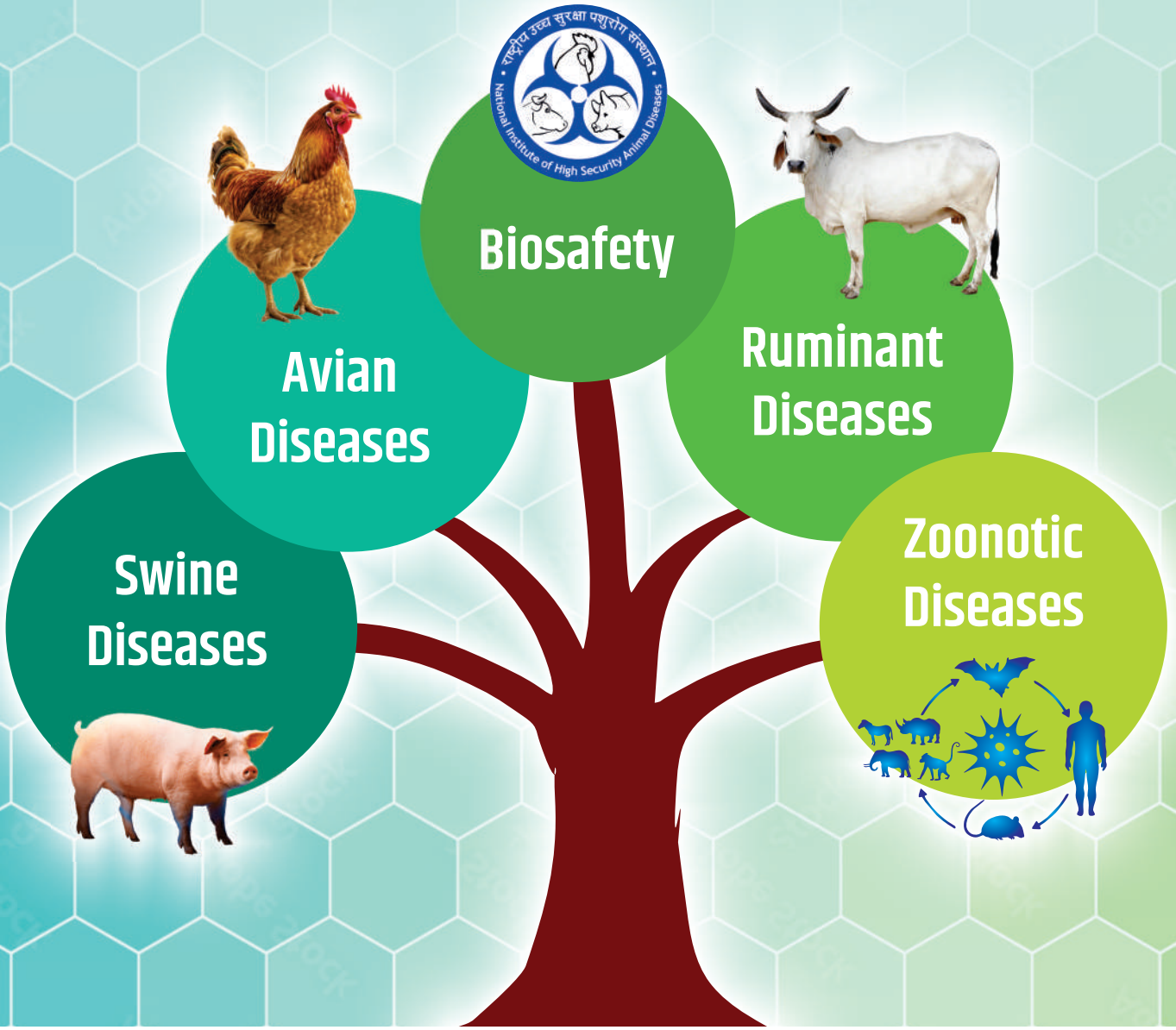
Annual Report 2024



ICAR-National Institute of High Security Animal Diseases
Anand Nagar, Bhopal-462022 (M.P.)

Annual Report 2024

ICAR-National Institute of High Security Animal Diseases
Anand Nagar, Bhopal-462022 (M.P.)

Published by

Dr. Aniket Sanyal, Director
ICAR-National Institute of High Security Animal Diseases
Anand Nagar, Bhopal – 462022 M.P. India

Compilation, Editing & Designing

Gandhale PN, Pateriya AK, Senthilkumar D, Nagarajan S, Sudhakar SB, Fateh Singh & Bhatia S

Citation

Gandhale PN, Pateriya AK, Senthilkumar D, Nagarajan S, Sudhakar SB, Fateh Singh & Bhatia S (2025). ICAR-National Institute of High Security Animal Diseases, Bhopal, Annual Report 2024, Pages 112.

Technical Assistance

R.K. Shukla and S.B. Somkuwar

Printed by

M/S Print Bajar, Plot no. 210, Zone 1,
MP Nagar, Bhopal-462011

CONTENTS

DIRECTOR'S FOREWORD

It is with great pride and a sense of accomplishment that I present the Annual Report of ICAR-NIHSAD for the year 2024. The year has witnessed exceptional progress in our core mandate areas of high-security animal disease research, diagnostics, and preparedness for emerging and re-emerging threats to animal and public health.

This year was marked by several landmark scientific achievements. The institute successfully released the inactivated bovine viral diarrhoea (BVD) vaccine, adding a critical tool for the control of this economically important disease in cattle. Following its earlier licensing, the low pathogenic H9N2 avian influenza vaccine was commercially launched by Indian manufacturers, reflecting the translational strength and stakeholder confidence in our vaccine development programs.

A major highlight of the year has been the development of an inactivated SARS-CoV-2 vaccine candidate employing a novel adjuvant, which promises enhanced immune responses in animal models. Additionally, significant headway has been made in the development of a CRISPR/Cas-based gene-deleted subunit vaccine candidate for African swine fever (ASF), showing promising results in pre-clinical phases. Our research has also led to noteworthy advances in understanding host susceptibility and resistance to SARS-CoV-2 in different animal species, contributing important knowledge to India's One Health preparedness. The first-ever detection of H5N1 avian influenza virus in wild mammalian species such as tiger and leopard in India, reported by the institute, emphasizes our pivotal role in cross-species surveillance of zoonotic viruses. Furthermore, our efforts have uncovered novel possibilities for developing a neuraminidase-based universal vaccine for avian influenza—an innovation that could pave the way for broader protection against evolving AIV strains.

The institute continues to discharge its national mandate through timely diagnosis and surveillance of animal diseases from across the country and also provides diagnostic testing services to the Animal Quarantine and Certification Services (AQCS) under the Department of Animal Husbandry and Dairying, facilitating the screening of imported animals and animal products for emerging and exotic diseases. In addition, ICAR-NIHSAD's scientific and advisory role within the National One Health Mission has become increasingly vital amid growing zoonotic threats, exemplifying the institute's expanding influence on national health policies and biosafety preparedness.

Beyond research, the institute actively engaged with stakeholders through capacity-building programs, awareness campaigns, and observance of national initiatives such as Swachh Bharat Abhiyan, Hindi Pakhwada, Women Farmers' Day, International Yoga Day, and Vigilance Awareness Week. These outreach activities have reinforced our commitment to public engagement and institutional responsibility.

As we look back on these achievements, I wish to place on record my deep appreciation to Dr. Himanshu Pathak, Secretary, DARE and DG, ICAR; Dr. Raghavendra Bhatta, DDG (AS); Dr. Ashok Kumar and D. Hemadri, ADG (AH); for their constant guidance and encouragement throughout the year. I also extend my heartfelt thanks to the dedicated scientists, technical staff, and administrative personnel of ICAR-NIHSAD whose unwavering efforts have made these milestones possible. My sincere gratitude goes to our collaborators, stakeholders, and the scientific community who continue to partner with us in our mission.

I trust that this annual report will serve as a valuable resource for our readers, including farmers, veterinarians, scientists in NARES, entrepreneurs, policymakers, and other stakeholders. We welcome your feedback and suggestions as we strive to elevate our impact and address future challenges in the domain of animal health and biosafety.

ICAR-NIHSAD, Bhopal
December 31, 2024

(ANIKET SANYAL)
Director

INSTITUTE PROFILE

The ICAR–National Institute of High Security Animal Diseases (ICAR-NIHSAD), Bhopal, is India's apex institute dedicated to the diagnosis, research, surveillance and containment of exotic, emerging and reemerging animal diseases, with strong implications for national food security and One Health. The BSL-4 facility established in 1998 as High Security Animal Disease Laboratory (HSADL) under the aegis of the Indian Veterinary Research Institute (IVRI), was formally dedicated to the nation on 23rd June, 2000 and elevated to the status of a National Institute on 8th August 2014 by the Indian Council of Agricultural Research (ICAR), assuming its current name and expanded mandate.

ICAR-NIHSAD plays a critical national role in protecting animal and public health by undertaking comprehensive surveillance, outbreak investigations, and providing timely diagnostic and advisory services for emerging, re-emerging, and transboundary exotic animal diseases. The institute conducts screening of animal samples and animal-derived products for over 23 exotic and emerging viral pathogens, enabling early detection, risk assessment, and strategic response to prevent incursions of foreign animal diseases. This year, the institute was pivotal in monitoring avian influenza outbreaks across multiple states, including detection of H5N1 virus in mammalian species, underscoring its front-line role in pandemic preparedness.

ICAR-NIHSAD has BSL-3 laboratory and animal containment facilities certified by the Inter-Ministerial Committee, Government of India. The institute is designated as Reference Laboratory for Avian Influenza by the World Organisation for Animal Health (WOAH) since 2009 and National Referral Facility for emerging & exotic animal diseases. The Avian Influenza Testing Laboratory is accredited under ISO/IEC 17025:2017 by NABL. The institute also maintains a Specific Pathogen Free (SPF) poultry unit, essential for controlled vaccine and pathogenicity trials.

The ICAR-NIHSAD research ecosystem spans development of next-generation diagnostics and vaccines, molecular epidemiology, genomic and environmental surveillance, host-pathogen interaction and immunological response studies and risk analysis under the One Health paradigm. The Institute is actively involved in the indigenous development of diagnostics and vaccines. The institute has successfully developed and validated multiple technologies. So far a total of six diagnostic technologies and two vaccines have been released by the institute, out of which one diagnostic kit and one vaccine have been commercialized. This year the Inactivated Bovine Viral Diarrhea Virus (BVDV-1) Vaccine for cattle developed at ICAR-NIHSAD was released by Sri Shivraj Singh Chouhan, Hon'able Union Minister of Agriculture and Farmers Welfare on 96th ICAR Foundation day on 16th July, 2024. The diagnostic kits and vaccines developed by ICAR-NIHSAD will reduce reliance on imported products and strengthen veterinary disease control infrastructure in the country aligning with the "Make in India" initiative of Government of India.

In addition to its research mandates, ICAR-NIHSAD functions as a premier center for capacity building, routinely organizing specialized hands-on trainings in biosafety, biosecurity, molecular diagnostics, and outbreak response for scientists, veterinarians, and stakeholders. The institute actively engages in field-level training and extension activities to raise awareness among farmers about emerging animal diseases, their prevention and control strategies, and the importance of implementing biosecurity measures at the farm level.

Recognized for its scientific excellence and global engagement, ICAR-NIHSAD continues to collaborate with WHO-GOARN, OFFLU, ILRI, FAO and other global partners in disease surveillance and pandemic response planning.

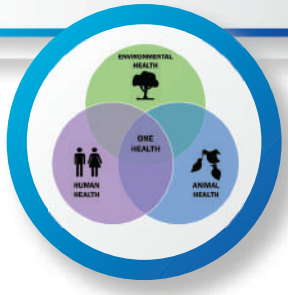
As it is going to complete 25 years of institutional service in the next year, ICAR-NIHSAD reaffirms its commitment to safeguard animal health, enabling zoonotic disease preparedness, and contributing to national and global food security through innovation, vigilance, and scientific leadership.

MANDATE

- Basic and strategic research on exotic, emerging and re-emerging animal diseases.
- Biorisk management and capacity building in the areas of biosafety, biosecurity and bio-containment for handling high risk pathogens.

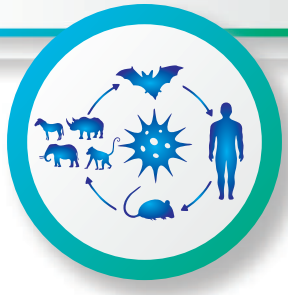
VISION

"Mitigating risks of known and unknown emerging infectious diseases in animals including zoonotic infections at human-animal interface through forecast, early detection of pathogens, emergency preparedness with diagnostics and vaccines while keeping vigil on changing host pathogen and environment interactions and creating understanding of potential bio-risks and disease threats among stakeholders."

