodent-associated soils, indicating active environmental persistence and potential transmission risk.

Molecular analysis of 83 serum samples from suspected human cases demonstrated 15.7% PCR positivity, confirming infection with pathogenic *Leptospira*. The majority of positive cases were reported from Mangaluru taluk,

followed by Bantwal and Belthangady. Thirteen PCR-positive samples were further subjected to amplification and sequencing of a partial 16S rRNA gene fragment (~331 bp) using Lep1/ Lep2 primers. Phylogenetic analysis revealed the co-circulation of multiple *Leptospira* species, including *L. interrogans*, *L. kirschneri*, *L. weilii*, and *L. fai*nei (Fig 25). Notably, the detection of the intermediate species *L. fainei* suggests an expanded pathogenic spectrum contributing to febrile illness and underscores the complexity of the regional epidemiology.

A One Health integrated surveillance and intervention, like awareness, identification of human cases, capacity building, coordination etc., implemented since 2019, demonstrated measurable impact, with human seropositivity declining from 26.7% in 2020 to 12.7% in 2023. Surveillance identified bovines as important reservoirs, while rodent studies confirmed the presence of highly virulent strains. The establishment of a regional diagnostic laboratory enhanced rapid detection and reporting in this region. However, challenges persist, including fragmented surveillance systems, limited diagnostic access, and low uptake of animal vaccination.

Overall, the findings provide comprehensive evidence of interconnected transmission across animal, environmental, and human interfaces in DK. They emphasize the importance of integrated surveillance, molecular diagnostics, and coordinated One Health strategies for effective control and managements of leptospirosis in endemic settings.

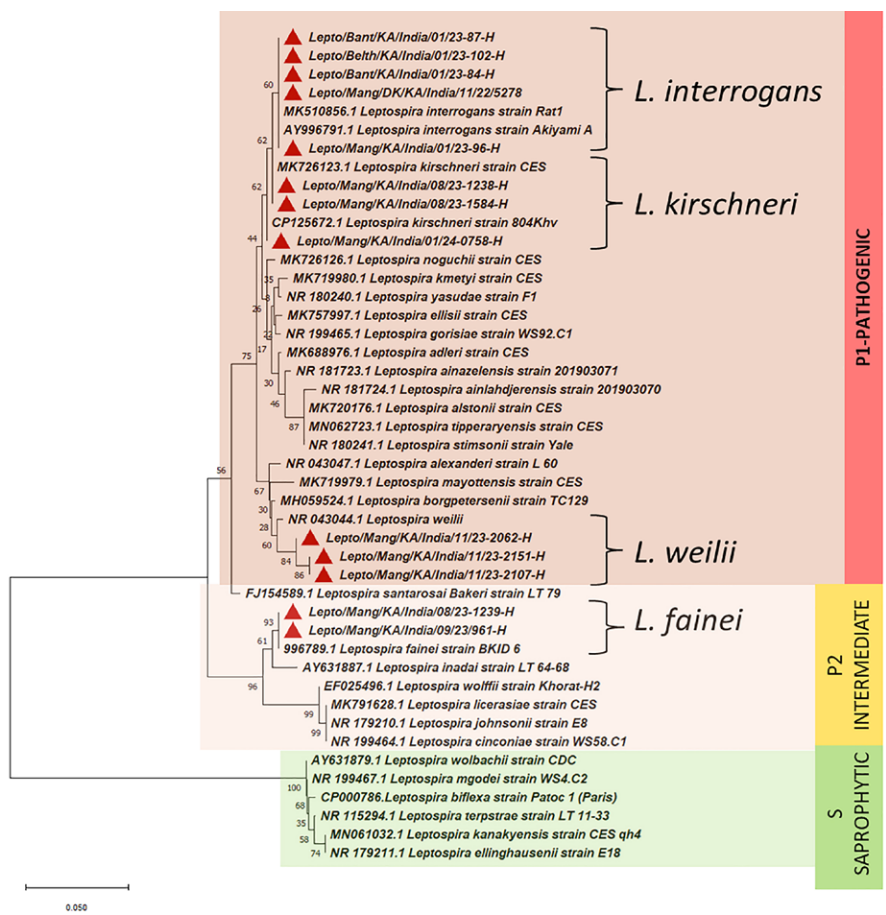


Fig 25: Phylogenetic analysis of Leptospira species detected in febrile patients from Dakshina Kannada, Karnataka, India. Partial 16S rRNA gene sequences (~331 bp) from PCR-positive samples were aligned and analyzed using MEGA 11. The phylogenetic tree shows clustering of isolates with pathogenic and intermediate species: Leptospira interrogans (n = 5), L. kirschneri (n = 3), L. weilii (n = 3), and L. fainei (n = 2).

(Balamurugan V, Chethan Kumar HB, Nagalingam M and Gulati BR)

Comparative Metabolomics Reveals Antagonistic Metabolic Networks Underpinning the Transition between Planktonic and Biofilm States of Leptospira

Leptospira species alternate between planktonic and biofilm lifestyles, both of which are critical for environmental persistence, host colonization, and transmission. While biofilm formation is known to enhance survival under adverse conditions, the metabolic mechanisms governing the transition between planktonic growth and biofilm-associated persistence remain poorly understood. This study employed a comparative metabolomics approach to systematically investigate metabolic differences between planktonic and biofilm states of pathogenic and intermediate Leptospira species.

Cultures were grown under defined planktonic and biofilm-inducing conditions, and intracellular metabolites were extracted using a methanol:acetonitrile:water (4:4:2, v/v/v) solvent system. Metabolic profiling was performed using ultra-high-performance liquid chromatography coupled with Q Exactive Orbitrap mass spectrometry (UHPLC–HRMS), with chromatographic separation on a Phenomenex Kinetex C18 column and polarity-switching data acquisition. Metabolite detection, annotation, and quantification were carried out using Compound Discoverer 3.2 against the mzCloud database, with reserpine and taurocholate-D8 used as internal standards for normalization. Multivariate statistical analyses, including principal component analysis (PCA), hierarchical clustering, and pathway enrichment analysis, were conducted using MetaboAnalyst 6.0.

A total of 70 metabolites were identified as significantly differentially abundant between planktonic and biofilm states. Planktonic cultures showed enrichment of metabolites associated with active growth and energy metabolism, including oleoyl ethanolamide, linoleic acid, oleic acid, glycerol-3-phosphate, and adenosine, implicating lipid metabolism, nucleotide metabolism, and central energy pathways. In contrast, biofilm-associated cultures were characterized by increased levels of signaling and stress-adaptive metabolites such as dodecanesulfonic acid, jasmonic acid, abscisic acid, and naringenin, linked to secondary metabolite biosynthesis, stress response, and environmental adaptation.

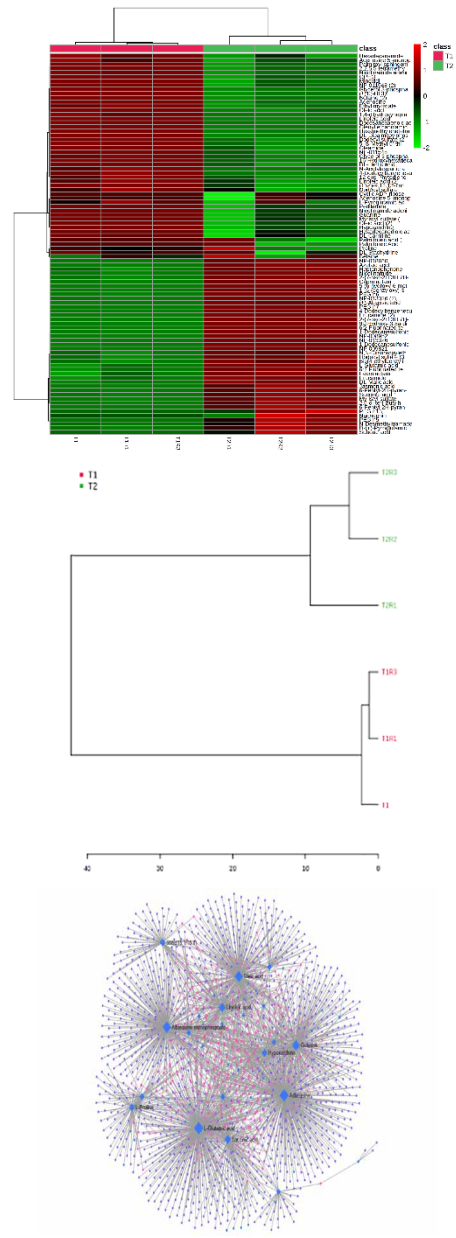


Fig 26: Integrated Heatmap and Clustering Analysis Highlight Divergent Metabolomic Profiles in Planktonic and Biofilm Conditions; Differential Pathway Activation and Network-Level Metabolite Connectivity Distinguishing Planktonic and Biofilm Leptospira Metabotypes.

Although these metabolites are classically described as plant-associated compounds, their identification here is based on spectral similarity and pathway enrichment analyses, and they likely represent structurally analogous or functionally related metabolites reflecting conserved stress-response mechanisms that remain underexplored in microbial systems. PCA and clustering analyses revealed clear separation between planktonic and biofilm metabolomes, indicating antagonistic metabolic reprogramming between growth-oriented and persistence-oriented lifestyles (Fig 26).

This study elucidates distinct metabolic signatures underlying Leptospira lifestyle transitions and provides novel insights into biofilm biology. The identified antagonistic metabolic networks highlight potential metabolic targets for disrupting biofilm formation and improving strategies for leptospirosis control. The putatively identified analogous or functionally related metabolites warrant further validation through in-depth MS/MS analysis to confirm their identity and biological relevance.

(Balamurugan V)

Standardization of Multiplex PCR (mPCR) for Detection and Differentiation of Leptospira

Leptospirosis is a re-emerging zoonotic disease caused by pathogenic *Leptospira* species and poses a significant public health challenge in endemic regions. Rapid, sensitive, and precise diagnostic tools are essential for effective disease management and control. Diagnostic methods often lack serogroup-level resolution, and most serological assays—except the microscopic agglutination test (MAT)—also offer limited discrimination, limiting their usefulness in epidemiological investigations and targeted interventions. This study aimed to develop and standardize a multiplex PCR (mPCR) assay for the simultaneous detection and differentiation of major pathogenic *Leptospira* serogroups, thereby strengthening diagnostic and surveillance capabilities. Well-characterized reference *Leptospira* cultures maintained at ICAR–NIVEDI were used for assay development. Published and optimized primers targeting conserved and virulence-associated genes (LipL32, 16S rRNA, and LigB), along with serogroup-specific target genes representing Icterohaemorrhagiae, Autumnalis, Sejroe, Canicola, and Grippotyphosa, were employed. Reaction conditions were optimized through systematic adjustment of annealing temperatures, primer concentrations, and primer combinations to achieve distinct and reproducible amplification patterns (Fig 27).

The standardized assay was configured as a two-tube mPCR system: one tube containing serogroup-specific primers and the second targeting conserved and virulence-associated *Leptospira* genes. Analytical sensitivity was evaluated using tenfold serial dilutions of *Leptospira* genomic DNA, while specificity was assessed against a panel of non-target organisms, including *Brucella* spp., *Pasteurella* spp., sheep pox virus, goat pox virus, Orf virus, and *Orientia tsutsugamushi*. The optimized mPCR assay demonstrated analytical specificity, with no non-specific amplification observed with other pathogens. All primer sets consistently amplified their respective targets at a 10^{-2} dilution (0.6 ng of target DNA), indicating that this range supports reliable multiplex amplification.

Evaluation of the assay was performed using twelve suspected field samples collected during a leptospirosis outbreak in Kanakapura, Karnataka. Six samples tested positive for pathogenic *Leptospira*, with several showing amplification of multiple serogroup-specific markers, suggesting possible mixed infections.

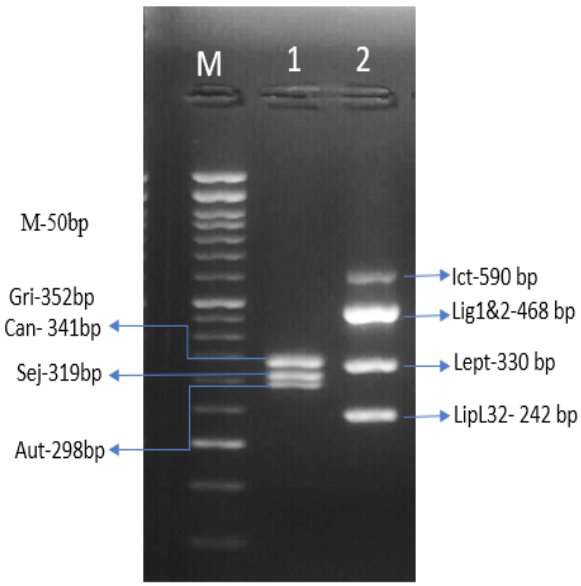


Fig 27: Agarose gel showing the optimization of mPCR using reference Leptospira strains. M: 50 bp DNA ladder; Lane 1: amplification with primer set 1 (serogroup-specific primers); Lane 2: amplification with primer set 2 (conserved and virulence-associated gene primers, including LipL32, 16S rRNA, and LigB). Distinct, reproducible bands indicate assay standardization.

The standardized mPCR assay exhibited good specificity and reproducibility. This assay provides a rapid and reliable tool for serogroup-level detection, supporting outbreak investigations, epidemiological surveillance, and targeted control strategies for leptospirosis in both human and animal populations.

(Balamurugan V, Chethan Kumar HB and Nagalingam M)

Detection of zoonotic pathogens from slaughterhouse environment

Increasing interactions between animals and humans in slaughterhouse environments pose a significant risk for zoonotic spillover events. The present study aimed to develop a surveillance framework using a One Health approach to detect potential zoonotic pathogens from environment of the selected slaughterhouses. Environmental surveillance was conducted in Chengicherla slaughterhouse (n = 498) and, Amberpet slaughterhouse (n = 511). All together 1009 test were performed and 147 (14.57%) samples were found to be positive for different pathogens (Table 6 & 7).

Table 6: Section wise testing of samples and their results.

Section	No. of samples tested	Positive	No. of samples tested	Positive
	Amberpet SH		**Chengicherla SH**	
Lairage	158	20	143	20
Slaughtering Hall	159	31	158	28
Sludge Plant	46	6	45	7
Unloading Pen	148	19	152	16
Total	**511**	**76**	**498**	**71**

Table 7 : Sample-wise testing of samples and their results

Type of sample	No of samples tested	Positive	No of samples tested	Positive
	Amberpet SH		Chengicherla SH	
Drainage water	105	11	100	15
Animal drinking water	17	01	19	1
Soil sample	20	00	20	00
Swab	291	44	291	47
Sludge water	76	19	64	6
Human drinking water	-	-	01	01
Washing water	02	01	03	01
Total	**511**	**76**	**498**	**71**

The pathogens identified were *E. coli* including three diarrhoeagenic *E. coli* (69), non-typhoidal *Salmonella* (16), *Leptospira* (12), *Listeria* (5), *S. aureus* (4), *Brucella* (9), *Toxoplasma* (24), *Entamoeba histolytica* (1), *Giardia* spp. (5) and *Echinococcus* spp. (2). *Brucella* spp. were detected in low numbers, with five isolates from Chengicherla and four from Amberpet; among these, five samples were identified as *Brucella abortus* and four as *B. melitensis*. Additional work on parasitological examination revealed the presence of eggs of *Haemonchus contortus*, *Trichuris* spp., *Toxocara* spp., and *Strongyloides* spp. PCR assays for buffalo pox virus and rotavirus were standardized; however, all tested samples were negative for these pathogens. Overall, the findings demonstrate significant microbial and parasitic contamination in slaughterhouse environments and highlight the importance of integrated One Health surveillance systems to monitor zoonotic risks at the animal–human interface.

(Dubal ZB, Suresh KP and Gulati BR)

Surveillance of Bovine Tuberculosis in Dairy Cattle of Karnataka, India

Bovine tuberculosis (bTB) is a chronic and debilitating disease that leads to significant but often undetected production losses in the dairy sector and poses an important zoonotic risk. Herd-level screening for bTB is commonly performed using delayed hypersensitivity tests and the Interferon Gamma Release Assay (IGRA).

In 2025, cattle farms in Hassan district of Karnataka, India, were surveyed using a multi-stage stratified cluster sampling design. A total of 813 cattle from 36 villages across seven taluks were screened.

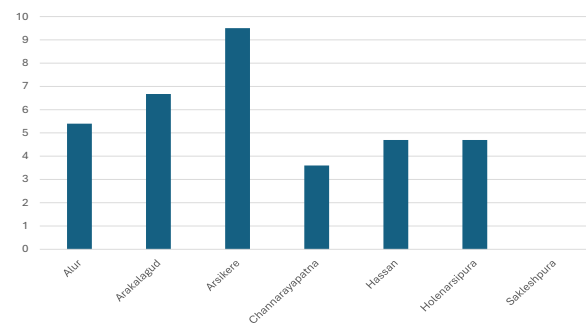


Fig 28: IGRA Positivity (%) for bovine tuberculosis in the taluks of Hassan District, Karnataka.

The results revealed an overall IGRA positivity rate of 4.67% (Fig 28). Breed-wise analysis

indicated a higher prevalence in crossbred cattle (4.8%) compared to indigenous breeds (2.3%). Age-wise analysis showed IGRA positivity of 6.2% among calves (<1 year), 5.1% among young adults (<3 years), and 4.2% among older cattle (≥3 years). These findings highlight the continued presence of bovine tuberculosis in the region and emphasize the need for strengthened surveillance, early detection, and targeted control strategies to mitigate the disease burden and reduce zoonotic transmission risks.

(*Nagalingam M, Krishnamoorthy P, Shome R, Balamurugan V and Gulati BR*)

Prevalence of Zoonotic Tuberculosis in Humans in India: A Meta-analysis

Zoonotic tuberculosis (zTB) is an important public health concern in India, arising from transmission of *Mycobacterium* species from animals to humans. To estimate the prevalence of zTB in humans in India, a meta-analysis study was conducted. A total of ten studies published between 1992 and 2020 were retrieved from online and offline databases and included in the analysis. Meta-analysis was performed using R software with the meta package. The overall pooled prevalence of zTB in humans in India was estimated at 3.0% (95% confidence interval [CI]: 1.0–6.0%; prediction interval [PI]: 0.0–29.0%) based on 2,288 samples tested. Temporal analysis revealed fluctuating trends in zTB prevalence across different years. Regional analysis indicated that the northern zone had the highest prevalence (7%), while the southern zone reported the lowest prevalence (0.9%) (Fig 29). State-wise analysis showed that Bihar recorded the highest prevalence (8.2%), whereas Tamil Nadu reported one of the lowest prevalence rates (0.9%).

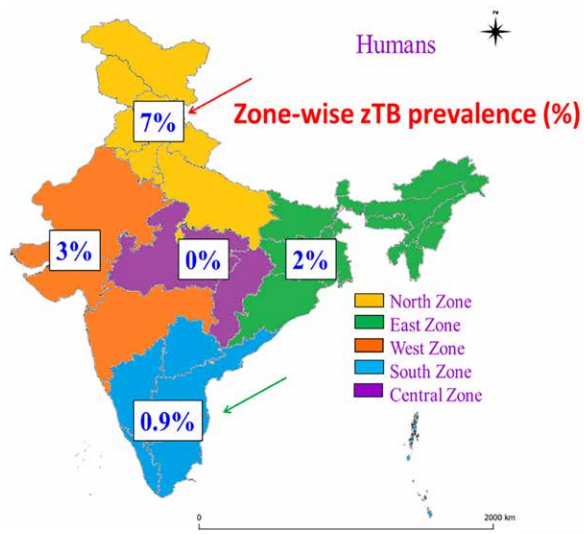


Fig 29: Zone-wise prevalence of zoonotic tuberculosis in humans of India.

Diagnostic method–based analysis indicated a higher prevalence detected by molecular methods (4%) compared with culture-based methods (0.1%). Among sample types, blood samples showed the highest zTB prevalence (11.6%), followed by tissue samples (1%), while clinical samples showed a comparatively lower prevalence (0.08%). Species-level confirmation revealed that *Mycobacterium bovis* had the highest prevalence (5%), followed by *M. orygis* (3%) and other *Mycobacterium* species. Notably, a greater number of studies reported zTB from extra-pulmonary sites compared with pulmonary tuberculosis cases. Overall, this meta-analysis provides valuable insights into the prevalence and distribution of zoonotic tuberculosis in humans in India. The findings can support policymakers in strengthening surveillance, improving diagnostic strategies, and implementing targeted interventions to reduce the burden of zoonotic tuberculosis under a One Health framework.

(Krishnamoorthy P, Nagalingam M, Suresh KP and Gulati BR)

Small Ruminant Diseases Epidemiology

Nationwide Surveillance and Diagnosis of Small Ruminant Diseases in India: Insights from 2025

In 2025, an extensive surveillance and diagnostic effort was undertaken to monitor major diseases affecting small ruminants across India. A total of 2,118 clinical and trade samples were received and analyzed, comprising serum, blood, fecal material, multiple swab types, and tissue specimens. These samples originated from diverse geographic regions, reflecting a broad representation of disease scenarios across the country.

Laboratory diagnosis revealed a wide spectrum of infectious diseases affecting sheep and goats. Among bacterial diseases, pasteurellosis (8.33%), enterotoxaemia (7.69%), and brucellosis (6.11%) were detected at moderate levels, while mycoplasmosis showed a notably high positivity (40.32%), indicating its significant role in small ruminant morbidity. Sheep pox (36.36%) and Peste des Petits Ruminants (PPR) also emerged as major viral diseases, with PPR showing a 32.87% overall positivity. Serological analysis further indicated widespread exposure to PPR virus, with 63.56% antibody positivity, while antigen detection confirmed active infections in a subset of cases. Among parasitic infections, haemoprotozoan diseases such as anaplasmosis (15.22%) and theileriosis (11.54%) were prominent, whereas babesiosis was comparatively low (1.1%). Sporadic but significant occurrences of anthrax (8.69%) were also confirmed, including successful isolation of the pathogen in select cases. The details of the samples tested for different diseases and their results are presented in Table 8.

Table 8: The details of the samples tested for different diseases.

Disease	Total Clinical Samples Tested	Positive	Percent Positives (%)	Agent Isolation	Isolates
Pasteurellosis in Sheep and goat	396	33	8.33	-	-
Enterotoxaemia (ET) in Sheep and goat	117	09	7.69	-	-
Anthrax in Sheep and goat	23	02	8.69	02	-
Mycoplasmosis in Sheep and Goats	186	75	40.32	-	-
Brucellosis Sheep & Goat	720	44	6.11	-	-
BT Sheep & Goat	42	02	4.76	-	-
Sheep Pox in Sheep & Goat	33	12	36.36	-	-
PPR in Sheep and goat	1290	424	32.87	-	1
PPR V antibodies	568	361	63.56	-	-
PPRV antigen	722	63	8.73	-	1
Theileriosis	184	21	11.54		
Anaplasmosis	184	28	15.22		
Babesiosis	184	2	1.1		

In parallel, 60 outbreak events were reported during the year, of which 44 were laboratory-confirmed, involving diseases such as PPR, mycoplasmosis, enterotoxaemia, haemoprotozoan infections, brucellosis, sheep pox, anthrax, and mixed infections. A subset of outbreaks associated with abortion and high mortality was directly investigated in the field, providing critical insights into disease dynamics under real-world conditions. Overall, the findings highlight the continued burden of both endemic and emerging diseases in small ruminants, with PPR and mycoplasmosis being particularly prominent. The high seroprevalence of PPR suggests widespread exposure despite control efforts, while the diversity of pathogens detected underscores the need for integrated disease surveillance and timely diagnostics. These results reinforce the importance of sustained monitoring, rapid outbreak response, and targeted control strategies to improve small ruminant health and productivity in India.

(Balamurugan V, Shivachandra SB, Sridevi R, Chanda MM, Nagalingam M, Manjunatha Reddy GB and Siju SJ)

Epidemiological and Molecular Investigation of a Mixed Haemoprotozoan Outbreak in Sheep at a Government Breeding Farm, Karnataka

Tick-borne haemoprotozoan diseases pose a significant threat to small ruminant production, particularly under organized farm conditions where animal movement and vector exposure can amplify disease transmission. In March 2025, an outbreak characterized by high morbidity and mortality was reported at a government sheep breeding farm in Kudapura, Chitradurga district. Clinically affected sheep exhibited fever, dyspnea, neurological signs, recumbency, diarrhea, and high mortality, particularly among newly introduced stock. Epidemiological analysis revealed an attack rate of 10.8%, a mortality rate of 5.8%, and a case fatality rate of 54%. The epidemic curve demonstrated a propagated pattern with multiple peaks following animal introduction in early January 2025, with a marked decline in mortality after implementation of intervention measures in mid-March 2025 (Fig 30).

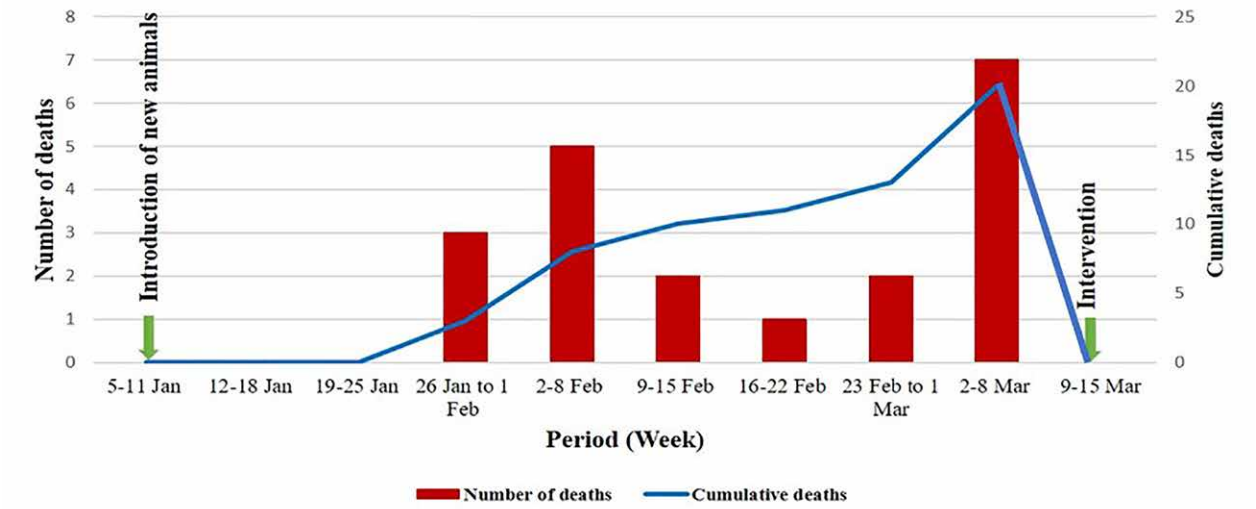


Fig 30: Epidemic curve showing the temporal pattern of mortality during the hemoprotozoan outbreak in sheep.

Blood and tissue samples were screened for haemoprotozoan parasites using microscopy and Polymerase Chain Reaction (PCR). PCR screening confirmed high positivity

for *Theileria* spp. (97.8%) and *Anaplasma* spp. (91.1%), along with moderate detection of Babesia spp. (40%), indicating a mixed haemoprotozoan infection. Subgroup analysis showed higher pathogen detection in Deccani sheep and newly introduced animals, while females exhibited higher *Babesia* positivity (Table 1). Concurrent infection with *Clostridium perfringens type* D was detected in two cases. Genetic characterization of *Theileria* and *Anaplasma* species was performed through sequencing and phylogenetic analysis. Descriptive subgroup analysis was conducted to assess associations with breed, sex, and animal source Molecular characterization identified *Theileria luwenshuni* and *Anaplasma ovis*.

This investigation highlights the critical role of animal introduction and tick exposure in driving propagated haemoprotozoan outbreaks under organized farm conditions. The findings underscore the need for stringent biosecurity measures, quarantine of newly introduced animals, integrated tick control strategies, and molecular surveillance to prevent similar outbreaks in organized sheep farms.

(Siju SJ, Nagalingam M, Shivachandra SB and Balamurugan V)

Assessment of Population Immunity against Peste des Petits Ruminants in Goats and Sheep in India after the Second Annual Mass Vaccination under the National PPR Eradication Programme

This study assessed population immunity against Peste des Petits Ruminants (PPR) in sheep and goats in India following the second annual round of mass vaccination implemented under the National PPR Eradication Programme, launched in 2023 as per the national strategic plan. A cross-sectional post-vaccination evaluation (PVE) was conducted during 2024–2025 to assess vaccine effectiveness and herd immunity under field conditions, in alignment with the WOAH/FAO Global Control and Eradication Strategy (GCES) of the PPR Global Eradication Programme (PPR-GEP) targeting eradication by 2030.

A total of 41,498 serum samples were collected within 90 days post-vaccination from sheep and goats across three age groups: 6–12 months (n = 14,372), 1–2 years (n = 13,826), and >2 years (n = 13,300). These samples represented 1,273 epidemiological units (villages) across multiple taluks and districts in 13 Indian states. All sera were tested for PPR virus (PPRV) antibodies using an indigenous monoclonal antibody-based competitive ELISA targeting the hemagglutinin (H) protein.

The results revealed an overall population immunity of 76% CI 95%: (74 to 76) with an estimated vaccine effectiveness of 72 % CI 95%: (70 to 72). PPRV antibodies prevalence distribution (Seroconversion and population immunity) in small ruminants after the Second Annual Mass Vaccination provided in Table 9. In general, at the epidemiological unit level, < 20% villages across the studied states remained below 30%, highlighting specific areas requiring intensified vaccination efforts. Overall vaccination coverage exceeded 95% among small ruminants aged above 3–4 months, approaching the critical herd immunity threshold of 70–80%.

Substantial heterogeneity in seroconversion and population immunity was observed across states and epidemiological units, with a small proportion of villages (<20%) remaining below 30% immunity despite high overall vaccination coverage. These immunity gaps highlight the need for targeted, risk-based vaccination and intensified surveillance to ensure uniform herd immunity and prevent persistent virus circulation. The findings underscore the importance of sustained, successive mass vaccination campaigns combined with targeted surveillance to achieve and maintain protective immunity, thereby supporting India's commitment to national and global PPR eradication goals.

Table 9: PPRV antibody prevalence and population immunity in small ruminants across 13 Indian States/UTs post-second mass vaccination round in India.

Name of States/Union Territories	Population Immunity			Sero-monitoring / Seroconversion		
	No. of serum samples screened	No. of samples positive in ELISA	Prevalence (%)	No. of serum samples screened	No. of samples positive in ELISA	Prevalence (%)
Andhra Pradesh	4935	3922	79.5	1650	1287	78
Chhattisgarh	2700	2026	75	927	687	74.1
Goa	1140	707	62	403	233	57.8
Gujarat	2236	1698	75.9	744	546	73.4
Karnataka	4543	3486	76.7	1522	1138	74.8
Odisha	2650	2169	81.8	857	696	81.2
Puducherry	2688	1859	69.2	1320	955	72.3
Punjab	1965	1440	73.3	659	454	68.9
Tamil Nadu	4417	3678	83.3	1487	1198	80.6
Telangana	7126	6083	85.4	2439	2057	84.3
Uttarakhand	1974	1236	62.6	659	405	61.5
Bihar	3202	1869	58.4	1066	639	59.9
Maharashtra	1922	1380	71.8	639	449	70.3
Grand Total	**41498**	**31553**	**76**	**14372**	**10744**	**74.8**
Chi-squared value (x^2): p-value and Prevalence at 95% CI	x^2: 1514.3, P <0.005		CI 95%: 76-76	x^2: 444.2, p <0.005		CI 95%: 74-75

(Balamurugan V, Suresh KP, Govindaraj G and Chandrasekar S)

Advancing Towards PPR Eradication in India: Assessment of Vaccination Impact on Population Immunity in Goats and Sheep in Odisha

This study evaluates population immunity and vaccine performance under the PPR EP implemented in Odisha, India. The assessment focuses on seroconversion, vaccine efficacy, and population immunity following annual mass vaccination, in alignment with WOAH and FAO guidelines for Post-Vaccination Evaluation under the Global Control and Eradication Strategy. A cross-sectional study was conducted for different purposes from 2023 to 2025. In the pre-vaccination phase (2023), 3,466 serum samples from sheep and goats across 120 epidemiological units (epi-units) in 82 taluks spanning 28 districts were analyzed. Three strata of age-wise group (6-12M, 1-2 Y and >2 Y) seropositivity ranged from 60% to 66%, with an overall seroprevalence of 61.1%; 43% of epi-units achieved ≥70% antibody prevalence. Following the first mass vaccination (2023), 1,125 samples from goats (6–12M collected within 90 days post-vaccination showed 76.9% seroconversion,

with ≥70% seroprevalence in over 68% of epi-units. After the second round in 2024, 2,650 samples across all age groups from 90 epi-units demonstrated improved herd immunity, with over 80% of epi-units achieving ≥70% immunity and vaccine effectiveness reaching 81.85%. The results from the third round of vaccination (2025) indicate sustained progress, with vaccine efficacy of ~75%, effectiveness of 74%, and population immunity of 78%. Among tested 3750 samples from 107 epi-units, more than 71% of villages achieved ≥70% immunity (Fig 31). These findings highlight the critical role of successive annual mass vaccination in achieving herd immunity. The Odisha PPR control programme has achieved >95% vaccination coverage in small ruminants (>3–4 months), approaching the herd immunity threshold (~80%). This study supports Odisha as a model for national PPR eradication and reinforces India's commitment to global eradication by 2030.

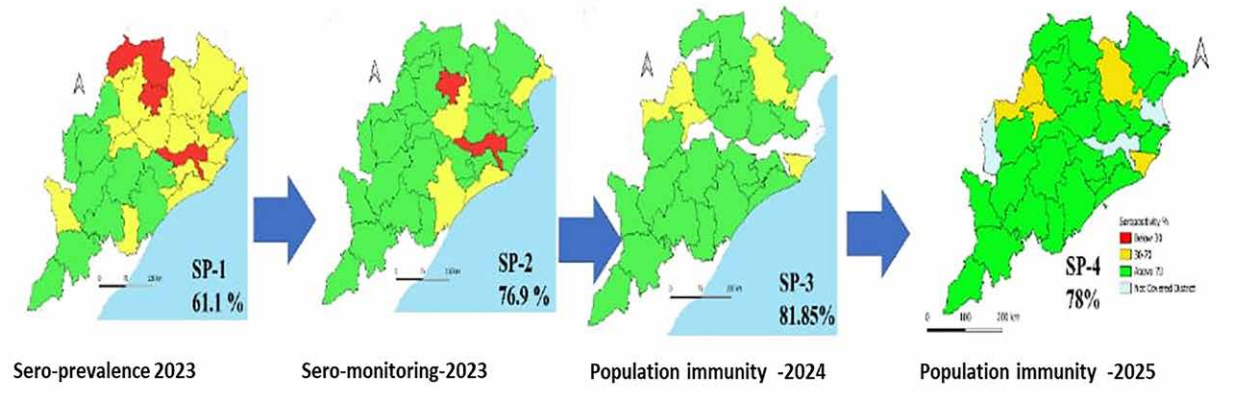


Fig 31: Evaluating vaccination impact on her immunity for PPR eradication in Odisha, India.

(Balamurugan V, Govindaraj G, Suresh KP and Chandrasekar S)

Molecular Surveillance of PPRV Reveals Persistent Lineage IV Circulation in India

Peste des Petits Ruminants (PPR) is a highly contagious viral disease that primarily affects sheep and goats, caused by the *Morbillivirus caprinae* species. Understanding the genetic variability and distribution of PPRV is critical for tracking viral evolution, especially in vaccinated regions, to develop effective diagnostic tools and control strategies. Detecting potential viral mutations and understanding transmission patterns are essential for refining disease control measures and ensuring the success of the PPR eradication program. Two PPR outbreaks were confirmed through passive surveillance in goat flocks from Mandi district of Himachal Pradesh (HP) (May 2024) and Betul district of Madhya Pradesh (MP) (February 2025). Both outbreaks resulted in high morbidity (84% in HP and 23% in MP) and considerable mortality, with 60% mortality and 71% case fatality rate (CFR) reported in HP, raising concerns about ongoing viral circulation despite control and eradication efforts. Clinical samples (blood/serum, swabs, and tissues) collected from affected animals and submitted to the laboratory were tested using ELISA for antibody detection, as well as RT-PCR and qRT-PCR, confirming the presence of the PPRV genome. A total of 10 out of 24 samples from HP and 4 out of 8 samples from MP were found positive. Highly positive tissue and swab samples were selected (2 samples from HP and one sample from MP outbreaks) for virus isolation in Vero cell cultures. The PPR virus was successfully isolated by blind passages, confirming its characteristics CPE of PPRV in Vero cells in laboratory conditions. To further validate the results and rule out the possibility of laboratory contamination, nucleocapsid (N) gene-specific RT-PCR products were

subjected to sequencing. This molecular characterization confirmed the authenticity of the detected virus, and subsequent NCBI BLAST analysis of the sequences verified that the isolates were indeed PPRV. Subsequent sequencing and phylogenetic analysis of partial N gene sequences using Maximum Likelihood method in MEGA 11 software, revealed that the isolates belong to Asian lineage IV (Fig 32). These isolates exhibit strong genetic similarity to Asian PPRV Lineage IV strains reported in India from 2005 to 2022, as described previously. The findings reaffirm the continued circulation of lineage IV PPRV in India, underscoring the need for ongoing genetic surveillance. This study contributes valuable insights into the molecular characterization of PPRV, supporting national and global efforts to eliminate the disease.

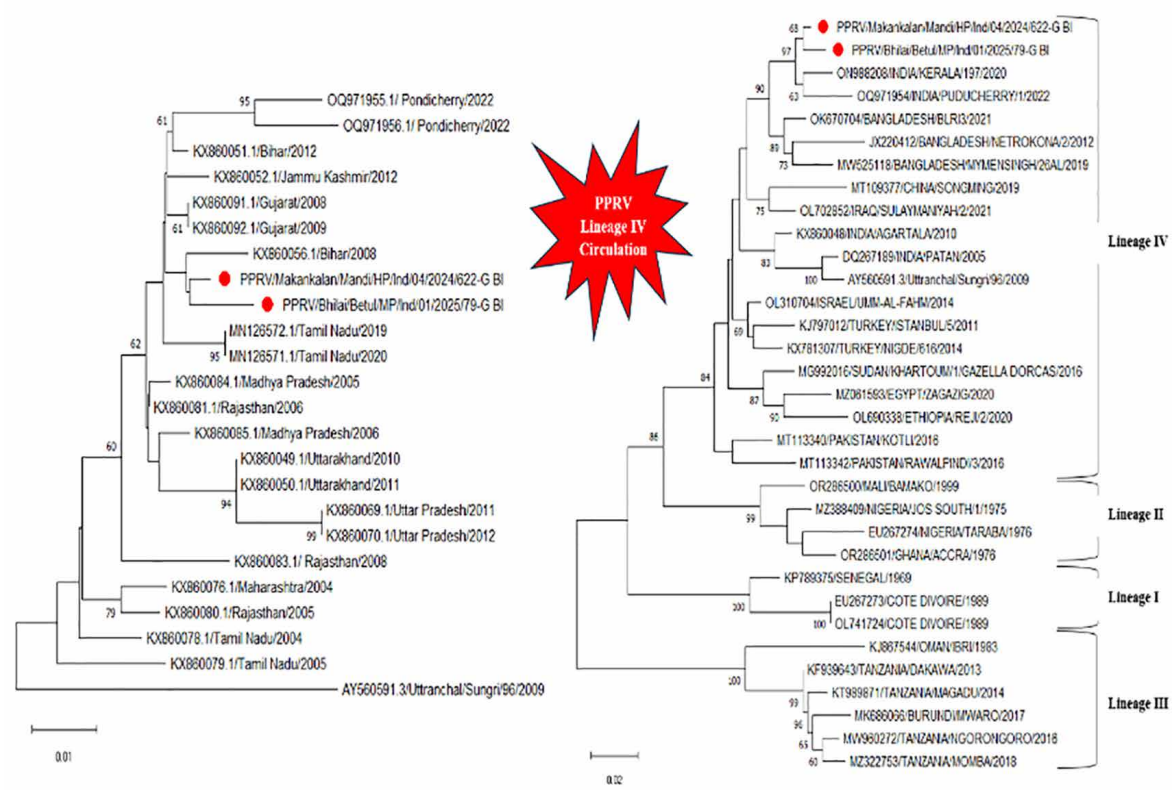


Fig 32: Phylogenetic analysis of PPRV isolates from field outbreaks in India.

(Balamurugan V)

Whole Genome Sequencing of Peste des Petits Ruminants Virus to Uncover Epidemiological Insights from Different Episystems of India

PPR is a highly contagious and economically devastating disease of sheep and goats caused by PPR virus (PPRV), a member of the family *Paramyxoviridae*, genus *Morbillivirus* (*Morbillivirus caprinae*). Continuous monitoring of the genetic diversity and spatiotemporal evolution of PPRV across different episystems is crucial for identifying emerging variants, understanding virus circulation, and developing effective diagnostics and episystem-based control strategies aligned with national PPR eradication programs.

This study aimed to generate and analyze whole genome sequences of 13 PPRV isolates obtained from cases in sheep and goats across Himachal Pradesh, Madhya Pradesh, Arunachal Pradesh, Mizoram, and Karnataka between June 2022 and March 2025, representing the Northern, North-Eastern (Eastern Himalayan), Central, and Southern episystems of India (Fig 33).

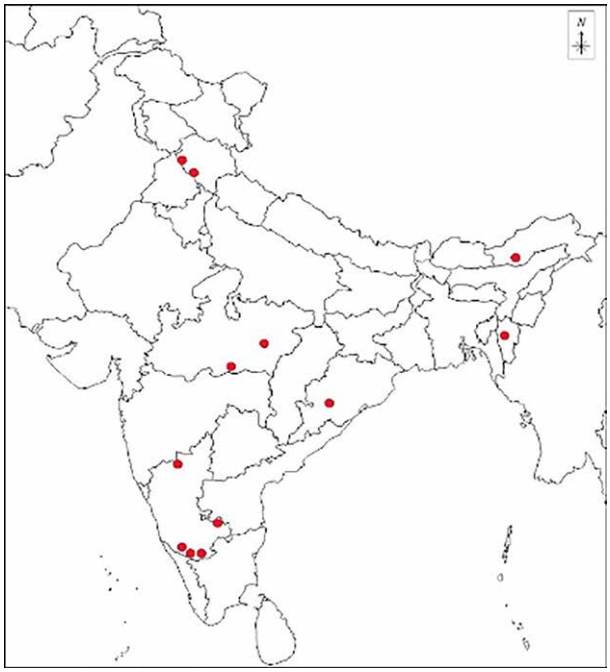


Fig 33: Spatial distribution of Peste des Petits Ruminants virus (PPRV) sampling sites across India. Red dots indicate sites from which serologically confirmed PPRV samples were collected for whole genome sequencing.

PRV-positive samples were confirmed by RT-PCR and sequencing, followed by virus isolation in Vero cells and whole-genome sequencing (Illumina NovaSeq 6000, ~100× coverage). Genomes were assembled (Prokka), compared (BLAST), and phylogenetically analyzed in MEGA 12 using the Neighbor-Joining method with reference lineages I–IV.

Complete genomes of 15,948 bp were done in GBRC, Gujarat, and assembled as single contigs for all nine isolates, with GC content ranging from 46–48%. The sequences shared ~96.05% nucleotide identity with the Indian vaccine strain Sungri-96. Phylogenetic analysis revealed clustering of all isolates within Lineage IV, closely related to strains from China, Tibet, and Bangladesh (Fig 34).

This study reports the first full genome characterization of Lineage IV PPRV from multiple episystems in India, confirming its continued dominance. Notably, viruses from the Northeastern episystem show close genetic association with strains circulating in neighboring regions, including Tibet, China, and Bangladesh. These findings emphasize the importance of sustained episystem-based genomic surveillance to support PPR control and global eradication efforts targeted for 2030.

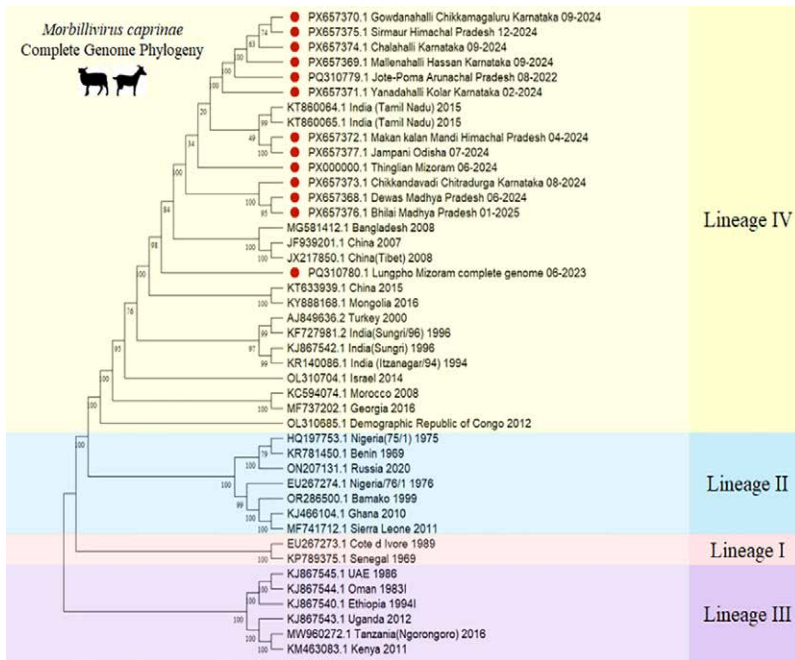


Fig 34: Phylogenetic analysis of PPRV isolates from multiple Indian episystems. Whole genome sequences of thirteen outbreak isolates were compared with 30 reference PPRV genomes representing all four lineages using the Neighbor-Joining method in MEGA 12.

(Balamurugan V)

Multiplex One-step PCR detection and differentiation of mixed infections of Capripox in Sheep and Goats

Small ruminants, which are vital to the livelihoods of marginal farmers in India, are frequently affected by co-infections involving multiple pathogens. Due to overlapping clinical manifestations, conventional diagnostic methods often fail to accurately detect and differentiate these infections, especially in mixed infection scenarios. Under the PPR surveillance programme, particularly during the eradication phase, it is critical that suspected outbreak samples from sheep and goats testing negative for PPR are further investigated for other etiological agents to accurately confirm the cause of the outbreak. To address this diagnostic gap, initially, a sensitive, specific, and rapid novel multiplex one-step PCR assay was developed for the simultaneous detection of PPRV and CaPV in a single reaction, using target RNA and DNA extracted simultaneously from the same samples using Nucleospore kit.

The assay demonstrated high analytical performance, with detection limits of 10^2 copies per reaction for PPRV (targeting the N gene) and 10^3 copies per reaction for CaPV (targeting the 13L gene). Specificity testing against a panel of pathogens, including *Bacillus anthracis*, *Babesia*, *Brucella*, *Leptospira*, and *Orientia tsutsugamushi, Bluetongue, Mycobacterium*, showed no cross-reactivity.

Further enhancement of the assay incorporated additional targets, including Orf virus (ORFV), Canine distemper virus (CDV) (Fig 35), N gene enabling broader detection of pathogens affecting domestic small ruminants and wild animals, with sensitivity of 10^2 to 10^3 copies/reaction. Ongoing standardization aims to include *Mycoplasma* spp. And *Pasteurella* spp., in a two-tube format to expand diagnostic coverage of related diseases. Field application of this standardized assay during 2025 identified mixed infections of PPRV and CaPV in 3 out of six outbreaks across Karnataka, Madhya Pradesh, Chhattisgarh, Goa, and Himachal Pradesh. Notably, these mixed infections were confirmed from nasal swabs and tissue samples collected from affected animals, demonstrating the suitability of this sample type for detecting co-infections under field conditions. Furthermore, a sheep pox outbreak in the Bengaluru Rural district revealed a triple infection involving PPRV, CaPV, and ORFV, highlighting the complexity of disease ecology in outbreak settings.

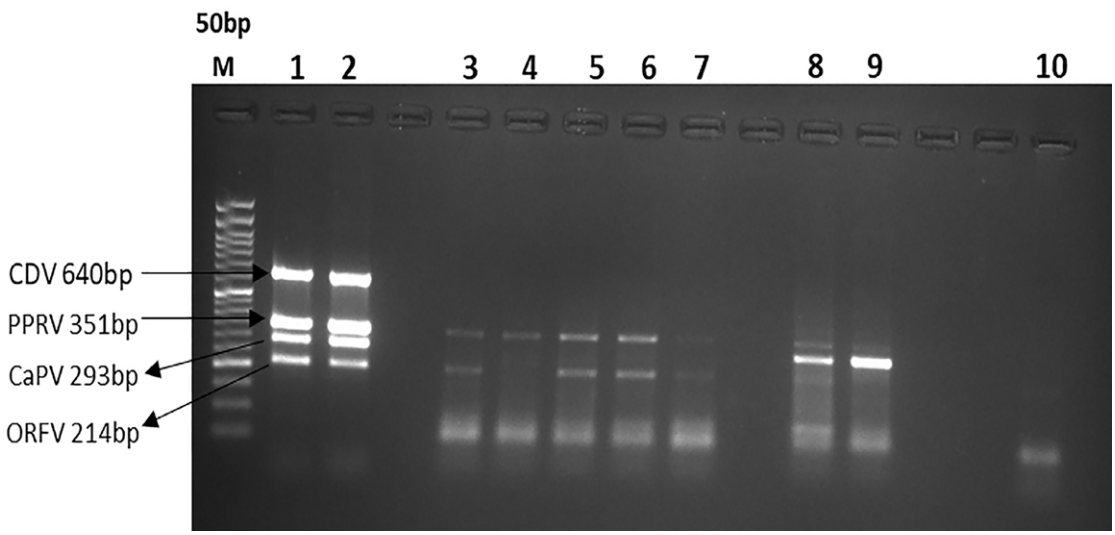
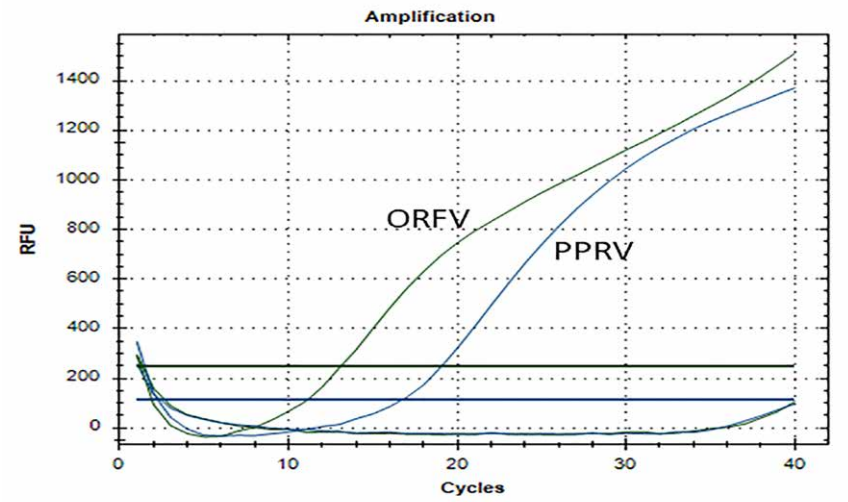


Fig 35: Agarose Gel Electrophoresis of One-Step Multiplex PCR: lane M: 100bp plus Marker, Lane 1 and 2 : Positive controls; Lane 3 -7: Clinical samples, showing amplification of target PPRV and ORFV: Lane 8-9: Clinical samples, showing amplification of target PPRV and CaPV: Lane 10: NTC.

Further, a duplex real-time PCR assay for PPRV and ORFV has already been successfully established with detection limit of 10^2 copies/ reaction, and further optimization is ongoing to incorporate additional targets for broader field applicability (Fig 36). The multiplex assays demonstrated the ability to detect both single and mixed infections in field samples, including cases missed by ELISA, and showed strong concordance with standard uniplex RT-PCR assays. This approach provides a robus t and practical tool for confirmatory diagnosis during outbreaks, particularly in regions where multiple viral and bacterial pathogens co-circulate.

Overall, this multiplex diagnostic strategy offers significant potential for expansion to include a wider range of pathogens, enabling precise detection and differentiation of co-infections. Such an integrated approach enhances diagnostic accuracy, generates valuable epidemiological insights, and strengthens surveillance and control efforts for small ruminant diseases in India under the ongoing PPR eradication programme.



Fluor	Target	Content	Cq
FAM	PPR	NTC	N/A
HEX	ORF	NTC	N/A
FAM	PPR	Pos Ctrl	16.66
HEX	ORF	Pos Ctrl	13.05

Fig 36: One step Duplex Real-time PCR of PPRV and ORFV.

(Balamurugan V)

Surveillance and Economic Impact Assessment of Bluetongue Disease in India

A comprehensive surveillance study of Bluetongue caused by the Bluetongue virus (BTV) was undertaken across four Indian states under the All India Network Programme on Control of Emerging and Re-emerging Animal Diseases programme. A total of 285 serum samples were tested using Competitive ELISA, revealing an overall seropositivity of 88.77% (253/285), indicating widespread circulation of BTV in the surveyed regions. State-wise analysis showed consistently high seroprevalence, with Jammu and Kashmir recording the highest positivity at 92.0% (23/25), followed by Rajasthan at 88.81% (119/134), Gujarat at 88.24% (30/34), and Karnataka at 88.04% (81/92). Rajasthan contributed the largest proportion of samples (47% of the total samples), while maintaining positivity levels comparable to the other states (Table 10).

Table 10: State wise samples tested for the presence of Bluetongue virus by RT-PCR.

State/Region	Total Samples Tested	Positive Samples	Positivity Rate (%)
Karnataka	92	81	88.04
Gujarat	34	30	88.24
Jammu & Kashmir	25	23	92.00
Rajasthan	134	119	88.81
TOTAL	**285**	**253**	**88.77**

Notably, Rajasthan reported bluetongue cases after a prolonged gap of more than 20 years, according to local records. A total of 140 clinically suspected samples were received from six districts-Balotara, Jaipur, Jalore, Pali, Jodhpur, and Didwana-Kuchaman-of which 119 samples tested positive by Reverse Transcription Polymerase Chain Reaction. Village-wise analysis demonstrated extensive virus circulation, with 100% positivity observed in locations such as Chirota village (Jaipur district; 8/8 samples) and Chanod village (Pali district; 8/8 samples). Serological testing using Indirect ELISA further showed 81% seropositivity (30/37 samples), confirming substantial population-level exposure to BTV.

(Chanda MM and Sathish Gowda CS)

Development of a Recombinant Non-Structural Protein (NS1–NS3)–Based DIVA-Compliant Competitive ELISA for Bluetongue Population Surveillance

A DIVA-compliant Competitive ELISA based on recombinant non-structural proteins (NS1–NS3) of the Bluetongue virus was optimized for the detection of antibodies against Bluetongue. The assay was standardized through systematic optimization of critical parameters, followed by rigorous evaluation of its analytical and diagnostic performance. Analytical sensitivity and specificity were determined initially, and diagnostic sensitivity (95.52%) and specificity (94.4%) were subsequently assessed using well-characterized positive and negative reference serum samples. The optimized cELISA was evaluated using 267 field serum samples collected from eight districts of Karnataka, namely Sira, Tumakuru, Chitradurga, Koppal, Bellahalli, Challakere, Belagavi, and Vijayapura. The large and geographically diverse sample set enabled robust assessment of assay performance under field conditions, supporting its suitability for population-level surveillance of bluetongue disease.

For assay development, large-scale production of the monoclonal antibody 6F7B5 was successfully achieved through expansion of the corresponding hybridoma clone under optimized *in vitro* culture conditions. To ensure sustainable and cost-effective antibody production, the hybridoma clone 6F7B5 was successfully adapted to serum-free culture conditions through a stepwise reduction of fetal bovine serum (FBS). During the adaptation process, cell viability, growth kinetics, and antibody titres were closely monitored to ensure consistent performance and stable monoclonal antibody yield. The successful serum-free adaptation supports scalable manufacturing and long-term production of the cELISA kit for national bluetongue surveillance programmes.

(Chanda MM)

Epidemiology of Chandipura Virus Infection in Gujarat, India

During the reporting period (2025), a total of 51 livestock samples were collected and processed from two Chandipura virus (CHPV)–affected villages in Gujarat. Village 1, Hathipura (Kheda district), contributed 29 cattle samples, while Village 2, Mota Jampur (Banaskantha district), provided 22 multi-species samples, comprising 8 cattle, 7 buffalo, and 7 goats. All blood samples were tested for CHPV using Reverse Transcription Polymerase Chain Reaction, and none were found positive. However, the Plaque Reduction Neutralization Test detected neutralizing antibodies in five samples, including four buffalo and one cattle, indicating prior exposure to CHPV in livestock. Expanded epidemiological surveillance of CHPV was initiated in Panchmahal district, involving systematic sampling of 688 livestock animals across 47 villages. We collected 542 blood samples, 542 serum samples, and 542 nasal swabs, along with 90 vector pools, enabling a comprehensive One Health–based investigation (Fig 37).

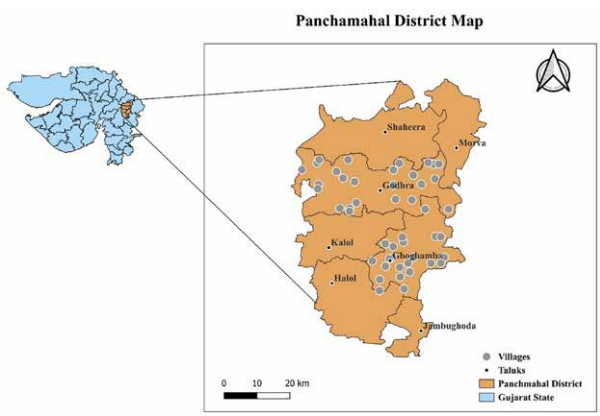


Fig 37: Sites for seroprevalence study on Chandipura virus in Panchmahal district of Gujarat.

Species-wise representation was well balanced, with cattle accounting for 34% (234 animals), buffalo 33% (230 animals), and goats 32% (223 animals) of the sampled population, while sheep representation was minimal (9 animals).

Spatial risk mapping of Chandipura virus in Gujarat was done using past CHPV occurrences and remotely sensed variables was done. It revealed a distinct geographical gradient in transmission probability. The highest-risk zones (red zones; probability ~0.97) were concentrated in the eastern and central districts, particularly in tribal and forested regions, consistent with historical outbreak patterns. In contrast, the western coastal districts predominantly exhibited low to moderate risk levels (green zones; probability ~0.06–0.40), while northern border districts showed variable risk with scattered medium-risk pockets (Fig 38).

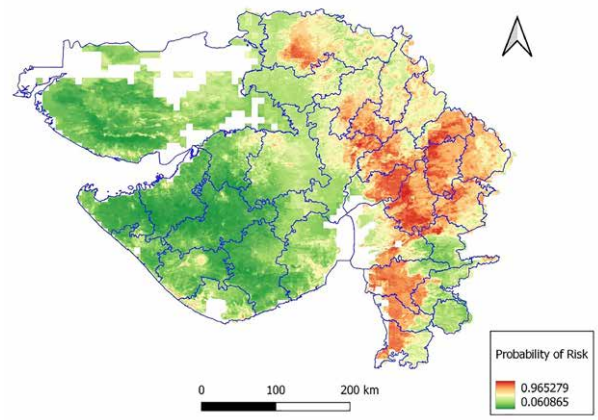


Figure 38: Spatial risk map of Chandipura virus (CHPV) in Gujarat.

This spatial risk distribution correlates strongly with ecological factors conducive to vector breeding and virus transmission, including forest cover, humidity, and favorable temperature conditions. The identified high-risk eastern corridor—encompassing Panchmahal, Dahod, and parts of Kheda and Banaskantha districts—overlaps with the current study sites, underscoring its relevance for targeted surveillance and control interventions.

(Chanda MM, Chethan Kumar HB and Gulati BR)

Climate-Driven Spatial Risk Mapping of Kyasanur Forest Disease and Crimean-Congo Hemorrhagic Fever in India Using GIS, Remote Sensing and Advanced Modelling Approaches

Kyasanur Forest Disease (KFD) and Crimean-Congo Hemorrhagic Fever (CCHF) are emerging tick-borne viral zoonoses in India, with transmission dynamics strongly influenced by climatic and ecological factors..

During the reporting period, predictive ecological niche models were developed for the Kyasanur Forest Disease virus (KFDV) and its primary vector Haemaphysalis spinigera using past occurrence data and remotely sensed variables, demonstrating excellent performance (ROC > 0.99 for KFDV and > 0.96 for the vector). Current risk mapping indicated that KFDV suitability is confined to approximately 7.2% of India, predominantly within the Western Ghats region covering Karnataka, Kerala, Goa, and Tamil Nadu, whereas *H. spinigera* exhibited a wider ecological niche (16.5%), extending into central and northeastern regions. Future climate projections suggested a marginal contraction of KFDV suitability with persistent hotspots along the Western Ghats and emerging risk zones in northeastern India, while the vector is projected to maintain its current range with further geographical expansion. Isothermality emerged as the most influential environmental variable (59% contribution), highlighting the critical role of temperature stability in shaping disease distribution.

In parallel, DNA barcoding protocols were optimized using Aedes aegypti samples, revealing high genetic diversity and signatures of population expansion, with flower pots identified as the dominant breeding habitat. The optimized protocol was subsequently applied to the molecular characterization of 1,400 tick samples collected from Goa and Karnataka. Ongoing and future work will extend these approaches to CCHF risk modelling and comprehensive phylogenetic analysis of tick populations, with the ultimate goal of establishing standardized climate–disease modelling frameworks to strengthen India's One Health preparedness against emerging vector-borne diseases.

(Chanda MM, Shivachandra SB and Chethan Kumar HB)

Quantifying Zoonotic Disease Spillover Risk at the Wildlife–Livestock–Human Interface

Zoonotic diseases emerging at the wildlife–livestock–human interface pose a growing public health challenge in India. This study aimed to identify high-risk areas for zoonotic spillover, characterize transmission pathways, and support the development of evidence-based risk mitigation strategies using a One Health framework. During the reporting period, intensive entomological and serological surveillance was conducted across multiple ecological interfaces. A total of 996 tick samples were collected from the wildlife–livestock interface in Sattari taluk. The collection comprised 789 adult ticks and 207 larvae belonging to Haemaphysalis and Rhipicephalus species, primarily from cattle and goats across nine villages. Reverse Transcription Polymerase Chain Reaction targeting the NS5 gene of Kyasanur Forest Disease virus detected virus presence in 155 samples, yielding an overall positivity rate of 15.6%, indicating active virus circulation within livestock-associated tick populations and a significant zoonotic risk.

Vector surveillance at Bannerghatta Biological Park between September 2025 and January 2026 yielded 223 *Culicoides* specimens across nine collection events, with peak abundance observed in December. Culicoides oxystoma was the dominant species (35.9%), followed by *Culicoides arakawae* and *Culicoides peregrinus*. Among the *Avaritia* subgenus, key arbovirus vectors such as *Culicoides orientalis, Culicoides imicola,* and *Culicoides fulvus* were predominant, highlighting the potential for arboviral transmission at wildlife interfaces. Serological surveillance of 1,665 cattle serum samples collected from buffer and core zones of tiger reserves in Madhya Pradesh revealed seroprevalence rates of 17.30% for Kyasanur Forest Disease (KFD) and 16.10% for Crimean-Congo Hemorrhagic Fever (CCHF). Notably,

9.55% of samples were seropositive for both pathogens, indicating overlapping exposure to multiple tick-borne zoonoses.

Quantitative risk assessment based on 1,063 responses from 56 veterinary professionals across six tiger reserves identified Pench Tiger Reserve as the highest-risk site for zoonotic spillover. Shared water sources, close grazing proximity to forests, and frequent wildlife–livestock contact emerged as critical transmission pathways. The findings underscore the urgent need for strengthened intersectoral One Health coordination among animal health, forest, and human health sectors to mitigate zoonotic disease risks and protect forest-dependent communities.

(Chanda MM, Shivachandra SB and Chethan Kumar HB)

National Livestock Disease Epidemiology and Disease Modelling Program

This progress report covers activities undertaken under the Gates Foundation-funded programme for building India's national capacity in livestock disease surveillance, epidemiological modelling, and disease informatics. The programme implemented by ICAR-NIVEDI in partnership with leading national and international institutions-is organized into three inter-linked work packages (WPs): WP1 (National Framework Development), WP2 (Disease Informatics System), and WP3 (Capacity Building and Fellowships).

The reporting period was marked by four key achievements. First, substantial analytical progress was made on FMD modelling, with spatio-temporal epidemiological analysis completed for Tamil Nadu and comparative epidemiological regimes identified across Karnataka, Tamil Nadu, and Kerala revealing that FMD transmission in southern India follows three distinct patterns, each demanding a tailored control response. Second, a preliminary risk advisory on FMD serotype SAT-1 was developed and communicated to DAHD, drawing on FAO's 2025 risk assessment and India's border exposure, representing an early and high-impact policy output of the programme. Third, the ten-day "Foundations of Livestock Disease Epidemiology" training programme was successfully delivered (16–25 February 2026), drawing 22 participants from 11 states and achieving a mean post-assessment score of 94.6%-a 12.6 percentage-point improvement over pre-training levels. Fourth, the INLEAD Fellowship Programme was launched, attracting 75 applications from 24 states and UTs across India within the first cycle, with interviews completed and results announced for the first batch of 10 MVSc and 10 PhD fellows.

The next quarter will focus on deploying subsequent training modules, enrolling the first fellowship batch formally, and advancing the disease modelling framework towards predictive outputs for Karnataka and Kerala. Exploratory work on milk-based disease surveillance-a potential high-impact extension of the programme in alignment with NADCP's 2030 targets-is also progressing through a structured feasibility design in partnership with Stellapps Technologies.

Sridevi R, Shivasharanappa N, Siju SJ and Chethan Kumar HB)

Whole-Genome Analysis of Indian *Bacillus anthracis* Strains

Anthrax, caused by the bacterial pathogen Bacillus anthracis, is a lethal disease affecting both livestock and humans. Anthrax is endemic among livestock in several states of India, and its surveillance has gained increasing priority following reported human cases in certain regions. However, phylogenetic information on *B. anthracis* strains circulating in India and their relationship to global and regional lineages remains limited. Likewise, studies examining local phylogenetic patterns and the genetic diversity of *B. anthracis* during outbreaks within India are scarce. Understanding these phylogenetic patterns

is essential for improving our knowledge of the diversity and evolution of *B. anthracis* lineages in the country. Two independent anthrax outbreaks occurred in geographically distinct regions of India and affecting different animal host species were investigated. The first outbreak occurred in cattle in Kannigalli village, Chamarajanagar district, during 2015. The second outbreak occurred in sheep in Kallumadi village, Singanamala Mandal, Anantapur district, during 2024. The present study focused on the revival of *B. anthracis* from glycerol stock which were previously isolated from clinical samples and the exploration of genetic relationships among *B. anthracis* strains originating from animals across different states of India, along with their comparison with global strains.

The study involved comparative whole-genome analysis of two virulent Indian *B. anthracis* strains recovered from anthrax cases in cattle (NIVEDIAX3) and sheep (NIVEDIAX61). These genomes were analysed in comparison with 55 publicly available genomes retrieved from the National Center for Biotechnology Information database. Phylogenetic analysis based on Average Nucleotide Identity clustered the 57 strains into three major groups. Both NIVEDIAX strains clustered within Group III, alongside the Ames ancestor strain (Fig 39).