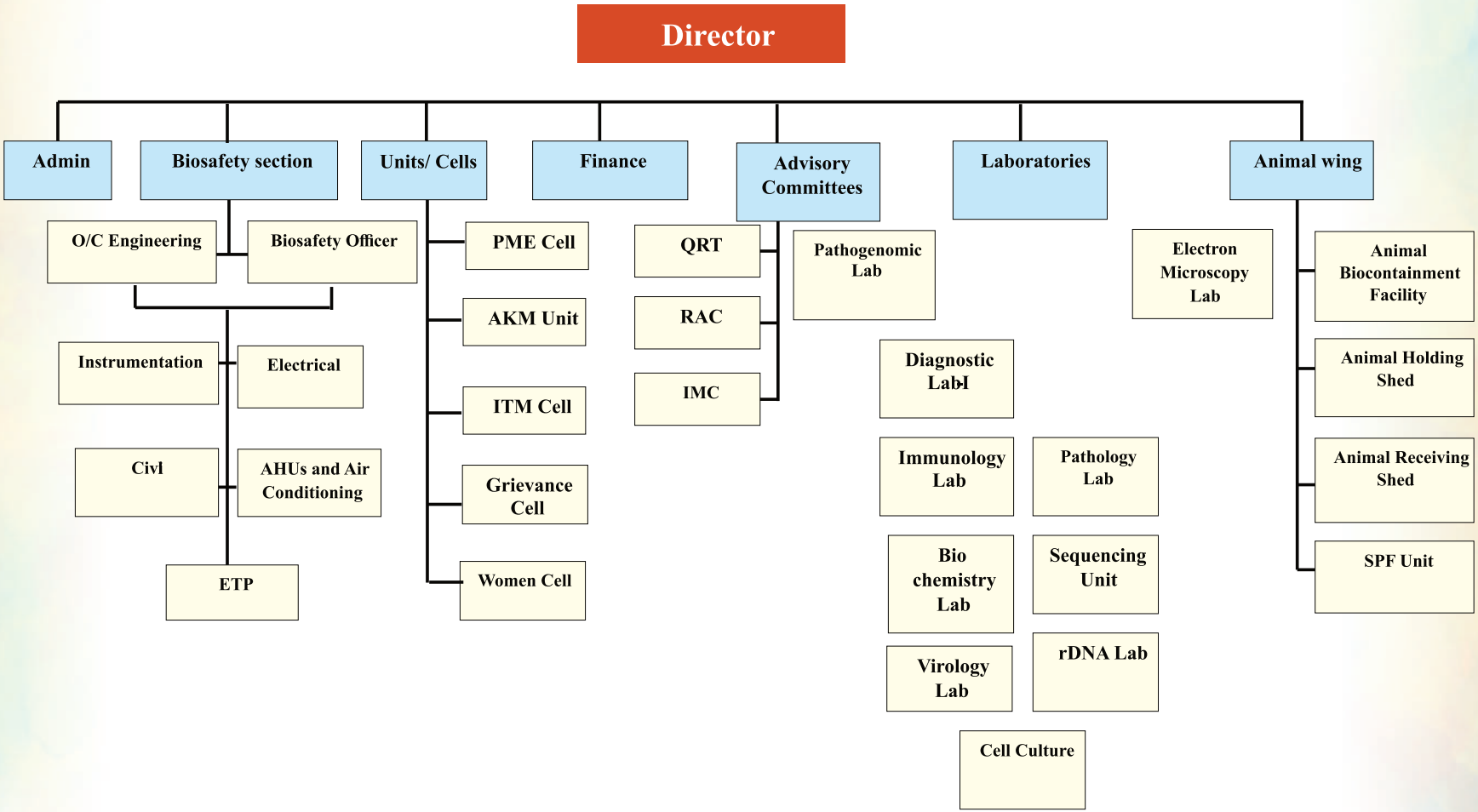


MISSION

Reducing threats of emerging and new pathogens for sustainable animal husbandry sector and safeguarding public health



ORGANIZATIONAL SETUP OF NIHSAD



Annual Report -2024

Executive Summary

Development of Vaccines

☞ **Selection of Candidate vaccine H5N1 virus strain:** Phylogeny was constructed using HA gene sequence of 73 H5Nx sequences from India. These included, 38 clade 2.3.2.1a H5N1, 11 clade 2.3.4.4b H5N1 and 25 clade 2.3.4.4b H5N8 viruses isolated over a period of 2011-2024. Based on the phylogeny, a total of 14 H5Nx viruses (6 from 2.3.2.1a and 8 from 2.3.4.4b clades) were chosen for antisera generation. Cross neutralization studies have revealed one of the clade 2.3.4.4b virus isolated from quail from Kerala as a probable candidate vaccine H5N1 virus strain. The virus was inactivated in 0.1% BPL as per the standard procedure and Water in Oil emulsion prepared with Montanide ISA 71 RVG (Sepic). The animal experimentation for potency testing are underway.

☞ **Monitoring of antigenic divergence of H9N2 field isolates with the approved vaccine strain:** A total of eight H9N2 viruses isolated during 2024 from chickens and the environment in the states of Chhattisgarh, Jharkhand, Madhya Pradesh, and Odisha were tested for antigenic monitoring. The results indicated close antigenic relationship of the currently circulating H9N2 viruses with the approved H9N2 vaccine strain.

☞ **Evaluation of safety and immunogenicity of inactivated BVDV (BVDV-1) monovalent vaccine:** Field trial showed that the vaccine is safe, immunogenic in cattle and can provide clinical protection against challenge-infection with homologous virus. The BVD vaccine technology developed is ready for transfer and commercialization.

☞ **Development of Vaccine for ASF:**

- Successfully generated and purified gene-deleted African swine fever virus using CRISPR/Cas 9 gene editing technology, with similar in vitro growth kinetics as that of the parental wild type virus. The genetically engineered mutant virus is being evaluated for virulence attenuation in piglets for its potential as a vaccine candidate.
- As part of a viral vector-based approach for generating ASFV vaccine candidates, successfully generated recombinant adenovirus expressing E183L gene (encodes the P54 structural protein of ASF virus).
- Two inactivated ASFV vaccine formulations (with or without immunostimulant) were prepared and evaluated for their immunogenicity and protective efficacy in pigs. The results showed that both the vaccine formulations were highly immunogenic but not protective against virulent ASFV challenge.

☞ **Development of Vaccine for SARS-CoV-2:** An inactivated SARS-CoV-2 vaccine was successfully developed using a Delta variant isolate, enhanced with alum and CpG adjuvants. The formulation elicited strong neutralizing antibody responses and a balanced Th1/Th2 immune profile in both mice and hamster models, providing robust protection against SARS-CoV-2 challenge. These results underscore the vaccine's potential for further preclinical and clinical advancement.

Development of Diagnostics

☞ **Selection of Monoclonal Antibody pair towards development of Lateral Flow Assay for Rapid Detection of Avian Influenza Virus:** Monoclonal antibodies (MAbs) generated against the recombinant nucleoprotein (rNP) of avian influenza (AI) virus were evaluated for their suitability in a lateral flow assay format. The assay was able to detect the recombinant protein at a concentration as low as 0.5μg/ml. This optimization marks a critical milestone toward the development of a lateral flow assay for avian influenza.

☞ **Polyclonal antibody purification using C- and N- terminal domains of avian influenza nucleoprotein for enhanced sensitivity in Lateral Flow Assays:** To support the development of a broad-reactive lateral flow assay (LFA) for avian influenza (AI) virus detection, recombinant expression of AI nucleoprotein and production of polyclonal antibodies was carried out using a targeted strategy. Polyclonal sera were raised in chickens against the full-length AI nucleoprotein, and the resulting antibodies were selectively purified using these region-specific affinity columns. The purified antibodies were further validated by ELISA and western blot analysis, confirming

specificity to the corresponding terminal regions. The purified polyclonal antibodies against rNP-N and rNP-C were then conjugated to gold nanoparticles and evaluated as detector and capture antibodies in LFA format. Optimization and validation studies are underway.

- **Probe-based one-step reverse transcription (RT) real-time PCR:** The test was developed to detect the genome of Porcine Epidemic Diarrhea virus (PEDV) using IVT-RNA prepared from synthetic gene construct. The developed assay demonstrated an analytical sensitivity of ~2 RNA copies at 10^{-12} dilutions of IVT-RNA. Specificity was confirmed by testing against TGEV, SIV, CSFV, and PRRSV and known PEDV-negative swine faecal or rectal swab samples (n = 250) collected from the field. The assay exhibited specific amplification for PEDV without cross-reactivity to TGEV, SIV, CSFV, PRRSV, or field samples.

- **Probe-based one-step reverse transcription real-time PCR:** The test was optimised to detect the Transmissible Gastroenteritis virus (TGEV) genome. The developed assay demonstrated an analytical sensitivity of ~10 RNA copies by testing in 10-fold dilutions of IVT-RNA. Specificity was confirmed by testing against PEDV, SIV, CSFV, and PRRSV and known TGEV-negative swine faecal or rectal swab samples (n = 250) collected from the field. The assay exhibited specific amplification for TGEV without cross-reactivity to PEDV, SIV, CSFV, PRRSV, or field samples.

- **RPA-CRISPR/Cas9 based lateral flow assay:** The assay was developed for sensitive detection of African Swine Fever virus (ASFV) genome. The assay involved forming a labeled Cas9–sgRNA ribonucleoprotein complex that binds to the ASFV target DNA, with detection via streptavidin-coated lateral flow strips. The assay showed high sensitivity and specificity, with no cross-reactivity with other important swine viruses.

- **Development of One Step RT-PCR for Ganjam:** As in-house diagnostic assay for genomic detection of Ganjam virus, one step RT-PCR assay for detection of Ganjam virus (GANV) genome in ticks using in-house designed primers targeting the conserved region of 'N' gene was developed. The reaction conditions like, annealing temperature, primer concentration and limit of detection was determined. The developed assay was used to screen the tick samples along with published assay.

- **Nucleocapsid antigen capture ELISA for SARS-CoV-2:** A cost-effective, high-throughput ELISA test was developed and validated for large-scale screening in humans and animals, showing diagnostic sensitivity of 67.78 %, diagnostic specificity (100%) and substantial diagnostic agreement with RT-qPCR and rapid antigen tests. This in-house ELISA offers a practical alternative for COVID-19 surveillance in low-resource settings.

- **Label-free colorimetric biosensor for SARS-CoV-2:** A label-free colorimetric biosensor for SARS-CoV-2 using gold nanoparticles functionalized with peptide dendrimers was developed to visually detect breakthrough COVID-19 infections by targeting antibodies against the SARS-CoV-2 nucleocapsid protein. The assay demonstrated high sensitivity (88.89%) and specificity (100%) in human serum samples, offering a simple and rapid tool for monitoring post-vaccination infections, especially from emerging variants.

Pathogen Characterization

- **Co-circulation of H5N1 clades 2.3.2.1a and 2.3.4.4b avian influenza viruses in India, 2024:** Highly Pathogenic Avian Influenza (HPAI) H5N1 virus was detected in poultry in Andhra Pradesh, Jharkhand, and Odisha; domestic ducks and poultry in Kerala; poultry, tigers, and leopards in Maharashtra; and wild birds in Rajasthan during 2024. The complete genome sequences were determined for comparison. Analysis of the HA gene cleavage region revealed the presence of multiple basic amino acid motifs PQKERRRKR/G, PLREKRRKR/G and PQRERRRKR/G. The H5N1 viruses isolated from chicken, tiger, and leopard in Andhra Pradesh, Jharkhand, Maharashtra and Odisha belonged to clade 2.3.2.1a, and the H5N1 virus isolated from duck, chicken, quails and wild birdsin Kerala and Rajasthan belonged to clade 2.3.4.4b, indicating co-circulation of both genetic clades in India during 2024.Two H5N1 clade 2.3.2.1a chicken isolates possessed a genetic mutation N295S (N1 numbering), indicating resistance to neuraminidase inhibitors. The detection of H5N1 virus in wild mammals for the first-time in India indicated an expanding host range of the virus implying the need for continuous surveillance and early detection and control of H5N1 virus outbreaks.

- **Genetic and phylogenetic analysis of LSDVs infecting water buffaloes during 2020-2024:** The study revealed circulation of wild-type strains of two divergent LSDV lineages (1.2.1 and 1.2.2) in Indian buffaloes with evidence of co-circulation of multiple LSDV sub-clusters in the same area.

- Genetic characterization of border disease virus (BDV) originating from persistently infected migratory sheep reveals high genetic diversity of BDV-3 strains circulating in India.

- Laboratory confirmed cases (n=3) of buffalopox have been detected in LSD-negative buffaloes in Maharashtra and genetic characterization of buffalopox virus (BPXV) isolate in ATI, B5R and C18L genes revealed high sequence homology with the previously reported BPXV strains from human and buffaloes in India, highlighting the need of monitoring the zoonotic impact of BPXV.

- **Genomic analysis of ASFV:** complete genome sequences of ASFV isolates of domestic pig (189,390 base pairs) and wild boar (190,489 base pairs) origin from Mizoram state were analysed. Alignment of the complete genome sequence of ASFV isolated from wild boar with the reference strain Georgia/2007 revealed notable mutations including nucleotide deletions, insertions which led to frame shifts and protein truncations across various genes of ASFV. The analysis revealed a unique mutation in MGF-360-21R gene (a 50-nucleotide deletion that resulted in a 30-amino-acid truncationin the carboxyl terminus). Comparative analysis with other ASFV isolates of domestic pig and wild boar origin indicated the susceptibilityof the MGF-360-21R geneto genetic changes during evolutionary adaptation in wild boars.

- **Exploring the Therapeutic Potential of Cordycepsmilitaris against SARS-CoV-2 through *In-silico* and *in-vitro* approach:** The Molecular docking analysis revealed that the Cordycepin, a bioactive compound inCordycepsmilitaris, has the highest binding affinity to the SARS-CoV-2 spike protein. The crude aqueous extract of *C. militaris* at 100 μg/mL in Vero E6 cells could reduce to 50.24% reduction in viral particles in-vitro. These findings suggest that *C. militaris* has promising anti-SARS-CoV-2 activity and may be explored as traditional medicine for other viruses of public/animal health importance.

Disease Surveillance and Monitoring

Avian influenza:

- A total of 66,702 samples (53,532 morbid materials and 13,170 sera) received from various parts of the country were tested as part of avian influenza virus surveillance during this year. In the passive surveillance, out of 1192 suspected samples tested, a total of 487 samples from five States (Andhra Pradesh – 07, Jharkhand-02, Kerala-392, Maharashtra – 01, Odisha - 81 and Rajasthan-04) have tested positive for H5N1 notifiable AIV and 3 sera samples from Kerala tested positive for H5 virus antibodies. Twenty samples from Kerala were found positive for NDV.