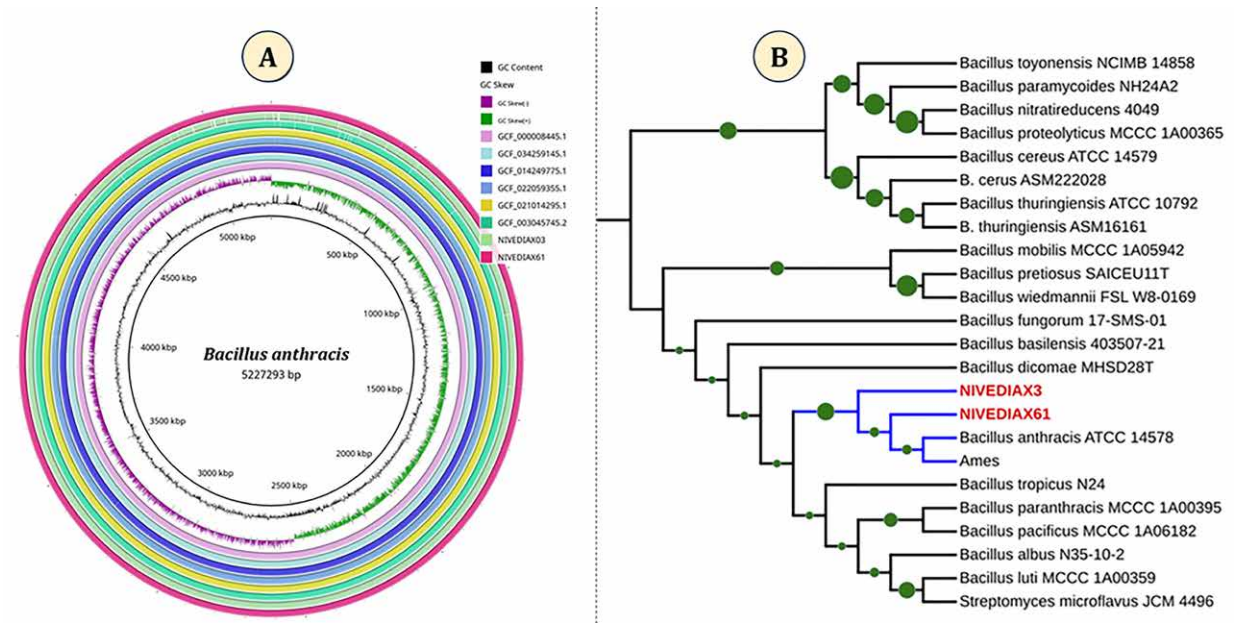


Fig 39: Comparative circular chromosome segments and phylogenetic tree.

Panel A. BLAST Ring Image Generator (BRIG) diagram showing homologous chromosome segments of Bacillus anthracis strains with genomes of strains Ames Ancestor as references. Innermost circles represent the GC content (black) and GC skew (purple/green). Panel B. Phylogenetic tree based on whole genomes Whole genome based phylogenetic tree inferring the evolutionary relationships amongst Bacillus species strains and the sequenced draft genome strains.

The ANI-based phylogenetic analysis demonstrated a high degree of genomic similarity among *B. anthracis* strains from different hosts and geographical locations. The BLAST Ring Image Generator (BRIG) was used to visualize coding sequence identity among strains of Indian origin, revealing a highly conserved genomic structure. Multilocus Sequence Typing assigned the strains to *B. cereus* sequence type ST1, *B. anthracis* cgMLST ST284, and plasmid ST12 based on the typing scheme. A total of 5,217 orthologous gene clusters and 468 single-copy gene clusters shared between the NIVEDIAX strains and the Ames ancestor strain were identified.

Based on core genome MLST (cgMLST) analysis, the NIVEDIAX strains were classified

as *B. anthracis* cgST284 with plasmid ST12. Notably, ST284 represents a unique sequence type identified among the analysed *B. anthracis* strains of animal origin in India. Strains from Tamil Nadu and Maharashtra were predicted to belong to cgMLST ST266, while a strain from Odisha was classified as ST312. Similarly, plasmid ST12 was also reported in isolates from Tamil Nadu, whereas plasmid ST13 was identified in the Odisha strain. The potential transfer of anthrax plasmids among members of the *Bacillus cereus* group can complicate classical typing approaches. Therefore, cgMLST-based genomic analysis is essential for accurate identification of clonal *B. anthracis* lineages, which is critical for epidemiological investigations, outbreak tracing, and microbial forensic applications.

A single-nucleotide polymorphism (SNP)–based phylogeny was constructed using the CSI Phylogeny v1.4 web service with the Ames Ancestor strain of Bacillus anthracis used as the reference genome. All phylogenetic trees were visualized using the Interactive Tree Of Life (iTOL) v5 online tool. The SNP-based analysis grouped the strains into multiple clusters that were not strictly associated with host species or geographical origin (Fig 40).

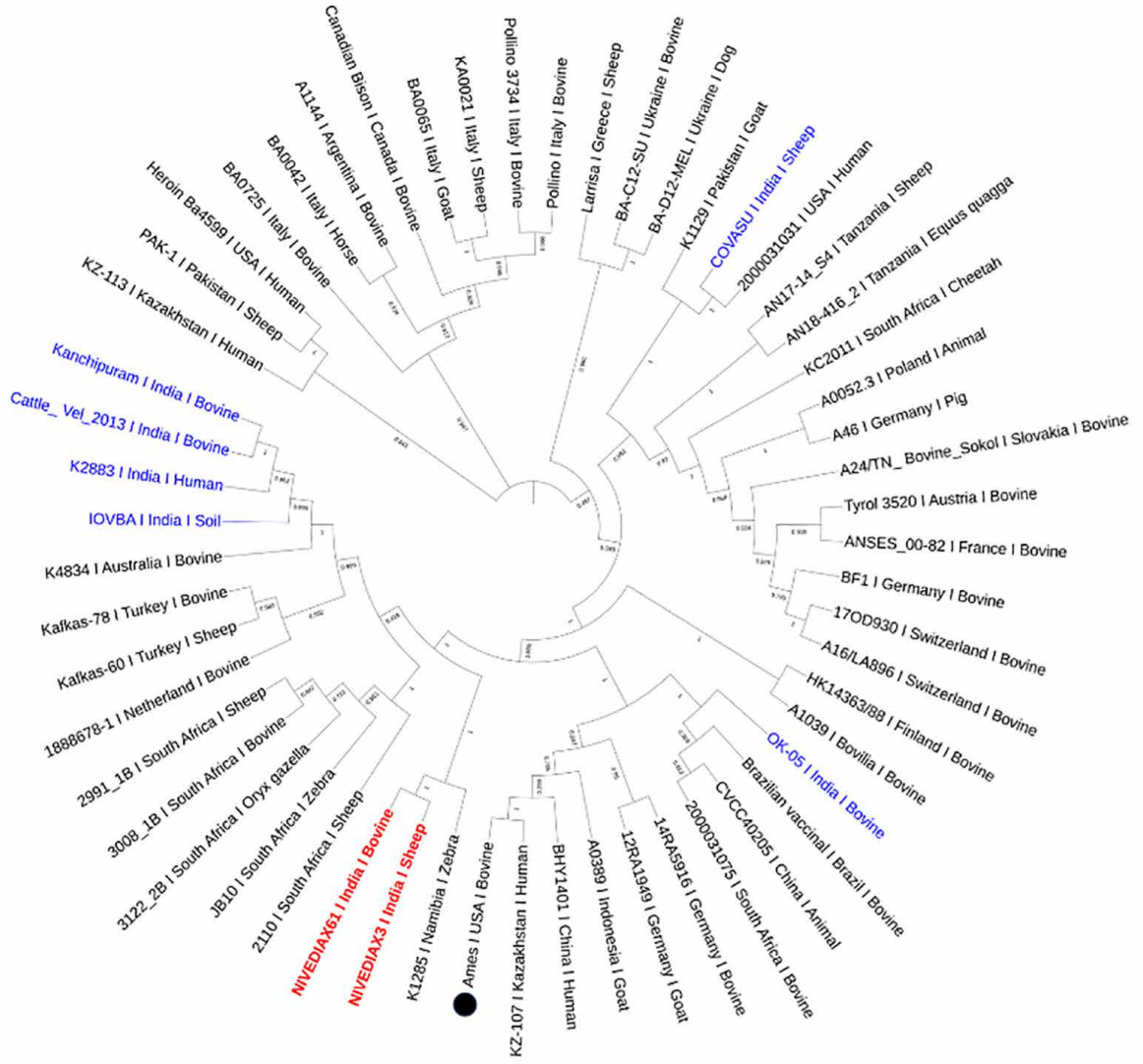


Fig 40: Phylogenetic tree based on core genome-SNPs in Bacillus anthracis strains.

Canonical SNP (canSNP) profiling indicated that both study strains belonged to the ABr.003 lineage (A.Br.Aust94 sublineage). Further analysis of 50 livestock genomes and five human *B. anthracis* isolates revealed the presence of diverse canSNP types, among

which ABr.003 was the most prevalent lineage detected in animal isolates. In India, the reported canSNP lineages include A.Br.002 (A.Br.001/002 sublineage), A.Br.003 (A.Br. Aust94 sublineage), and A.Br.007 (A.Br.Vollum sublineage)

The phylogenetic tree was constructed using the core SNPs identified from 57 genome sequences of *Bacillus anthracis* strains including NIVEDIAX strains (in red color), other Indian strains (in blue color) and *Bacillus anthracis* Ames ancestor (in black colored round dot) reference genome downloaded from NCBI to understand evolutionary relationship. The analysis was performed using CSI Phylogeny 1.4 with the Maximum Likelihood method and a default bootstrap replication value of 100.

Geographically, ABr.003 has been identified in strains from Karnataka, Tamil Nadu, and Andhra Pradesh, whereas ABr.002 has been reported from Odisha and ABr.007 from Maharashtra. Species-wise distribution of canSNP types among animal hosts revealed considerable diversity. In bovines, multiple lineages were detected, including A.Br.001, A.Br.002, A.Br.003, A.Br.004, A.Br.008, A.Br.009, and B.Br.004. In sheep, A.Br.003, A.Br.007, and A.Br.008 were observed, while goats carried A.Br.002, A.Br.007, and A.Br.008. Single canSNP types were reported in other species such as zebra (A.Br.003), pig (B.Br.004), antelope (A.Br.003), horse (A.Br.008), dog (A.Br.008), and cheetah (*Acinonyx jubatus*) (B.Br.002). Analysis of the 57 *B. anthracis* genomes confirmed that A.Br.003 was the dominant canSNP lineage among animal-derived isolates. Overall, multiple *B. anthracis* sublineages have been reported from India, indicating significant genetic diversity among circulating strains. The findings demonstrate the circulation of diverse *B. anthracis* sublineages among livestock populations in southern and eastern regions of India.

In conclusion, global comparative genome analysis of *Bacillus anthracis* strains, including Indian isolates from animals, provided deeper insights into the molecular epidemiology of circulating strains. Both study strains (NIVEDIAX3 and NIVEDIAX61) shared similar cgMLST and canSNP profiles despite originating from different host species and geographical locations. canSNP analysis grouped the Indian strains into one major clonal lineage with three distinct sublineages. The A.Br.003 (A.Br.Aust94) lineage was more frequently detected in southern Indian states, while Group B strains have not yet been reported in India and appear to be restricted to specific countries and host species. Identification of such lineages could assist in tracing potential transboundary transmission events. These findings highlight the need for broader genomic sampling of *B. anthracis* isolates from diverse domestic animal species and geographical regions, particularly from southern and eastern India, to better understand the genotypic diversity and distribution patterns of this important zoonotic pathogen. The phylogenetic tree was constructed using core SNPs identified from 57 genome sequences of Bacillus anthracis, including NIVEDIAX strains (shown in red), other Indian strains (shown in blue), and the Ames Ancestor reference genome (represented by a black circular node) downloaded from the National Center for Biotechnology Information. The analysis was performed using CSI Phylogeny v1.4 with the Maximum Likelihood method, applying a bootstrap replication value of 100 to infer the evolutionary relationships among the strains.

(Shivachandra SB and Chanda MM)

Development of an Indirect ELISA Based on Recombinant Protective Antigen of *Bacillus anthracis*

Anthrax, caused by *Bacillus anthracis*, is a highly fatal disease affecting herbivorous animals and occasionally humans. Although an effective live spore vaccine is widely used to immunize susceptible livestock, pre- and post-vaccination antibody titres are rarely monitored, despite their immunological importance in endemic areas. Monitoring antibody responses is essential for evaluating vaccine-induced immunity and field-level vaccine efficacy. The protective antigen (PA), a major exotoxin component of *B. anthracis*, plays a crucial role in anthrax pathogenesis and is known to induce protective neutralizing antibodies following vaccination. Therefore, the present study aimed to develop a simple and rapid indirect ELISA based on recombinant protective antigen for detecting anti-PA–specific IgG antibodies in sheep serum samples, providing serological evidence of anthrax exposure or vaccination.

A recombinant protective antigen (603 amino acids; ~67 kDa) was expressed, and a truncated PA antigen (~63 kDa) was purified from *Escherichia coli* under denaturing conditions for assay development and optimization (Fig 41).

The standardized indirect ELISA, using 200 ng of recombinant PA antigen per well, demonstrated excellent diagnostic performance with an area under the curve (AUC) of 0.980 (95% CI: 0.932–0.992). The assay showed a diagnostic sensitivity of 93.7% and specificity of 94.9% ($p < 0.001$) at an optimal cut-off value of >25.3 percent positivity (PP) or >0.46 OD (Fig. 2). The average intra-plate and inter-plate % Coefficients of Variance (CV) were 4.118 and 7.007, respectively, which was less than the prior precision criteria of 10 % and 15 % CV, respectively (Table 11) Further evaluation indicated that the assay could reliably detect antibodies in serum samples diluted up to 1:800, demonstrating high analytical sensitivity. Importantly, the assay specifically detected anti-anthrax antibodies without cross-reactivity with other sera. Repeatability testing showed acceptable intra-plate and inter-plate variation, with coefficients of variation (CV) below 10% and 15%, respectively. However, a limitation of this immunoassay is the lack of validation against standard reference assays, such as the Toxin Neutralization Assay or validated commercial ELISA kits. Future studies involving comparative validation with established assays will further strengthen the diagnostic applicability of the developed indirect ELISA for serological monitoring of anthrax vaccination and exposure in livestock populations.

Table 11: Analytical Precision / Repeatability of the inter-plate and intra-plate % co-efficient of variation.

Degree of Reactivity	Intra-plate				Inter-plate		
	Mean	SD	%CV		Mean	SD	%CV
Negatives	0.239	0.011	4.953		0.229	0.029	12.873
Low positives	0.835	0.031	3.811		0.829	0.036	4.382
Medium positives	1.173	0.042	3.601		1.185	0.064	5.471
High positives	1.873	0.077	4.110		1.857	0.098	5.303
Average	**1.03**	**0.040**	**4.118**		**1.025**	**0.056**	**7.007**

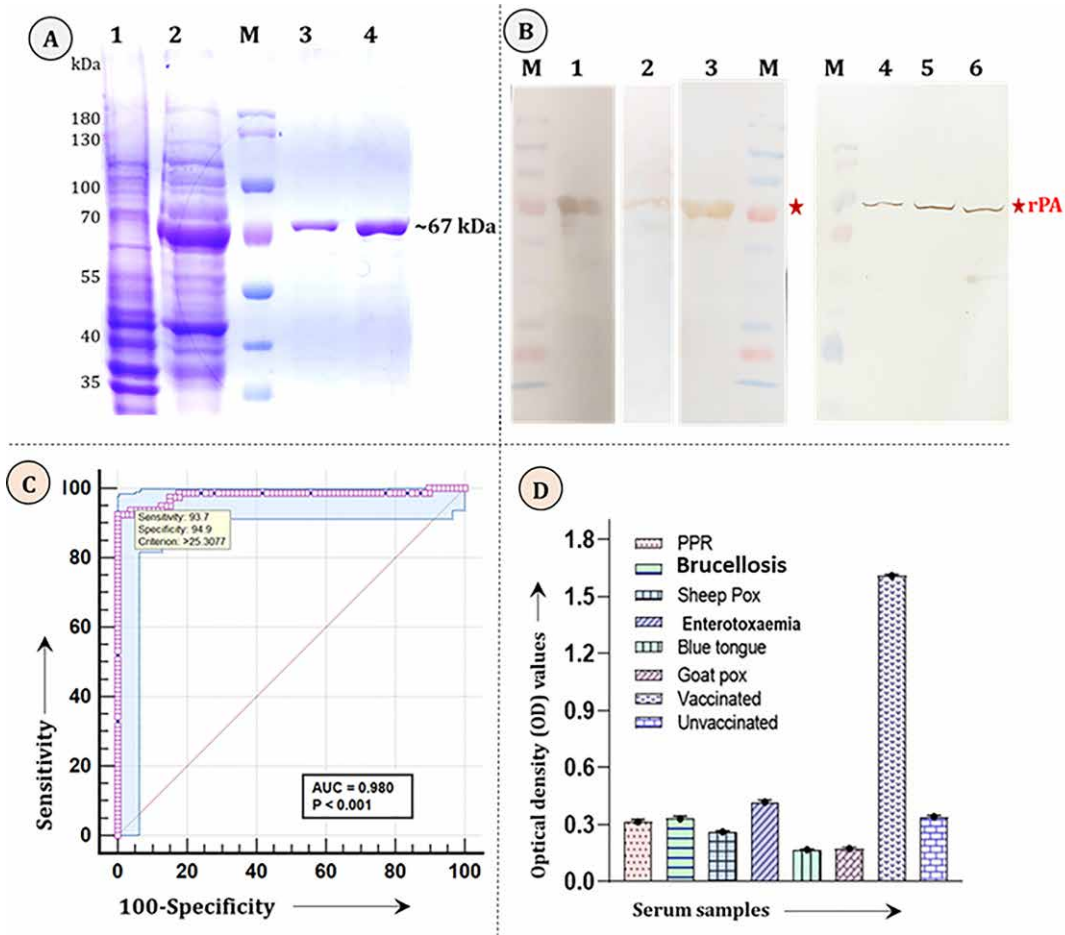


Fig 41: Production and Standardization of recombinant PA based indirect ELISA.

Panel A: Expression and production of recombinant rPA antigen. Lane M: Pre-stained protein ladder; Panel B: Western blot of recombinant PA and native PA. Lane M: Pre-stained protein ladder; Panel C: ROC curve showing diagnostic sensitivity and diagnostic specificity. Panel D: Cross-reactivity of indirect-ELISA with other infections positive sera. Note: A red colored star denotes the location of recombinant and native PA in Western blot.

(Shivachandra SB and Chanda MM)

Sero-Monitoring of Anti-PA–Specific IgG Antibodies in Sheep from Anthrax-Endemic and Non-Endemic States

In India, the incidence of Anthrax varies considerably across agro-climatic zones, with the highest occurrence reported in the southern region, followed by the eastern, western, and northeastern zones. Despite routine vaccination programs, anthrax cases continue to be reported in several endemic areas, highlighting the need to evaluate anti-protective antigen (PA) antibody titres and assess vaccine-induced immunity under field conditions. Furthermore, the immune status or seropositivity of PA-specific antibodies among susceptible hosts in endemic regions is rarely monitored. In the present study, an in-house developed recombinant PA–based ELISA (rPA-ELISA) was used for sero-monitoring in endemic and non-endemic regions to further validate the assay under field conditions. The optimized rPA-ELISA was used to evaluate anti-PA–specific IgG antibody titres in 1,289 randomly collected sheep serum samples from three states representing anthrax-endemic and non-endemic regions of India: Telangana (endemic), and Punjab and Haryana (non-endemic).

The screening results revealed the highest seropositivity in Telangana (66.98%), followed by Haryana (15.95%) and Punjab (6.83%) (Fig 42). Stratification of percent positivity (PP) values for Telangana showed >80 PP in 10.58%, >40–80 PP in 36.44%, and >26–40 PP in 19.74% of samples. In Haryana, antibody positivity was observed in >40–80 PP (5.66%) and >26–40 PP (9.69%) categories. Similarly, in Punjab, positivity was recorded at >40–80 PP (4.24%) and >26–40 PP (2.42%), with no samples showing titres above 80 PP. Overall, higher antibody titres were observed in the anthrax-endemic state of Telangana, whereas lower titres were detected in the non-endemic states of Punjab and Haryana. Serological analysis indicated substantial positivity for anti-PA–specific IgG antibodies among sheep in Telangana, with approximately 50% of the population showing relatively high antibody titres, likely reflecting vaccine-induced immunity. However, the relationship between observed antibody titres and vaccination status in endemic districts could not be definitively established due to the lack of reliable field-level vaccination records.

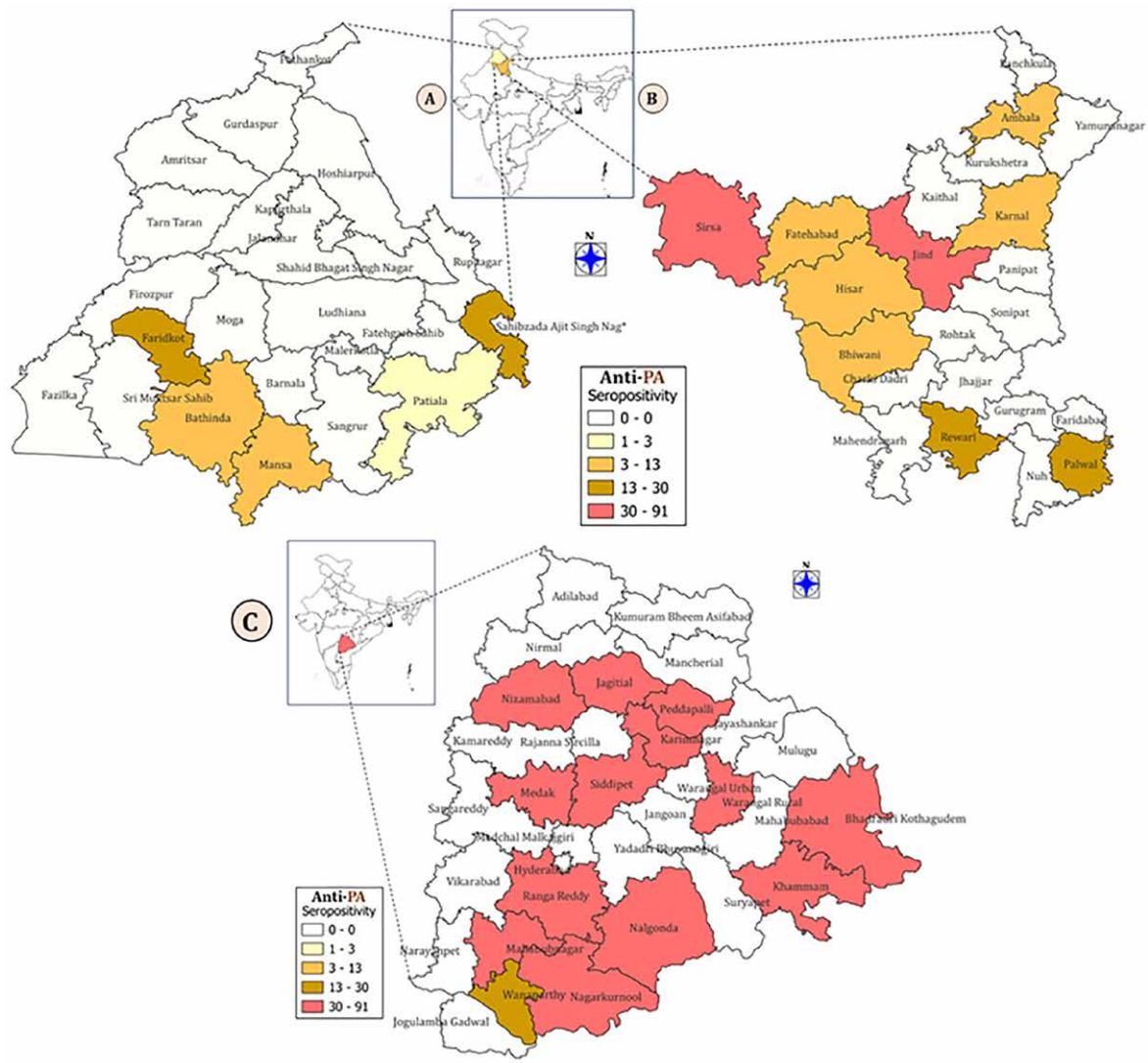


Fig 42: Geographical map of Anthrax endemic and non-endemic states showing percentage Sero-positivity in sheep using rPA-iELISA. Panel A: non-endemic state. Panel B: non-endemic state. Panel C: endemic state. Note: No serum samples from 'light /white' colored districts/areas tested using rPA-iELISA.

(Shivachandra SB and Chanda MM)

Production and Characterization of Recombinant Epsilon Toxin of *Clostridium perfringens*

Enterotoxaemia (ET), caused primarily by exotoxins—particularly epsilon toxin—secreted by *Clostridium perfringens* Type D strains, is a highly fatal disease of small ruminants, especially lambs, often leading to sudden death. The disease causes substantial economic losses to the small ruminant farming industry in India. Epsilon toxin (Etx) is one of the major exotoxins (among ~18 toxins) produced by this spore-forming bacterium and plays a critical role in the pathogenesis of enterotoxaemia. Currently, a chemically inactivated epsilon toxoid is used as a vaccine for the prevention of ET in animals. However, non-toxic mutant forms of Etx have potential applications in the development of improved immunoassays and alternative subunit vaccine formulations for effective disease control.

During the present study period, a codon-optimized synthetic quadruple point mutant (Y30A, H106P, H149A, and Y196A) of the *etx* gene of *Clostridium perfringens* was expressed in *Escherichia coli* to produce a recombinant epsilon toxin mutant protein consisting of 331 amino acids (~36 kDa). The recombinant mutant epsilon toxin (rEtx-mutant) protein was purified using single-step affinity chromatography under both non-denaturing and denaturing–renaturing conditions. The purified rEtx-mutant protein was subsequently functionally characterized through in vitro and in vivo assays. Structural analysis indicated that the quadruple point mutant retained structural similarity to the wild-type epsilon toxin, suggesting its suitability as a non-toxic antigenic candidate for diagnostic assay development and potential vaccine applications against enterotoxaemia in small ruminants.

As a candidate antigen for subunit vaccine development or immuno-diagnostic assays, the recombinant epsilon mutant toxin (rEtx) was subjected to functional characterization through both in vitro and in vivo assays. In vitro cytotoxicity studies: Both the rEtx mutant protein and wildtype Etx/prototoxins were activated by purified porcine trypsin. Serial dilutions (100 µL per well) of activated proteins were applied to confluent monolayers of Madin-Darby bovine kidney (MDBK) cells. Morphological changes were monitored every 2 h for up to 24 h, and cell viability was assessed using the MTT colorimetric assay. Cells treated with wildtype Etx exhibited nuclear condensation, cell disintegration, and detachment (Fig 43). In contrast, cells treated with the rEtx mutant remained intact with no observable morphological alterations, even at higher protein concentrations. Quantitative analysis confirmed that cell viability was significantly higher in rEtx-treated cells compared to wildtype Etx-treated cells.

In vivo toxicity studies: The rEtx mutant protein was administered subcutaneously at doses of 15 µg, 25 µg, and 50 µg to Swiss albino mice (n = 2 per dose), which were monitored daily for one week. Additionally, two-fold serial dilutions of trypsin-activated rEtx mutant and wildtype Etx proteins were injected intraperitoneally into BALB/c mice, and clinical signs and mortality were monitored hourly for up to 48 h. Kaplan–Meier survival curves were plotted using GraphPad Prism software. Polyclonal sera from guinea pigs and ET-vaccinated sheep neutralized wildtype Etx toxicity in a dose-dependent manner (up to 1:24 dilution), whereas sera from naïve lambs failed to neutralize the toxin (Fig. 1, Panel H). Mice inoculated with activated wildtype Etx succumbed within 24 h at higher dilutions and within 2 h when undiluted. In contrast, mice, rabbits, and guinea pigs inoculated with rEtx mutant protein—either soluble or insoluble fractions—showed no clinical signs, side effects, or mortality, even after trypsin activation. These results demonstrate that the rEtx mutant protein is non-toxic in vitro and in vivo, confirming its suitability as a safe candidate for subunit vaccine formulations and immuno-diagnostic applications.

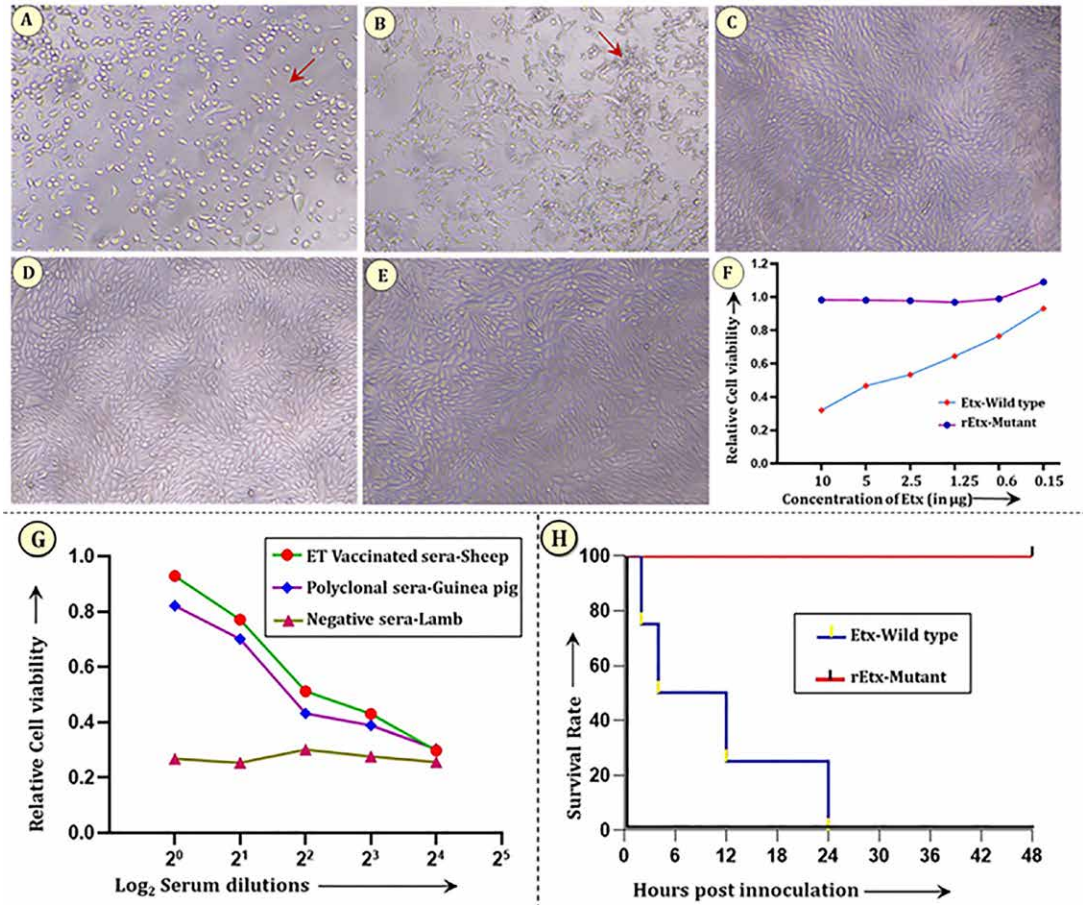


Fig. 43. Cytotoxicity analysis of rEtx-mutant protein

A confluent of MDBK monolayer showing morphological changes (10x) following12 h post-treatment with; Panel A: Trypsin activated Clostridium perfringens Etx-Wt (~10 µg), Panel B: Trypsin activated Clostridium perfringens Etx-Wt (~5 µg), Panel C: Control cell, 12 h post treatment with PBS, Panel D: Trypsin activated rEtx-mutant protein (~10 µg), purified under non-denaturing (native) condition (soluble form), showing no visible morphological changes, Panel E: Trypsin activated rEtx-mutant protein (~10 µg), purified under denaturing-renaturing condition (insoluble form), showing no visible morphological changes, Panel F: The graph denoting cell viability/cytotoxicity of MDBK cells treated with the activated Etx-Wt and rEtx-mutant protein on a time scale. Panel G: Graph showing inhibition of cytotoxicity using various sera samples in Etx-toxin neutralization assay, Panel H: The Kaplan-Meier survival curve showing probability of post inoculation survival of mice Note: The 'red' colored arrows in Panels A and B indicate morphological changes (nuclear condensation, cell disintegration, and detachment) in cell monolayer caused by Etx-Wt.

(Shivachandra SB and Chanda MM)

Development of indirect-ELISA based on recombinant Epsilon antigen of *Clostridium perfringens*

The rEtx-mutant protein–based indirect-ELISA was optimized using a two-fold checkerboard titration following established protocols. Optimal assay conditions were: rEtx antigen at 125 ng/well, primary antibody dilution at 1:100, donkey anti-sheep IgG HRPO conjugate at 1:2000, and rabbit anti-goat IgG HRPO conjugate at 1:5000. Diagnostic performance: Receiver operating characteristic (ROC) analysis showed an area under the curve (AUC) of 0.997, with diagnostic sensitivity of 98.7% and diagnostic specificity of 96.2% (95% CI: 93.2–99.2%; $p < 0.0001$) at a cut-off percentage positivity (PP) of 10.42 (Fig 44, Panel A). Using sera from 100 unvaccinated animals, a cut-off threshold of 12% was determined,

with negative OD values ranging from 0.147 to 0.46. Therefore, test samples with OD >0.46 or PP >12% were considered positive for Etx-specific antibodies.

Analytical sensitivity and specificity: The assay reliably detected antibodies up to 1:800 serum dilution, with OD values significantly higher than negatives. In analytical specificity tests, OD values of vaccinated positive sera were above the cut-off (0.46), while sera from unvaccinated or animals with other common infections were below the cut-off (Fig 44, Panel B).