- In the active surveillance, out of the 48,125 morbid samples, 171 samples from ten States/UTs (Andhra Pradesh – 01, Bihar-04, Chhattisgarh -17, Himachal Pradesh-01, Jharkhand-10, Madhya Pradesh-35, Maharashtra-12, Odisha-62, Punjab-06 and Rajasthan-23) tested positive for H9N2 avian influenza virus and 109 samples from nine States (Andhra Pradesh – 03, Gujarat-30, Himachal Pradesh-04, Jammu-03, Kerala-20, Mahrashtra-12, Odisha-24, Punjab-08 and Rajasthan-05) tested positive for Newcastle disease virus. Out of 11,170 sera samples tested, a total of 55 sera samples from six States (Andhra Pradesh-01, Gujarat-09, Kerala- 02, Odisha-36 and Rajasthan-07)were positive for H9 antibodies. A total of 124 sera from nine States/UTs (Andhra Pradesh-18, Chhattisgarh- 46, Gujarat-03, Jharkhand -03, Kerala- 02, New Delhi-04, Odisha-29 Rajasthan-06 and West Bengal-13) were positive against NDV antibodies. A total of six sera samples from Chhattisgarh were positive to both H9 and NDV antibodies. A total of4315 swab samples received under POSP, 22 samples (Jharkhand-10 and Maharashtra-12) were tested positive for H9N2 avian influenza virus. A total of fifteen samples including 12 from Maharashtra and 03 from Odisha were found positive for NDV. Out of 1,900 sera samples received under POSP, 06 samples from Kerala were found positive against H9 virus antibodies and 03 samples from Jharkhand and 02 samples from Kerala were positive against NDV antibodies.

Lumpy Skin Disease:

- Emergence of lumpy skin disease (LSD) in domestic water buffaloes reported for the first time in India, indicating susceptibility of Indian buffaloes to natural LSDV infection. Molecular evidence of LSDV infection in buffaloes was found in three states, while serological evidence of LSDV infection was found in six states.
- During the year 2024, laboratory confirmed cases of lumpy skin disease (LSD) have been detected in cattle of four States (Tamil Nadu, Punjab, West Bengal, Andhra Pradesh and Madhya Pradesh).

Swine diseases:

- Out of 204 porcine samples from 9 states, 68 samples tested positive for ASFV. The positive samples were from Andhra Pradesh (2), Haryana (6), Karnataka (6), Kerala (15), Madhya Pradesh (7), Maharashtra (15), Rajasthan (11), and Sikkim (6).
- Faecal metavirome sequencing and analysis of swine faecal samples, from Madhya Pradesh and Assam, revealed high diversity of families of viruses.
- A total of 148 pig samples received from Chhattisgarh, Madhya Pradesh, Maharashtra and Sikkim were tested for the PRRSV genome by RT-PCR. All samples were found to be negative.
- 234 swine nasal swabs tested by real-time PCR and were negative for Influenza A viruses of Swine. 28 out of 265 swine serum samples from 7 states were found positive for presence of H1 antibodies by Haemagglutination Inhibition test.
- A total of 160 swine faecal samples, collected from Assam (n=80), Meghalaya (n=22), Chhattisgarh (n=35), and Kerala (n=23), were tested for the genome of PEDV and TGEV and found to be negative.

Zoonotic diseases:

- A total of 73 samples of wild and domestic animals from Kerala, Madhya Pradesh and Assam and were tested for SARS CoV-2, West Nile Virus, Monkey pox, Kysannur Forest disease and Hepatitis E. All samples were found negative.
- **Surveillance of zoonotic pathogens in rodent population of Central India:** A total of 74 rodent intestine and organs pools were collected from Nagpur and Udgir of Maharashtra and screened for Monkeypox virus, Hanta virus, Crimean-Congo haemorrhagic fever virus (CCHFV), Kyasanur Forest disease virus (KFDV), SARS-CoV-2, Coxiella burnetii (Q fever), Orientia tsutsugamushi (Scrub typhus), Rickettsia genera spp. The former 7 were screened by Real- time PCR while the later was screened by conventional PCR. All samples were found to be negative for the pathogens tested.
- As investigation of Nipah in animals and environment post human cases, National Joint Outbreak Response Team (NJORT) conducted a comprehensive investigation, involving an inter-departmental team comprising experts from the human, livestock, and wildlife sectors. A total of 39 samples from different animal species and 26 environmental samples from Malappuram district, Kerala were tested for Nipah and were found negative.
- **Sero-prevalence of Crimean-Congo Haemorrhagic Fever virus in livestock population of Wayanad, Kerala:** The CCHFV sero-prevalence study consisting of 300 serum samples comprising of cattle, goats and buffaloes revealed overall CCHFV seroprevalence of 2.34% with species-wise seropositivity of 1.01% and 5.10% in cattle and goats, respectively.
- **Viral diversity in ticks collected from the Madhya pradesh:** The virome analysis of Rhipicephalus and Hyalomma tick pools collected from the Madhya Pradesh revealed genetic evidence of important viruses belonging to families of Rhabdoviridae, Flaviviridae, Orthomyxoviridae, Reoviridae, Nairoviridae, Parvoviridae, Phlebovirus, Arenaviridae, and simbu serogroup viruses.

Host-Pathogen Interaction Studies

- **H5 transmission in Guinea pigs:** The in-contact transmission potential of a clade 2.3.4.4b virus was assessed in guinea pigs. Viral RNA was detected by RT-qPCR in nasal washings of infected guinea pigs till 7 dpi. All the infected guinea pigs seroconverted against H5N1 virus. However, only one in-contact showed seroconversion against the virus. This study highlights that H5N1 clade 2.3.4.4b virus could transmit from infected to in-contact guinea pigs without prior adaptation in mammalian host.
- Trancriptome analysis of SARS CoV-2 infected cat and dog lung explant cultures of dogs displayed activation of reparative response genes at 24 hpi, suggesting potential for tissue recovery, whereas cats did not show similar activation, indicating a potentially higher susceptibility to lung injury.
- Metabolomics analysis of H5N1 infected chicken lungs revealed altered levels of critical metabolites in sphingolipid metabolism, tryptophan metabolism, and arginine-proline metabolism. Influenza virus possibly exploits sphingolipid metabolism to facilitate critical host pathogen interactions.

Diagnostic Services

- A total of 8890 samples of imported livestock, poultry and related products received from different Animal Quarantine & Certification Services were tested for exotic and emerging diseases including Avian Influenza (6920), Porcine Reproductive and Respiratory Syndrome (298), African Swine Fever (323), Malignant Catarrhal Fever (53), Nairobi Sheep Disease (53), Rift Valley Fever (41), Caprine Arthritis and Encephalitis (52), Bovine Viral Diarrhea (257), Swine Influenza (237), Aujesky's Disease (217), Porcine epidemic diarrhea (216), Transmissible gastroenteritis (216) Lumpy Skin Disease (06) and Rabbit Haemorrhagic Disease (01) and found negative.

कार्यकारी सारांश

टीकों का विकास

- **कैंडिडेट वैक्सीन H5N1 वायरस स्ट्रेन का चयन:** भारत से 73 H5Nx अनुक्रमों के HA जीन अनुक्रम का उपयोग करके फाइलोजेनी का निर्माण किया गया। इनमें 2011-2024 की अवधि में पृथक किए गए 38 क्लेड 2.3.2.1a H5N1, 11 क्लेड 2.3.4.4b H5N1 और 25 क्लेड 2.3.4.4b H5N8 वायरस शामिल थे। फाइलोजेनी के आधार पर, कुल 14 H5Nx वायरस (2.3.2.1a से 6 और 2.3.4.4b क्लेड से 8) एंटीसेरा उत्पन्न करने के लिए चुने गए। क्रॉस न्यूट्रलाइजेशन अध्ययनों से पता चला है कि केरल से बटेर से पृथक किए गए क्लेड 2.3.4.4b वायरस में से एक संभावित कैंडिडेट वैक्सीन H5N1 वायरस स्ट्रेन है। मानक प्रक्रिया के अनुसार 0.1% बीपीएल में वायरस को निष्क्रिय किया गया और मोंटेनाइड आईएसए 71 आरवीजी (सेपिक) के साथ पानी में तेल पायस तैयार किया गया। क्षमता परीक्षण के लिए जानवरों पर प्रयोग चल रहे हैं।

- **स्वीकृत वैक्सीन स्ट्रेन के साथ H9N2 फील्ड आइसोलेट्स के एंटीजेनिक डायवर्जेंस की निगरानी:** छत्तीसगढ़, झारखंड, मध्य प्रदेश और ओडिशा राज्यों में मुर्गियों और पर्यावरण से 2024 के दौरान अलग किए गए कुल आठ H9N2 वायरस का एंटीजेनिक निगरानी के लिए परीक्षण किया गया। परिणामों ने वर्तमान में प्रचलित H9N2 वायरस के स्वीकृत H9N2 वैक्सीन स्ट्रेन के साथ घनिष्ठ एंटीजेनिक संबंध का संकेत दिया।

- **निष्क्रिय BVDV (BVDV-1) मोनोवैलेंट वैक्सीन की सुरक्षा और प्रतिरक्षात्मकता का मूल्यांकन:** मवेशी परीक्षण से पता चला है कि वैक्सीन सुरक्षित, प्रतिरक्षात्मक है और होमोलॉगस वायरस के साथ चुनौती-संक्रमण के खिलाफ नैदानिक सुरक्षा प्रदान कर सकती है। विकसित BVD वैक्सीन तकनीक हस्तांतरण और व्यावसायीकरण के लिए तैयार है।

- **अफ्रीकी स्वाइन फीवर वैक्सीन**

  - CRISPR/Cas 9 जीन संपादन तकनीक का उपयोग करके जीन- विलोपित अफ्रीकी स्वाइन फीवर वायरस को सफलतापूर्वक उत्पन्न और शुद्ध किया गया, जिसमें पैतृक वाइल्ड प्रकार के वायरस के समान इन विट्रो विकास कैनेटीक्स है। आनुवंशिक रूप से रूपांकित उत्परिवर्ती वायरस का वैक्सीन कैंडिडेट के रूप में इसकी क्षमता के लिए घेंटा में विषाणु क्षीणन के लिए मूल्यांकन किया जा रहा है।

  - वायरल वेक्टर-आधारित दृष्टिकोण के अनुसार ASFV वैक्सीन कैंडिडेट को उत्पन्न करने के लिए, E183L जीन (ASF वायरस के P54 संरचनात्मक प्रोटीन को एनकोड करता है) को व्यक्त करने वाले पुनः संयोजक एडेनोवायरस को सफलतापूर्वक उत्पन्न किया गया।

  - दो निष्क्रिय ASFV वैक्सीन फॉर्मूलेशन (इम्यूनोस्टिमुलेंट के साथ या बिना) तैयार किए गए और सूअरों में उनकी प्रतिरक्षात्मकता और सुरक्षात्मक प्रभावकारिता के लिए उनका मूल्यांकन किया गया। परिणामों से पता चला कि दोनों वैक्सीन फॉर्मूलेशन अत्यधिक प्रतिरक्षात्मक थे, लेकिन विषमय ASFV चुनौती के खिलाफ सुरक्षात्मक नहीं थे।

- **SARS-CoV-2 वैक्सीन:** डेल्टा वेरिएंट आइसोलेट का उपयोग करके एलम और CpG एडजुवेंट्स के साथ एक निष्क्रिय SARS-CoV-2 वैक्सीन सफलतापूर्वक विकसित की गई । इस फॉर्मूलेशन ने चूहों और हम्सटर मॉडल दोनों में मजबूत न्यूट्रलाइजिंग एंटीबॉडी प्रतिक्रियाएं और संतुलित Th1/Th2 प्रतिरक्षा प्रोफ़ाइल प्राप्त की, जो SARS-CoV-2 चुनौती के खिलाफ मजबूत सुरक्षा प्रदान करता है। ये परिणाम आगे के प्रीक्लिनिकल और क्लिनिकल उन्नति के लिए वैक्सीन की क्षमता को रेखांकित करते हैं।

डायग्नोस्टिक का विकास

- **एवियन इन्फ्लूएंजा वायरस का तेजी से पता लगाने के लिए लेटरल फ्लो परख के विकास की दिशा में मोनोक्लोनल एंटीबॉडी जोड़ी का चयन:** एवियन इन्फ्लूएंजा (एआई) वायरस के पुनः संयोजक न्यूक्लियोप्रोटीन (आरएनपी) के खिलाफ उत्पन्न मोनोक्लोनल एंटीबॉडी (एमएबी) का लेटरल फ्लो परख प्रारूप में उनकी उपयुक्तता के लिए मूल्यांकन किया गया। परख 0.5µg/ml जितनी कम सांद्रता पर पुनः संयोजक प्रोटीन का पता लगाने में सक्षम थी। यह अनुकूलन एवियन इन्फ्लूएंजा के लिए लेटरल फ्लो परख के विकास की दिशा में एक महत्वपूर्ण मील का पत्थर है।

- **लेटरल फ्लो एसेज़ में उच्च संवेदनशीलता के लिए एवियन इन्फ्लूएंजा न्यूक्लियोप्रोटीन के सी- और एन- टर्मिनल डोमेन का उपयोग करके पॉलीक्लोनल एंटीबॉडी शुद्धिकरण:** एवियन इन्फ्लूएंजा (एआई) वायरस का पता लगाने के लिए एक व्यापक-प्रतिक्रियाशील लेटरल फ्लो एसे

(एलएफए) के विकास का समर्थन करने के लिए, एआई न्यूक्लियोप्रोटीन की पुनः संयोजक अभिव्यक्ति और पॉलीक्लोनल एंटीबॉडी का उत्पादन एक लक्षित रणनीति का उपयोग करके किया गया था। पॉलीक्लोनल सीरा को पूर्ण-लंबाई वाले एआई न्यूक्लियोप्रोटीन के खिलाफ मुर्गियों में उत्पन्न किया गया था, और परिणामी एंटीबॉडी को इन क्षेत्र-विशिष्ट आकर्षण कालम का उपयोग करके चुनिंदा रूप से शुद्ध किया गया था। शुद्ध किए गए एंटीबॉडी को एलिसा और वेस्टर्न ब्लॉट विश्लेषण द्वारा आगे मान्य किया गया, जो संबंधित अंतिम क्षेत्रों की विशिष्टता की पुष्टि करता है। आरएनपी-एन और आरएनपी-सी के विरुद्ध शुद्ध पॉलीक्लोनल एंटीबॉडी को फिर स्वर्ण नैनोकणों के साथ संयुग्मित किया गया और एलएफए प्रारूप में डिटेक्टर और कैप्चर एंटीबॉडी के रूप में मूल्यांकन किया गया। अनुकूलन और सत्यापन अध्ययन चल रहे हैं।

- **प्रोब आधारित वन-स्टेप रिवर्स ट्रांसक्रिप्शन रियल-टाइम आरटी-पीसीआर:** सिंथेटिक जीन निर्माण से तैयार आईवीटी आरएनए का उपयोग करके पीईडीवी के जीनोम का पता लगाने के लिए प्रोब जांच-आधारित वन-स्टेप रिवर्स ट्रांसक्रिप्शन रियल-टाइम आरटी-पीसीआर विकसित किया गया । विकसित जांच ने आईवीटी आरएनए के 10-12 तनुकरण पर ~2 RNA प्रतियों की विश्लेषणात्मक संवेदनशीलता का प्रदर्शन किया। टीजीईवी, एसआईवी, सीएसएफवी, और पीआरआरएसवी और क्षेत्र से एकत्र किए गए ज्ञात पीईडीवी -नकारात्मक सूअर के मल या मलाशय के स्वाब नमूनों (n = 250) के विरुद्ध परीक्षण करके विशिष्टता की पुष्टि की गई। जांच ने टीजीईवी, एसआईवी, सीएसएफवी, पीआरआरएसवी, या क्षेत्र के नमूनों के लिए क्रॉस-रिएक्टिविटी के बिना पीईडीवी के लिए विशिष्ट प्रवर्धन प्रदर्शित किया।

- **प्रोब आधारित वन-स्टेप रिवर्स ट्रांसक्रिप्शन रियल-टाइम पीसीआर:** टीजीईवी जीनोम का पता लगाने के लिए अनुकूलित किया गया था। विकसित जांच ने आईवीटी-आरएनए के 10 गुना तनुकरण पर परीक्षण करके ~10 आरएनए प्रतियों की विश्लेषणात्मक संवेदनशीलता का प्रदर्शन किया। क्षेत्र से एकत्र किए गए पीईडीवी, एसआईवी, सीएसएफवी और पीआरआरएसवी और ज्ञात टीजीईवी-नकारात्मक सूअर के मल या मलाशय के स्वाब नमूनों (एन = 250) के खिलाफ परीक्षण करके विशिष्टता की पुष्टि की गई। जांच ने पीईडीवी, एसआईवी, सीएसएफवी, पीआरआरएसवी या क्षेत्र के नमूनों के लिए क्रॉस-रिएक्टिविटी के बिना टीजीईवी के लिए विशिष्ट प्रवर्धन प्रदर्शित किया।

- **आरपीए-सीआरआईएसपीआर/कैस9 आधारित पार्श्व प्रवाह जांच:** एएसएफवी जीनोम के संवेदनशील पहचान के लिए एक आरपीए-सीआरआईएसपीआर/कैस9 आधारित पार्श्व प्रवाह जांच विकसित की गई । इस परीक्षण में लेबलयुक्त Cas9-sgRNA राइबोन्यूक्लियोप्रोटीन कॉम्प्लेक्स बनाना शामिल था जो ASFV लक्ष्य डीएनए से जुड़ता है, जिसका पता स्ट्रेप्टाविडिन-लेपित पार्श्व प्रवाह पट्टियों के माध्यम से लगाया जाता है। परीक्षण में उच्च संवेदनशीलता और विशिष्टता दिखाई गई, अन्य महत्वपूर्ण स्वाइन वायरस के साथ कोई क्रॉस-रिएक्टिविटी नहीं थी।

- **गंजम के लिए वन स्टेप आरटी-पीसीआर का विकास:** गंजम वायरस के जीनोमिक पता लगाने के लिए इन-हाउस डायग्नोस्टिक जांच के रूप में, 'एन' जीन के संरक्षित क्षेत्र को लक्षित करके इन-हाउस डिज़ाइन किए गए प्राइमरों का उपयोग करके टिक्स में जीएएनवी जीनोम का पता लगाने के लिए वन स्टेप आरटी-पीसीआर जांच विकसित की गई। प्रतिक्रिया की स्थिति जैसे, एनीलिंग तापमान, प्राइमर सांद्रता और पता लगाने की सीमा निर्धारित की गई । विकसित जांच का उपयोग प्रकाशित जांच के साथ टिक नमूनों की स्क्रीनिंग के लिए किया गया।

- **SARS-CoV-2 न्यूक्लियोकैप्सिड एंटीजन कैप्चर ELISA:** मनुष्यों और जानवरों में बड़े पैमाने पर स्क्रीनिंग के लिए एक लागत प्रभावी, उच्च-थ्रूपुट SARS-CoV-2 न्यूक्लियोकैप्सिड एंटीजन कैप्चर ELISA विकसित और मान्य किया गया था, जिसमें 67.78% की डायग्नोस्टिक संवेदनशीलता, डायग्नोस्टिक विशिष्टता (100%) और RT-qPCR और रैपिड एंटीजन परीक्षणों के साथ पर्याप्त डायग्नोस्टिक एग्रीमेंट दिखाया गया। यह इन-हाउस ELISA कम संसाधन वाली सेटिंग्स में COVID-19 निगरानी के लिए एक व्यावहारिक विकल्प प्रदान करता है।

- **लेबल-मुक्त वर्णमिति बायोसेंसर:** पेप्टाइड डेंड्रिमर्स के साथ क्रियाशील सोने के नैनोकणों का उपयोग करके एक लेबल-मुक्त वर्णमिति बायोसेंसर विकसित किया गया, जो SARS-CoV-2 न्यूक्लियोकैप्सिड प्रोटीन के खिलाफ एंटीबॉडी को लक्षित करके सफल COVID-19 संक्रमणों का आँखों से देखकर पता लगाने के लिए विकसित किया गया । जांच ने मानव सीरम नमूनों में उच्च संवेदनशीलता (88.89%) और विशिष्टता (100%) का प्रदर्शन किया, जो टीकाकरण के बाद के संक्रमणों की निगरानी के लिए एक सरल और तेज़ उपकरण प्रदान करता है, विशेष रूप से उभरते वेरिएंट से।

रोगज़नक़ विश्लेषण

- **भारत में एच5एन1 विषाणु के 2.3.2.1a और 2.3.4.4b वंशों का सह-परिसंचरण (वर्ष 2024):** वर्ष 2024 में भारत में उच्च रोगजनक एवियन इन्फ्लुएंजा (एचपीएआई) एच5एन1 विषाणु की पुष्टि कई राज्यों में की गई। यह विषाणु आंध्र प्रदेश, झारखंड और ओडिशा में मुर्गियों में; केरल में घरेलू बत्तखों और मुर्गियों में; महाराष्ट्र में मुर्गियों, बाघों और तेंदुओं में तथा राजस्थान में वन्य पक्षियों में पाया गया। इसके पूर्ण जीनोम अनुक्रम निर्धारित किए गए ताकि विभिन्न नमूनों की तुलना की जा सके। एचए (हीमैग्लूटिनिन) जीन के क्लिवेज क्षेत्र के विश्लेषण में यह पाया

गया कि इनमें अनेक मूल अम्लीय अनुक्रम उपस्थित थे, जैसे: PQKERRRKR/G, PLREKRRKR/G तथा PQRERRRKR/G, जो इसकी उच्च रोगजनकता को दर्शाते हैं। आंध्र प्रदेश, झारखंड, महाराष्ट्र और ओडिशा से मुर्गियों, बाघ और तेंदुए से पृथक किए गए एच5एन1 विषाणु वंश 2.3.2.1a से संबंधित थे, जबकि केरल और राजस्थान से बत्तख, मुर्गी, बटेर और वन्य पक्षियों से पाए गए एच5एन1 विषाणु वंश 2.3.4.4b से संबंधित पाए गए। इससे यह स्पष्ट होता है कि वर्ष 2024 में भारत में एच5एन1 विषाणु के दोनों वंश एक साथ परिसंचारित हो रहे थे। इसके अतिरिक्त, वंश 2.3.2.1a से संबंधित दो मुर्गी विषाणु नमूनों में N295S उत्परिवर्तन (न्यूरामिनीडेस जीन की क्रम संख्या अनुसार) पाया गया, जो न्यूरामिनीडेस अवरोधकों के प्रति प्रतिरोधकता का संकेत देता है। भारत में पहली बार एच5एन1 विषाणु की पहचान वन्य स्तनधारियों (बाघ और तेंदुआ) में हुई, जो इस विषाणु के होस्ट रेंज (आमंत्रक दायरा) में विस्तार को दर्शाती है। यह स्थिति देश में एच5एन1 विषाणु के प्रकोप की लगातार निगरानी, प्रारंभिक पहचान तथा नियंत्रण की आवश्यकता को अत्यंत महत्वपूर्ण बनाती है।

- **जल भैंसों को संक्रमित करने वाले एलएसडीवी का आनुवंशिक और फ़ायलोजेनेटिक विश्लेषण:** वर्ष 2020 से 2024 के दौरान भैंसों में लंपी स्किन डिज़ीज़ वायरस (एलएसडीवी) से संक्रमित मामलों के आनुवंशिक और वंशवृत्तीय विश्लेषण में यह पाया गया कि भारतीय भैंसों में एलएसडीवी की दो भिन्न वंशावलियों (1.2.1 और 1.2.2) के वाइल्ड-टाइप विषाणु परिसंचारित हो रहे हैं। इसके साथ ही, एक ही क्षेत्र में एलएसडीवी के एकाधिक उप-समूहों (सब-क्लस्टर्स) के सह-परिसंचरण के प्रमाण भी मिले हैं।

- **बॉर्डर डिज़ीज़ वायरस का आनुवंशिक विश्लेषण:** लगातार संक्रमित प्रवासी भेड़ों से उत्पन्न बॉर्डर डिज़ीज़ वायरस (बीडीवी) के आनुवंशिक विश्लेषण से यह स्पष्ट हुआ कि भारत में परिसंचारित बीडीवी-3 वंश के विषाणु में उच्च आनुवंशिक विविधता पाई जाती है, जो इसके व्यापक प्रसार और विकास को दर्शाता है।

- **महाराष्ट्र में एलएसडी**-निगेटिव भैंसों में बफैलोपॉक्स के प्रयोगशाला द्वारा पुष्टि किए गए तीन मामले सामने आए हैं। बफैलोपॉक्स विषाणु (बीपीएक्सवी) के ATI, B5R और C18L जीनों में किए गए आनुवंशिक विश्लेषण से यह ज्ञात हुआ कि इसके अनुक्रम भारत में पूर्व में मानव और भैंसों से प्राप्त बीपीएक्सवी नमूनों से अत्यधिक मिलते-जुलते हैं। यह स्थिति बीपीएक्सवी के संभावित जूनोटिक प्रभाव की निगरानी की आवश्यकता को स्पष्ट रूप से रेखांकित करती है।

- **सम्पूर्ण जीनोम अनुक्रमण:** मिज़ोरम राज्य से प्राप्त घरेलु शूकर तथा वन्य शूकर के नमूनों से पृथक किए गए अफ्रीकी स्वाइन फीवर वायरस के पूर्ण जीनोम (189,390 bp and 190,489 bp) अनुक्रम का विश्लेषण किया गया। वन्य शूकर से पृथक किए गए एएसएफवी जीनोम (190,489 bp) का जॉर्जिया/2007 संदर्भ विषाणु से तुलनात्मक अनुक्रमण करने पर अनेक महत्वपूर्ण उत्परिवर्तन देखे गए, जिनमें न्यूक्लियोटाइड की हानियाँ (डिलीशन), समावेशन (इन्सर्शन) शामिल थे, जो कि कई जीनों में फ्रेम-शिफ्ट और प्रोटीन के समय से पहले समाप्त होने (प्रोटीन ट्रंकेशन) का कारण बने। विश्लेषण में एक विशिष्ट उत्परिवर्तन एमजीएफ-360-21आर जीन में पाया गया, जिसमें 50 न्यूक्लियोटाइड की हानि हुई, जिसके फलस्वरूप कार्बॉक्सिल अंतिम छोर (सी-टर्मिनस) पर 30 अमीनो अम्लों की कटौती हुई। घरेलु शूकर और वन्य शूकर मूल के अन्य एएसएफवी नमूनों के साथ की गई तुलना से यह संकेत मिलता है कि एमजीएफ-360-21आर जीन वन्य शूकरों में विकासीय अनुकूलन की प्रक्रिया के दौरान आनुवंशिक परिवर्तनों के प्रति संवेदनशील होता है।

- **सार्स कोरोना वायरस-2 के विरुद्ध कॉर्डिसेप्स मिलिटैरिस की औषधीय संभावनाओं की खोज:** इन-सिलिको एवं इन-विट्रो अध्ययन: कॉर्डिसेप्स मिलिटैरिस में पाए जाने वाले जैवसक्रिय यौगिक कॉर्डिसेपिन की सार्स कोरोना वायरस-2 स्पाइक प्रोटीन से बाँधने की क्षमता का मूल्यांकन आणविक डॉकिंग (मॉलिक्यूलर डॉकिंग) तकनीक द्वारा किया गया। विश्लेषण से यह ज्ञात हुआ कि कॉर्डिसेपिन की स्पाइक प्रोटीन से सबसे अधिक बाँधने की प्रवृत्ति (बाइंडिंग एफिनिटी) है। वेरो-ई6 कोशिकाओं में कॉर्डिसेप्स मिलिटैरिस के कच्चे जलीय अर्क (100 माइक्रोग्राम प्रति मिलीलीटर) के प्रयोग से इन-विट्रो परिस्थितियों में विषाणु कणों की संख्या में 50.24% की कमी देखी गई। यह निष्कर्ष संकेत देते हैं कि कॉर्डिसेप्स मिलिटैरिस में प्रतिसंक्रामक (एंटी-वायरल) गतिविधि की पर्याप्त संभावना है और इसे न केवल सार्स कोरोना वायरस-2 बल्कि जनस्वास्थ्य एवं पशु स्वास्थ्य के दृष्टिकोण से अन्य महत्वपूर्ण विषाणुओं के विरुद्ध परंपरागत औषधि के रूप में भी विकसित किया जा सकता है।