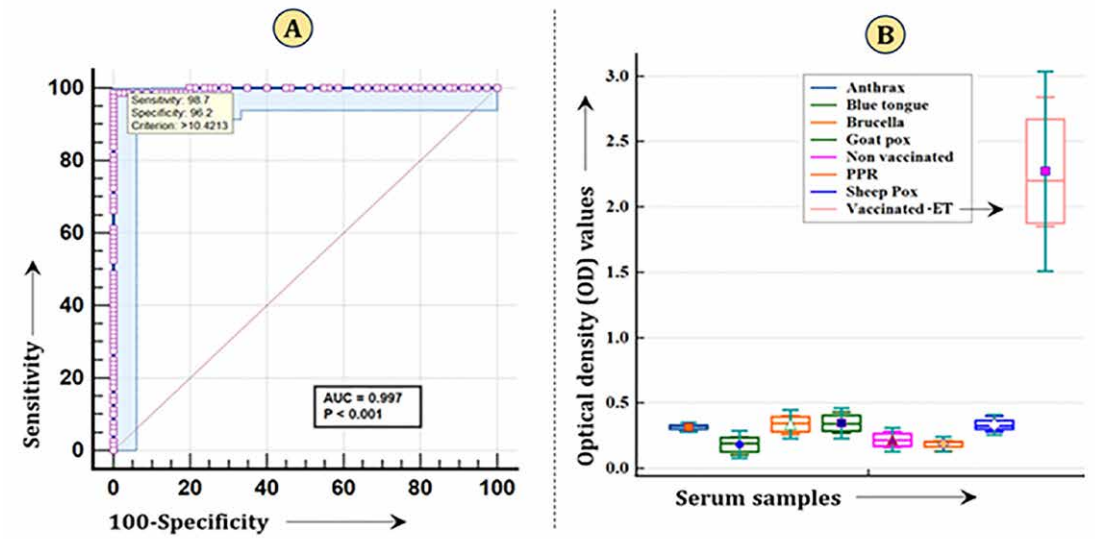


Fig 44: ROC analysis and cross-reactivity of rEtx-ELISA Panel A: ROC curve showing diagnostic sensitivity and diagnostic specificity Panel B: Cross-reactivity of indirect-ELISA with other infections positive sera.

One-way ANOVA confirmed statistically significant differences in OD readings ($P < 0.05^*$, $P < 0.01^{**}$). Precision and reproducibility: Inter-plate and intra-plate coefficients of variation (% CV) were 2.35% and 6.9%, respectively, well within the acceptable limit of 10% CV. Comparison with commercial kit: A total of 160 field sera samples were tested with both the in-house rEtx-ELISA and a commercial kit. Eighty-five samples were positive and 67 samples were negative in both assays, with seven samples showing discordant results. The degree of agreement between the assays was high, with a kappa value of 0.91, indicating strong concordance between the in-house and commercial ELISA formats (Table 12).

Table 12: Comparison of rEtx-ELISA with Commercial kit.

Serum samples	rEtx-ELISA			Commercial Kit		
	Positives	Negatives	Total	Positives	Negatives	Total
Vaccinated (n=90)	89	1	90	85	5	90
Unvaccinated (n=70)	0	70	70	3	67	70
Total (n=160)	89	71	160	88	72	160
Kappa value Standard error 95% Confidence interval	0.912 0.033 0.847- 0.976					

(Shivachandra SB and Chanda MM)

Serosurveillance of Contagious Caprine Pleuropneumonia (CCPP) in North-Eastern States of India

During the study period, a total of 638 serum samples from small ruminants, collected under PPR-CP from Assam and Meghalaya were tested for CCPP antibodies using a commercial ELISA kit. Samples originated from nine districts in Assam and seven districts in Meghalaya (Fig 45). Overall, 27.5% of the sample seropositivity indicating notable % of CCPP exposure. Seropositive animals were distributed in all seven districts of Meghalaya, demonstrating likely widespread disease circulation. The highest seropositivity was recorded in the East Garo Hills and East Khasi Hills districts of Meghalaya. District-wise percent seropositivity are depicted below.

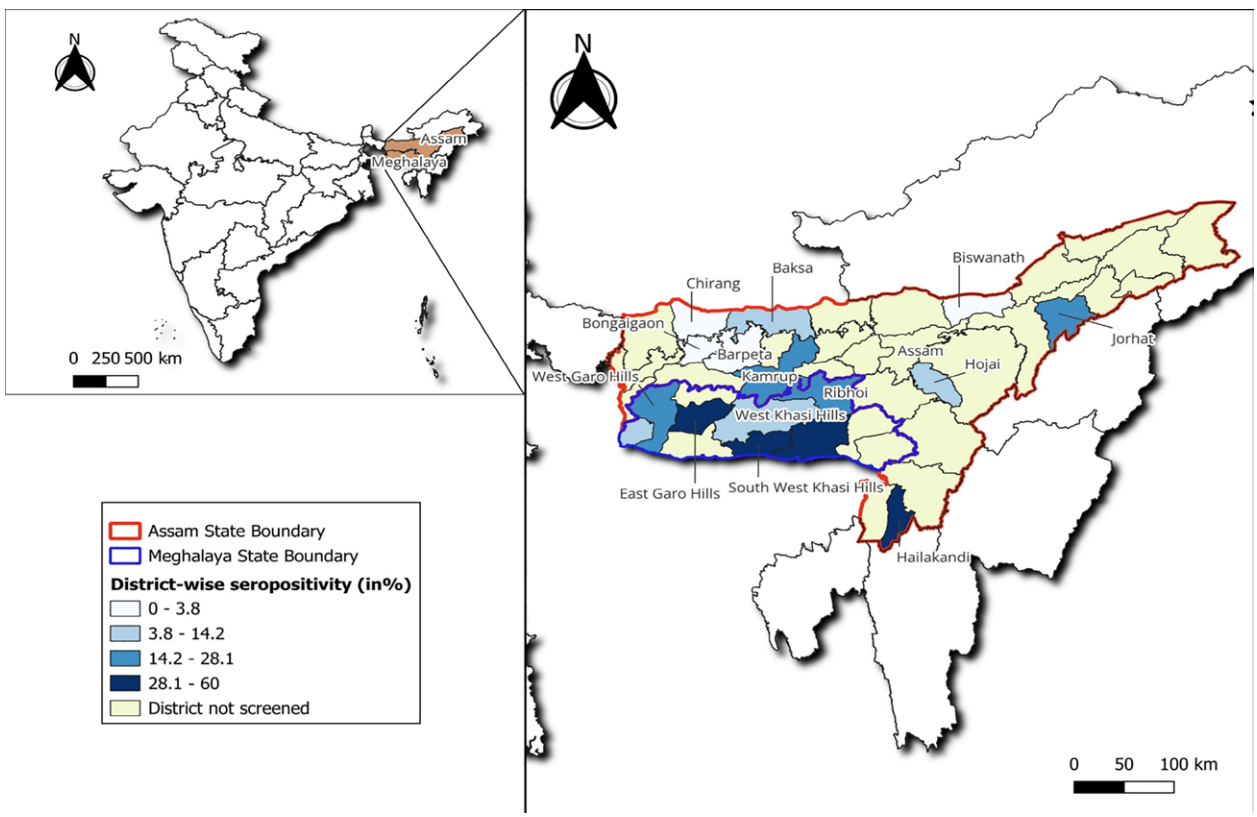


Fig 45: Serosurveillance of Contagious Caprine Pleuropneumonia in North-Eastern States of India.

(Sridevi R, Balamurugan V, Patil SS and Gulati BR)

Molecular Epidemiology of Goat and Sheep Mycoplasmosis in Southern States of India

A total of 1,200 small ruminants were examined for clinical respiratory illness across four southern states—Puducherry, Tamil Nadu, Telangana, and Kerala—to screen for caprine and ovine mycoplasmal respiratory infections. One fourth of the examined animals exhibited respiratory symptoms and revealed an overall positivity rate of 23.9% among symptomatic animals by Mycoplasma genus-specific PCR. Further analysis identified three species *Mycoplasma ovipneumoniae*, *Mycoplasma arginini*, and *Acholeplasma laidlawii* as the causative agents. Sequencing and phylogenetic analysis of partial 16S rRNA gene sequences by MEGA11 software showed that the *M. ovipneumoniae* isolates clustered closely with sheep isolates earlier reported from China and United States, indicating closer evolutionary relatedness nature (Fig 46).

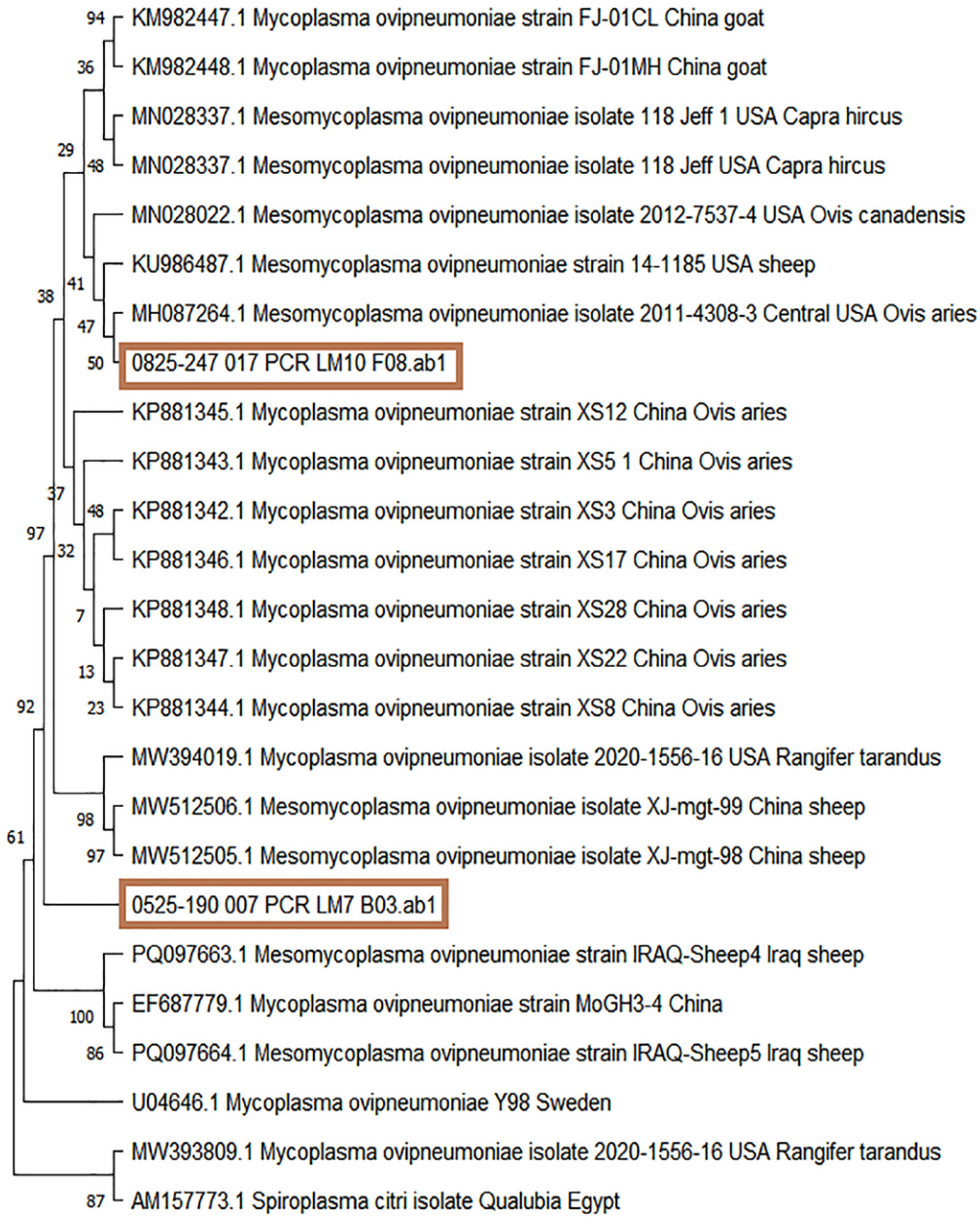


Fig 46: Phylogenetic analysis of partial 16S rRNA gene sequences of M. ovipneumoniae.

(Sridevi R)

Contractual testing and revenue generation

In the case of trade samples, a total of 155 samples received from the Government of India–Animal Quarantine and Certification Services (GoI-AQCS) were tested by real-time PCR, of which 143 were screened for PPR, 132 for sheep pox, and 3 for goat pox. None of the samples tested positive in real-time PCR. Trade samples primarily consisted of leather/skin/wool/processed samples Additionally, another set of 31 samples received from Ykitra Life Sciences were tested for Mycoplasma by PCR, and all 31 samples were found to be positive for Mycoplasma. In total, 155 diagnostic reports were issued to different stakeholders through the Small Ruminants Disease Epidemiology Group, generating revenue exceeding ₹ 3.5 lakhs from commercial sample testing.

Swine Diseases Epidemiology

Sero-monitoring and Molecular Surveillance of Classical Swine Fever in India

Classical Swine Fever (CSF) is a highly contagious viral disease causing major economic losses in the swine sector. Sero-monitoring and molecular surveillance are essential for assessing disease status and vaccination effectiveness under the CSF Control Programme. During 2025, 16,072 pre-vaccination samples were tested, with 7,573 positives (30.12%). Post-vaccination, 12,706 samples were tested, of which 9,872 were positive (77.70%), indicating a strong improvement in herd immunity (Fig 47). Post-vaccination seropositivity across states ranged from 46.67% to 91.84%, with higher responses observed in Kerala, Mizoram, Goa, and Telangana (Table 13).

A total of 618 clinical samples (blood, serum, swabs, and tissues) were collected from Andhra Pradesh, Karnataka, Tamil Nadu, Odisha, and Jharkhand (Fig 48).

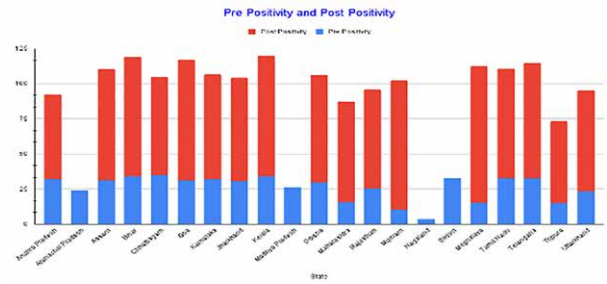


Fig 47: Pre and post vaccination positivity across different states.

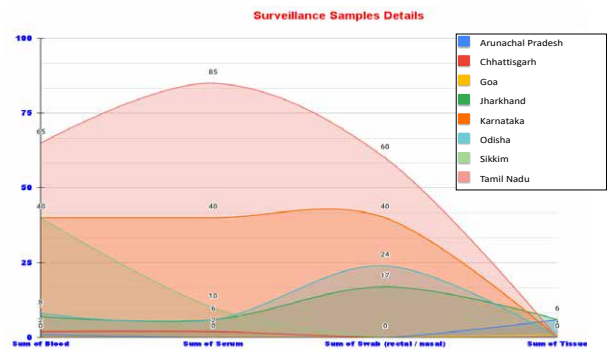


Fig 48: CSF Surveillance sample details during 2025.

Table 13: State-wise post-vaccination seropositivity.

State	Samples Tested	Samples Positive	Positivity (%)
Karnataka	1543	1151	74.6
Chhattisgarh	1559	1060	67.9
Odisha	1409	1032	73.2
Andhra Pradesh	1332	806	60.51
Assam	2262	1793	79.27
Jharkhand	353	260	73.65
Maharashtra	364	248	68.13
Telangana	1066	874	81.99
Kerala	1139	981	86.13
Rajasthan	47	33	70.21
Goa	525	452	86.1
Tripura	405	189	46.67
Bihar	1456	1024	70.33
Mizoram	711	653	91.84
Meghalaya	260	163	62.69
Tamil Nadu	92	68	73.91

All samples tested negative by RT-PCR, indicating that no CSF virus was detected in the samples tested. However, given the large pig population in India (~9 million) and the targeted sampling approach, these findings should be interpreted cautiously and do not confirm absence of the virus at the population level. There is a marked increase in seropositivity following vaccination, demonstrating the effectiveness of the CSF Control Programme. Continued surveillance is essential for sustained disease control.

(Patil SS, Jagadish Hiremath, Shivasharanappa N, Sridevi R, Narayanan G, Suresh KP, Chethan Kumar HB and Sathish Gowda CS)

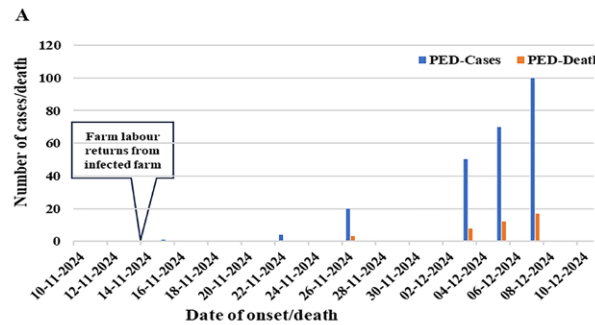
First Evidence of Porcine Epidemic Diarrhoea Virus and African Swine Fever Virus Co-Infection in Pigs from Karnataka, India: An Epidemiological Investigation

This study reports a diarrhoeal outbreak in pigs in Karnataka, India, primarily caused by Porcine Epidemic Diarrhoea Virus (PEDV), with concurrent infection by African Swine Fever Virus (ASFV), representing the first documented natural PEDV–ASFV co-infection in India. The outbreak was reported during December 2024 and epidemiological investigation was completed during February 2025. This finding is significant because the two diseases require fundamentally different control responses — PED through management and supportive care, ASF through stamping out and movement restrictions — and their co-occurrence complicates both clinical diagnosis and outbreak response.

Distinct clinical signs were observed: the majority of pigs exhibited profuse yellow watery diarrhoea and vomiting characteristic of PED, whereas a few showed high fever, systemic haemorrhages, and coffee-coloured diarrhoea indicative of ASF (Fig 49). The outbreak persisted for 25 days and followed a propagated epidemic curve, suggesting pig-to-pig transmission (Fig 50). Epidemiological investigation implicated farm labourers returning from ASF- and PEDV-affected premises as potential sources of disease introduction. Using defined case definitions and snowball sampling, five additional affected farms across two districts were traced, demonstrating the utility of this approach for outbreak mapping in settings with limited cooperation.

Molecular testing confirmed the presence of both PEDV and ASFV in sampled pigs. PEDV detection was further confirmed in faecal samples using the fluorescent antibody test (FAT) on Vero cell monolayers. Phylogenetic analysis placed PEDV isolates within the G2a genotype, closely related to previously reported Indian, Chinese, and South Korean strains, while ASFV isolates clustered within Genotype II, consistent with Indian and East Asian lineages. This first evidence of natural PEDV–ASFV co-infection in India highlights the diagnostic complexity of pig diarrhoeal outbreaks and underscores the urgent need for integrated surveillance, improved diagnostic capacities, and strengthened biosecurity measures to prevent the spread of these economically important swine pathogens.

Fig 49: Clinical observation recorded during outbreak investigation.



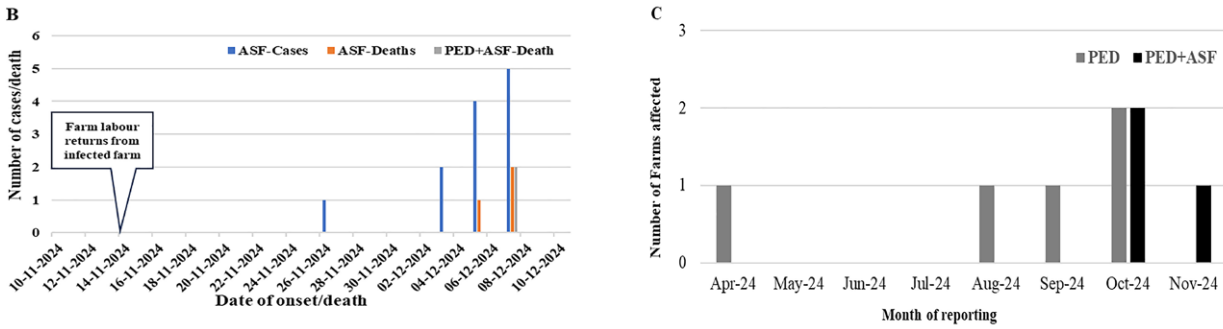


Fig 50: Epidemic curve of co-infection of PEDV and ASFV.

(Jagadish Hiremath, Chethan Kumar HB, Siju SJ Shivashararanapp N, Sathish Gowda CS, Suresh KP and Patil SS)

Epidemiological Investigation of a Porcine Epidemic Diarrhoea Outbreak in a Commercial Pig Farm, Karnataka, India

In June 2025, an acute diarrhoeal outbreak consistent with Porcine Epidemic Diarrhoea (PED) was investigated in a commercial pig farm in Karnataka. The outbreak was traced to pigs purchased from Srinivaspura, Kolar district, on 12 June 2025, which served as the primary source of infection. Clinical progression of faecal changes was observed from normal brown faeces (0–1 days post-infection) to soft, mushy yellow-brown faeces (1–2 days), followed by watery, foamy, grayish-yellow to clay-coloured diarrhoea during 2–4 days post-infection, accompanied by dehydration, feed refusal, and strong odour. By 5–7 days post-infection, faeces gradually became pasty to formed, with recovery of appetite and activity.

The first cases appeared on 13 June 2025 in the index pen, followed by secondary spread to adjacent pens between 16–17 June. A peak in cases occurred on 21 June, indicating rapid within-farm propagated transmission, followed by a decline from 22–29 June (Fig 51). The farm housed approximately 320 weaned pigs across 12 pens. Epidemiological assessment identified direct pig-to-pig contact and indirect transmission via labourers and shared equipment as key modes of spread. Biosecurity lapses included absence of quarantine for incoming pigs, ineffective disinfection, and unrestricted human movement between pens. The outbreak was classified as a point-source introduction followed by propagated transmission within the farm. This investigation highlights that co-infections can obscure clinical presentation, reinforcing the need for panel-based molecular diagnostics in pig disease outbreaks rather than reliance on syndromic diagnosis alone.

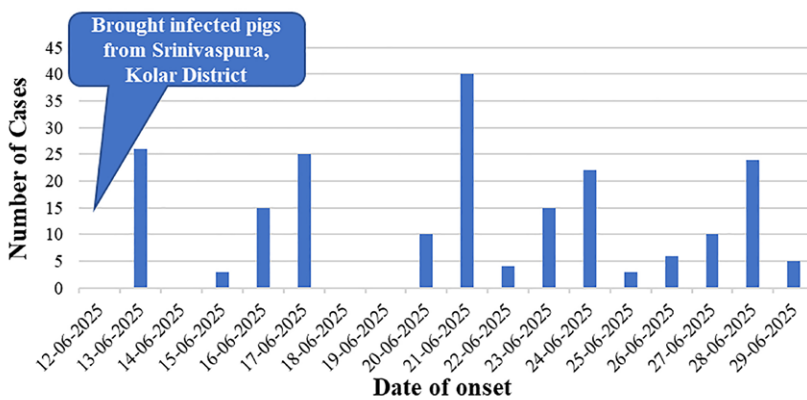


Fig 51: Daily distribution of PED cases showing point-source introduction following purchase of infected pigs from Srinivaspura, Kolar district, and subsequent propagated within-farm spread with a peak around 21 June 2025.

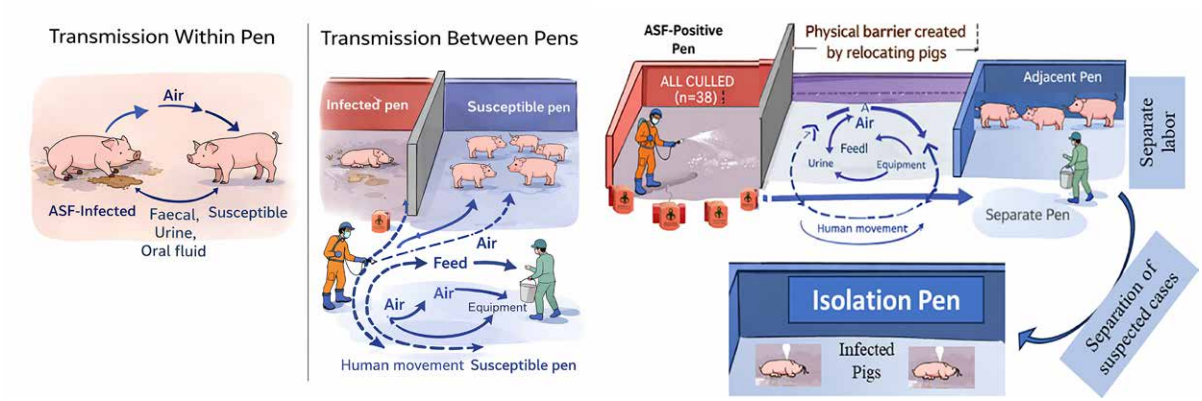
(Jagadish Hiremath, Chethan Kumar HB, Siju SJ, Shivashararanapp N, Sathish Gowda CS, Suresh KP and Patil SS)

Epidemiological Investigation and Implementation of Targeted Biosecurity to Limit African Swine Fever Spread in Intensive Pig Production

An outbreak of African Swine Fever (ASF) was investigated in a multi-pen commercial pig farm to elucidate transmission pathways and evaluate the effectiveness of risk-based biosecurity interventions. Suspected ASF cases were first observed on 21 July 2025, presenting with high fever, cyanotic ears, and mortality in a single pen. Clinical samples collected from affected pigs on 7 August 2025 were laboratory-confirmed as ASF virus, identifying the index pen as the primary source of infection. Epidemiological assessment indicated rapid within-pen transmission, facilitated by close animal contact and environmental contamination through faeces, urine, oral fluids, and shared airspace (Fig 52). Prior to laboratory confirmation, routine human movements, shared equipment, and operational activities contributed to inter-pen spread, resulting in suspected cases in adjacent pens, consistent with propagated transmission rather than multiple introductions. Three clinically affected pigs were immediately isolated.

Following confirmation, targeted risk-based biosecurity measures were implemented. All pigs (n = 38) in the ASF-positive pen were culled to eliminate the infection source. Susceptible pigs in adjoining pens were relocated, creating a physical buffer of one pen between infected and healthy groups (Fig 52). Separate labourers were assigned for cleaning and disinfection of the affected pen to prevent mechanical transmission. Enhanced disinfection protocols and strict movement control were enforced. These interventions lead to no further new cases resulting in control of outbreak effectively.

This investigation highlights the critical role of human-mediated spread in inter-pen transmission of ASF and demonstrates that timely, pen-level segregation, controlled personnel movement, and rapid depopulation are essential components of outbreak containment in intensive pig production systems.



A B

Fig 52: ASF transmission within the Farm. Panel A. Modes of transmission within and between pens. Panel B. Schematic representation of risk-based biosecurity measures to prevent the between pen transmission of ASFV.

(Jagadish Hiremath, Chethan Kumar HB, Siju SJ, Shivashararanapp N, Sathish Gowda CS, Suresh KP and Patil SS)

Development and Evaluation of Recombinant ASFV Antigen–based Serological Assays for African Swine Fever Surveillance in India

African swine fever (ASF) poses a significant threat to pig production in India, necessitating robust diagnostic tools for both early detection and large-scale sero-surveillance, particularly in the context of evolving disease presentation. While molecular assays are highly effective for detecting active infection, their utility in identifying prior exposure, recovered, or subclinical infections at the population level remains limited. Accordingly, an indigenous, cost-effective, and scalable serological assay was developed to support surveillance in settings transitioning towards endemicity and post-outbreak phases.

In this study, recombinant ASFV structural proteins p32 and p72 were successfully expressed, purified, and validated for antigenic reactivity using field sera, confirming their diagnostic applicability. Subsequently, a recombinant p22-based indirect ELISA (p22 iELISA) was developed, optimized, and standardized for serological screening. The diagnostic performance of the p22 iELISA was assessed using receiver operating characteristic (ROC) analysis, demonstrating a sensitivity of 87.8% and specificity of 96.4%, indicative of high overall assay accuracy (Fig 53). However, the observed sensitivity, while acceptable for surveillance applications, suggests the need for further optimization to enhance detection, particularly in low-antibody or heterogeneous field conditions.

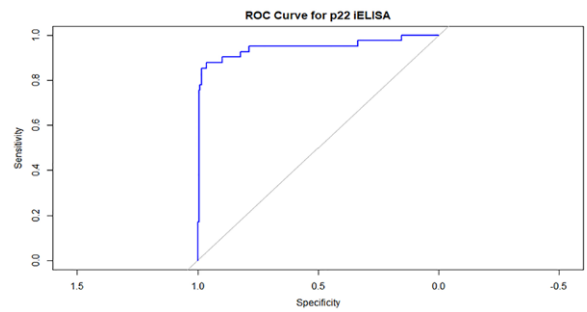


Fig 53: ROC curve for p22 ELISA.

(Jagadish Hiremath)

Standardization of Aseptic Isolation, Yield Characterization, and Organoid Culture of Porcine Lymphoid Immune Cells from Abattoir Sources

To strengthen preparedness against emerging and re-emerging swine diseases, ICAR-NIVEDI has initiated the development of porcine immune cell culture systems as *in vitro* platforms for studying host–pathogen interactions and evaluating vaccines. This is particularly relevant for priority diseases such as African swine fever (ASF), classical swine fever (CSF), and swine influenza, where standardized experimental models are limited and reliance on live animal studies poses ethical and logistical challenges.

During the reporting period, robust and contamination-free protocols were established for the aseptic collection and processing of porcine lymphoid tissues sourced from slaughterhouses, ensuring an ethically compliant and scalable source of biological material. Importantly, animal-level parameters were documented to standardize expectations for cell recovery. Lungs from pigs with mean age of 7 months and mean body weight of 44 kg yielded an average of ~258.9 million cells per organ, demonstrating high recovery even from post-slaughter tissues. Similarly, spleens from pigs (mean age 5 months, mean body weight 23.8 kg) yielded ~9.9 million cells per gram, tonsils (mean age 4.7 months, mean body weight 31.7 kg) yielded ~52.2 million cells per gram, and lymph nodes (mean age 4.3 months, mean body weight 25 kg) yielded ~19.3 million cells per gram.

These data provide a practical reference framework for anticipating cell yields based on animal age, body weight, and tissue type, thereby enhancing reproducibility and scalability across laboratories. Building on these optimized yields, using standardized

cell inputs, a proof-of-concept vaccine (CSF) stimulation model was developed and monitored over a 9-day period, demonstrating the functional responsiveness of the system. Supporting methodologies were also established to characterize immune cell composition and spatial organization, ensuring biological relevance of the organoid model.

This platform offers significant translational potential for pre-clinical evaluation of vaccines and immunological studies for ASF, CSF, and swine influenza. The use of slaughterhouse-derived tissues aligns with ethical principles by reducing dependence on experimental animals, while also enabling scalability. Furthermore, the standardized protocols and yield benchmarks facilitate reproducibility and open avenues for collaboration, industry engagement, and potential technology transfer.

(Jagadish Hiremath, Chethan Kumar HB, Shivashararanapp N, Girish Halemani and Yoganand SM)

Isolation and Characterization of Japanese Encephalitis Virus Genotype I from a Pig in Assam, India

Japanese encephalitis (JE) remains a leading cause of viral encephalitis among children in many Asian countries despite the availability of effective vaccines. Five JE virus (JEV) genotypes (GI–GV) have been recognized, with GIII historically the most prevalent. Although co-circulation of GI and GIII has been reported previously in India through molecular approaches, all previous JEV isolations from pigs were of the GIII genotype.

In this study, we report the first isolation and characterization of a JEV GI from a nasal swab of a naturally infected pig in Assam, India. The isolate was designated JEV/Pig/Assam/NIVEDI-1/2025 (GI) (Fig 54).

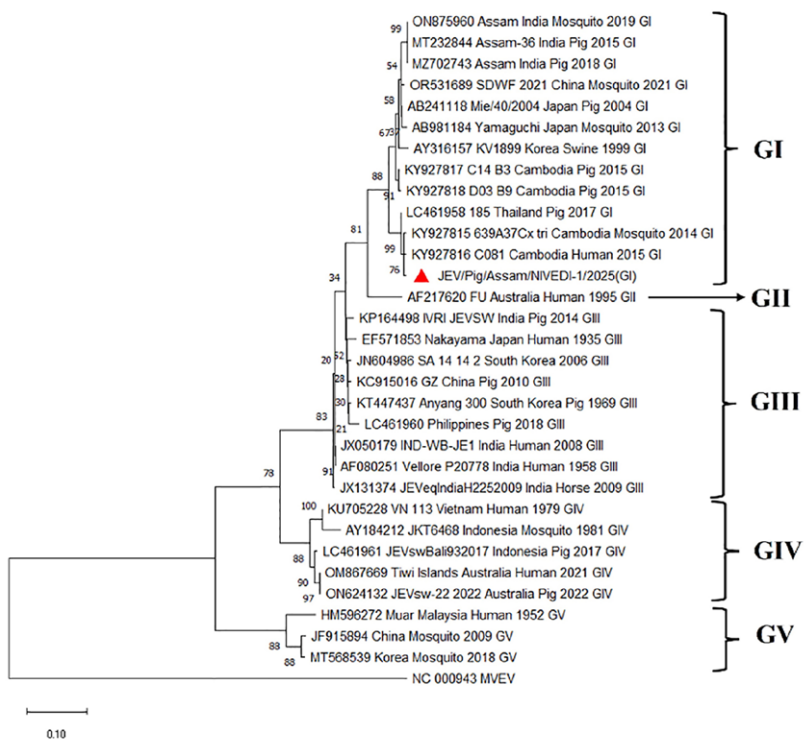


Fig 54: Phylogenetic tree of JEV isolate based on 5' UTR–prM region nucleotide sequence. The scale bar indicates the nucleotide substitution per site. Red triangle indicates JEV sequence from the current study.

Detection and isolation of JEV from nasal swabs provides evidence for the presence of the JEV in oro-nasal secretion in naturally infected pigs and also demonstrates the feasibility of using nasal swabs for virus detection and isolation for surveillance and diagnosis purposes. These findings underscore the need for enhanced surveillance in swine populations to monitor genotype shifts, understand viral evolution, and generate field isolates critical for vaccine evaluation and preparedness against emerging JEV genotypes.