रोग निगरानी

☞ एवियन इन्फ्लूएंजा

- एवियन इन्फ्लूएंजा वायरस निगरानी के तहत देश के विभिन्न भागों से प्राप्त कुल 66,702 नमूनों (53,532 रोगसूचक पदार्थ और 13,170 सीरा) का परीक्षण किया गया। निष्क्रिय निगरानी में, परीक्षण किए गए 1192 संदिग्ध नमूनों में से, पाँच राज्यों (आंध्र प्रदेश - 07, झारखंड-02, केरल- 392, महाराष्ट्र-01, ओडिशा- 81 और राजस्थान-04) से कुल 487 नमूने H5N1 नोटिफ़ायबल AIV के लिए सकारात्मक पाए गए

और केरल से 3 सीरा नमूने H5 वायरस एंटीबॉडी के लिए सकारात्मक पाए गए। केरल से बीस नमूने NDV के लिए सकारात्मक पाए गए।

- सक्रिय निगरानी के दौरान, 48,125 रोगग्रस्त नमूनों में से, दस राज्यों/केंद्र शासित प्रदेशों (आंध्र प्रदेश-01, बिहार-04, छत्तीसगढ़-17, हिमाचल प्रदेश-01, झारखंड-10, मध्य प्रदेश-35, महाराष्ट्र-12, ओडिशा-62, पंजाब-06 और राजस्थान-23) के 171 नमूने एच9एन2 एवियन इन्फ्लूएंजा वायरस के लिए सकारात्मक पाए गए और नौ राज्यों (आंध्र प्रदेश-03, गुजरात-30, हिमाचल प्रदेश-04, जम्मू-03, केरल-20, महाराष्ट्र-12, ओडिशा-24, पंजाब-08 और राजस्थान-05) के 109 नमूने न्यूकैसल रोग वायरस के लिए सकारात्मक पाए गए। परीक्षण किए गए 11,170 सीरा नमूनों में से, छह राज्यों (आंध्र प्रदेश-01, गुजरात-09, केरल-02, ओडिशा-36 और राजस्थान-07) से कुल 55 सीरा नमूने एच9 एंटीबॉडी के लिए सकारात्मक थे। नौ राज्यों/केंद्र शासित प्रदेशों (आंध्र प्रदेश-18, छत्तीसगढ़- 46, गुजरात-03, झारखंड-03, केरल- 02, नई दिल्ली-04, ओडिशा-29 राजस्थान-06 और पश्चिम बंगाल-13) से कुल 124 सीरा एनडीवी एंटीबॉडी के प्रति पॉजिटिव थे। छत्तीसगढ़ से कुल छह सीरा नमूने एच9 और एनडीवी दोनों एंटीबॉडी के लिए पॉजिटिव थे। पीओएसपी के तहत प्राप्त कुल 4315 स्वाब नमूनों में से 22 नमूने (झारखंड-10 और महाराष्ट्र-12) एच9एन2 एवियन इन्फ्लूएंजा वायरस के लिए पॉजिटिव पाए गए। महाराष्ट्र से 12 और ओडिशा से 03 सहित कुल पंद्रह नमूने एनडीवी के लिए पॉजिटिव पाए गए। पीओएसपी के तहत प्राप्त 1,900 सीरा नमूनों में से केरल के 06 नमूने एच9 वायरस एंटीबॉडी के खिलाफ पॉजिटिव पाए ।

☞ लम्पी स्किन डिजीज (एलएसडी)

- भारत में पहली बार घरेलू भैंसों में गांठदार त्वचा रोग (एलएसडी) के उभरने की सूचना मिली, जो भारतीय भैंसों में प्राकृतिक एलएसडीवी संक्रमण के प्रति संवेदनशीलता को दर्शाता है। भैंसों में एलएसडीवी संक्रमण के आणविक सबूत तीन राज्यों में पाए गए, जबकि एलएसडीवी संक्रमण के सीरोलॉजिकल सबूत छह राज्यों में पाए गए।
- वर्ष 2024 के दौरान, चार राज्यों (तमिलनाडु, पंजाब, पश्चिम बंगाल, आंध्र प्रदेश और मध्य प्रदेश) के मवेशियों में गांठदार त्वचा रोग (एलएसडी) के प्रयोगशाला द्वारा पुष्टि किए गए मामलों का पता चला है।

☞ स्वाइन रोग

- देश के 9 राज्यों से एकत्रित कुल 204 शूकर नमूनों में से 68 नमूने अफ्रीकी स्वाइन फीवर वायरस के लिए पॉज़िटिव पाए गए। यह संक्रमण आंध्र प्रदेश (2 नमूने), हरियाणा (6), कर्नाटक (6), केरल (15), मध्य प्रदेश (7), महाराष्ट्र (15), राजस्थान (11) और सिक्किम (6) राज्यों के शूकरों में पाया गया।
- मध्य प्रदेश और असम से प्राप्त सूअरों के मल के नमूनों के मल मेटावायरोम अनुक्रमण और विश्लेषण से वायरस के परिवारों में उच्च विविधता का पता चला।
- छत्तीसगढ़, मध्य प्रदेश, महाराष्ट्र और सिक्किम से प्राप्त कुल 148 शूकर नमूनों की पीआरआरएस वायरस जीनोम की जांच आरटी-पीसीआर तकनीक द्वारा की गई। परीक्षण परिणामों में सभी नमूने निगेटिव पाए गए।
- मध्य प्रदेश, असम, केरल और छत्तीसगढ़ राज्यों से एकत्रित कुल 234 शूकर नैसल स्वैब नमूनों की रीयल-टाइम पीसीआर विधि द्वारा जांच की गई, जिसमें सभी नमूने शूकर इन्फ्लुएंजा ए वायरस के लिए निगेटिव पाए गए। इसके अतिरिक्त, सिक्किम, बिहार, झारखंड, असम, मध्य प्रदेश, केरल और छत्तीसगढ़ से प्राप्त कुल 265 शूकर सीरम नमूनों की हीमैग्लूटिनेशन इनहिबिशन परीक्षण द्वारा जांच की गई, जिसमें 28 नमूने H1 एंटीबॉडी की उपस्थिति के लिए पॉज़िटिव पाए गए।
- असम (80 नमूने), मेघालय (22), छत्तीसगढ़ (35) और केरल (23) से एकत्रित कुल 160 शूकर मल नमूनों की जांच पोर्साइन एपिडेमिक डायरिया और ट्रांसमिसिबल गैस्ट्रोएंट्राइटिस वायरस के जीनोम की उपस्थिति के लिए की गई। सभी नमूने इन दोनों वायरस के लिए निगेटिव पाए गए।

☞ जूनोटिक रोग

- केरल, मध्य प्रदेश और असम से प्राप्त कुल 73 वन्य और घरेलु पशु नमूनों की जांच सार्स कोरोना वायरस-2, वेस्टनाइल वायरस, मंकीपॉक्स, क्यासनूर फारेस्ट डिजीज तथा हेपाटाइटिस ई विषाणुओं के लिए की गई। सभी नमूने इन पांचों विषाणुओं के लिए निगेटिव पाए गए।
- मध्य भारत की कृंतक आबादी में जूनोटिक रोगजनकों की निगरानी: महाराष्ट्र के नागपुर और उदगीर क्षेत्रों से कुल 74 कृंतकों (रोडेंट्स) की आंतों और अंगों के नमूनों का संग्रह किया गया। इन नमूनों की जांच मंकीपॉक्स वायरस, हंटा वायरस, क्रीमियन-कांगो हेमोरेजिक फीवर वायरस,

क्यासानुर फारेस्ट डिजीज वायरस, सार्स कोरोना वायरस-2, कॉक्सिएला बर्नेटी (क्यू फीवर), ओरिएंटिया त्सुत्सुगामुशी (स्क्रब टाइफस), और रिकेट्सिया जीनस प्रजातियों के लिए की गई। इनमें से पहले सात रोगजनकों की जांच रीयल-टाइम पीसीआर द्वारा तथा अंतिम रोगजनक की जांच पारंपरिक पीसीआर तकनीक से की गई। जांच किए गए सभी नमूनों में कोई भी रोगजनक उपस्थित नहीं पाया गया।

- मानव संक्रमण के पश्चात पशुओं एवं पर्यावरण में निपाह वायरस की जांच के लिए राष्ट्रीय संयुक्त प्रकोप प्रतिक्रिया दल द्वारा एक व्यापक जांच अभियान चलाया गया। इस जांच में मानव, पशुपालन एवं वन्यजीव क्षेत्रों के विशेषज्ञों की एक अंतर्विभागीय टीम सम्मिलित थी। केरल के मलप्पुरम ज़िले से विभिन्न पशु प्रजातियों के 39 नमूने तथा पर्यावरण से 26 नमूने एकत्र कर निपाह वायरस की जांच की गई। सभी नमूने निपाह वायरस के लिए निगेटिव पाए गए।
- केरल की पशुधन जनसंख्या में क्रीमियन-कांगो हेमोरेजिक फीवर वायरस (सीसीएचएफ वायरस) की सेरो-प्रचलन स्थिति का अध्ययन : सीसीएचएफवी सीरो-प्रचलन अध्ययन में मवेशियों, बकरियों और भैंसों के 300 सीरम नमूनों के परिक्षण से पता चला कि सीसीएचएफवी सीरो-प्रचलन 2.34% है, तथा मवेशियों और बकरियों में प्रजाति-वार सीरोपॉजिटिविटी क्रमशः 1.01% और 5.10% है।
- मध्य प्रदेश से एकत्रित टिक्स में वायरल विविधता: मध्य प्रदेश से एकत्र किए गए राइपिसिफेलस और हायलोमा वंश की किलनियों के संकलित नमूनों के विषाणु समूह (वायरोम) का विश्लेषण में अनेक प्रमुख विषाणु कुलों जैसे कि फ्लैविविरिडी, ऑर्थोमिक्सोविरिडी, रियोविरिडी, नैरोविरिडी, पार्वोविरिडी, फ्लीबोवायरस, एरेनाविरिडी तथा सिम्बू सेरोग्रुप विषाणु से संबंधित आनुवंशिक प्रमाण प्राप्त हुए।

पोषक-रोगजनक अंतःक्रिया अध्ययन

- **एच5 विषाणु का गिनी पिग में संचरण:** क्लेड 2.3.4.4b के एच5एन1 विषाणु के संपर्क-संचरण की क्षमता का मूल्यांकन गिनी पिग में किया गया। छह गिनी पिग को विषाणु से संक्रमित किया गया और 24 घंटे बाद छह अन्य गिनी पिग को संपर्क समूह में शामिल किया गया। संक्रमित गिनी पिग की नासिका से एकत्र धोवन (नेज़ल वॉश) में विषाणु का आरएनए आरटी-क्यूपीसीआर द्वारा पाया गया। संक्रमित समूह के सभी पशुओं में 7 दिनों तक लगातार विषाणु जीनोम की उपस्थिति दर्ज की गई। सभी संक्रमित गिनी पिग में एच5एन1 के प्रति एंटीबॉडी निर्मित हुई (सेरो-कन्वर्ज़न), जबकि संपर्क में आए समूह में केवल एक पशु में ही एंटीबॉडी प्रतिक्रिया देखी गई। यह अध्ययन दर्शाता है कि एच5एन1 क्लेड 2.3.4.4b विषाणु स्तनधारियों में किसी पूर्व अनुकूलन (एडेप्टेशन) के बिना भी संक्रमित पशु से संपर्क पशु में संचरित हो सकता है।
- **कोविड-19 संक्रमित बिल्ली और कुत्ते के फेफड़ों के एक्सप्लांट कल्चर का ट्रांसक्रिप्टोम विश्लेषण:** बिल्ली एवं कुत्ते के फेफड़ों की ऊतक-संस्कृति (लंग एक्सप्लांट) में कोविड-19 के रोगजनन तंत्र को समझने हेतु ट्रांसक्रिप्टोम विश्लेषण किया गया। विश्लेषण में यह पाया गया कि संक्रमण के 24 घंटे पश्चात कुत्तों में ऊतक पुनरुत्थान (टिशू रिपेयर) से संबंधित जीन सक्रिय हो गए थे, जो ऊतक सुधार की संभावना को दर्शाता है। इसके विपरीत, बिल्लियों में ऐसा कोई जीन सक्रियण नहीं पाया गया, जिससे संकेत मिलता है कि वे फेफड़ों की क्षति के प्रति अधिक संवेदनशील हो सकती हैं।
- **एच5एन1 से संक्रमित मुर्गियों का मेटाबोलोमिक्स विश्लेषण:** मुर्गियों के फेफड़ों में किए गए मेटाबोलोमिक्स विश्लेषण से यह ज्ञात हुआ कि संक्रमण के दौरान स्फिंगोलिपिड चयापचय, ट्रिप्टोफेन चयापचय, तथा आर्जिनीन-प्रोलिन चयापचय में महत्वपूर्ण बदलाव हुए। विश्लेषण से यह संकेत मिला कि इन्फ्लुएंज़ा विषाणु स्फिंगोलिपिड चयापचय का उपयोग पोषद- रोगजनक अंतःक्रिया को नियंत्रित करने हेतु करता है। ट्रिप्टोफेन चयापचय में बदलाव से सूजन तथा केन्द्रीय तंत्रिका तंत्र से जुड़ी जटिलताएँ उत्पन्न हो सकती हैं, जो एच5एन1 संक्रमण की विशेषता है।

नैदानिक सेवाएं

- विभिन्न पशु संगरोध एवं प्रमाणीकरण सेवाओं से प्राप्त कुल 8890 नमूनों (आयातित पशुधन, कुक्कुट एवं संबंधित उत्पादों) की जांच विभिन्न विदेशज एवं नवागत रोगजनकों की उपस्थिति के लिए की गई। इनमें एवियन इन्फ्लुएंजा (6920 नमूने), पोर्सिन रिप्रोडक्टिव एंड रेस्पिरेटरी सिंड्रोम (298), अफ्रीकी स्वाइन फीवर (323), मैलिग्नेंट कैटर्रल फीवर (53), नैरोबी शीप डिज़ीज़ (53), रिफ्ट वैली फीवर (41), कैप्राइन आर्थ्राइटिस एवं एन्सेफेलाइटिस (52), बोवाइन वायरल डायरिया (257), स्वाइन इन्फ्लुएंजा (237), ऑजेस्की रोग (217), पोर्साइन एपिडेमिक डायरिया (216), ट्रांसमिसिबल गैस्ट्रोएंट्राइटिस (216), लंपी स्किन डिज़ीज़ (06), तथा रैबिट हेमोरेजिक डिजीज (01) जैसे रोग शामिल थे। सभी नमूने इन रोगों के लिए नकारात्मक (निगेटिव) पाए गए ।

Research Achievements

Development of vaccines

☞ Selection of Candidate vaccine H5N1 virus strain:

Phylogeny was constructed using HA gene sequence of 73 H5Nx sequences from India. These included, 38 clade 2.3.2.1a H5N1, 11 clade 2.3.4.4b H5N1 and 25 clade 2.3.4.4b H5N8 viruses isolated over a period of 2011-2024. Based on the phylogeny, a total of 14 H5Nx viruses (6 from 2.3.2.1a and 8 from 2.3.4.4b clades) were chosen for antisera generation. The viruses were revived in 9-11 day old embryonated SPF chicken eggs. The viruses were inactivated in 0.1% BPL as per the standard procedure. The inactivation was confirmed by passaging three times in embryonated chicken eggs. Emulsion of FCA and allantoic fluid was prepared and three birds were inoculated with 0.5 ml of emulsion each for every virus for antisera raising. The birds were boosted with 0.5 ml emulsion of FIA and allantoic fluid on 21st day. Serum was collected on 35th day of primary inoculation. The antisera has been raised against seven 2.3.4.4b viruses and seven 2.3.2.1a viruses. Cross neutralization studies have revealed one of the clade 2.3.4.4b virus isolated from quail from Kerala as a probable candidate vaccine H5N1 virus strain. The growth kinetics of the virus studied in 9-11 day old embryonated chicken eggs revealed a peak HA titre of 211 in 48 hours – aliquoted (0.5 ml) and stored under -800C. The virus was inactivated in 0.1% BPL as per the standard procedure. The inactivation was confirmed by passaging three times in embryonated chicken eggs. Emulsified with Montanide ISA 71 RVG (Sepic) in the ratio of 40:60 as per standard procedure (antigen dose 29 per 0.5 ml). The animal experimentation for potency testing is underway.

☞ Monitoring of antigenic divergence of H9N2 field isolates with the approved vaccine strain:

A total of eight H9N2 viruses isolated during 2024 from chickens and the environment in the states of Chhattisgarh, Jharkhand, Madhya Pradesh, and Odisha were tested for antigenic monitoring by Hemagglutination inhibition (HI) assay using chicken antisera raised against the approved vaccine strain A/chicken/India/22213/06 (H9N2). The HI titre of the serum of the approved vaccine strain against homologous virus is 29 and the HI titres against the H9N2 isolates ranged from 28 to 211. These results indicate close antigenic relationship of the currently circulating H9N2 viruses with the approved H9N2 vaccine strain.

☞ Evaluation of BVD vaccine safety, immunogenicity and efficacy in experimental and field cattle

As BVD is one of the major causes of reproductive disease in cattle, vaccination against BVD is advocated as it enhances herd level immunity, reduces clinical disease and prevents fetal infection and generation of PI calf. However, BVD vaccine is not available in India so far. To prevent BVDV infection in cattle, ICAR-NIHSAD has developed an inactivated BVDV whole virus vaccine using a BVDV-1 field isolate. The vaccine passed the sterility test and showed no adverse effects in guinea pigs when tested for safety by injecting 1.0 ml vaccine by intramuscular route followed by booster on 28th day. To evaluate vaccine safety, immunogenicity and efficacy in experimental cattle, BVDV vaccine was inoculated in 9-12 months cattle calves intramuscularly followed by booster on 28th day of primary dose. The vaccine was found to be safe, immunogenic, potent and efficacious in preventing clinical disease upon challenge with BVDV-1. It provides protective immunity (neutralizing antibody titre of 1:128) up to 12 months following booster vaccination (Figure: 1) and covers divergent strains of BVDV-1 circulating in India, besides providing partial protection against BVDV-2 and HoBiPeV. Fetal protective antibody titre (1:512) was persisted for 5 months post vaccination. Vaccine safety and immunogenicity trial in field cattle also showed promising results, as demonstrated by protective antibody titre (1:128) in 74% cattle, fetal protective titre (1:512) in 48% cattle and 1: 64 titre in 91.0% cattle up to the assessed period of 6 months following the booster vaccination (Figure: 2 and Figure: 3).

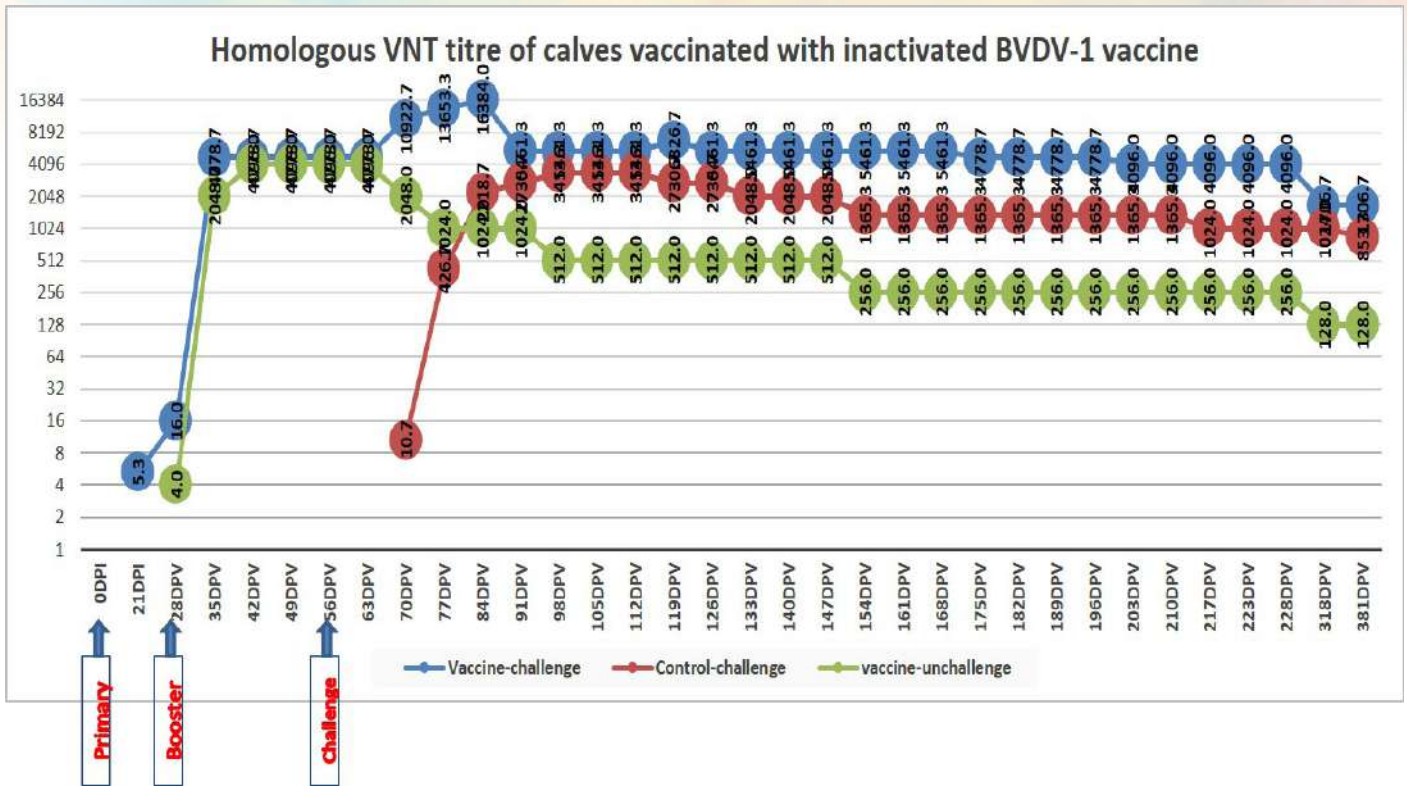


Figure:1. *Immunogenicity of inactivated BVD vaccine in experimental cattle.*

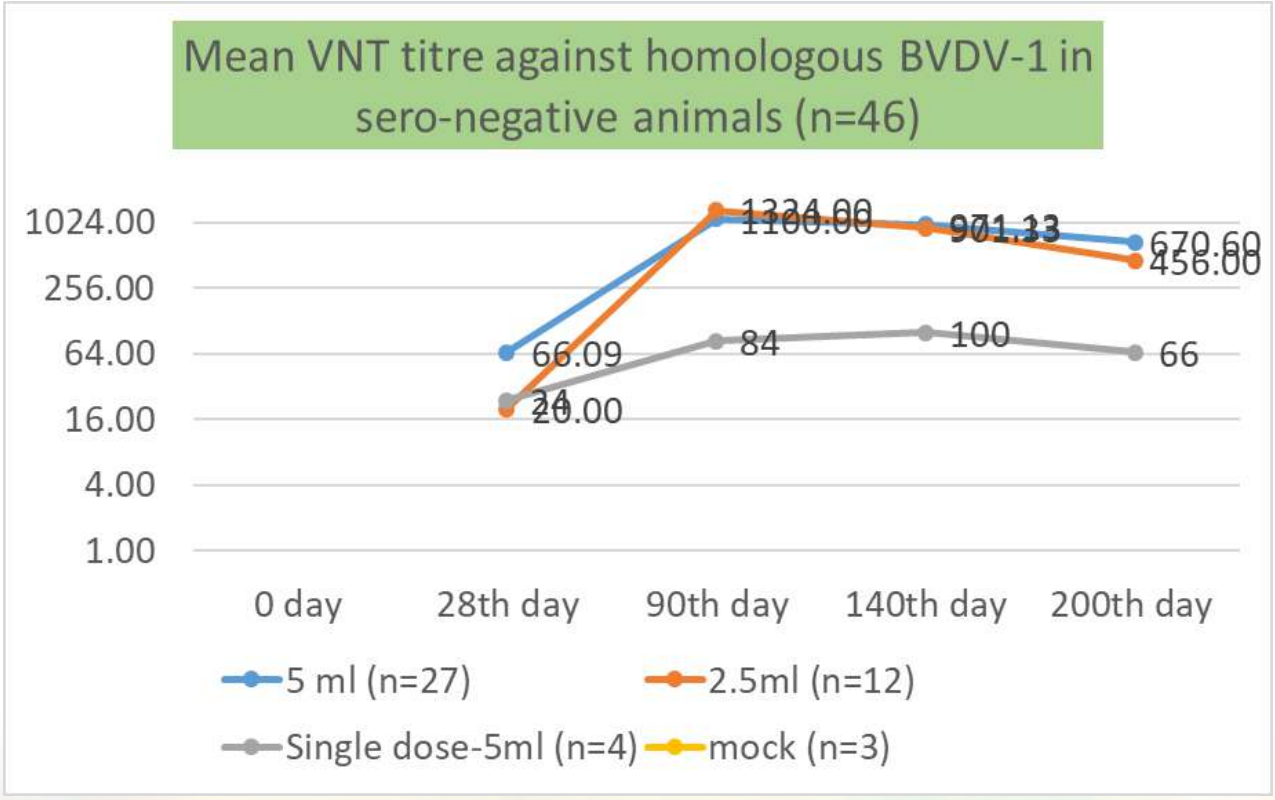


Figure:2. *Immunogenicity of inactivated BVD vaccine in BVD sero-negative field cattle.*

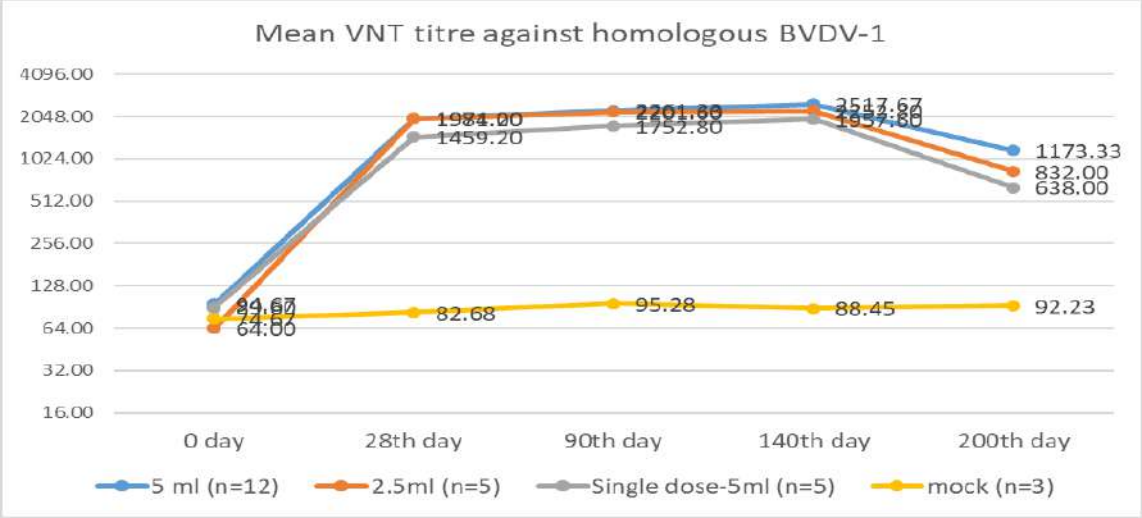
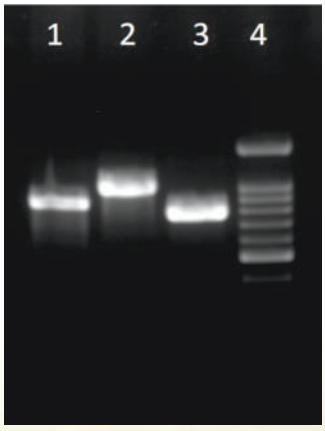


Figure: 3. *Immunogenicity of inactivated BVD vaccine in BVD sero-positive field cattle.*

☞ Generation of a gene-deleted African swine fever virus using CRISPR/Cas9 gene editing technology

African swine fever is the most dreaded disease confronting the swine farmers worldwide. Due to lack of effective treatment or vaccination, control measures mainly revolve around culling of all pigs in the affected premises and implementation of biosecurity protocols. To identify vaccine candidates, deletion of genes related to the virulence of the virus is a promising approach. We report the successful deletion of a virulence related gene of Indian ASFV using the CRISPR/Cas 9 gene editing technology. Plasmid vector constructs capable of expressing cas9 protein, GFP and target gRNA were prepared for deletion of the desired target gene (not disclosed) of ASFV. For facilitating homology directed repair (HDR) after CRISPR/cas9 induced DNA break and for visualization of the mutant virus in cell culture, a reporter gene template containing left and right homology arms and a reporter gene (red) was designed. The arms and the reporter gene were amplified by PCR using specific primers (Figure: 4). Fusion PCR was carried out to prepare the HDR template, and the fusion product was cloned in to pUC19 linearized vector.Transfection grade plasmids containing HDR template were prepared. ASFV infected cells were co-transfected with both the plasmids and observed for fluorescence. Appearance of green and red fluorescence within 72 hours post transfection (hpt) (Figure: 5A), and expansion of red fluorescence on subsequent passages (Figure: 5B) indicated the generation of gene deleted mutant ASF virus. Deletion of the target gene was confirmed by PCR (Figure: 6) and nucleotide sequencing. The mutant virus was purified using a combination of limiting dilutions and plaque purification (Figure: 5C). The mutant virus is being assessed for their virulence attenuation in piglets.