(Chethan Kumar HB, Jagadish Hiremath, Patil SS, Manjunatha Reddy GB and Gulati BR)

Production of Recombinant Antigens of Nipah virus for Development of Diagnostics for Pigs

Nipah virus (NiV), an emerging bat-borne viral disease of zoonotic significance causing fatal encephalitis in South-East and South-Asia including India. Pigs are reckoned to play a pivotal role in maintaining and transmission of NiV in zoonotic cycle. Surveillance for NiV specific antigen or antibodies in sentinel animal host such as pigs is of paramount relevance to develop spillover risk of human infection in any given geographical area. For serological detection of NiV specific antibodies, native viral antigen-based ELISAs are widely used as screening assays in animals and humans during the NiV outbreaks. However, the zoonotic risk of handling NiV and requirement of high containment laboratories (BSL-4) precluded general practice to use native antigen-based immunoassays.

Since, recombinant antigen based immuno-assays overcome these challenges, we targeted two candidate genes (N gene and Glycoprotein gene) of Nipah virus (NiV) for cloning and expression from prokaryotic expression. The codon optimized synthetic gene(s) were cloned in to pET28a vector and purified by affinity chromatography. The purified recombinant nucleocapsid (rN) (~62 kDa) and glycoprotein (rGtr) (~51 kDa) were noted on 10% SDS-PAGE (Fig 55). Subsequently, these two recombinant proteins used to raise hyper-immune sera in rabbit and guinea pig model as per standard protocol. The immunoreactivity of both the recombinant proteins was confirmed by Western blot using rabbit and guinea pig hyperimmune sera as well as field sera collected from pigs belonging to the Nipah cases reported states of India. Further, sero-diagnostic potential of two recombinant proteins in indirect-ELISA format for detection of NiV specific antibodies in pig serum samples along with all the standardization protocols /parameters are currently being evaluated.

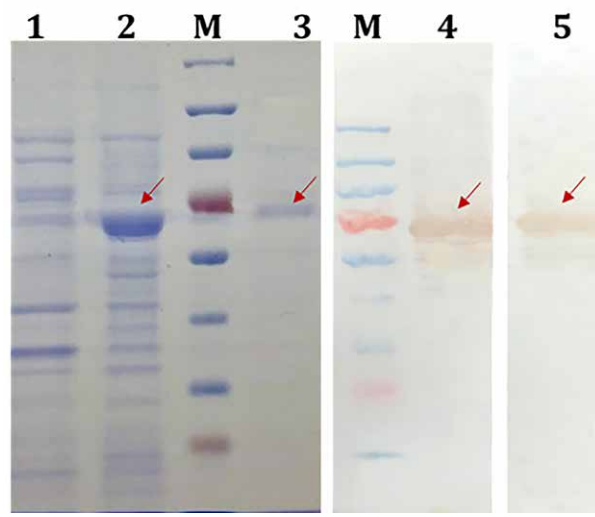


Fig 55: Production of recombinant protein of NiV. Lane M: Protein standard marker, Lane 1: Uninduced E. coli cell lysate, Lane 2: Induced E. coli cell lysate with rN protein, Lane 3: Purified rN protein, Lane 4: Western blot of rN using Rabbit HIS, Lane 5: Western blot of rN using Guinea pig HIS.

(Shivachandra SB, Chanda MM, Chethan Kumar HB and Patil SS)

Swine Disease Diagnosis and Sero-Surveillance Across Multiple States in India

Comprehensive diagnostic and sero-surveillance activities were conducted to assess viral and parasitic diseases of major importance in pigs across India. For African swine fever (ASF), 48 tissue, 129 blood, 8 nasal swab, and 24 serum samples collected from six states were tested, with 42 tissue samples, 6 blood samples, and 4 nasal swabs testing positive, while all serum samples were negative. During a porcine epidemic diarrhoea (PED) outbreak in Karnataka, 32 of 48 faecal samples were confirmed positive.

As part of ongoing Japanese encephalitis (JE) surveillance and diagnostic efforts, a total of 738 pig serum samples were screened from nine states (Table 14). These samples were either submitted by state animal husbandry departments for JE surveillance or collected as part of broader animal disease control programs. Serum samples were tested for anti-JEV antibodies using the virus neutralization test. The overall seropositivity in pigs was 35.6%, with state-wise prevalence ranging from 0% to 84.2%. Sero-surveillance in pigs provides a crucial tool to estimate JE prevalence and to map the spatial and temporal distribution of the virus.

Table 14.: JEV neutralizing antibody positivity in pigs across different states

State	No. Tested	No. Positive	% Positivity
Andhra Pradesh	19	16	84.2
Arunachal Pradesh	13	7	53.8
Assam	18	10	55.6
Chhattisgarh	471	192	40.8
Jammu	26	0	0
Karnataka	104	3	2.8
Madhya Pradesh	44	12	27.2
Odisha	19	8	42.1
Tamil Nadu	24	15	62.5
Grand Total	**738**	**263**	**35.6**

In addition, 37 pig samples from apparently healthy pigs of four states were screened for JEV RNA, of which 6 pigs from Assam and Tripura states tested positive for JEV by RT-PCR, demonstrating active viral circulation in selected regions. These findings identify specific states with evidence of ongoing JEV amplification in swine and can inform targeting of vector control and human vaccination efforts in coordination with public health authorities.

Parasitic surveillance using the indigenously developed indirect ELISA kit (Cystisure) for *Taenia solium* cysticercosis in 120 pig serum samples from Tripura detected antibodies in 8 samples (6.6%), indicating ongoing exposure to zoonotic parasites. These findings highlight the importance of integrated viral and parasitic surveillance to inform disease control strategies and mitigate zoonotic risks in pig populations.

(Jagadish Hiremath, Chethan Kumar HB, Siju SJ, Shivashararanapp N, Sathish Gowda CS, Suresh KP and Patil SS)

Disease Informatics and Socio-economics

AI-Enabled Two-Month Advance Forecasting of Livestock Disease Risks

The National Animal Disease Referral Expert System v2.0 was further strengthened as a climate-driven Artificial Intelligence (AI) and Machine Learning (ML)–enabled livestock disease forecasting and forewarning platform capable of predicting disease risk up to two months in advance. The system integrates long-term livestock disease incidence data, livestock census information, and an expanded set of 56 predictors, including meteorological variables, remote-sensing indicators, ecological variables, and climate-extreme indicators.

During 2025, the modelling framework was enhanced by incorporating additional ecological risk parameters such as elevation and soil pH, and by expanding the ensemble from 20 to 22 machine learning models, including LSTM and Bayesian regression approaches. A major methodological advancement involved agro-climatic zonal-level disease prediction, followed by systematic downscaling to state and district levels, enabling risk mapping across 15 Agro-climatic zones, 36 States/UTs, and 755 districts.

During 2025, NADRES processed approximately 4.88 million data points per month and forecasted 900–1,200 district-level high-risk disease events monthly across the country. Model performance validation using ground-truth data indicated good agreement between forecasted and reported cases, demonstrating the reliability of the system. A representative district-level risk forecast map is provided in Fig 56.

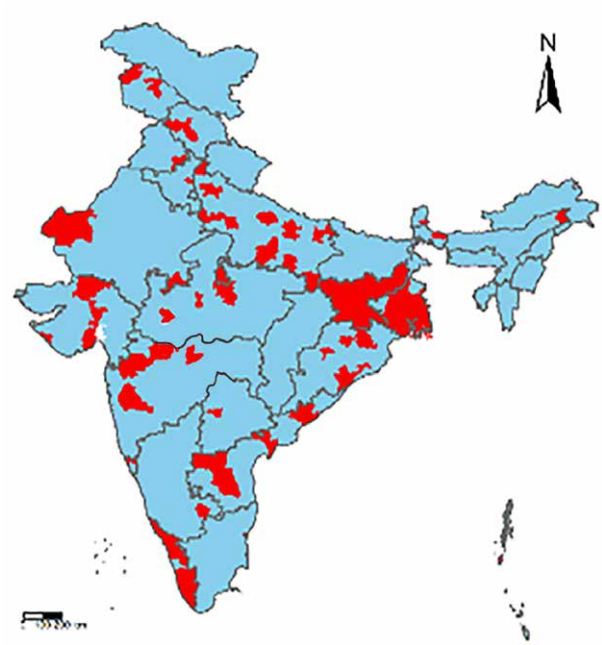


Fig 56: District-level risk prediction of Theileriosis in India for December 2025.

Risk advisories disseminated during 2025 through SMS alerts, monthly bulletins, and disease risk maps strengthened early warning, targeted surveillance, and evidence-based livestock disease preparedness nationwide. A total of 3.20 crore SMS alerts were disseminated to farmers in Karnataka through the FRUITS platform, while 2.12 lakh SMS alerts were sent to veterinarians across the country, ensuring timely communication to key stakeholders.

(Suresh KP, Shome R, Patil SS, Jagadish Hiremath, Krishnamoorthy P, Siju SJ, Narayanan G and Gulati BR)

Climate-Driven Analytics for Understanding Livestock Disease Risks across India

Understanding the influence of climate variability on livestock disease dynamics is critical for developing climate-resilient disease management strategies.

During the year, spatial epidemiological and analytical approaches were applied to examine climate–disease relationships across agro-climatic regions of India.

Spatial interpolation-based Kriging models were developed for key climatic variables including rainfall, wind speed, specific humidity, land surface temperature (LST), and the Normalized Difference Vegetation Index (NDVI) to assess spatial patterns and long-term climate variability, with detailed analysis for Agro-climatic Zones 14 and 15. The results indicated increasing temperature and humidity trends in these zones, along with rising variability in rainfall patterns suggesting heightened climate stress conditions in southern and coastal regions (Fig 57). Bland–Altman analysis showed good agreement with small mean differences, confirming the reliability of interpolated datasets. The consistently negative mean differences observed across time periods indicate that predicted rainfall values are slightly higher than observed values; however, the narrow limits of agreement demonstrate strong consistency and robustness of the spatial interpolation approach (Table 15).

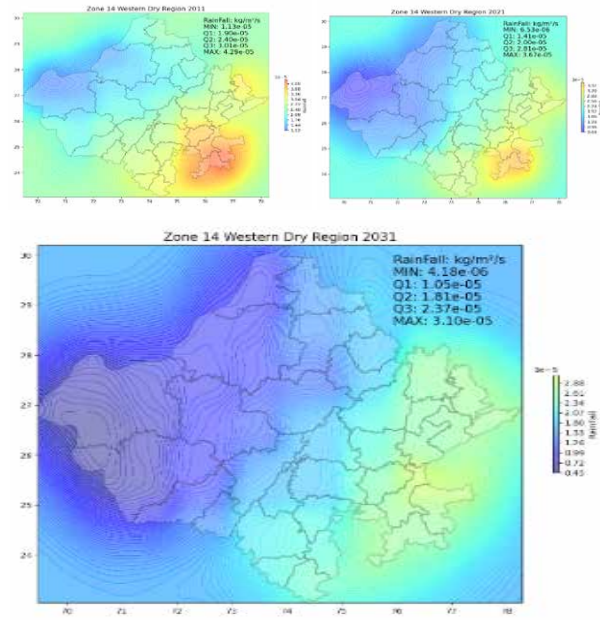


Fig 57: Spatial Interpolation of Rainfall Patterns in Agro-climatic Zone 14 (2001–2031).

Table 15.: Bland–Altman analysis of rainfall data agreement in agro-climatic zone 14.

Year	Mean Difference	Lower Limit	Upper Limit	Trend
2001-2011	-1.2272e-05	-1.7503e-05	-7.0406e-06	Negative
2001-2021	-1.2839e-05	-1.9999e-05	-5.6790e-06	Negative
2001-2031	-1.3540e-05	-1.6340e-05	-1.0739e-05	Negative

Thermal stress conditions affecting livestock were assessed using the Temperature–Humidity Index (THI), derived from temperature and humidity parameters and spatially interpolated across all 15 agro-climatic zones In the Southern Plateau and Hills region (Zone 10), integrated THI modelling with disease distribution (2001–2012 vs. 2013–2024) revealed a strong climate–disease relationship. Overlay of 15 endemic diseases (viral, bacterial, parasitic) showed that within THI range 62–71, disease incidence declined with decreasing THI, indicating a positive association between THI and disease occurrence.District-level analysis for Foot and Mouth Disease (FMD) further showed significant negative THI–risk correlations ($r < -0.108$) in districts such as Karimnagar, Vizianagaram, Nizamabad, Virudhunagar, and Uttara Kannada, while near-zero correlations in Chikkaballapura and Guntur indicated non-climatic drivers, highlighting spatial heterogeneity.

Field-level surveys involving 514 farmers across 61 villages in 12 taluks of Karnataka (Table 16) confirmed increasing heat stress, erratic rainfall, and rising disease incidence. The survey findings provide ground-level evidence supporting climate–disease linkages observed in analytical models. Farmer-experience documentation and awareness initiatives promoted adaptive practices such as farm ponds, early warning advisories, and livestock insurance, strengthening climate-resilient livestock disease preparedness.

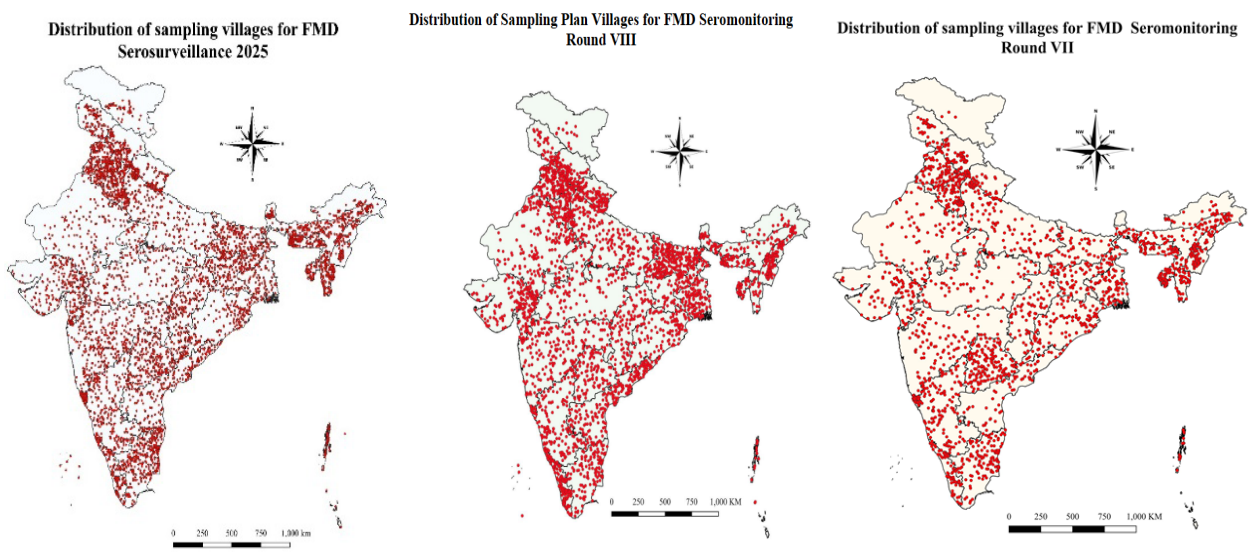
Table 16: District-wise Farmer Survey Details (2025).

Name of the districts	No of Taluks	No of Villages	Number of Farmers Interviewed
Koppal	1	15	148
Davangere	4	28	199
Ramanagara	2	3	38
Tumakuru	3	7	79
Vijayanagara	2	8	50
Total	12	61	514

(Suresh KP, Krishnamoorthy P and Siju SJ)

Nationwide Serosurveillance and Seromonitoring Framework for Strengthening Livestock Disease Control

Extensive seromonitoring and serosurveillance activities were undertaken during 2025 to strengthen national livestock disease surveillance under the Livestock Health and Disease Control Programme and the National Animal Disease Control Programme. Statistically robust sampling frameworks were developed and implemented for priority livestock diseases using a two-stage stratified random sampling design, including Foot-and-Mouth Disease (FMD), Brucellosis, Classical Swine Fever (CSF), and Peste des Petits Ruminants (PPR). Under FMD seromonitoring, the sampling intensity was expanded from 34,797 samples in Round VII (2,432 villages) to 53,016 samples in Round VIII (3,538 villages), while large-scale FMD serosurveillance encompassed 95,572 samples from 5,548 villages. Similarly, nationwide monitoring was undertaken for Brucellosis (46,398 samples from 3,528 villages), CSF (32,355 samples from 2,477 villages), and PPR (83,424 samples under Sampling Plan III and 77,412 samples under Sampling Plan IV), demonstrating sustained and adequate coverage for programme evaluation. The spatial distribution of the selected sampling villages across states and districts is presented below, highlighting the geographic coverage and representativeness of the sampling framework (Fig 58).



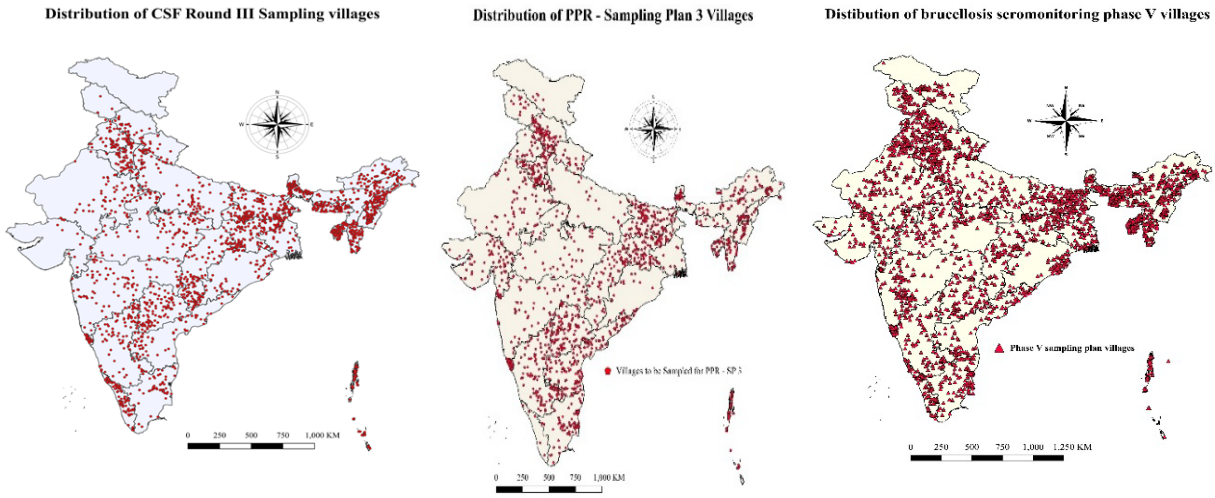


Fig 58: The spatial distribution of the selected sampling villages across states and districts of sampling plans.

Post-vaccination impact assessments indicate a substantial reduction in disease occurrence following the implementation of mass vaccination strategies. FMD cases declined from 121,305 during 2000-2019 to 38,464 during 2020-2025. Similarly, Brucellosis cases decreased from 20,170 to 4,770; CSF cases declined from 11,887 to 7,665; and PPR cases decreased from 65,864 to 38,773 over the same period.

For the year 2025, the reported cases were 641 for FMD, 38 for Brucellosis, 87 for CSF, and 3,359 for PPR. These data were utilized for forecasting using advanced statistical modelling approaches, including Generalized Autoregressive Moving Average (GARMA) and Generalized Additive Models (GAM), which demonstrated a consistent declining trend, indicating reduced transmission intensity and attenuation of seasonal outbreak patterns, these findings suggest the current monitoring and surveillance framework provides adequate statistical precision to assess vaccination effectiveness, track temporal disease dynamics, and support evidence-based, targeted disease control interventions.

A key methodological advancement was the integration of official village codes into all sampling plans, uniquely linking villages with district, block, and state identifiers. This eliminated ambiguity arising from duplicate village names and enabled seamless integration with GIS-based mapping and digital data platforms. Dissemination through the NADRES v2 portal and integration with the LHDCP portal enabled real-time monitoring of sampling progress and strengthened evidence-based livestock disease control strategies.

(Suresh KP and Patil SS)

Spatial Risk Mapping of Lumpy Skin Disease in India Using Case Data and Climate-Driven Machine Learning Models

District-wise Lumpy Skin Disease (LSD) outbreak records (December 2019–December 2024) were analyzed alongside key environmental variables, including air temperature, land surface temperature (LST), normalized difference vegetation index (NDVI), enhanced vegetation index (EVI), specific humidity, wind speed, potential evapotranspiration (PET), soil moisture, and surface pressure. These variables showed significant associations ($p \leq 0.05$), indicating their influence on vector survival and disease transmission dynamics (Table 17).

Table 17: Key environmental risk factors associated with LSD incidence derived through LDA.

Parametes	Mean	SD	F-value	p-value	95 % CI
Air temperature	23.05	6.33	47.46	6.59×10^{-12}*	22.85 - 23.25
EVI	0.36	0.14	27.29	1.84×10^{-7}*	0.36 - 0.36
LST	24.82	11.04	19.97	8.11×10^{-6}*	24.46 - 25.18
LAI	0.3	0.49	0.07	0.79	0.28 - 0.32
NDVI	0.6	0.19	7.83	5.16×10^{-3}*	0.59 - 0.61
Potential evaporation rate	191.59	67.61	0.55	0.46	189.41 - 193.77
PET	737.49	1111.7	6.49	1.08×10^{-2}*	701.69 - 773.29
Rainfall precipitation rate	4.34	4.15	1.79	0.18	4.21 - 4.47
Soil moisture	28.11	7.33	27.73	1.48×10^{-7}*	27.87 - 28.35
Specific humidity	0.0134	0.004775	31.62	2.01×10^{-8}*	0.0132 - 0.014
Surface pressure	94488.69	11071.27	32.33	1.40×10^{-8}*	94132.15 - 94845.23
Wind speed	2.35	1.22	71.78	3.42×10^{-17}*	2.31 - 2.39

Risk prediction was carried out using Random Forest (RF), Classification Tree (CT), and Support Vector Machine (SVM) models, and an ensemble approach combining these models was used to improve prediction reliability. The resulting risk probability maps (0–1 scale) revealed strong spatial heterogeneity in LSD distribution across India. High-risk districts (risk probability >0.7) were predominantly concentrated in Rajasthan, Madhya Pradesh, Maharashtra, eastern Uttar Pradesh, and Bihar, aligning with regions that experienced severe outbreaks during 2022 (Fig 59).

Comparative assessment indicated that Rajasthan and Maharashtra contributed the highest number of high-risk districts, reflecting persistent transmission potential and favorable environmental conditions. In contrast, southern and northeastern regions largely exhibited low to moderate risk (<0.5), though localized moderate-risk pockets suggest potential vulnerability under conducive climatic conditions.

Overall, the results highlight that LSD risk is driven by a combination of environmental suitability and historical outbreak intensity. The identified high-risk zones provide a quantitative basis for prioritizing targeted vaccination, vector control, and surveillance strategies, supporting efficient resource allocation and improved outbreak preparedness.

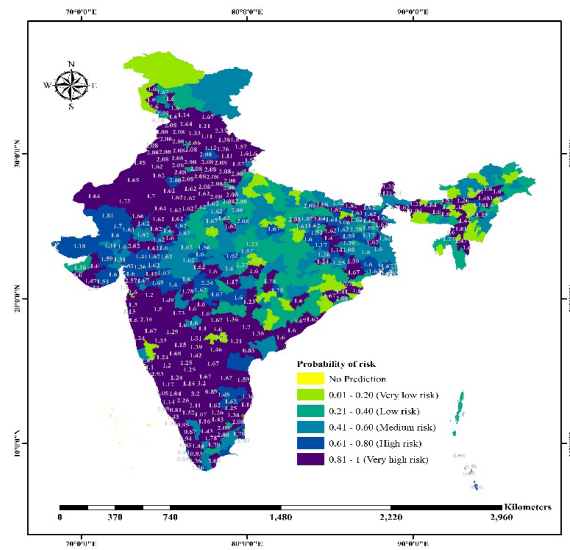


Fig 59: Spatial overlay of the basic reproduction number (R_0) on the risk map (depicted in white) for Lumpy Skin Disease (LSD) for December 2019 and December 2024.

(Suresh KP, Shome R, Patil SS, Jagadish Hiremath, Siju SJ, Narayanan G and Gulati BR)

Epidemiological Risk Assessment and Genomic Analysis of Anthrax under a One Health Framework in Karnataka

A comprehensive investigation of anthrax was conducted under the One Health Approach Initiative (OHAI) to assess epidemiological risk factors, farmers' knowledge, and mitigation practices across multiple districts of Karnataka, including Chikkaballapura, Tumakuru, Koppal, Bengaluru Rural, and Davanagere. In Koppal taluk, field investigations were conducted in nine villages. The investigations documented eight laboratory-confirmed anthrax cases along with four control cases; the disease was reported in 2018. The preliminary diagnosis was done by a local veterinary doctor based on clinical symptomatology and postmortem findings. This was subsequently confirmed through laboratory analysis at the Regional Animal Disease Diagnostic Laboratory and Information Centre (ADDL&IC), Bellary (part of IAH&VB), using standard diagnostic protocols, enabling a detailed assessment of vaccination coverage, shepherd migration routes, community awareness, and socioeconomic determinants of disease risk.

Complementary surveys were conducted across several villages in Chikkaballapura, Tumakuru, and Bengaluru Rural districts, encompassing both anthrax-affected and unaffected herds. Structured interviews captured farmers' perceptions of climate variability and its potential influence on livestock health. In total, epidemiological data from 1,025 farmers across diverse agro-ecological zones of Karnataka were compiled. All datasets were curated and analysed using a binomial modelling framework to estimate the village-level risk of anthrax; however, the analysis is ongoing, and the findings are preliminary.

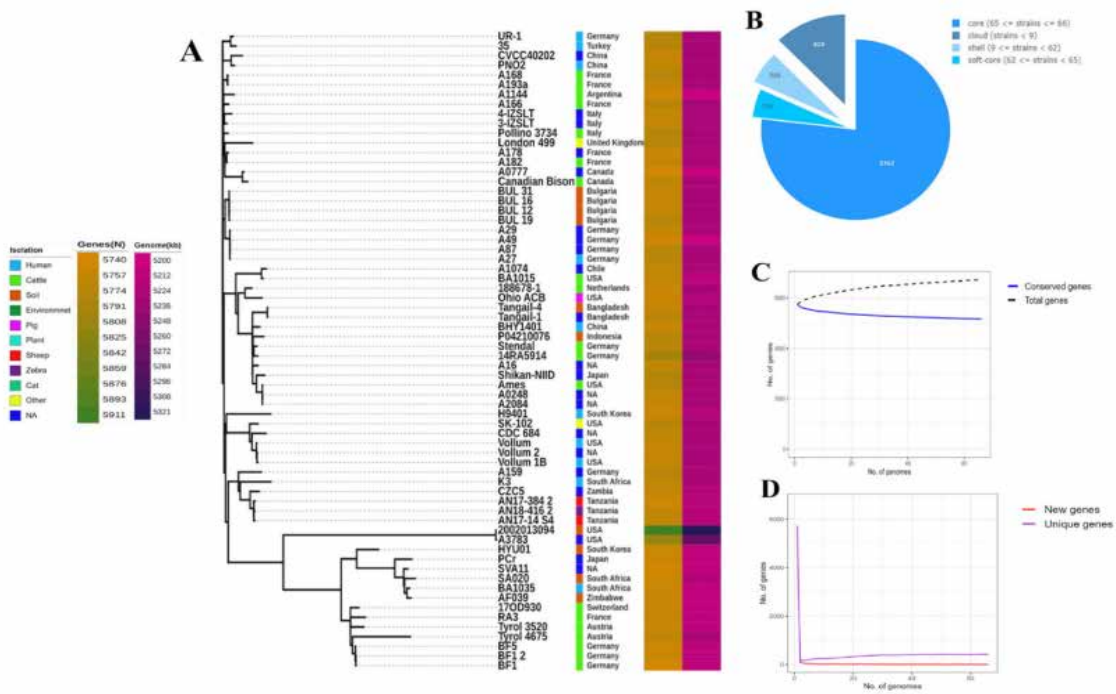


Fig 60: Phylogenomic trees of 66 B. anthracis isolates were constructed based on SNPs(A). The MCL algorithm reveals the number of genes within the soft core, cloud, shell, and core genome categories of B. anthracis isolates (B). Additionally, the conserved gene content (C) and the presence of new and unique genes (D) are illustrated.

Under the OHAI project, genomic investigation was conducted to address the limited understanding of *Bacillus anthracis* evolutionary dynamics, metabolic genes, and plasmid-driven virulence mechanisms across globally diverse isolates. To achieve

this, performed a partitioned pan-genomic analysis of the chromosome and key virulence plasmids (pXO1 and pXO2) using a functionally curated dataset of genomes. Integrated advanced computational approaches, including modularity-optimized Markov Clustering (MCL), ortholog prediction, and core genome SNP alignment, to evaluate gene family divergence and structural variations. Furthermore, machine learning techniques and metabolic network analyses were applied to differentiate isolates based on toxin profiles and to pinpoint crucial metabolic hub genes relevant to host-pathogen interactions.

Comprehensive genomic and comparative analyses of Bacillus anthracis revealed a dual pattern of conserved virulence determinants and plasmid-driven genetic variability shaping its pathogenicity. The thiol-activated cytolysin BAS3109 was found to be highly conserved across all isolates, indicating its fundamental role alongside canonical toxin genes (*pagA, lef,* and *cya*) in maintaining core virulence functions (Fig 60).

In contrast, substantial variation in the pXO1 and particularly pXO2 plasmids highlighted their critical contribution to strain-specific virulence, immune evasion, and environmental adaptation, despite the overall chromosomal genome remaining highly stable and monomorphic. Machine learning–based clustering and network analyses further identified GuaA as a central metabolic hub gene, with high connectivity in protein–protein interaction networks, suggesting its essential role in nucleotide biosynthesis and its potential as a diagnostic biomarker and therapeutic target. Additionally, clustering of BAS3109 variants based on virulence scores and molecular characteristics revealed distinct strain groupings associated with host and geographic diversity, reinforcing the role of subtle genetic variation in ecological adaptation. Focusing on the Indian context, the representative Indian isolate analyzed in this study (strain CVCC40205, originally sourced from the Indian Veterinary Research Institute in Uttar Pradesh) demonstrated notable genomic plasticity, grouping within the most globally diverse and adaptable isolates (Cluster 0). Together, these findings demonstrate that while conserved core genes underpin essential biological functions, plasmid variability and metabolic network centrality collectively drive the evolutionary adaptability and virulence of B. anthracis in endemic regions like India and worldwide.

(Suresh KP, Patil SS and Gulati BR)

A Multi-Host Mathematical Model for Analysing Transmission Dynamics of Japanese Encephalitis

A multi-host mathematical model was employed to analyse the transmission dynamics of Japanese Encephalitis (JE) across human, animal, and vector populations. The compartmental structure of the model, illustrating transmission pathways between humans, pigs, mosquitoes, and wading birds, is presented in Fig 61, which highlights the role of vector–host interactions and intervention pathways such as vaccination and biosecurity.

The analysis revealed that JE transmission is primarily driven by interactions between mosquito vectors and amplifying hosts, particularly pigs, which play a critical role in sustaining the infection cycle. The estimated basic reproduction number (R_0) indicated that the disease persists in settings with high vector density and frequent host–vector contact. Sensitivity analysis identified key parameters influencing transmission intensity, including mosquito biting rate, vector survival probability, and transmission efficiency between pigs and mosquitoes.

Further quantitative analysis showed that infection peaks occurred within 3–5 days under different transmission scenarios. In the Udupi district, infections peaked at approximately 694,719 cases by Day 3 with a low reproduction number (R_0 = 0.27), followed by a rapid decline, indicating a disease-free equilibrium represented in Fig 62.

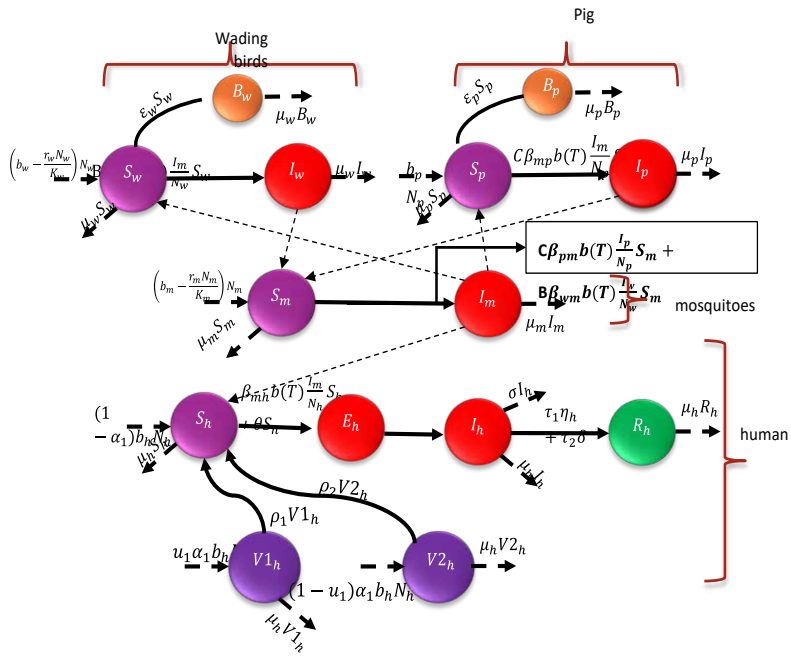


Fig 61: JE Transmission Pathways in a Multi-Host with SVIIR in humans, SI in mosquitos, SISB in pigs and SIB framework in wading birds.