Lane 1- Left arm, Lane 2- reporter gene, Lane 3 – Right arm, Lane 4 – 100 bp DNA ladder
Figure: 4. PCR amplification products of target gene arms and reporter gene

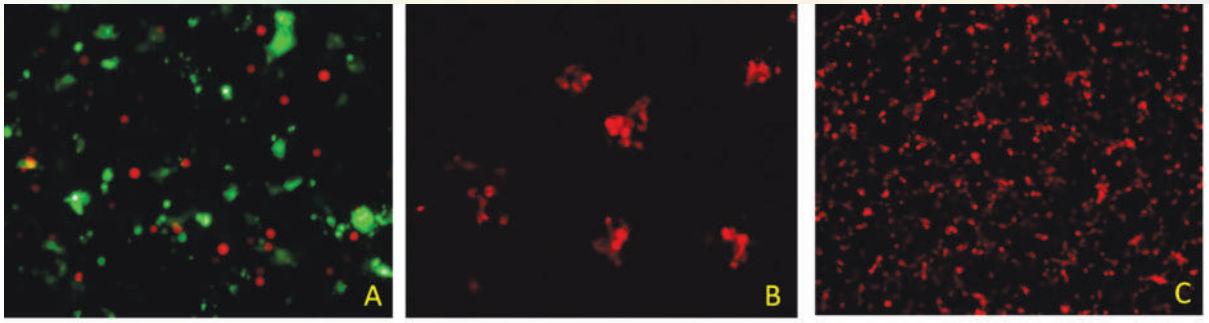
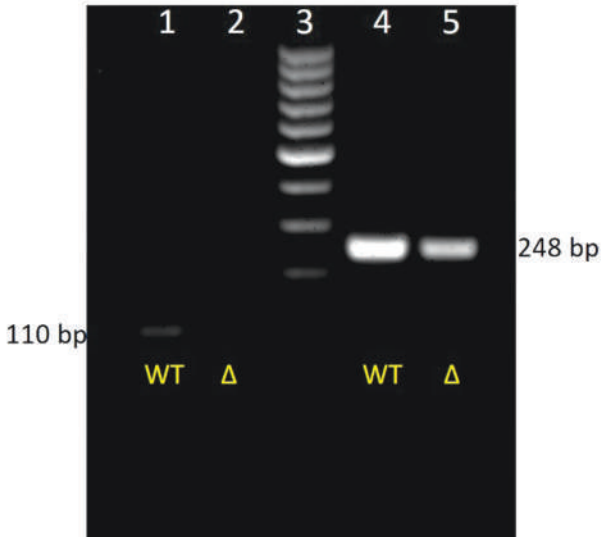


Figure: 5A. *Transfected ASFV infected cells showing green and red fluorescence within 72 hpt, B. Expanding plaques of mutant ASFV, P3, 72 hpi; C. Purified gene-deleted mutant ASF virus showing red fluorescence, P9*



Lane 1 – Wild type ASFV showing PCR amplification with internal primers of target gene, Lane 2- gene-deleted mutant ASFV showing absence of amplification with internal primers of target gene, Lane 3 – 100 bp DNA ladder, Lane 4 and 5 – Both wild type and mutant ASFV showing amplification with a non-target gene

Figure: 6. *Confirmation of target gene deletion in mutant ASF virus by PCR*

☞ Generation of a recombinant Adenovirus expressing ASFV protein

As part of a viral vector-based approach for generating ASFV vaccine candidates, the E183L gene, which encodes the P54 structural protein of ASFV, was amplified from an Indian ASFV isolate using gene-specific primers. The amplified gene was cloned into a commercial adenoviral shuttle vector and transformed into *E. coli* competent cells for plasmid propagation. Successful transformation was confirmed through colony PCR, and NheI and XhoI restriction enzyme digestion analysis (Figure: 7), validating the correct insertion of the E183L gene. The recombinant plasmid was then bulk propagated and linearized using the PacI restriction enzyme to expose the inverted terminal repeats (ITRs), essential for adenoviral genome packaging. The linearized plasmid was transfected into AdenoX™ 293 cells to rescue the recombinant adenovirus expressing the E183L gene. The recombinant adenovirus was successfully rescued, as indicated by the appearance of cytopathic effects (CPE) and green fluorescence in transfected cells, confirming expression from the GFP reporter cassette (Figure: 8). Confirmation of adenovirus production was done using a lateral flow assay targeting the adenoviral hexon protein. Further characterization of rescued recombinant adenovirus for expression of ASFV protein and immunogenicity evaluation is under progress.

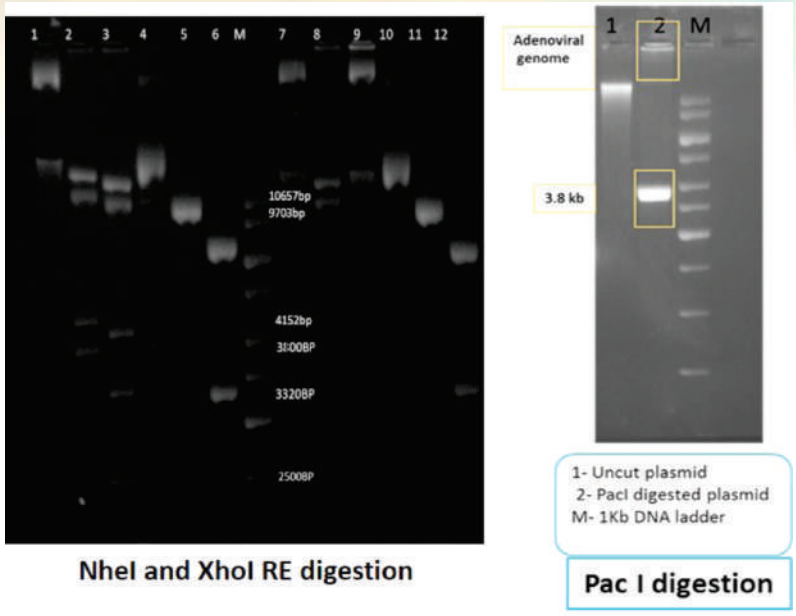


Figure :7. *Confirmation of recombinant adenoviral construct by RE digestion and linearization to expose ITR.*

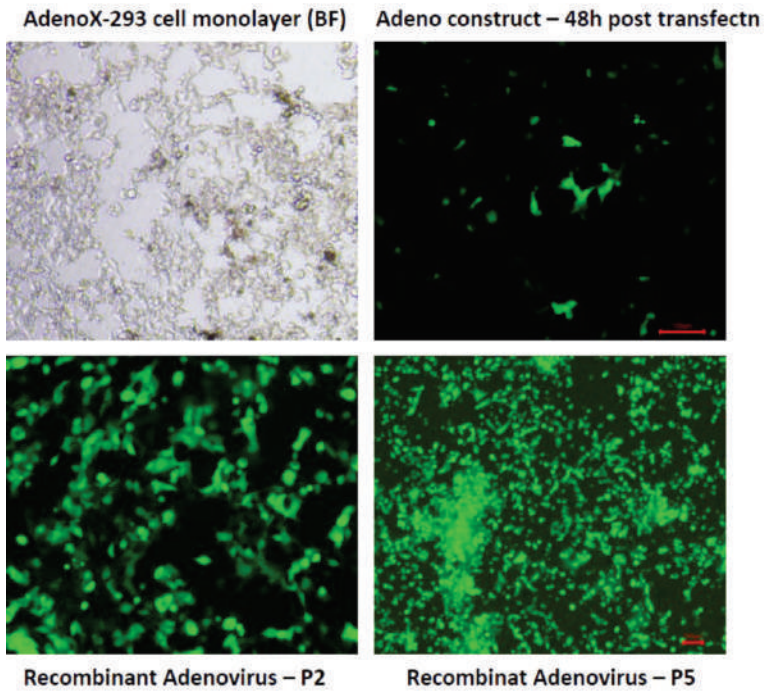


Figure:8. *Rescue of Recombinant Adenovirus after transfection on to AdenoX-293 cell and its propagation.*

☞ Inactivated ASFV vaccine formulations with or without immunostimulant were immunogenic but not protective against virulent ASF virus in pigs

An Indian ASF virus (Ind/NIHSAD/Sw-2022/1055) isolated from clinical samples received from Punjab, propagated to a titre of 106.83 HAD 50/ml, was inactivated using 3mM BEI and absence of residual infectivity was confirmed by 3 blind serial passages in MA-104 cells. Two vaccine formulations were prepared. One contained the inactivated ASFV (IA) adjuvanted with Montanide ISA 206 (IA-1) and the other formulation contained adjuvanted IA plus an immunostimulant (Poly I:C) (IA-2).

12 ASFV genome and antibody negative piglets aged between 2 to 3 months were divided into groups (G) of three animals each viz., G-1 (IA-1), G-2 (IA-2), G-3 (challenge control) and G-4 (healthy uninfected unimmunized control). Piglets in Groups 1 and 2 were inoculated with 2 ml of the respective immunogen formulation through intra-muscular route. Booster doses were administered on 21st and 56th day post-priming (dpp). Five out of the 6 immunized animals seroconverted by 28 dpp (except one animal in G-1). All the immunized pigs developed ASFV specific antibodies by 56th dpp (Figure: 9). None of the pigs in groups G-3 and G-4 seroconverted. Complete neutralization was not observed in any of the animals, although a reduction in the number of HAd positive cells was observed, indicating partial neutralization.

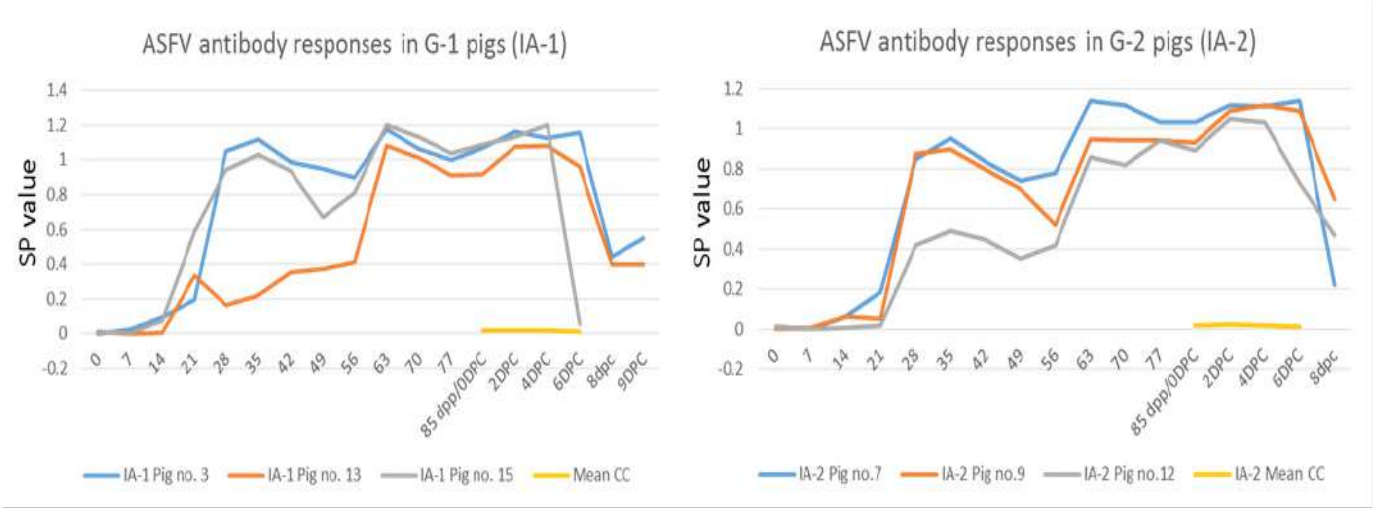
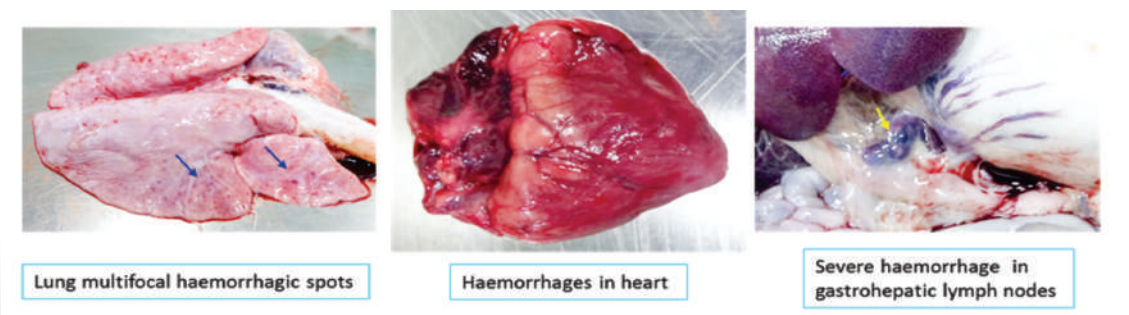


Figure: 9. *Antibody responses in groups of pigs immunized with inactivated vaccine formulations*

To evaluate protective efficacy, G1, G2 and G3 were challenged with 100 HAD 50 of virulent ASFV intra-muscularly. All the animals had fever which started around 5 dpc. There was a significant reduction in the ELISA SP values by 6 to 8 dpc. There was no significant difference in the serum viral copy numbers between the two immunized groups, whereas there was a significant difference between the serum viral copy numbers of immunized pigs and the challenge control pigs on 4 dpc. All pigs in G-1, G-2 and G-3 died between 8 and 11 dpc. On necropsy, all the pigs challenged with ASFV showed severe haemorrhagic lymph nodes. Moderate to severe splenomegaly, small multifocal haemorrhagic foci in lungs, petechial haemorrhages in kidneys, haemorrhages in small and large intestine were the other gross lesions observed in immunized and challenged pigs (Figure: 10). The challenge control pigs showed more severe haemorrhages in heart. Spleen, tonsils and lungs were the organs which had highest viral load whereas brain had the lowest. The results showed that both the inactivated vaccine formulations were immunogenic but not protective against virulent ASFV challenge.