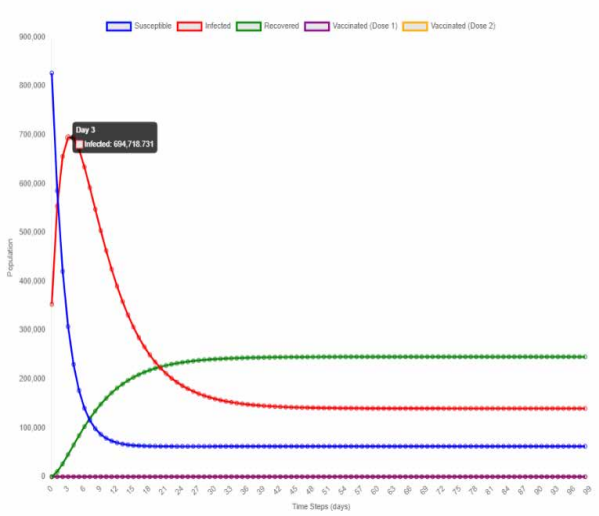


Fig 62: Simulation for Udupi district.

In contrast, Raichur district exhibited a higher transmission scenario, with infections peaking at approximately 1.35 million cases by Day 5 and R_0 increasing to 2.86, indicating endemic persistence. Under moderate transmission conditions (R_0 = 0.74), the outbreak showed a declining trend without long-term persistence, as presented in Fig 63.

The model further demonstrated that increasing vector abundance and host density significantly elevated infection prevalence, while reductions in vector population or host–vector contact substantially decreased transmission potential.

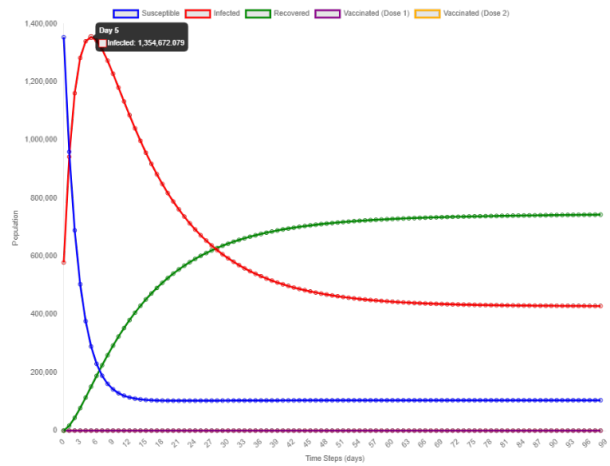


Fig 63: Simulation for Raichur district.

Herd immunity thresholds were estimated at approximately 17.4% under moderate transmission and 65.03% under high transmission scenarios, highlighting the critical role of vaccination in outbreak control. These findings quantitatively confirm the dominant role of vector ecology and reservoir hosts in shaping JE dynamics and provide evidence-based insights into factors driving disease persistence and spread.

(Suresh KP, Sengupta PP, and Krishnamoorthy P)

Farm-Level Economic Impact of African Swine Fever in India: Evidence from Multi-State Field Surveys and System Dynamics Modeling

A cross-sectional economic assessment was conducted to quantify the farm-level financial impact of African Swine Fever (ASF) outbreaks in major pig-producing states of India. Primary data were collected from 807 pig farms through structured field surveys conducted in Karnataka (n = 202), Assam (n = 200), Jharkhand (n = 204) and Meghalaya (n = 201). The details of the ASF infection (%) and mortality (%) of crossbred and indigenous pig population in surveyed states are presented in Fig 64.

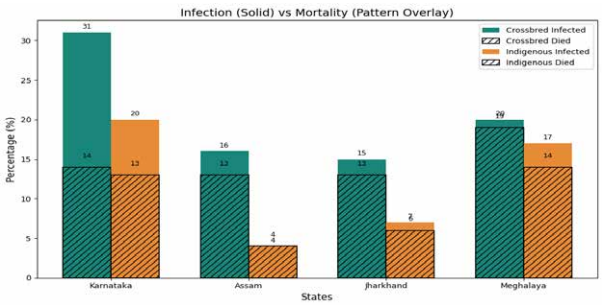


Fig 64: Infection (%) and mortality (%) among surveyed states.

Economic losses due to ASF were substantial across all surveyed states. The pooled mean mortality loss per animal was highest in Meghalaya i.e., 11,569 (95% CI: 9,309 – 13,830), followed by INR 11,242.40 (95% CI: 8,627-13,857) in Jharkhand, INR 11140 (95% CI: 8,760 – 13,520) in Assam and INR 8,778 (95% CI: 7,991 – 9,565) in Karnataka. Distress sale losses ranged from INR 1,250–6,000 for indigenous pigs and INR 2,691–10,000 for crossbred pigs, with additional variation in labour and treatment costs.

System Dynamics Model simulations for Assam state over a 10-year period showed that biosecurity measures (fencing, footbaths, isolation of sick animals, protective clothing, feed management, waste disposal, disinfection, veterinary care, swill heating, vector control, and pen cleaning) improved pig population stability. Market hub interventions (centralized pig collection centres, basic health screening, and regulated animal movement) reduced distress sales and improved price realization. Combined (bio security and Markert hub) implementation had the greatest impact, reducing ASF-related mortality by 49.3% and outbreak frequency by 75%, while improving price stability and market efficiency. These findings provide evidence-based insights for designing effective ASF control strategies and strengthening resilience in pig production systems in endemic regions.

(Govindaraj G, Narayanan G and Sathish Gowda CS)

Livestock-Based Livelihood Interventions for Socio-Economic Empowerment of Scheduled Caste Farming Households

Livestock-based livelihood interventions on sheep and goat production, scientific dairy farming, and fodder management were implemented in three drought-prone districts of Karnataka—Bidar, Kolar, and Tumakuru—to enhance livelihood resilience among Scheduled Caste farming households. In each district, 50 beneficiary households were covered in one selected village, while a socio-economically comparable village was identified as a control with 50 non-beneficiaries by the implementing agencies to enable outcome assessment. By targeting dryland areas, where agricultural income is often inadequate and unstable, the intervention sought to generate more reliable livestock-based livelihood opportunities and provide an evidence-based framework for assessing programme impact.

The interventions resulted in measurable improvements in livestock productivity, management practices, and household economic outcomes. Based on recall-based baseline and endline assessment conducted before and after programme implementation, covering 50 beneficiary households and 50 households from socio-economically comparable control villages, participating households reported that income from livestock activities increased by approximately 15% due to increased milk yield and weight gain.

(Narayanan G and Sathish Gowda CS)

Hands-on Training on Laboratory Diagnosis of Leptospirosis under the NCDC – NOHPPCZ during 11-14th August 2025

Capacity Development, Education and Trainings

4

During 2025, the institute strengthened collaborations with national and international organizations to support research, training, and outreach in veterinary epidemiology and livestock health.

India–Brazil Agri-Tech Collaboration Strengthened through Maitri 2.0

ICAR–NIVEDI hosted a Brazilian delegation (29 Sept–1 Oct 2025) under Maitri 2.0: India–Brazil Cross-Border Agri-Tech Incubators' Program through its NaaViC Agri-Business Incubation Centre. Discussions focused on agri-tech innovation, livestock technologies, and bioinputs, with visits to ICAR institutes and interactions with incubatees. The visit opened avenues for co-incubation, student exchange, technology validation, and joint R&D collaborations.

Workshop on Climate-Sensitive Zoonotic Disease Prioritization

A two-day workshop in Kochi on prioritizing climate-sensitive zoonotic and high-threat pathogens was jointly organized by ICAR–NIVEDI, the World Bank, the University of Queensland, and ICMR–RMRC Bhubaneswar under the One Health framework. Experts and officials identified priority diseases, assessed climate-related risks, and developed an evidence-based ranking to strengthen Kerala's integrated surveillance and rapid response system.

National Workshop on Strengthening AMR Surveillance

ICAR–NIVEDI organized a one-day national workshop during World AMR Awareness Week 2025 on "Strengthening AMR Surveillance and Research Linkages." Experts from human, animal, and environmental health sectors discussed integrated surveillance, laboratory networks, diagnostics, and innovation under the One Health framework. The workshop emphasized scaling up AMR surveillance, strengthening research–policy linkages, and enhancing national–state coordination to combat antimicrobial resistance.

Field Veterinary Epidemiology Training for Odisha Veterinary Officers

A five-day training programme (1–5 December 2025) on Field Veterinary Epidemiology was conducted at ICAR–NIVEDI, Bengaluru for 16 Veterinary Officers from Odisha. The programme provided hands-on training in outbreak investigation, GIS-based disease mapping, questionnaire design, and data analysis using Epi Info to strengthen field-level disease surveillance and response capacity.

National Training on Leptospirosis Diagnostics

ICAR–NIVEDI conducted a four-day national training programme (11–14 August 2025) on laboratory diagnosis of Leptospirosis in collaboration with NCDC, Delhi under the National One Health Programme for Prevention and Control of Zoonoses. The programme trained 30 participants from 14 States/UTs through hands-on sessions on biosafety, outbreak investigation, serological and molecular diagnostics (MAT, ELISA, PCR) to strengthen national diagnostic capacity and One Health preparedness.

International Training Strengthens Global Leptospirosis Response

ICAR–NIVEDI conducted a month-long international training (4 August–3 September 2025) on *Leptospira* diagnosis at its WOAH Reference Laboratory, under the IAEA Fellowship. The programme provided hands-on training in microbiological, serological, and molecular techniques, strengthening global diagnostic capacity and One Health collaboration.

Awareness Session on NABL Accreditation

ICAR–NIVEDI, in collaboration with NABL, Bengaluru, conducted a one-day awareness session on 16 December 2025 for scientists and KVK Subject Matter Specialists. The programme covered the NABL accreditation framework, procedures, and requirements, highlighting its importance for strengthening laboratory quality and standards.

Workshop on ASF Biosecurity at Kannur

ICAR–NIVEDI in collaboration with the Animal Husbandry Department, Kerala, conducted a one-day workshop at Kannur on risk-based farm biosecurity to prevent African Swine Fever (ASF). The programme provided farmer-oriented training on biosecurity practices, risk assessment, and ASF prevention, with participation from veterinarians, farmers, and state officials.

World AMR Awareness Week 2025

ICAR–NIVEDI observed World AMR Awareness Week (18–24 November 2025) with activities promoting responsible antibiotic use and One Health awareness. The programme included student outreach, farmer interactions, and a national workshop on strengthening AMR surveillance and research linkages.

Meetings on African Swine Fever Surveillance and Control

ICAR–NIVEDI conducted a Focus Group Discussion on ASF (20 November 2025) in Guwahati under a World Bank-supported project to assess its status, economic burden, and mitigation strategies. Additionally, a brainstorming workshop (24 October 2025) at College of Veterinary Science, Khanapara, Guwahati, Assam discussed ASF epidemiology, surveillance, and control measures, strengthening regional preparedness and coordinated response.

Memorandum of Understandings (MoUs)

The ICAR-NIVEDI executed Memoranda of Understanding (MoUs) with the following institutions:

- Garden City University, Bengaluru-560049, Karnataka on 28.02.2025.
- Foundation for Bengaluru Science and Technology, Bengaluru-560003, Karnataka on 01.04.2025.
- Siksha 'O' Anusandhan, Bhubaneswar-751030, Odisha on 21.05.2025.
- Neuberg Anand Academy of Laboratory Medicine Private Limited, Bengaluru-560001, Karnataka on 23.05.2025.
- Indian Academy Degree College, Autonomous, Bengaluru-560043, Karnataka on 06.08.2025.
- India Meteorological Department, Mausam Bhawan, Lodhi Road, New Delhi – 110003 on 16.09.2025.
- Vellore Institute of Technology, Vellore-632014, Tamil Nadu on 16.09.2025.

ICAR–NIVEDI and IMD Sign MoU for Climate-Based Disease Forecasting

ICAR–NIVEDI and the India Meteorological Department (IMD) signed an MoU on 16 September 2025 to integrate climate data with the NADRES system for improved livestock disease forecasting. The collaboration will enhance block-level advisories, data sharing, and early warning systems to support livestock health and farmer livelihoods.

Training/Capacity building programs organized by NaaVic

Sl #	Name of Seminar /Workshop /EDP/ Training	Venue	Duration (Days)	Date
1	Orientation Program on importance of startups, innovation and entrepreneurship	GKVK, Bengaluru	1	17th Jan, 2025
2	Orientation Program on importance of startups, innovation and entrepreneurship for Veterinary Doctors	ICAR-NIVEDI	1	10th Mar, 2025
3	Orientation Program on Entrepreneurship opportunities in Animal Husbandry & Livestock Sector	Veterinary College, Gadag	1	9th April, 2025
4	Orientation Program on Entrepreneurship opportunities in Animal Husbandry & Livestock Sector	ICAR-NIVEDI	1	20th June, 2025
5	Orientation Program on Entrepreneurship opportunities in Agri & Allied sector	Veterinary College, Hebbal	1	20th June, 2025
6	Orientation Program on Entrepreneurship opportunities in Agri & Allied sector	Veterinary College, Hebbal	1	23rd June, 2025
7	Orientation Program on Entrepreneurship opportunities in Agri & Allied sector	Veterinary College, Hebbal	1	24th June, 2025
8	Orientation Program on Entrepreneurship opportunities in Agri & Allied sector	Veterinary College, Hebbal.	1	24th June, 2025
9	Three days 'Maitri 2.0 India Brazil Cross Border Agri-Tech Incubators Program'	ICAR-NIVEDI Bengaluru	3	29th Sep, 2025 to 1st Oct 2025
10	Orientation Program on ''Entrepreneurship opportunities in Agri & Allied sector''	ICAR-NIVEDI	1	10th Oct, 2025
11	Orientation Program on ''Entrepreneurship opportunities in Agri & Allied sector''	ICAR-NIVEDI	1	19th Oct, 2025
12	Agripreneurship Awareness Program for Farmers in Medihala Village, Kolar District.	Medihala Village, Kolar	1	23rd Dec, 2025
13	One Month training on Agripreneurship Orientation Program [For the 9th cohort startups]	ICAR-NIVEDI	31	1st Dec, to 31st Dec, 2025

Entrepreneurship Development Programs (EDP) in collaboration with different Institutes				
1	EDP on Entrepreneurship in Sheep and Goat Farming	Veterinary College, Hebbal, Bengaluru	3	6th to 8th Jan, 2025
2	EDP on Entrepreneurship in Sheep and Goat Farming	KSNUAHS, Shivamogga	3	9th to 11th Jan, 2025
3	EDP on Entrepreneurship in Sheep and Goat Farming	Veterinary College, Hebbal, Bengaluru	1	24th March 2025
4	EDP on Entrepreneurship in Piggery Healthcare	Veterinary College, Hassan	1	11th Nov 2025
5	EDP on Entrepreneurship Opportunities in the Livestock Sector for undergraduate Students.	Veterinary College, Gadag	1	19th Nov 2025
Meetings				
1	SIC Meeting (9th cohort)	Virtual	1	4th Feb, 2025
2	RKVY-RAFTAAR Review Meeting	Krishi Bhawan, New Delhi	1	8th July 2025
3	1st RIC meeting (10th cohort)	Virtual	1	13th Oct 2025
4	1st RIC meeting (10th cohort)	Virtual	1	14th Oct 2025
5	1st RIC meeting (10th cohort)	Virtual	1	17th Oct 2025

Post-Graduate Teaching and Research Academic Activities of IVRI-Deemed University Bengaluru Hub at ICAR-NIVEDI

ICAR-NIVEDI, as a recognized Centre under the Bengaluru Hub of the Indian Veterinary Research Institute-Deemed University (IVRI-DU), continues to actively contribute to postgraduate education through both offline and online modes of instruction. During the academic year 2025–26, the institute admitted seven students, including six in the M.V.Sc. programme and one in the Ph.D. programme. The M.V.Sc. cohort comprises three students in Veterinary Microbiology and three in Veterinary Public Health & Epidemiology, while the Ph.D. scholar is enrolled in Veterinary Public Health & Epidemiology. All students have been provided with on-campus hostel accommodation, along with access to essential amenities such as purified drinking water, geysers, smart classrooms, and sports facilities, ensuring a comfortable and conducive academic environment.

Students undertaken PG Research in ICAR-NIVEDI during 2025

Sl.No.	Name of student	University	Name of supervisor	Degree Awarded
1.	Mr.Thushar, H.C	Dayananda Sagar University	Dr. V. Balamurugan,	M.Sc.Biotech
2.	Ms. Anusha K.S	Dayananda Sagar University	Dr. V. Balamurugan	M.Sc. Biotech
3.	Ms.Namratha	REVA University	Dr. Jagdish Hiremath	M.Sc. Biotech
4.	Ms.Malini	REVA University	Dr. GBM Reddy	M.Sc. Biotech
5.	Ms.Vaishnavi	REVA University	Dr. Siju Susan Jacob	M.Sc. Biotech
6.	Ms.Moulya	REVA University	Dr.M.Nagalingam	M.Sc. Biotech
7.	Ms.Deepu	REVA University	Dr.Shivasharanappa	M.Sc. Biotech
8.	Ms. Bhoomika	JSS AHER University	Dr.K.P.Suresh	M.Sc. Medical Statistics
9.	Ms. Chaithanya Shetty	JSS AHER University	Dr.K.P.Suresh	M.Sc. Medical Statistics
10.	Ms. Likitha,R.	JSS AHER University	Dr.K.P.Suresh	M.Sc. Medical Statistics
11.	Ms. Keerthana.K.S.	Kannur University	Dr.K.P.Suresh	M.Sc. Bioinformatics
12.	Ms. Keerthana.C.K	Kannur University	Dr.K.P.Suresh	Bioinformatics
13.	Ms. Anupama. M.	Kannur University	Dr.K.P.Suresh	M.Sc. Bioinformatics
14.	Ms.Geethika.B	Kannur University	Dr.K.P.Suresh	Bioinformatics
15.	Ms. Nafala,C.K.,	Kannur University	Dr.K.P.Suresh	M.Sc. Bioinformatics
16.	Ms.Sahana	REVA University	Dr.Sridevi.R,	M.Sc. Biotech
17.	Ms.Gagana Deepa.C.S	Dayananda Sagar University	Dr.Shivasharanappa	M.Sc. Biotech
18.	Ms. Keerthana.M	Dayananda Sagar University,	Dr.Jagadish Hiremath	M.Sc. Biotech
19.	Mr. VENKAT, S.N	Vellore Institute of Technology,TN	Dr.Jagadish Hiremath	M.Tech. Biotechnology
20.	Mr. Yadhu Soman P	Kannur University, Kerala	Dr.K.P.Suresh	M.Sc. Computational Biology
21.	Mr.Navadeep Chandran	Kannur University, Kerala	Dr.K.P.Suresh	M.Sc. Computational Biology
22.	Mr. Selva Pradeesh	Bharathiar University,TN	Dr.K.P.Suresh	M.Sc. Bioinformatics

Participation in Training/Workshop/ Conference 5

Conference/Symposium/Conclave

1. Dr. K.P. Suresh attended the International Symposium on One Health and Emerging Infectious Diseases, held at Sun Pharma Science Foundation in collaboration with NIAB, Hyderabad, on 3 February 2025.
2. Dr. M.M. Chanda attended the 18th HISICON (Hospital Infection Society–India) Conference, held at SGPGIMS, Lucknow, during 6–8 February 2025.
3. Dr. S.B. Shivachandra, Dr. G.B. Manjunath Reddy and Dr. Narayanan G attended the National Horticulture Fair-2025, held at ICAR-IIHR, Bengaluru, during 27 February–1 March 2025.
4. Dr. M. Nagalingam attended the National Conference on Trends and Transcends in Zoological Sciences (NCTTZS), held at St. Joseph's University, Bengaluru, during 17–18 March 2025.
5. Dr. P. Krishnamoorthy participated in the CCSEA Seminar on "Laboratory Animal Welfare and Ethics", held at CCMB, Hyderabad, on 27 March 2025.
6. Dr. K.P. Suresh attended the World Health Summit Regional Meeting 2025, held at Bharat Mandapam, New Delhi, during 25–27 April 2025.
7. Dr. Siju Susan Jacob and Dr. Chethan Kumar H.B. attended National Space Day Celebration 2025, held at A.P. Shinde Symposium Hall, NASC Complex, New Delhi, on 23 August 2025.
8. Dr. K.P. Suresh attended the 28th National Conference on e-Governance (NCeG), organized by DARPG & MeitY, held at Visakhapatnam, Andhra Pradesh, during 22–23 September 2025.
9. Dr. Jagadish Hiremath attended the 5th Annual Conference of Animal Physiologists Association and National Symposium on "Next-Generation Physiological Approaches for Climate-Adaptive Livestock Production", held at KVAFSU, Bidar, during 9–10 October 2025.
10. Dr. S.B. Shivachandra and Dr. G.B. Manjunath Reddy attended the Krishi Mela, held at UAS, Bengaluru, during 13–16 November 2025.
11. Dr. Rajeswari Shome, Dr. K.P. Suresh, Dr. V. Balamurugan, Dr. S.B. Shivachandra, Dr. M.M. Chanda, Dr. Jagadish Hiremath, Dr. M. Nagalingam, Dr. Siju Susan Jacob and Dr. Chethan Kumar H.B. attended the National One Health Assembly 2025: "Translating Knowledge to Practice – One Earth, One Health, One Future", held at Bharat Mandapam Convention Centre, New Delhi, during 20–21 November 2025.
12. Dr. P.P. Sengupta and Dr. Siju Susan Jacob attended CLIMATECON 2025: Conference-cum-Workshop on "Climate Resilient Livestock Production: Emerging Concepts and Technologies for Sustenance", held at ICAR-NIANP, Bengaluru, during 23–24 November 2025.
13. Dr. Narayanan G attended the 12th International Conference on "Emerging Issues in Agricultural, Food Technology, Biological & Applied Sciences for Global Development (EIAFTBASGD-2025)" which is scheduled to be held on November 15-17, 2025 at Maharana Pratap University of Agriculture and Technology, Udaipur, Rajasthan, India.

14. Dr. P. Krishnamoorthy participated in the 42nd Annual Conference of Indian Association of Veterinary Pathologists on "Bridging Conventional and AI-Based Digital Pathology for Veterinary Disease Diagnosis", held at Ranchi during 4–6 December 2025.

15. Dr. Z.B. Dubal attended the IAVPHSCON-2025 (Annual Conference of Indian Association of Veterinary Public Health Specialists), held at GADVASU, Ludhiana, during 11–12 December 2025.

16. Dr. M. Nagalingam attended the International Symposium on "Advancing One Health: Concept to Action for Promoting Human, Animal and Environmental Health" & XXI IAVPHS Conference, held at GADVASU, Ludhiana, during 11–12 December 2025.

17. Dr. P. Krishnamoorthy participated in the International Symposium of IAVPHS on "Advancing One Health: Concept to Action for Promoting Human, Animal and Environmental Health", held at Ludhiana during 11–12 December 2025.

18. Dr. Siju Susan Jacob and Dr. P.P. Sengupta attended the 34th National Congress of Veterinary Parasitology (NCVP-2025) & National Symposium on "Parasitology in the Digital Era: Innovations for One Health and Farmers' Prosperity", held at Udgir, Maharashtra, during 17–19 December 2025.

19. Dr. P. Krishnamoorthy participated in the 13th International Conference of Laboratory Animal Scientists Association (India) on "Preclinical Insights from Animal Studies on Drug Discovery and Translational Research", held at GITAM University, Visakhapatnam, during 18–20 December 2025.

Workshops

1. Dr. Shivasharanappa N attended the 7th Annual Meeting of the PPR Global Research and Expertise Network (PPR-GREN), organized by FAO-PPR Secretariat, held during 20–22 January 2025 (Virtual).

2. Dr. Shivasharanappa N attended the FAO ATLASS Workshop on "Assessment Tool for Laboratories and Antimicrobial Resistance Surveillance Systems", organized by FAO-ECTAD India at ICAR-CIFT, Kochi, during 20–22 January 2025.

3. Dr. Chethan Kumar H.B. attended the Capacity Building for Virus Disease Outbreak Response and Collaborative Research: Proposal Development Workshop, organized by NIV (South Zone), Bengaluru, during 13–15 March 2025.

4. Dr. P. Krishnamoorthy participated in the FAO Workshop on "Cross-border Harmonization and Mano River Episystem for PPR Eradication in West Africa", held at Abidjan, Ivory Coast, during 23–25 June 2025.

5. Dr. K.P. Suresh attended the Workshop on "Pandemic Preparedness and Response", held at Mahabalipuram, Chennai, on 25 June 2025.

6. Dr. S.S. Patil attended the Immersion Workshop on "Animal Health Security: Strengthening India for Pandemic Preparedness and Response", organized by DAHD, held at Sheraton Grand, Mahabalipuram, Tamil Nadu, on 26 June 2025.

7. Dr. Jagadish Hiremath attended the Brainstorming-cum-Workshop on "Strengthening Preparedness and Control of African Swine Fever in North East India: Policy, Biosecurity and Pig Movement Management", organized by ICAR-RC NEH, Umiam, Meghalaya, on 24 October 2025.

8. Dr. M. Nagalingam attended the Workshop and Panel Discussion on "Strengthening AMR Surveillance and Research Linkages", organized by ICAR–NIVEDI, Bengaluru, on 24 November 2025.
9. Dr. V. Balamurugan attended the Workshop on "Recent Developments in Control and Containment of Animal Diseases" under ASCAD Awareness Programme, held on 3 December 2025.

Trainings

1. Dr. P. Krishnamoorthy attended the Training Programme on "Laboratory Quality Management System and Internal Audit as per ISO/IEC 17025:2017", held at NITS, BIS, Noida, during 5–8 May 2025.
2. Dr. Chethan Kumar H.B. attended the Training Programme on "Inter-Laboratory Comparison, Proficiency Testing, and Evaluation of Scores (ILCPT)", conducted by NITS, BIS, Noida, organized by WHO India in collaboration with NCDC and ICMR, during 25–26 June 2025.
3. Dr. Jagadish Hiremath attended the 21-day Online Training Programme on "Advanced Statistical and Machine Learning Techniques for Data Analysis Using Open-Source Software for Abiotic Stress Management in Agriculture", organized by ICAR-NIASM, during 16 July–5 August 2025.
4. Dr. Siju Susan Jacob attended the Online National Training Programme on "Advances in Survey Research and Data Analysis Using Open-Source Software", organized by ICAR-NIFMD, Bhubaneswar, during 15–24 September 2025.
5. Dr. S.S. Patil attended the Two-day Training Programme on "ISO 17025:2017 for Quality Managers", organized by NABL, held at Bengaluru, during 25–26 September 2025.
6. Dr. Chethan Kumar H.B. attended the Awareness Session on "NABL Accreditation – Gunvatta Yatra", held at ICAR–NIVEDI on 16 December 2025.

International Meetings/Workshop Participation

1. Dr. V. Balamurugan and Dr. G. Govindaraj attended the 7th PPR Global Research and Expertise Network (GREN) Meeting, held at ADAFSA, Abu Dhabi, UAE, during 20–22 January 2025.
2. Dr. G. Govindaraj attended the Socioeconomic Thematic Group Meeting of PPR-GREN, organized by FAO at ILRI, Nairobi, Kenya, during 12–13 May 2025.
3. Dr. Narayanan G attended (Virtual) the Socioeconomic Thematic Group Meeting of PPR-GREN, organized by FAO at ILRI, Nairobi, Kenya, during 12–13 May 2025.
4. Dr. V. Balamurugan participated in the Global Laboratory and Epidemiology Networking Workshop on TADs (GLENW 2025), organized by FAO/IAEA, Vienna, Austria, during 17–19 June 2025.
5. Dr. V. Balamurugan and Dr. G. Govindaraj attended the 8th PPR Global Research and Expertise Network (GREN) Meeting, held at Qingdao, China, during 25–27 November 2025.
6. Dr. P. Krishnamoorthy, attended the FAO "Cross-border Harmonization and Mano River Episystem for PPR Eradication" workshop held at Abidjan, Ivory Coast, during 23–25 June 2025


राष्ट्रीय पशुरोग जानपदिक एवं सूचना विज्ञान संस्थान
NATIONAL INSTITUTE OF VETERINARY EPIDEMIOLOGY AND DISEASE INFORMA
DAPST Launch Workshop at ICAR-NIVEDI on 18th July 2025
ICAR-National Institute of Veterinary Epidemiology and Disease Informatics (ICAR-NIVEDI), Bengaluru-560 119, Karnataka, India
DAPST Launching Workshop
on
ವಾಯಕ್ಕಾಗಿ ಸುಧಾರಿತ ಪಶುಸಂಗೋಪನೆ ಪದ್ಧತಿಗಳು
dvanced Animal Husbandry Practices for Sustainable Income
ದಿನಾಂಕ: 18/07/2025 (ಶುಕ್ರವಾರ,10:30 AM)

Outreach, Extension and Institutional Activities

6

Secretary DARE Inaugurates Facilities at ICAR–NIVEDI

Dr. Himanshu Pathak, Secretary (DARE) & DG (ICAR) visited ICAR–NIVEDI on 2 January 2025, inaugurating the 'Hoof & Health Gate' and the WOAH Reference Laboratory for Leptospirosis. He reviewed institute activities and appreciated NIVEDI's contributions in disease epidemiology, modelling, AMR surveillance, and zoonotic research, highlighting its role as a leading centre in livestock health research.

WOAH Expert Mission Reviews PPR Eradication Programme

A WOAH expert delegation led by Dr. Henry M. Wamwayi visited ICAR–NIVEDI on 18 February 2025 to review India's PPR control and eradication programme. The team visited the WOAH Reference Laboratory for PPR at ICAR-NIVEDI and discussed surveillance, vaccination monitoring, and outbreak investigations. ICAR–NIVEDI highlighted its key contributions and technical capabilities, supporting strengthened strategies for national PPR eradication.

INLEAD Program Launched to Strengthen Disease Modelling

ICAR–NIVEDI launched the INLEAD (National Livestock Epidemiology and Disease Modelling) Program with support from the Gates Foundation, marked by a two-day international workshop (24–25 June 2025). The programme focuses on disease modelling, surveillance, and data integration for priority diseases such as FMD, PPR, LSD, ASF, and Avian Influenza, promoting collaborative and evidence-based approaches for improved disease forecasting and control.

Seminar on Bovine Antibody Gene Technology

ICAR–NIVEDI hosted a Seminar Club lecture on 10 March 2025 by Dr. Azad Kumar Kaushik on bovine antibody gene technology and its applications in livestock health. The session, attended by scientists and students, featured interactions with Dr. Inderjeet Singh and Prof. A.C. Varshney on emerging trends in veterinary science.

NaaViC Promotes Agri-Startups and Entrepreneurship

NaaViC, the agri-business incubator at ICAR–NIVEDI, supported startup funding (₹38.5 lakh) and launched its 10th cohort, receiving 300+ applications and student innovations. It also conducted entrepreneurship programmes for farmers and students and expanded outreach through major expos and academic platforms, strengthening innovation-driven agri-entrepreneurship.

76th Republic Day Celebrated at ICAR–NIVEDI

ICAR–NIVEDI celebrated the 76th Republic Day on 26th January 2025, with flag hoisting by Dr. B.R. Gulati. In his address, he emphasized strengthening the livestock sector through modern tools in disease diagnosis, surveillance, and epidemiology.

Celebration of International Women's Day

ICAR–NIVEDI celebrated International Women's Day (20th March 2025) with participation of ~100 women staff, focusing on the theme "Accelerate Action." The programme featured expert talks on women's empowerment, career development, and entrepreneurship, reinforcing the institute's commitment to gender equality and capacity building.

Celebration of the 25th Foundation Day

ICAR–NIVEDI celebrated its 25th Foundation Day on 1st July 2025, highlighting its contributions to veterinary epidemiology, disease informatics, and One Health. The event featured lectures, awards, and farmer felicitation, recognizing achievements of scientists, staff, and progressive livestock farmers.

World Zoonoses Day 2025 Awareness Programme

ICAR–NIVEDI, in collaboration with the Department of Animal Husbandry and Veterinary Services, organized a zoonoses awareness programme on 8th July 2025 under the NCDC–NOHPPZ initiative. The event educated 150 students and teachers on zoonotic diseases, their transmission, and prevention, promoting hygiene, vaccination, and One Health awareness.

Observance of World Zoonoses Day with an Expert Visit

On World Zoonoses Day (6th July 2025), ICAR–NIVEDI hosted eminent veterinary leaders who reviewed ongoing initiatives in in rsearch on epidemiology of zoonotic diseases. The visit highlighted the need for stronger collaborations, disease surveillance, and coordinated efforts toward national disease control programmes, including FMD eradication.

AMR Stewardship Drive 2025 Promotes One Health Collaboration

ICAR–NIVEDI hosted the AMR Stewardship Drive 2025 (11th July 2025) in collaboration with CII-FACE and INFAH, bringing together stakeholders from government, academia, and industry. The event emphasized responsible antibiotic use, strengthened AMR surveillance, and multi-sector partnerships under the One Health framework to combat antimicrobial resistance.

Celebration of the 79th Independence Day

ICAR–NIVEDI celebrated the 79th Independence Day on 15 August 2025 with flag hoisting by Dr. B.R. Gulati. In his address, he emphasized strengthening the livestock sector through modern tools in disease diagnosis, surveillance, and veterinary epidemiology.

Celebration of Teachers' Day by PG Scholars

PG scholars of the IVRI Bengaluru Education Hub (NIVEDI Campus) celebrated Teachers' Day on 4th September 2025. The event featured cultural activities and student–faculty interactions, fostering stronger mentor–student bonding and marking the beginning of an annual tradition.

Completion of the NABL ISO/IEC 17025 Renewal Audit

ICAR–NIVEDI successfully completed the ISO/IEC 17025:2017 NABL renewal audit (1–2 November 2025) for its Livestock Disease Diagnosis Laboratory (LDDL). The audit reaffirmed quality standards, technical competence, and compliance, strengthening reliable diagnostic services under the One Health framework.

Seminar on Strengthening AMR Surveillance

On 17 September 2025, ICAR–NIVEDI hosted a Seminar Club lecture by Dr. Sweta Raghavan on the State Action Plan for AMR. The session emphasized robust surveillance, responsible antimicrobial use, and collaborative efforts for effective AMR containment.

Hindi Saptah Celebrated

ICAR–NIVEDI celebrated Hindi Saptah (14–19 September 2025) with competitions including essay writing, debates, poetry, and singing. The event promoted Hindi in official and scientific communication while fostering cultural unity and linguistic pride.

Vigilance Awareness Week 2025

ICAR–NIVEDI observed Vigilance Awareness Week (27 October–3 November 2025) with activities including an integrity pledge, quiz competition, poster displays, and essay writing on AI in governance. The programme encouraged active participation of staff and students and reinforced values of transparency, accountability, and ethical conduct.

Rashtriya Ekta Diwas Observed

ICAR–NIVEDI observed Rashtriya Ekta Diwas on 31 October 2025 with an integrity pledge administered by the Director, along with banner display and video screening on Sardar Vallabhbhai Patel's legacy. The programme reinforced national unity, teamwork, and institutional commitment to collective responsibility.

DAHD Secretary Visits ICAR–NIVEDI Launches Toll Free Helpline and Sampling Plan

Shri Naresh Pal Gangwar, Secretary (DAHD), visited ICAR–NIVEDI on 6 & 8 November 2025, reviewing key research facilities and ongoing projects. He launched a toll-free helpline (1800-599-4233) and released the National Sero-Monitoring Sampling Plan for Brucellosis and FMD, while emphasizing collaboration under NDLM and NADICC to strengthen disease surveillance and forecasting.

Observance of World AMR Awareness Week 2025

ICAR–NIVEDI observed World AMR Awareness Week (18–24 November 2025) with activities including an integrity pledge, student outreach, farmer interactions, and a national workshop. The programme promoted responsible antibiotic use, AMR surveillance, and One Health collaboration.

Constitution Day (*Samvidhan Diwas*) Observed at ICAR–NIVEDI

ICAR–NIVEDI observed Constitution Day on 26 November 2025 with a pledge ceremony, reaffirming commitment to justice, liberty, equality, and fraternity. The programme emphasized constitutional values and collective responsibility toward national progress.

Expert Lecture on Avian Influenza H5N1 Epidemiology

ICAR–NIVEDI organized a Continuing Epidemiology Education (CEE) lecture on 16 December 2025 on Avian Influenza H5N1 Clade 2.3.4.4b epidemiology and public health implications, delivered by Dr. Suresh V. Kuchipudi. The session enhanced awareness, preparedness, and scientific dialogue on avian influenza threats.

NaaViC Strengthening Agri-Startups and Entrepreneurship

NaaViC promoted agri-startups under NEO, NEST, and NUZEN, releasing ₹36 lakh to 7 startups (9th cohort) and launching the 10th cohort (421 proposals; 25 shortlisted), alongside MoUs, reviews, and national-level engagements with MoAFW and the Union Agriculture Minister. It also strengthened the ecosystem through training 1700+ youths/startups and 200+ farmers, global collaboration (Maitri 2.0), and support to 75 startups generating significant employment. Further, NaaViC expanded outreach through stakeholder meetings, expert visits, institutional collaborations, and agripreneurship programmes, including a dairy entrepreneurship training (50+ farmers) and awareness initiatives with academic institutions and KMF, further promoting innovation, entrepreneurship, and technology adoption in livestock and agriculture.

Union Minister Appreciates NIVEDI's Disease Forecasting System

At the National Horticulture Fair 2025, Bengaluru, Ms. Shobha Karandlaje visited the ICAR–NIVEDI stall and appreciated its livestock disease forecasting system. She encouraged nationwide digital expansion to enhance farmer outreach and reduce economic losses. ICAR–NIVEDI also participated in the VKSA Pre-Kharif 2025 campaign (8 June 2025) at ICAR-IIHR, Bengaluru, showcasing its animal disease forecasting system. The exhibit received appreciation from Union Minister Shri Shivraj Singh Chouhan.

NIVEDI Promotes Livestock Health Awareness during VKSA

During the VKSA Pre-Kharif Campaign (29 May–12 June 2025), ICAR–NIVEDI scientists conducted awareness programmes across 11 districts of Karnataka, addressing region-specific livestock issues such as mastitis, repeat breeding, AMR, and disease surveillance. The initiative identified key field challenges and emphasized location-specific, science-based solutions to strengthen livestock health and farmer livelihoods.

Strengthening Livelihoods of SC & ST Farmers through Livestock Interventions

ICAR–NIVEDI implemented training, input distribution, and awareness programmes under DAPSC and DAPST to support SC and ST farmers in Karnataka. Activities included biosecurity training, distribution of livestock inputs, backyard poultry promotion, and health camps, enhancing livestock productivity, disease prevention, and rural livelihoods.

DAPST Launch Workshop on Advanced Animal Husbandry for Tribal Farmers

ICAR–NIVEDI organized a workshop on 18 July 2025 under the DAPST initiative to promote advanced animal husbandry practices for Scheduled Tribe farmers. The programme focused on capacity building, sustainable livestock practices, and livelihood improvement, along with distribution of essential livestock inputs and expert sessions on pig farming, backyard poultry, and ethnoveterinary medicine.

Empowering SC Women Farmers through Dairy Entrepreneurship

ICAR–NIVEDI, in collaboration with TANUVAS, conducted a one-day capacity-building workshop (27 March 2025) for 40 Scheduled Caste women farmers in Tamil Nadu. The programme focused on sustainable dairy farming, animal nutrition, disease management, and technology-driven livelihoods, along with distribution of essential livestock inputs.

Union Agriculture Minister Visits ICAR–NIVEDI to Strengthen Livestock Health and Farmer Empowerment

Shri Shivraj Singh Chouhan MoA&FW visited ICAR–NIVEDI on 29 August 2025, where he reviewed advanced disease informatics, AI-based forecasting systems, NADRES advisories, and WOAH reference laboratories. He appreciated the institute's farmer-centric innovations, including SMS-based disease alerts, and emphasized expanding digital advisory services and precision livestock management across India. The Minister interacted with scientists, farmers, entrepreneurs, and NaaViC-supported startups, showcasing innovations in diagnostics, disease control, and agri-tech incubation. He also addressed farmers under the DAPSC initiative, promoting integrated farming, self-reliance, and technology adoption, while reaffirming government support for strengthening national livestock health systems and improving farmer livelihoods.

Launch of the 'Swachhata Hi Seva 2025' Campaign

ICAR–NIVEDI launched the Swachhata Hi Seva campaign (17th September to 2nd October 2025) under the theme "Swachhotsav", promoting cleanliness, waste management, and sustainability. The initiative included staff pledges, GIS-based waste mapping, awareness drives, and coordination with local bodies, ensuring community impact and long-term behavioural change.

Live Telecast of the Release of the 21st Instalment of PM-KISAN Samman Nidhi

ICAR–NIVEDI organized a programme under the DAPSC initiative on 19th November 2025 to facilitate farmers' participation in the live telecast of the 21st PM-KISAN installment release. The event was attended by 448 farmers from Yelahanka, along with sessions on livestock health management, disease prevention, and productivity enhancement, strengthening farmer awareness and outreach.

Swachhata Pakhwada 2025: Cleanliness and Awareness Drive

ICAR–NIVEDI conducted a 16-day Swachhata Pakhwada (16–31 December 2025) focusing on cleanliness, sanitation, and sustainable waste management. Activities included pledges, campus and community drives, awareness programmes, and farmer engagement, along with institutional measures like record weeding and digitalization. The initiative reinforced public health, environmental sustainability, and long-term behavioural change.

Kisan Diwas Celebration for SC Livestock Farmers

ICAR–NIVEDI celebrated Kisan Diwas on 23 December 2025 under Swachhata Pakhwada, engaging 103 Scheduled Caste livestock farmers from Tumakuru district. The programme promoted hygiene, biosecurity, and improved animal husbandry practices, along with distribution of Kaveri chicks to support backyard poultry and livelihood enhancement.

Zoonotic Disease Awareness and Health Camp for SC Farmers

ICAR–NIVEDI organized a zoonotic disease awareness programme and health camp on 2 December 2025 at Budughavahalli village, Chikkaballapura, under the SCSP of ICAR–AINP on One Health. The programme educated Scheduled Caste dairy farmers on prevention of diseases such as brucellosis, leptospirosis, rabies, and anthrax, along with hygiene and vaccination practices. A medical health camp and distribution of hygiene materials further promoted One Health awareness among farmers.

World Rabies Day 2025 Awareness Programmes

ICAR–NIVEDI organized rabies awareness programmes on 19 September and 13 November 2025 at Bengaluru North and Chikkaballapura, reaching over 300 students and teachers. The sessions covered rabies transmission, prevention, wound care, vaccination, and One Health approaches, along with leaflet distribution and interactive activities, promoting community awareness and responsible animal handling.

Awareness Programme on Zoonotic Diseases for School Students

On World Zoonoses Day (8 July 2025), ICAR–NIVEDI, in collaboration with the Department of Animal Husbandry and Veterinary Services, Doddaballapura, organized an awareness programme for students of Government schools in Doddaballapura Taluk under the NCDC–NOHPPZ project. The session educated 150 students and teachers on the transmission, prevention, and control of major zoonotic diseases.

Ongoing Research Projects 7

Externally Funded Research Projects

1. ICMR-NOHM project on 'Exploring the Possibility of Utilizing Domestic Poultry as a Sentinel Host for Surveillance of Zoonotic Flaviviruses in India: A Pilot Study'; Investigators: Dr. Chethan Kumar H. B., Dr. S. S. Patil, Dr. J. Hiremath, Dr. M. M. Chanda, Dr. G. B. M. Reddy, Dr. Sathisha S. P.; Duration: February 2025–February 2028.
2. NLM project on 'Comparative Genomics and Epidemiology of Capripox Viruses in India; Investigators: Dr. G. B. M. Reddy, Dr. Shivasharanappa N., Dr. Chethan Kumar H. B.; Duration: April 2023–September 2026.
3. DBT project on 'Development of an Inactivated Homologous Vaccine to Control Lumpy Skin Disease in India'; Investigators: Dr. G. B. M. Reddy, Dr. Shivasharanappa N., Dr. Chethan Kumar H. B.; Duration: September 2023–September 2026.
4. NCBS project on 'Environmental Surveillance and Early Warning System for Animal Pathogen Surveillance'; Investigators: Dr. G. B. M. Reddy, Dr. B. R. Gulati, Dr. M. M. Chanda; Duration: August 2024–August 2026.
5. ICAR project on 'Development of CRISPR-Cas Platform Assays for Rapid Detection and Differentiation of Capripox Viruses'; Investigators: Dr. G. B. M. Reddy, Dr. Shivasharanappa N., Dr. M. Nagalingam; Duration: August 2024–August 2026.
6. ANRF DST project on 'Unraveling the Interactome Leading to Differential Host Response to LSDV'; Investigators: Dr. G. B. M. Reddy, Dr. Ravi Kumar Gandham; Duration: September 2025–September 2028.
7. NLM project on 'Characterization of Bluetongue Virus Strains/Serotypes and Vaccine Suitability'; Investigator: Dr. M. M. Chanda; Duration: March 2022–March 2026.
8. ICAR CRP V&D project on 'Development of NS1–NS3 Based DIVA ELISA Kit for Bluetongue Surveillance'; Investigators: Dr. M. M. Chanda, Dr. Madhusudan Hosamani, Dr. Karam Chand Negi; Duration: December 2022–March 2025.
9. AINP-CEDA project on 'Bluetongue Research Component'; Investigator: Dr. M. M. Chanda, Dr. C. S. Sathish Gowda; Duration: October 2024–March 2026.
10. ICMR-NOHM project on 'Quantifying Risk of Zoonotic Diseases at Wildlife–Livestock–Human Interface'; Investigators: Dr. M. M. Chanda, Dr. B. R. Gulati, Dr. S. B. Shivachandra, Dr. Chethan Kumar H. B.; Duration: February 2025–February 2028.
11. ICMR project on 'Epidemiology of Chandipura Virus Infection, Gujarat, India'; Investigators: Dr. M. M. Chanda, Dr. Chethan Kumar H. B., Dr. Amit Kanani, Dr. Vartika Chandra, Dr. Baldev Raj Gulati; Duration: July 2025–July 2026.
12. ICMR project on 'Identifying the association between Climatic Variables and Risk Mapping of CCHF, KFD Using GIS and Modelling'; Investigators: Dr. M. M. Chanda, Dr. S. B. Shivachandra, Dr. Chethan Kumar H. B.; Duration: January 2024–December 2026.
13. NLM project on 'Epidemiological Surveillance of antimicrobial use (AMU) and Antimicrobial Resistance (AMR) in Sheep, Goats and Poultry with one health approach in Karnataka

and Tamil Nadu'; Investigators: Dr. Shivasharanappa N., Dr. Rajeswari Shome, Dr. S. S. Patil, Dr. P. Krishnamoorthy, Dr. G. Narayanan, Dr. Chethan Kumar H. B.; Duration: April 2023–September 2026.

14. ICAR All India Network Project on AMR in Fisheries & Livestock (AINP-AMR/INFAAR); Investigators: Dr. Shivasharanappa N., Dr. Rajeswari Shome, Dr. P. Krishnamoorthy, Dr. Z. B. Dubal; Duration: November 2018–March 2027.
15. NLM project on 'Development of Recombinant antigen based Novel Epi diagnostics and Subunit Vaccines for Anthrax in Small Ruminants'; Investigators: Dr. S. B. Shivachandra, Dr. M. M. Chanda; Duration: April 2023–September 2025.
16. DBT project on 'Design and evaluation of new generation bivalent recombinant toxoid vaccine and companion immuno-diagnostic for Anthrax and Entertoxaemia in small ruminants'; Investigator: Dr. S. B. Shivachandra, Dr. M. M. Chanda; Duration: September 2023–September 2026.
17. ICMR project on 'Development of recombinant antigens based immuno-diagnostics for sero-surveillance of zoonotic tick-borne diseases (CCHF, GAN, AND KFD) among livestock under one health approach'; Investigator: Dr. S. B. Shivachandra, Dr. M. M. Chanda; Duration: January 2024–January 2027.
18. ICMR-NOHM project on 'Production of recombinant antigens of Nipah Virus (NiV) and evaluation of their utility in immuno-diagnostics for sero-surveillance among livestock under one health approach'; Investigator: Dr. S. B. Shivachandra, Dr. M. M. Chanda; Duration: February 2025–February 2028.
19. NCDC project on 'National One Health Program for Prevention and Control of Zoonotic Diseases (NOHPPCZ)'; Investigators: Dr. V. Balamurugan, Dr. B. R. Gulati, Dr. Chethan Kumar H. B., Dr. M. Nagalingam, Dr. Siju S. Jacob, Dr. K. P. Suresh, Dr. J. Hiremath, Dr. G. B. M. Reddy, Dr. M. M. Chanda, Dr. G. Govindaraj; Duration: February 2025–February 2028.
20. ICMR-NOHM project on 'Advanced diagnostic and omics strategies for surveillance and characterization of Leptospira carriers in livestock and their environments'; Investigators: Dr. V. Balamurugan, Dr. M. Nagalingam, Dr. Chethan Kumar H. B.; Duration: February 2025–February 2028.
21. ICMR-NOHM project on 'Development of Indigenous recombinant adenovirus vector-based oral rabies vaccine intended for free-roaming dogs'; Investigators: Dr. V. Balamurugan, Dr. Nagendra R. Hegde, Dr. S. Isloor; Duration: April 2025–March 2028.
22. DST-ANRF project on 'development and evaluation of a novel polymerized porin platform based nanoscaffold vaccine against Leptospirosis in Golden Syrian Hamster model'; Investigator: Dr. V. Balamurugan, Dr. Sabarinath T; Duration: August 2025–August 2028.
23. LH&DCP Programme Projects (Brucellosis/FMD seromonitoring, sampling plan, PPR surveillance, CSF surveillance); Investigators: Dr. V. Balamurugan, Dr. R. Shome, Dr. K. P. Suresh, Dr. S. S. Patil, Dr. Jagadish Hiremath, Dr. Shivasharanappa N., Dr. R. Sridevi, Dr. G. Narayanan, Dr. Chethan Kumar H. B., Dr. M. Nagalingam; Duration: January 2021–March 2026 & September 2022– September 2026.
24. ICAR project on 'Artificial Intelligence-driven predictive modelling of the effects of climate change on transmission of vector-borne/infectious livestock diseases in india (Phase-III)'; Investigators: Dr. K. P. Suresh, Dr. Siju Susan Jacob, Dr. P. Krishnamoorthy; Duration: February 2015–September 2026.
25. IIT-Bombay project on 'Assessing Japanese encephalitis vaccination impact: a mathematical modeling and risk mapping perspective'; Investigators: Dr. K. P. Suresh, Dr. P. P. Sengupta, Dr. P. Krishnamoorthy; Duration: April 2024–March 2026.

26. ICMR-NOHM project on 'Unified Artificial Intelligence and Machine Learning frameworks for risk prediction, disease modeling, and pathogen detection across human, animal, and environmental health systems'; Investigators: Dr. K. P. Suresh, Dr. B. R. Gulati; Duration: October 2025– October 2028.

27. ICAR All India Network Program on One Health (AINP-OH); Investigators: Dr. R. Shome, Dr. V. Balamurugan, Dr. G. B. M. Reddy, Dr. M. Nagalingam, Dr. Chethan Kumar H. B.; Duration: October 2024–October 2026.

28. ICMR-NOHM project on 'Development of novel Multiplex-Based Point of Care (M-POC) diagnostic for Brucellosis, Leptospirosis, Scrub Typhus and Coxiellosis (Q Fever) and to unravel zoonotic disease dynamics at human and animal interface in Assam, North East India; Investigator: Dr. R. Shome, Dr. V. Balamurugan, Dr. M. Nagalingam; Duration: April 2025–March 2028.

29. ICMR project on 'Building a surveillance model for detecting zoonotic spill over in increased animal-human interaction setting using a one health approach: a study at selected slaughterhouses'; Investigators: Dr. B. R. Gulati, Dr. K. P. Suresh, Dr. Z. B. Dubal, Dr. Rajeswari Shome, Dr. Shivasharanappa N., Dr. Siju Susan Jacob; Duration: August 2024–July 2026.

30. ICMR project on 'Mapping climate sensitive zoonotic diseases and non-zoonotic high threat pathogens in India; Investigator: Dr. B. R. Gulati, Dr. M. M. Chanda; Duration: September 2025–January 2026.

31. ICAR AINP-CEDA Mycoplasma and Theileriosis Research Component; Investigators: Dr. R. Sridevi, Dr. Siju S. Jacob; Duration: October 2024–September 2026.

32. DBT project on 'Development and validation of efficient multiplexed diagnostic platforms for early detection of African Swine Fever Virus'; Investigators: Dr. Jagadish Hiremath, Dr. Sonu Gandhi; Duration: June 2024–June 2027.

33. ICMR-NOHM project on 'Establishment and Characterization of Pig Lymphoid Organoids as Ex Vivo Preclinical Animal Model for Screening of Influenza Vaccines'; Investigators: Dr. Jagadish Hiremath, Dr. Chethan Kumar H. B., Dr. Shivasharanappa N., Dr. S. S. Patil, Dr. G. Halemani, Dr. Yogananda S.M; Duration: February 2025–February 2028.

34. ICMR-NOHM project on 'Surveillance and Genomic Profiling of Potential Zoonotic Pathogens in Indian Pig Population at Human Pig Interface; Investigator: Dr. Siju S. Jacob; Duration: October 2025–October 2028.

Institute Funded Research Projects

35. Host-Parasite dynamics of Theileria orientalis in Bovines: Linking genotype to pathogenicity and drug resistance; Investigators: Dr. Siju S. Jacob, Dr. P. P. Sengupta, Dr. G. B. M. Reddy, Dr. M. Nagalingam; Duration: April 2025–March 2028.

36. Epidemiology of Respiratory infections in small ruminants with reference to Mycoplasmosis; Investigators: Dr. R. Sridevi, Dr. M. Nagalingam, Dr. B. Sumathi; Duration: May 2023–July 2026.

37. Epidemiology of Major Pig Diseases in India; Investigators: Dr. Jagadish Hiremath, Dr. S. S. Patil, Dr. Shivasharanappa N., Dr. Chethan Kumar H. B., Dr. S. S. Gowda. Dr. K. P. Suresh, Dr. Siju S Jacob; Duration: April 2023–March 2027.

38. Development of mRNA Vaccine Against Leptospirosis; Investigators: Dr. V. Balamurugan, Dr. P. Krishnamoorthy, Dr. V. Rajesh Iyer; Duration: April 2024–September 2026.

39. Epidemiology of Infectious Diseases of Small Ruminants; Investigators: Dr. V. Balamurugan, Dr. M. M. Chanda, Dr. G. B. M. Reddy, Dr. S. B. Shivachandra, Dr. Shivasharanappa N., Dr. R. Sridevi, Dr. M. Nagalingam, Dr. Siju S. Jacob; Duration: September 2022–March 2027.

40. Integrating data-driven disease surveillance and predictive analytics for live-stock diseases (NADRES v2); Investigators: Dr. K. P. Suresh, Dr. Rajeswari Shome, Dr. S. S. Patil, Dr. P. Krishnamoorthy, Dr. Siju S. Jacob, Dr. G. Narayanan; Duration: April 2023–March 2027.

41. Socio-Economic Impact of Livestock Diseases in India; Investigators: Dr. G. Govindaraj, Dr. G. Narayanan, Dr. C. S. Sathish Gowda; Duration: April 2023–March 2026.

42. Active Surveillance of the important Haemoprotozoan parasites in large ruminants in Karnataka and Chhattisgarh; Investigators: Dr. P. P. Sengupta, Dr. Siju S. Jacob, Dr. P. Krishnamoorthy; Duration: July 2024–June 2026.

43. Epidemiology of Economically Important Bovine Diseases; Investigators: Dr. Rajeswari Shome, Dr. P. P. Sengupta, Dr. S. B. Shivachandra, Dr. V. Balamurugan, Dr. S. S. Patil, Dr. Shivasharanappa N., Dr. G. B. M. Reddy, Dr. Siju S. Jacob; Duration: April 2023–March 2027.

International Funded Research Projects

44. Bill and Melinda Gates Foundation (BMGF) project on 'National Livestock Disease Epidemiology and Disease Modelling Program': Investigators: Dr. B. R. Gulati, Dr. M. M. Chanda, Dr. Z. B. Dubal, Dr. Jagadish Hiremath, Dr. R. Sridevi, Dr. Shivasharanappa N., Dr. Siju S. Jacob, Dr. Chethan Kumar H. B., Dr. K. P. Suresh; Duration: May 2025–May 2030.

45. DTRA project on 'Risk Estimation, Prediction and Risk Mapping Communication of Anthrax using Artificial Intelligence systems'; Investigators: Dr. K. P. Suresh, Dr. S. S. Patil, Dr. B. R. Gulati; Duration: February 2023–March 2027.

46. Pennsylvania State University project on 'Estimates of risk and assessment of burden of zoonotic TB in India (ERAzTB); Investigators: Dr. B. R. Gulati, Dr. M. Nagalingam, Dr. P. Krishnamoorthy, Dr. Rajeswari Shome, Dr. V. Balamurugan; Duration: May 2024–September 2026.

47. World Bank project on 'System dynamic modelling for African Swine Fever and Lumpy Skin Disease in India'; Investigators: Dr. G. Govindaraj, Dr. G. Narayanan, Dr. C. S. Sathish Gowda; Duration: January 2025–August 2026.

48. DBT-BBSRC project on 'Understanding and controlling Lumpy Skin Disease in Indian cattle'; Investigators: Dr. B. R. Gulati, Dr. G. B. M. Reddy, Dr. M. M. Chanda; Duration: July 2025–July 2028.

Technology Development and Commercialization

8

Patents Filed

1. *Recombinant mutant epsilon (retx) fusion protein and the method of preparation thereof.* Shivachandra S. B., Hemanth R. A., Namrutha M. R., Bindu S., Prajapati A., Chanda M. M. Application No.: 202511062810. Date of Filing: 01.07.2025.
2. *Production of recombinant A27L protein and its utilities in immuno-diagnostics for lumpy skin disease in animals.* Reddy G. B. M., Yogisharadhya R., Shivachandra S. B., Chethan Kumar H. B., Gulati B. R. Application No.: 202511063083. Date of Filing: 02.07.2025.
3. *Polyclonal antibody-based Sandwich ELISA for detection of Capripoxvirus.* Reddy G. B. M., Chethan Kumar H. B., Shivachandra S. B., Gulati B. R. Application No.: 202511125506. Date of Filing: 11.12.2025.

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1. *NEST Logo.* Shivachandra S. B., Chanda M. M., Reddy G. B. M., Yogisharadhya R., Prajapathi A. Application No.: 7777/2024-CO/A Date of Filing: 12.03.2024 Registration No.: A-157835/2025 Date of Registration: 03.02.2025.
2. *NEO Logo* Shivachandra S. B., Chanda M. M., Reddy G. B. M., Yogisharadhya R., Prajapathi A. Application No.: 5786/2025-CO/A. Date of Filing: 13.12.2024 Registration No.: AT-20250160244 Date of Registration: 05.08.2025.

Technology Validation

1. Capripox-Detect sELISA (*A polyclonal sandwich ELISA for detection of Capripoxviruses: GPV/LSDV/SPV).*

Technology Released

The CYSTISURE Kit (a recombinant GP50 antigen-based indirect ELISA for the detection of antibodies against porcine cysticercosis) and the Flukevey Kit (a recombinant Cathepsin B-based indirect ELISA for the serodiagnosis of bovine tropical fasciolosis) were developed by ICAR-NIVEDI and officially released by the Hon'ble Deputy Director General (Animal Sciences), ICAR, New Delhi, on 21st July 2025 at ICAR-NIVEDI, Bengaluru. The CYSTISURE Kit was developed by Siju S. J., Sengupta P. P., and Patil S. S., while the Flukevey Kit was developed by Sengupta P. P. and Siju S. J.

Publications 9

ICAR-NIVEDI Publications

1. Amitkumar M, Prajapati A, Bindu S, Sairam S, Shirisha A, Namrutha MR, Hemanth RA, Yogisharadhya R, Chanda MM, Shivachandra SB. Comparative evaluation of indirect ELISAs based on native antigens of *Clostridium chauvoei* for detection of blackleg-specific antibodies in cattle. *Anaerobe*. 2025;94:102975. doi:10.1016/j.anaerobe.2025.102975.

2. Anand A, Mahadevappa S, Ojha R, Pal A, Priya S, D'Souza AH, Bokade PP, Vinod Kumar K, Hemadri D, Gulati BR, Balamurugan V. Molecular insights from 2023 and 2024 outbreaks reveal exclusive circulation of peste des petits ruminants virus lineage IV in India. *Arch Virol*. 2025;170:73.

3. Burthe SJ, Kumbar B, Schäfer SM, Purse BV, Vanak AT, Balakrishnan N, Hassall R, Hoti SL, Narayanaswamy D, Potadar S, Rahman M, Chanda MM. First evidence of transovarial transmission of Kyasanur Forest disease virus in *Haemaphysalis* and *Rhipicephalus* ticks in the wild. *Parasites Vectors*. 2025;18(1):14.

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Collaborative Publications

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ICAR-NIVEDI's Livestock Disease Diagnosis Laboratory Received NABL ISO/IEC 17025:2017 Accreditation

National Accreditation Board for Testing and Calibration Laboratories

NABL

CERTIFICATE OF ACCREDITATION

LIVESTOCK DISEASE DIAGNOSIS LABORATORY

has been assessed and accredited in accordance with the standard

ISO/IEC 17025:2017

"General Requirements for the Competence of Testing & Calibration Laboratories"

for its facilities at

ICAR-NIVEDI, YELAHANKA, RAMAGONDANAHALLI, BENGALURU, BENGALURU URBAN, KARNATAKA, INDIA

in the field of

TESTING

Certificate Number: TC-12705

Issue Date: 05/12/2025 Valid Until: 04/12/2029

This certificate remains valid for the Scope of Accreditation as specified in the annexure subject to continued satisfactory compliance to the above standard & the relevant requirements of NABL.
(To see the scope of accreditation of thislaboratory, you may also visit NABL website www.nabl-india.org)

Name of Legal Entity: ICAR-NATIONAL INSTITUTE OF VETERINARY EPIDEMIOLOGY AND DISEASEINFORMATICS

Signed for and on behalf of NABL

Srikanth R
Director

Chakravarthy T. Kannan
Chief Executive Officer

ICAR-NIVEDI Received STQC Certification for the Website (GIGW 3.0)

सत्यमेव जयते

STQC
गुणोत्कर्ष समृद्धि

WEBSITE QUALITY CERTIFICATION SCHEME

STQC Directorate
Ministry of Electronics and Information Technology
Electronics Niketan, 6, CGO Complex, Lodi Road, New Delhi – 110003

CERTIFICATE OF APPROVAL

Approval Number: **STQC/CQW/2025/37**

It is hereby certified that the website of
ICAR- National Institute of Veterinary Epidemiology and Disease Informatics
Ramagondanahalli, Yelahanka,
Post Box No. 6450, Bengaluru - 560119
URL of Website: https://nivedi.res.in/

Fulfills the requirements of the
Website Quality Certification Scheme

It is verified that the website meets the requirements of the
Guidelines for Indian Government Websites, Ver 3.0

This Certificate is valid upto: 15/02/2029 Date of Issue: 16/02/2026

Note 1:With 05 exemptions as per Annexure – I attached.
Note 2: Subject to compliance during the surveillance audit.
Note 3: Visit https://stqc.gov.in/website-quality-certification-0 for details of the scheme.

CQW

(A. K. Upadhyaya)
HEAD – WQCS &
SCIENTIST 'G'

Awards, Recognitions and Personal Milestones

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ICAR–NIVEDI Wins National e-Governance Award Gold for NADRES-v2.0

ICAR–NIVEDI received the National e-Governance Award 2025 (Gold) from DARPG, Government of India, presented by Dr. Jitendra Singh at the 28th National Conference on e-Governance, Visakhapatnam (22 September 2025). NADRES-v2.0, using GIS, AI, and ML to forecast 15 livestock diseases and issue district-level alerts, was recognized under "Innovation using AI and New-Age Technologies." Selected among 589 entries, the award included a trophy, certificate, and ₹10 lakh, received by the NADRES team led by Dr. B.R. Gulati.

ICAR–NIVEDI Scientists Conferred NABS Fellows

Dr. P.P. Sengupta and Dr. S.S. Patil of ICAR–NIVEDI were conferred the Fellowship of the National Academy of Biological Sciences (NABS) during the 14th NABS National Conference & AGM held at Agricultural College & Research Institute (TNAU), Kudumiyanmalai, Pudukottai, Tamil Nadu, on 29 January 2025.

NIVEDI Scientists Contribute to Global Dialogues on PPR and TADs

During 2025, ICAR–NIVEDI scientists actively participated in international forums across UAE, Kenya, Austria, and Ivory Coast, sharing India's expertise on PPR and transboundary animal diseases. Their contributions focused on disease control strategies, socio-economic impacts, surveillance, and global collaboration, strengthening India's leadership in international animal health initiatives.

ICAR–NIVEDI scientists Dr. V. Balamurugan and Dr. G. Govindaraj participated in the 8th PPR GREN Meeting (25–27 November 2025, Qingdao, China) organized by FAO/WOAH.

Dr. P. Krishnamoorthy, attended the FAO "Cross-border Harmonization and Mano River Episystem for PPR Eradication" workshop held at Abidjan, Ivory Coast, during 23–25 June 2025

NIVEDI Scientist Honoured at NAVS Convention 2025

At the NAVS Convention (22–23 December 2025, Patna), Dr. V. Balamurugan received the NAVS Fellowship and the Dr. K.K. Baxi Outstanding Scientist Award (2024) for his contributions to veterinary science.

NIVEDI Scientist Receives Kameshwar Sahai Bhargava Oration Award

At VIROCON-2025 (8–10 December 2025, Pune), Dr. V. Balamurugan was conferred the Kameshwar Sahai Bhargava Oration Award for his outstanding contributions to veterinary virology and infectious disease research.

NIVEDI Scientist Conferred IAVPHS Fellowship

At the IAVPHS Conference 2025 (11–12 December 2025, Ludhiana), Dr. Z.B. Dubal was awarded the Fellowship of the Indian Association of Veterinary Public Health Specialists in recognition of his contributions to veterinary public health.

ICAR–NIVEDI Scientists Win Multiple Awards at National and International Conferences

ICAR–NIVEDI scientists achieved multiple accolades across major scientific forums, with Dr. P.P. Sengupta and Dr. Siju Susan Jacob winning Best Oral Presentation Awards at CLIMATECON 2025 (Bengaluru), and Dr. Narayanan G. received Best Oral Presentation and Best Scientist (Extension Education) award at EIAFTBASGD-2025 held at Udaipur.

At VIROCON-2025, teams secured Best Oral and Poster Presentation awards across virology, One Health, tuberculosis, and leptospirosis research, including recognition to Dr. M. Nagalingam. At NCVP-2025 (17–19 December 2025, Udgir), the Parasitology team earned multiple Best Oral Presentation awards, further highlighting excellence in parasitology and epidemiological research.

ICAR–NIVEDI Excels at ICAR South Zone Sports Tournament

ICAR–NIVEDI delivered an outstanding performance at the ICAR South Zone Sports Tournament (8–11 April 2025, Coimbatore), winning 2 gold and 2 silver medals. Ms. Aachal Palewar was crowned Overall Athletic Champion (Women), highlighting the team's excellence among participants from 28 ICAR institutes.

WOAH Leptospirosis Reference Laboratory Inaugurated at ICAR–NIVEDI

The WOAH Reference Laboratory for Leptospirosis at ICAR–NIVEDI, Bengaluru was officially inaugurated by Dr. Himanshu Pathak, Secretary (DARE) & Director General (ICAR) on 2 January 2025.

ICAR–NIVEDI Excels at Inter-Zonal Sports Meet

ICAR–NIVEDI delivered a strong performance at the ICAR Inter-Zonal Sports Tournament (4–7 November 2025, Lucknow), with Ms. Aachal Palewar winning multiple medals and the Best Athlete (Women) title, and Mr. Abhishek Tomar securing gold in shot put. The institute achieved an impressive 6th position overall, reflecting excellence in sports and holistic development.

Participation in Global Livestock & Aquaculture Conclave

Dr. B.R. Gulati participated in the Livestock & Aquaculture Convening (2–4 December 2025, Cape Town) organized by the Gates Foundation, presenting on livestock disease status and modelling in India under INLEAD. He contributed to discussions on disease surveillance, risk assessment, and biosecurity, and engaged with global partners including FAO and WOAH to strengthen collaboration in transboundary disease preparedness and One Health research.

Staff of ICAR NIVEDI

Dr. Baldev Raj Gulati
Director

Scientific Staff

Dr. Rajeswari Shome
Principal Scientist

Dr. P. P. Sengupta
Principal Scientist

Dr. K.P. Suresh
Principal Scientist

Dr. V. Balamurugan
Principal Scientist

Dr. S.S.Patil
Principal Scientist

Dr. Sathish B Shivachandra
Principal Scientist

Dr. Z. B. Dubal
Principal Scientist

Dr. G.Govindaraj
Principal Scientist

Dr. Jagadish Hiremath
Principal Scientist

Dr. P. Krishnamoorthy
Principal Scientist

Dr. Sridevi R
Principal Scientist

Dr. Shivasharanappa N
Senior Scientist

Dr. Mohd Mudassar Chanda
Senior Scientist

Dr. Manjunatha Reddy G. B.
Senior Scientist

Dr. M. Nagalingam
Senior Scientist

Dr. G. Narayanan
Senior Scientist

Dr. Siju Susan Jacob
Senior Scientist

Dr. Chethan Kumar H. B.
Senior Scientist

Dr. Sathish Gowda C. S.
Scientist

Administrative Staff

Mr. Sadik Ali
F&AO

Mr. Navneet Agarwal
AO

Mrs. Aachal Palewar
AAO

Mrs. A. Saranya
PA

Ms. Aparna Kaushik
Assistant

Mr. Vivek Kumar
Assistant

Mr. Abhishek Tomar
Assistant

Mr.Pradeep Biradar
Assistant

Mrs. Sridevi G. C.
UDC

Mr. Umesh H. S.
LDC

Mr. B. Hanumantharaju
LDC

Technical Staff

Mr. Praveen
Technician (T-1)

Mr. Md Razi Ahmad
Technician (T-1)

Multitasking Staff

Mr. M. K. Ramu
MTS

Personnel Joined/Transferred/Promoted:

- Shri. K. Vijayaraj, Stenographer Grade 'D', was relieved from ICAR-NIVEDI on 1st January 2025 (A/N)
- Mr. Purushotam Yadav, Technician (T-1), was relieved from ICAR-NIVEDI on 17th January 2025 (A/N).
- Shri. Navneet Agarwal, Administrative Officer, Joined ICAR-NIVEDI on 17th April 2025 (F/N)
- Shri. Pradeep Biradar, Assistant, joined ICAR-NIVEDI on 8th August 2025 (F/N)
- Dr. P. Krishnamoorthy, Senior Scientist has been promoted as Principal Scientist under Career Advancement Scheme (CAS) with effect from 7th January 2024.
- Dr. R. Sridevi, Senior Scientist has been promoted as Principal Scientist under Career Advancement Scheme (CAS) with effect from 10th February 2024.

IRC, RAC and other Review Meetings

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17th RAC meeting provides road map for future research

The 17th RAC meeting of ICAR-NIVEDI, held on 13 May 2025, was attended by the Chairman, RAC members, Director, and Member Secretary, where the Director highlighted significant progress including 18 new projects worth ₹14.36 crore, international collaborations, ICAR-certified technologies, FAO recognition, and efforts toward ISO 17025 accreditation and FAO reference laboratory status. The RAC appreciated advancements in epidemiology, surveillance, modelling, and research, and approved the Action Taken Report of the 16th RAC. Presentations from various divisions were reviewed, and key recommendations included strengthening stakeholder outreach, enhancing zoonotic surveillance through medical collaborations, revising the epidemiology curriculum, expanding NADRES outreach, developing risk-based documents and mobile tools for farmers, intensifying national disease surveillance, preparing prevalence maps, improving institute visibility, and formulating strategic livestock disease control and eradication plans.

IRC Reviews Research Progress and Future Plans

ICAR–NIVEDI held the 19th IRC meeting (21–22 May 2025) and the Mid-Term IRC meeting (6 October 2025), chaired by Dr. B.R. Gulati, with Dr. S.C. Yadav as external expert. Scientists presented over 50 research projects (institute- and externally funded), which were reviewed for scientific merit, progress, and alignment with national priorities. The committee emphasized timeline-driven, target-oriented research, provided recommendations to improve impact, completed six projects, approved two new proposals, and reviewed progress of ongoing studies for 2025–26.

IBSC Reviews GMO Research and Strengthens Biosafety Compliance

The 12th IBSC meeting, held on 4 July 2025, at ICAR–NIVEDI reviewed nine proposals on GMOs, HMOs, and MTAs, including work on recombinant vaccines, zoonotic disease surveillance, and One Health risk assessment. Proposals were approved after evaluation of scientific merit, biosafety, and regulatory compliance, with emphasis on strict adherence to DBT guidelines and institutional biosafety protocols.

ITMC Reviews IP Proposals and Approves Technologies for Certification

Two Institute Technology Management Committee (ITMC) meetings were held to evaluate IP and technology certification proposals. The meeting on 26 March 2025 reviewed three patent and two copyright proposals, recommending revision and resubmission to the ITMU. The subsequent meeting on 26 May 2025 evaluated six diagnostic methodology proposals, approving five for submission to ICAR's Animal Science Division for certification. These reviews highlight the institute's focus on innovation, IP protection, and technology transfer.

IAEC Reviews Research Proposals

The 27th and 28th IAEC meetings were held on 22 January and 28 July 2025, chaired by Dr. B.R. Gulati, with CPCSEA nominees participating. The committee reviewed research proposals involving vaccines, point-of-care diagnostics (brucellosis, scrub typhus, coxiellosis), anthrax epidemiology, multiplex diagnostics for African swine fever, and studies using laboratory animals and livestock samples. All proposals were cleared after ensuring scientific merit and strict compliance with CPCSEA ethical guidelines for animal welfare.

NADEN Review Meeting Strengthens Livestock Disease Surveillance

The 3rd NADEN Annual Review Meeting (21–22 July 2025) at ICAR–NIVEDI, Bengaluru reviewed surveillance progress, outbreak trends, and future strategies. A new AICRP on Animal Disease Surveillance, strengthened data validation for elimination of FMD, PPR, Brucellosis, and Rabies by 2030, and the release of three diagnostic kits and key NADEN reports were highlighted.

Annual Review Meeting on Emerging Diseases and One Health

ICAR–NIVEDI organized the Annual Review Meeting (25–26 August 2025) of AINP-CEDA and AINP-OH, bringing together investigators nationwide. The meeting reviewed project progress, disease priorities, and One Health research strategies, emphasizing standardized diagnostics, systematic sampling, inter-sectoral collaboration, and efficient fund utilization to strengthen control of emerging and zoonotic diseases.

IMC Reviews Infrastructure Expansion and Human Resource Strengthening

The 23rd IMC meeting of ICAR–NIVEDI was held on 19 September 2025, chaired by Dr. B.R. Gulati, with participation of eminent members and experts. The committee reviewed proposals to strengthen infrastructure and human resources, recommending disposal of obsolete items, new laboratory construction, administrative block expansion, a walk-in cold room, initiation of AICRP-LEAD, and filling vacant posts to enhance research capacity and disease forecasting.

Distinguished Visitors

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Name & Designation	Date of visit
Dr. Himanshu Pathak, Secretary (DARE) & Director General (ICAR) accompanied with Dr. Pallab Chaudhuri, Joint Director, ICAR-IVRI, Bengaluru Campus, Bengaluru Dr. V. Venkatasubramanian, Director, ICAR-ATARI, Bengaluru Dr. S. N. Sushil, Director, ICAR- NBAIR, Bengaluru Dr. Tusar Kanti Behera, Director, ICAR-Indian Institute of Horticultural Research, Bengaluru Dr. Arindam Dhali, Head, SRS, ICAR-NDRI, Bengaluru Dr. Artabandhu Sahoo, Director, ICAR-NIANP, Hosur Main Road, Bengaluru	1-2nd January 2025
Shri Prashant Kumar Mittal, DDG, NIC	16th January 2025
Dr. Henry M. Wamwayi, WOAH expert accompanied with Dr. Michael D. Baron, WOAH expert Dr. Camilla Benfield, WOAH expert Dr. Sara Lysholm, PPR Status Officer	18th February 2025
Prof. AC Varshney, Former Vice-Chancellor, DUVASU accompanied with Dr. Inderjeet Singh, Vice Chancellor, Bihar Animal Sciences University, Patna Dr. Azad Kumar Kashik DSc (Paris)	10th March 2025
Mrs. Savithri S Mani (Retd. Director, Administrative Training Institute, Department of Atomic Energy, Government of India) accompanied with Mrs. Rampriya Manikandan, Director operations at Gremach Aerospace and Rotary Club, President, Rotary Bangalore Skyway Dr. R. Jayashree, Professor, Dept. of Animal Genetics and Breeding, Veterinary College, Hebbal, Bangalore	20th March 2025
Dr. Mandeep Sharma, Hon'ble Vice Chanceller, Nanaji Deshmukh Veterinary Science University (NDVSU), Jabalpur, M.P accompanied with Dr. Divakar Hemadri, Assistant Director General (AH), ICAR, Krishi Bhavan, New Delhi Dr. S. C. Dubey, Former Director, ICAR-NIHSAD, Bhopal Dr. Rajendra Singh, Former Head, Division of Pathology, ICAR-IVRI, Izatnagar Dr C. Madan Mohan, Head, Division of Veterinary Biotechnology, ICAR-IVRI, Izatnagar	13th May 2025
Dr. Eaknath B Chakurkar, Director, ICAR-CIARI, Sri Vijaya Puram	4th June 2025
Dr. J.P.S. Gill, Vice-Chancellor, GADVASU accompanied with Dr. Vivek Kapur, Penn State University Dr. Mahesh P.S, Joint Commissioner GoI & Director, Central Poultry Development Organisation & Training Institute, Bengaluru Dr. Nicholas Juleff from the Gates Foundation Dr. Alkesh Wadhwani from the Gates Foundation Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	24-25th June 2025

Dr. Sindura Ganapati, Visiting PSA Fellow, Office of the Principal Scientific Adviser (PSA), Government of India accompanied with Prof (Dr) Prabhdeep Kaur, Isaac Centre for Public Health, IISc, Bengaluru	24-25th June 2025 & 11th July 2025
Dr. Kamal Malla Bujarbaruah, Former Deputy Director General (Animal Science) and Former Vice-Chancellor of Assam Agricultural University accompanied with Dr. D.V.R Prakash Rao, President, National Academy of Veterinary Sciences (India) Dr. Triveni Dutt, Director, ICAR-Indian Veterinary Research Institute (IVRI)	6th July 2025
Mr. Suresh Chitturi, Chairman of the CII Animal Agriculture Committee and Managing Director of Srinivasa Farms accompanied with accompanied with Dr. Shirish Nigam, President of INFAH and Managing Director of EW Nutrition India Prof. (Dr.) P. K. Shukla, President of the Indian Poultry Science Association and Head of the Department of Poultry Science at DUVASU, Mathura	11th July 2025
Dr. Suresh Honnappagol, Former Animal Husbandry Commissioner, Government of India and Former Vice Chancellor, KVAFSU, Bidar	18th July 2025 & 24th November 2025
Dr. P. Srinivasu, Director, Department of Animal Husbandry and Veterinary Services, Karnataka accompanied with Dr. Raghavendra Bhatta, Deputy Director General (Animal Science)	21st July 2025
Shri Shivraj Singh Chouhan, Union Minister for Agriculture & Farmers' Welfare and Rural Development, Government of India accompanied with Shri V. Somanna, Union Minister of State (MoS) in Ministry of Railways and Ministry of Jal Shakti, Government of India Shri S. R. Vishwanath, Member of Legislative Assembly (MLA), Yelahanka Assembly constituency, Karnataka	29th August 2025
Dr. K.C. Veeranna, Vice Chancellor, KVAFSU, Bidar accompanied with Dr. Nitin Virmani, HoD, ICAR-NRC Equine, Hisar	19th September 2025
Brazilian delegates: Dr. Carlos Nabil Ghobril, Dr. Hamilton Humberto Ramos, Dr. Ana Eugenia, Dr. Priscilla Rocha Silva Fagundes, Mr. Sergio Tutui and Mr. Angelo Mauricio	29th September 2025
Prof. M.C. Sharma, Former Director cum Vice-Chancellor, Indian Veterinary Research Institute (IVRI), Izatnagar, India	15th October 2025
Shri S. K. Pathak, Joint Secretary (Finance), ICAR, New Delhi	3rd November 2025
Shri Naresh Pal Gangwar, Secretary, Department of Animal Husbandry and Dairying (DAHD), Government of India	6th & 8th November 2025
Ms. Varsha Joshi, Additional Secretary (CDD/Trade/CE&P), Department of Animal Husbandry and Dairying (DAHD), Government of India	8th November 2025
Dr. Sujit K. Dutta, Joint Commissioner (NLM), Department of Animal Husbandry and Dairying (DAHD), Government of India	8th November 2025
Dr. Taslimarif Saiyed, CEO of C-CAMP	24th November 2025

ICAR-NIVEDI in Media...

ಕನ್ನಡಪ್ರಭ

ಸ್ವಚ್ಛತೆ ಆರೋಗ್ಯಕ್ಕೆ ಮೂಲ: ಡಾ| ಬಲದೇವ್

ಸ್ವಚ್ಛತೆ ಕಾಪಾಡಿಕೊಳ್ಳುವುದು ಮುಖ್ಯ | ಪಖ್ವಾಡಾ ಅಭಿಯಾನ ಸಮಾರೋಪ ಸಮಾರಂಭದಲ್ಲಿ ಸಲಹೆ

• **ಕನ್ನಡಪ್ರಭ ವಾರ್ತೆ** ಯಲಹಂಕ

ವೈಯಕ್ತಿಕ ಮತ್ತು ಪರಿಸರ ಸ್ವಚ್ಛತೆ ಮನುಷ್ಯನ ಆರೋಗ್ಯದ ಮೂಲ ಸಾಧನವಾಗಿದ್ದು, ಕಾಪಾಡಿಕೊಳ್ಳುವುದು ಅತ್ಯವಶ್ಯಕ ಎಂದು ಐಸಿಎಆರ್-ನಿವೇದಿ ಸಂಸ್ಥೆಯ ನಿರ್ದೇಶಕ ಡಾ.ಬಲದೇವ್ ರಾಜ್ ಗುಲಾಟಿ ತಿಳಿಸಿದರು.

ರಾಮಗೊಂಡನಹಳ್ಳಿಯಲ್ಲಿರುವ ಐಸಿಎಆರ್-ನಿವೇದಿ ಸಂಸ್ಥೆಯ ವತಿಯಿಂದ ಡಿ.16 ರಿಂದ 31ರವರೆಗೆ ಆಯೋಜಿಸಿದ್ದ ಸ್ವಚ್ಛತಾ ಪಖ್ವಾಡಾ (ಸ್ವಚ್ಛತೆಯ 15 ದಿನಗಳು) ಅಭಿಯಾನದ ಸಮಾರೋಪ ಸಮಾರಂಭದಲ್ಲಿ ಮಾತನಾಡಿ, ಅಭಿಯಾನದ ಅಂಗವಾಗಿ ನಿವೇದಿ ಸಂಸ್ಥೆಯ ವಿಜ್ಞಾನಿಗಳು ಮತ್ತು ಸಂಶೋಧನಾ ವಿದ್ಯಾರ್ಥಿಗಳು ಸ್ವಚ್ಛತೆಯನ್ನೇ ಪ್ರಮುಖ ಧ್ಯೇಯವಾಗಿಸಿಕೊಂಡು ಕಳೆದ 15 ದಿನಗಳಲ್ಲಿ ಹಲವು ಕಾರ್ಯಕ್ರಮಗಳನ್ನು ಶ್ರದ್ಧೆಯಿಂದ ಕೈಗೊಂಡು ಸ್ವಚ್ಛತಾ ಪಖ್ವಾಡನ್ನು ಅರ್ಥಪೂರ್ಣವಾಗಿಯಶಸ್ವಿಗೊಳಿಸಿದ್ದಾರೆ ಎಂದರು.

ಸ್ವಚ್ಛತೆಯ ಬಗ್ಗೆ ಅರಿವು ಮೂಡಿಸಲು ಏರ್ಪಡಿಸಿದ್ದ

ರಾಮಗೊಂಡನಹಳ್ಳಿಯಲ್ಲಿರುವ ಐಸಿಎಆರ್ - ನಿವೇದಿ ಸಂಸ್ಥೆಯಿಂದ ಆಯೋಜಿಸಿದ್ದ ಸ್ವಚ್ಛತಾ ಪಖ್ವಾಡಾದ ಸಮಾರೋಪ ಸಮಾರಂಭ ಬುಧವಾರ ನಡೆಯಿತು. ಸಂಸ್ಥೆಯ ನಿರ್ದೇಶಕ ಡಾ.ಬಲದೇವ್ ರಾಜ್ ಗುಲಾಟಿ ಇದ್ದರು.

ಸ್ಪರ್ಧಾ ಚಟುವಟಿಕೆಗಳಲ್ಲಿ ಅತ್ಯುತ್ತಮ ಸಾಧನೆಗೈದ ಸಂಶೋಧನಾ ವಿದ್ಯಾರ್ಥಿಗಳಿಗೆ ಬಹುಮಾನ ವಿತರಿಸಲಾಯಿತು. ಈ ವೇಳೆ ನಿವೇದಿ ಸಂಸ್ಥೆಯ ವಿಜ್ಞಾನಿಗಳಾದ ಡಾ.ನಾರಾಯಣನ್, ಡಾ.ಚೇತನ್ ಕುಮಾರ್, ಡಾ.ಸತೀಶ್ ಗೌಡ, ಡಾ.ಪುನೀತ್ ರಾಜ್, ಡಾ.ಪ್ರೇಮ್ ಕಿಶೋರ್, ಸಂಶೋಧನಾ ವಿದ್ಯಾರ್ಥಿಗಳಾದ ಪವನ್ ಕಲ್ಯಾಣ್, ಮಹೇಶ್ ಕುಮಾರ್, ವರ್ಷಿತಾ, ಐಶ್ವರ್ಯ ಇದ್ದರು.

THE NEW INDIAN EXPRESS | KARNATAKA
06 BENGALURU TUESDAY 18.11.2025

BLACKBUCK DEATH TOLL IN BELAGAVI ZOO TOUCHES 31

Officials' laxity suspected, as infection appears to have spread unchecked for days

NAUSHAD BIJAPUR & SUNIL PATIL @ Belagavi

IN what experts describe as India's largest blackbucks mass death, the toll of the protected antelope species at Belagavi's Rani Channamma Mini Zoo has shot up from 8 to 31 in a span of only three days. With the seven remaining blackbucks battling for life, veterinarians fear the toll may climb further.

The suspected outbreak of haemorrhagic septicaemia (HS) – a fast-spreading bacterial infection – has raised concerns about zoo officials' negligence. Sources said the infection appears to have spread unchecked for days before containment began – a lapse now under scrutiny.

Virologist Dr Chandrashekhar said "There were extensive haemorrhagic lesions, suggesting a bacterial infection. Blackbucks are extremely sensitive, and even a sudden temperature drop or stress can speed up mortality," he said.

Karnataka Zoo Authority Chairman K Rangaswamy, who visited the enclosure on Monday, said, "There seems to be negligence at multiple levels. The veterinary and forest staff failed to respond when the first deaths occurred."

Rangaswamy said action will be taken once the final laboratory results confirm the cause of death. He also briefed District In-charge Minister Satish Jarkiholi and said further review meetings will be held with senior forest officials.

With a total of 226 animals housed inside the facility, including tigers, lions, leopards, hyenas, bears, crocodiles and deer species, experts have warned the infection could spread unless strict emergency protocols are enforced immediately.

Inside the infected enclosure, blackbucks were being fed a diet consisting of groundnut meal, lentils like soaked green gram and horse gram, carrots and napier grass. Whether the feed, water source, vector contamination, enclosure hygiene or staff handling contributed to the outbreak remains under investigation. "This scale of mortality is unprecedented. It should serve as a wake-up call. These animals can die within days unless immediate containment measures are taken," an expert said.

INMATES HEADCOUNT

TOTAL ANIMALS	226
BLACKBUCKS	38
DEATH TOLL	31
CRITICALLY ILL	07

Suspected cause: Haemorrhagic septicaemia

'Climate change, lack of hygiene behind infection'

CONTINUED FROM PAGE 1

"THE reasons for the spread of HS, which is a bacterial infection, include stress due to climate change (weather fluctuations, sudden dip in temperature), lack of good, clean shelters, hygiene etc. Animals develop respiratory distress due to weather fluctuations leading to HS. There are vaccines for the bacterial infection. An animal with HS should be isolated from the rest to prevent its spread," said sources. HS, however, is not a zoonotic disease.

The NADRES advisory included several preventive measures, including "disease surveillance, enforcing strict biosecurity protocols, controlled access, equipment disinfection and quarantine for newly introduced animals, vaccinating animals in endemic zones to prevent outbreaks, ensuring age-appropriate and serotype-specific vaccinations; conducting ring vaccination campaigns within a 5km radius in affected areas using suitable vaccines for specific diseases; administering primary vaccinations at the recommended age, followed by booster doses annually or as advised."

NADRES-NIVEDI was developed in 2015 to forecast potential threats (to livestock and wildlife) from pathogens two months in advance to provide the stakeholders a sufficient time line for awareness and preparedness to act.

"Disease surveillance has a significant contribution towards animal health and helps in taking precautionary measures during disease epidemics. NADRES is a weather-based forewarning system enabled with artificial intelligence (AIML) system developed by ICAR-NIVEDI that forecasts potential threats from pathogens two months in advance with 95 percent accuracy to provide the stakeholders sufficient time line for awareness and preparedness to act," said sources.

...ഷനി തടയാനുള്ള ശില്പശാല

..., കോഴിക്കോട്, കണ്ണൂർ, കാസർകോട് ജില്ലകളിലെ പന്നിവളർ...ഷകർക്കായി കണ്ണൂർ മൃഗസംരക്ഷണ പരിശീലനകേന്ദ്രത്തിൽ ... ശില്പശാലയിൽ നിന്ന്

...നാഷണൽ ഇൻസ്റ്റിറ്റ്യൂട്ട് ഓഫ് വെറ്ററിനറി എപ്പിഡമോ...

ಸಮಯ ಮಿತ್ರ

Samaya Mithra Kannada Daily

ಐಸಿಎಆರ್-ನಿವೇದಿ ಸಂಸ್ಥೆಗೆ ಕೇಂದ್ರ ಕೃಷಿ ಸಚಿವ ಶಿವರಾಜ್ ಸಿಂಗ್ ಚೌಹಾನ್ ಭೇಟಿ

NIVEDI gets leptospirosis lab

EXPRESS NEWS SERVICE @Bengaluru

A World Organisation for Animal Health (WOAH) reference laboratory for leptospirosis was opened at the ICAR-NIVEDI (National Institute of Veterinary Epidemiology and Disease Informatics) in the city on Thursday. Dr Himanshu Pathak, Secretary, Department of Agricultural Research & Education (DARE) and Director General (DG) of Indian Council of Agricultural Research (ICAR), inaugurated the lab.

Director, ICAR-NIVEDI, Baldev R Gulati and Dr Pallab Chaudhury, Joint Director, ICAR-IVRI (Indian Veterinary Research Institute), regional campus, Bengaluru, and other scientists and staff of both institutes were present on the occasion. "The laboratory is located within NIVEDI's state-of-the-art Biosafety Laboratory. It is equipped with advanced di-

Leptospirosis is a global zoonotic disease caused by bacteria called leptospira, affecting both humans and animals. "Each year, an estimated 1.03 million people are infected, leading to about 58,900 deaths worldwide. Adult males aged 20-49 are most commonly affected. In India, leptospirosis is a major concern with an annual rate of 19.7 cases per 100,000 people," said Dr V Balamurugan, in-charge, WoAH referral laboratory on Leptospirosis.

He added, "Between 2021 and 2024, 11,205 samples were screened across India, reflecting extensive surveillance for zoonotic diseases in livestock, domestic animals and humans. Karnataka contributed 3,267 samples, accounting for 29% of national screenings in 2024, demonstrating a proactive role in disease monitoring. Human samples dominated testing in Karnataka, with 2,790 analysed (85% of the state's total), emphasising the focus on zoonotic

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கறவைமாடு வளர்க்கும் பட்டியலின

விவசாயிகளுக்கு திறன் மேம்பாட்டு பயிற்சி

தர்மபுரி, மார்ச் 29: தர்மபுரி கால்நடை மருத்துவ பல்கலைக்கழக பயிற்சி மற்றும் ஆராய்ச்சி மையத்தில், கறவைமாடு வளர்க்கும் பட்டியலின விவசாயிகளுக்கு திறன் மேம்பாட்டு பயிற்சி முகாம் நடைபெற்றது.

தமிழ்நாடு கால்நடை மருத்துவ அறிவியல் பல்கலைக்கழகமும், இந்திய தேசிய வேளாண் ஆராய்ச்சி நிலையத்தின் தேசிய கால்நடை தொற்றுநோயியல் மற்றும் நோய் தகவல் நிறுவனமும் இணைந்து !"நிலைத்த ஆதாயம் தரும் கறவை மாட்டுப் பண்ணையத்திற்கான அறிவியல்பூர்வ கறவை மாடு வளர்ப்பு முறைகள் மற்றும் தானுவாசு தொழில்நுட்பங்களை பரவலாக்குதல் வழி பட்டியலின விவசாயிகளை மேம்படுத்துதல்!" என்ற தலைப்பில் மாவட்ட அளவிலான ஆராய்ச்சி திட்டத்தை தர்மபுரி, கால்நடை மருத்துவ பல்கலைக்கழக பயிற்சி மற்றும் ஆராய்ச்சி மையத்தின் மூலமாக செயல்படுத்தி வருகிறது. கால்நடை வளர்ப்பு தொழில்நுட்பங்களுக்கு தொலைவாக அமைந்து, கால்நடை வளர்ப்பு குறித்த சேவைகளை அளிக்கும் நிறுவனங்களின் சேவைகளை பெறுவதில் சிரமத்திற்குள்ளாகி வரும் பட்டியலின விவசாயிகள் பயன்பெறும் நோக்குடன் இத்திட்டம் கால்நடை மருத்துவ பல்கலைக்கழகத்தால் வகுக்கப்பட்டு, பட்டியலின மக்களுக்கான இந்திய வேளாண் ஆராய்ச்சி கழகத்தின் உபதிட்டத்தின்கீழ் நிதியுதவி பெறப்பட்டது.

▶ தர்மபுரி கால்நடை மருத்துவ பல்கலைக்கழக பயிற்சி மையத்தில் விவசாயிகளுக்கு திறன் மேம்பாட்டு கையேடு வழங்கப்பட்டது.

இத்திட்டம், கறவை மாடுகளை வளர்க்கும் பட்டியலின விவசாயிகளின் தொழில்நுட்பத் தேவைகளை ஆய்ந்தறிந்து, அத்தேவைகளை பூர்த்தி செய்யும் விதமாக தொழில்நுட்ப ஆலோசனைகள், இடுபொருட்கள் மற்றும் கள வழிகாட்டல் உள்ளிட்ட சேவைகளை வழங்கி, அதன்வழி கறவை மாடு உற்பத்தி மேம்பாடு, பட்டியலின விவசாயிகளின் சமூக பொருளாதார மேம்பாடு ஆகியவற்றை குறித்து ஆராய்ச்சி செய்வதை நோக்கமாகக் கொண்டது. இத்திட்டத்தில், தர்மபுரி மாவட்டத்தில் கால்நடைகளை வளர்க்கும் 40 பட்டியலின விவசாயிகள் தேர்வு செய்யப்பட்டு, இரண்டு நாள் திறன் மேம்பாட்டு பயிற்சி அளிக்கப்பட்டது. நிகழ்ச்சிக்கு பல்கலைக்கழகத்தின் விரிவாக்க கல்வி இயக்குனர் அப்பாராவ் தலைமை வகித்து பேசினார். பெங்களூரு, தேசிய கால்நடை தொற்றுநோயியல் மற்றும் நோய் தகவல் நிறுவனத்தின் முதுநிலை விஞ்ஞானி நாராயணன் முன்னிலை வகித்து பேசினார். பயிற்சியின் இறுதியில் விவசாயிகளுக்கு இடுபொருட்கள், சான்றிதழ் மற்றும் பயிற்சி கையேடு வழங்கப்பட்டன. பல்கலைக்கழகத்தின் பேராசிரியர்கள் பொன்.திலகர் மற்றும் கண்ணதாசன் ஆகியோர் ஒருங்கிணைத்தனர்.

ಐಸಿಎಆರ್-ನಿವೇದಿ ಸಂಸ್ಥೆಗೆ ಬ್ರೆಜಿಲ್ ನಿಯೋಗ ಭೇಟಿ

ಉದಯಕಾಲ ನ್ಯೂಸ್, ಯಲಹಂಕ:

ಭಾರತ ಮತ್ತು ಬ್ರೆಜಿಲ್ ನಡುವೆ ಕೃಷಿ ತಂತ್ರಜ್ಞಾನ ವಿನಿಮಯ ಮತ್ತು ಬಲಪಡಿಸುವ ದಿಸೆಯಲ್ಲಿ ಐಸಿಎಆರ್ (ಭಾರತೀಯ ಕೃಷಿ ಸಂಶೋಧನಾ ಮಂಡಳಿ)-ನಿವೇದಿ ಸಂಸ್ಥೆ ವತಿಯಿಂದ ಹೆಸರಘಟ್ಟದ ಕಚೇರಿಯಲ್ಲಿ ಆಯೋಜಿಸಿದ್ದ ಕಾರ್ಯಕ್ರಮದಲ್ಲಿ ಬ್ರೆಜಿಲ್ ಪ್ರತಿನಿಧಿಗಳು ಪಾಲ್ಗೊಂಡಿದ್ದರು. ಕಾರ್ಯಕ್ರಮದಲ್ಲಿ ಡಾ.ಕಾರ್ಲೋಸ್ ನಬಿಲ್ ಘೋಬ್ರಿಲ್, ಡಾ.ಹ್ಯಾಮಿಲ್ಟನ್ ಹಂಬರ್ಟೋ ರಾಮೋಸ್, ಡಾ.ಅನಾ ಯುಜೆನಿಯಾ, ಡಾ.ಪ್ರಿಸ್ಸಿಲ್ಲಾ ರೋಚಾ ಸಿಲ್ವ ಫಗುಂಡೆಸ್ ಅವರು ಬ್ರೆಜಿಲ್ ಕೃಷಿ ಕ್ಷೇತ್ರದಲ್ಲಿ ಯಾವೆಲ್ಲಾ ಭಾರತೀಯ ತಂತ್ರಜ್ಞಾನ ಅಳವಡಿಸಿಕೊಂಡಿದೆ ಎಂಬುದರ ಕುರಿತು ಸವಿವರವಾದ ವಿಚಾರ ಮಂಡಿಸಿದರು. ಐಸಿಎಆರ್-ನಿವೇದಿ ಸಂಸ್ಥೆಯ ನಿರ್ದೇಶಕ ಡಾ.ಬಲದೇವ್ ಆರ್.ಗುಲಾಟಿ ಮಾತನಾಡಿ 'ಜೈವಿಕ ತಂತ್ರಜ್ಞಾನ, ಡಿಜಿಟಲ್ ಪರಿಹಾರದ ಮೂಲಕ ನಿವೇದಿ ಸಂಸ್ಥೆಯು ಜಾನುವಾರುಗಳನ್ನು ರಕ್ಷಿಸುವಲ್ಲಿ ಮುಂಚೂಣಿಯಲ್ಲಿದೆ' ಎಂದರು. ಪಶುಸಂಗೋಪನೆ ಮತ್ತು ಜಾನುವಾರು ಉದ್ಯಮದಲ್ಲಿನ ಅವಕಾಶಗಳ ಕುರಿತು ಡಾ.ಸತೀಶ್ ಬಿ.ಶಿವಚಂದ್ರ, ಮಾಹಿತಿ ನೀಡಿದರು. ಆರ್ಥಿಕ ಪ್ರಾಮುಖ್ಯತೆ ಮತ್ತು ಕೃಷಿಗೆ ಸಂಬಂಧಿಸಿದಂತೆ ಭಾರತ ಮತ್ತು ಬ್ರೆಜಿಲ್ ತಂತ್ರಜ್ಞಾನ ವಿನಿಮಯದ ಅಗತ್ಯತೆ ಕುರಿತು ಡಾ.ಎಂ.ಎಂ.ಚಂದಾ, ಡಾ.ಜಿ.ಬಿ.ಮಂಜುನಾಥ್ ರೆಡ್ಡಿ ತಮ್ಮ ಅಭಿಪ್ರಾಯ ವ್ಯಕ್ತಪಡಿಸಿದರು. ಐಸಿಎಆರ್-ನಿವೇದಿ

ಕನ್ನಡಪ್ರಭ

ಯಲಹಂಕದಲ್ಲಿ ಪ್ರಗತಿಪರ ರೈತರಿಗೆ ಸನ್ಮಾನ

ಯಲಹಂಕ ಕ್ಷೇತ್ರದ ರಾಮಗೊಂಡನಹಳ್ಳಿ ಸಮೀಪದ ಐಸಿಎಆರ್ ನಿವೇದಿಯಲ್ಲಿ ಹಮ್ಮಿಕೊಂಡಿದ್ದ 'ರಾಷ್ಟ್ರೀಯ ರೈತ ದಿನಾಚರಣೆ' ಕಾರ್ಯಕ್ರಮದಲ್ಲಿ ಪ್ರಗತಿಪರ ರೈತರನ್ನು ಸನ್ಮಾನಿಸಲಾಯಿತು.

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