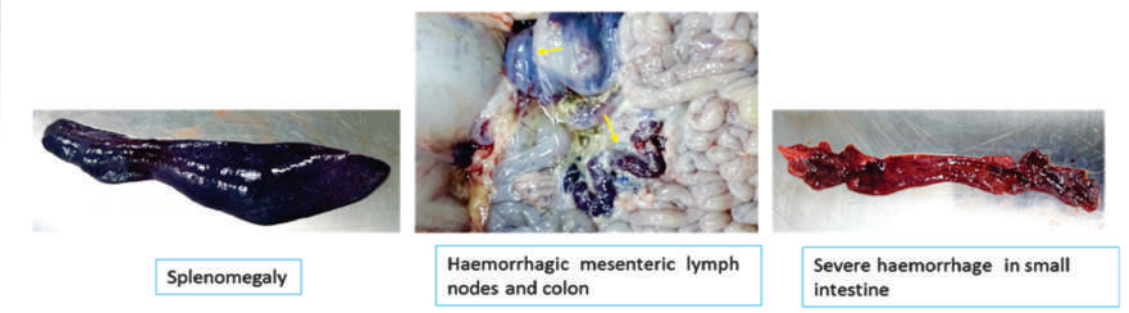


Figure: 10. *Representative pictures of gross lesions observed in pigs immunized with inactivated ASFV vaccine formulations after challenge with WT ASFV challenge*

☞ Development of an Inactivated SARS-CoV-2 Vaccine with Alum and CpG Adjuvants

The NASF-funded project entitled "Studies on host-pathogen interaction and development of vaccine against zoonotic coronaviruses" focused on the design and evaluation of an inactivated SARS-CoV-2 vaccine formulation. The vaccine development process emphasized optimizing antigen dose and adjuvant selection to elicit a robust and balanced immune response while minimizing adverse outcomes like vaccine-associated enhanced respiratory disease (VAERD).

The study began with the propagation of the SARS-CoV-2 Delta variant in VeroE6 cells, achieving a concentration of 2×10^3 TCID 50/ml. The virus was inactivated using beta-propiolactone, and its inactivation was confirmed across three consecutive passages. Protein concentration was enhanced over fivefold using Tangential Flow Filtration (TFF), yielding a preparation with a viral protein concentration of 1.0 μg/μl. SDS-PAGE analysis verified the presence of distinct nucleoprotein (55-60 kDa) and spike protein (150 kDa) bands, further validated by Western blotting. Dose optimization was conducted in a mouse model by administering varying doses (10 μg, 20 μg, and 30 μg) of inactivated virus with alum as an adjuvant, followed by boosting on Day 21. Immune responses, including antibody titers and virus-neutralizing assays, were assessed on Days 14, 28, and 35. The 20 μg dose consistently elicited the highest immune response with significant neutralizing antibody titers, establishing it as the optimal dose for subsequent experiments. The adjuvant evaluation study further tested the impact of CpG motifs, recognized as potent activators of Th1 responses via TLR9. Mice were divided into four groups, receiving antigen alone, antigen with alum, antigen with CpG, and antigen with a combination of alum and CpG. Blood samples collected on Days 21, 35, and 42 revealed that alum significantly enhanced antibody levels, while the addition of CpG promoted a pronounced Th1-biased response, as indicated by elevated mRNA levels of IFN-γ and IL-2. Importantly, the Antigen+Alum+CpG group demonstrated the most sustained immune response with high neutralizing titers and balanced Th1/Th2 cytokine profiles.

To validate these findings in a larger animal model, a parallel experiment was conducted in hamsters. Groups received similar treatments and were challenged with live SARS-CoV-2 on Day 50. Blood samples collected on Days 14, 21, 35, and 42 post-immunization, along with viral load assessments and lung pathology post-challenge, confirmed the superior efficacy of the Antigen+Alum+CpG formulation. By Day 56, this group exhibited the lowest viral RNA levels in lung tissues and absence of pathological lesions, suggesting strong protective efficacy. Cytokine analysis in hamsters corroborated the results observed in mice. IFN-γ and IL-2 levels were significantly elevated in the Antigen+Alum+CpG group, indicating a robust Th1 response. IL-4 levels were moderately enhanced, reflecting a maintained Th2 response, crucial for long-term humoral immunity. The vaccine formulation effectively balanced these immune pathways, providing comprehensive protection.

Overall, the study highlights the potential of combining alum and CpG adjuvants with an inactivated SARS-CoV-2 antigen to develop a vaccine with strong immunogenicity, a balanced immune profile, and robust protection against SARS-CoV-2 infection. These findings lay the foundation for advanced preclinical and clinical evaluations of this promising formulation.

Development of Diagnostics

☞ Selection of Monoclonal Antibody pair towards development of Lateral Flow Assay for Rapid Detection of Avian Influenza Virus

Monoclonal antibodies (MAbs) generated against the recombinant nucleoprotein (rNP) of avian influenza (AI) virus were evaluated for their suitability in a lateral flow assay (LFA) format to facilitate the development of an indigenous, rapid diagnostic test. A panel of previously characterized MAbs—10F8, 7E9, 2F12, 8E2, and 5D1—was screened in various combinations to identify the most effective capture and detector antibody pair. The combination of 10F8 as the capture antibody and 5D1 as the detector antibody demonstrated specific detection of the recombinant nucleoprotein with no false positive results, establishing it as a promising configuration for assay development (Figure:11). The assay was able to detect the recombinant protein at a concentration as low as 0.5 μg/ml, indicating a good preliminary sensitivity threshold (Figure: 11). The performance was consistent and specific, showing clean background and clear signal intensity. This optimization marks a critical milestone toward the development of a field-level diagnostic tool for avian influenza, offering an alternative to currently imported LFA kits that are often costly and less accessible in remote settings. Further work is underway to enhance the analytical sensitivity, improve stability under varied conditions, and validate the test using field samples. This monoclonal antibody-based LFA platform provides the foundation for a user-friendly, rapid, and specific detection system that can support early surveillance and response measures during outbreaks of avian influenza in poultry populations.

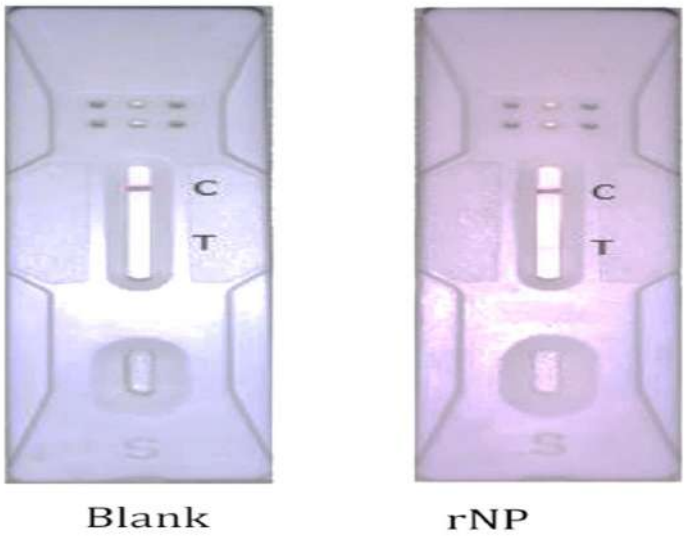


Figure: 11. *Lateral flow assay determining the capture & detection antibody pair detecting the rNP protein.*

☞ Polyclonal antibody purification using C- and N- terminal domains of avian influenza nucleoprotein for enhanced sensitivity in Lateral Flow Assays

To support the development of a broad-reactive lateral flow assay (LFA) for avian influenza (AI) virus detection, recombinant expression of AI nucleoprotein and production of polyclonal antibodies was carried out using a targeted strategy. The full-length recombinant nucleoprotein (rNP, ~61 kDa) of AI virus, along with its N-terminal (rNP-N, 36.71 kDa) and C-terminal (rNP-C, 30.88 kDa) halves, were successfully expressed in a bacterial system and purified through Ni-NTA affinity chromatography (Figure: 12). The purified proteins were confirmed via SDS-PAGE and characterized by western blot using reference anti-AI sera. To generate region-specific antibodies, affinity columns were developed by covalently coupling the purified rNP-N and rNP-C proteins to agarose bead supports. Polyclonal sera were raised in chickens against the full-length AI nucleoprotein, and the resulting antibodies were

selectively purified using these region-specific affinity columns (Figure: 13). The purified antibodies were further validated by ELISA and western blot analysis, confirming specificity to the corresponding terminal regions. The purified polyclonal antibodies against rNP-N and rNP-C were then conjugated to gold nanoparticles and evaluated as detector and capture antibodies in LFA format. The intent of this polyclonal approach is to increase the sensitivity and broaden the subtype coverage of the assay, potentially enabling detection of all H1–H16 subtypes of type A avian influenza viruses, irrespective of genetic drift or reassortment events. These developments represent a significant step toward integrating polyclonal antibody-based detection strategies within the LFA platform. Optimization and validation studies are ongoing to assess performance characteristics, and the approach is expected to complement the monoclonal-based format for improved field applicability and diagnostic robustness.

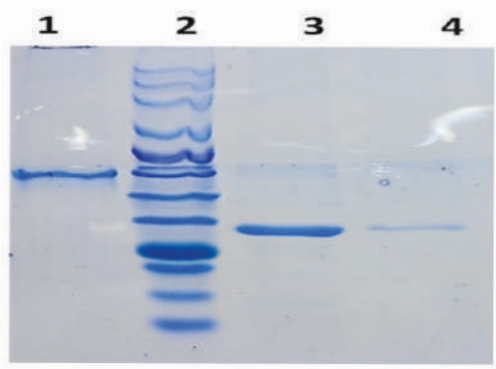


Figure: 12. *Expression and purification of rNP, rNP-N & rNP-C nucleoproteins of avian influenza virus. Lane# 1: Purified rNP, Lane# 2:Protein Ladder, Lane# 3: Purified rNP-N, Lane# 4: Purified rNP-C*

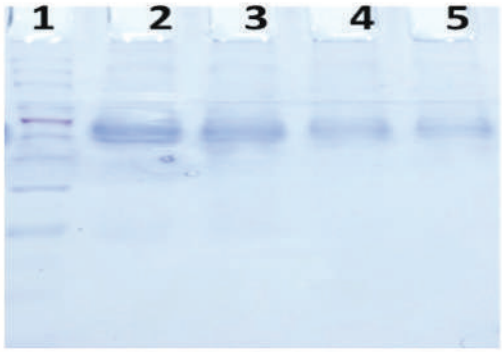


Figure:13. *Purification of polyclonal antibodies specific to rNP-N & rNP-C region of AI nucleoproteins. Lane# 1: Protein Ladder, Lane #2 & 3: Purified Polyclonal antibodies with INP-N Elution 1 & 2, Lane# 4 & 5: Purified Polyclonal antibodies with rNP-C Elution 1 & 2*

☞ Development of RT-qPCR for detection Porcine Epidemic Diarrhoea virus and Transmissible Gastroenteritis virus

A probe-based one-step reverse transcription (RT) real-time PCR was developed to detect the genome of PEDV. A gene construct, two pairs of primers, and a probe were designed by aligning N gene sequences from various PEDV strains, which were subsequently synthesized. The gene construct was sub-cloned into the pTZ57R/T vector, enabling the synthesis of in vitro transcribed (IVT) RNA, which served as a PEDV-positive control for RT-qPCR protocol optimization. The assay optimization involved systematic testing of various parameters, including annealing temperatures and other thermal variables, primer concentrations, probe concentration, and RNA template quantities. The analytical sensitivity was evaluated by examining serial 10-fold dilutions of IVT-RNA, both in actual form and when recovered from swine faeces after spiking with the same dilutions of IVT-RNA. The developed assay demonstrated an analytical sensitivity of ~2 RNA copies at 10-12 dilutions of IVT-RNA (Figure: 14). Specificity was confirmed by testing against TGEV, SIV, CSFV, and PRRSV and known PEDV-negative swine faecal or rectal swab samples (n = 250) collected from the field. The assay exhibited specific amplification for PEDV without cross-reactivity to TGEV, SIV, CSFV, PRRSV, or field samples. This one-step RT-qPCR assay proved to be both sensitive and specific for genomic detection of PEDV in pigs.

Similarly, a probe-based one-step reverse transcription real-time PCR was also optimised to detect the TGEV genome (Figure: 15). The developed assay demonstrated an analytical sensitivity of ~10 RNA copies by testing in 10-fold dilutions of IVT-RNA. Specificity was confirmed by testing against PEDV, SIV, CSFV, and PRRSV and known TGEV-negative swine faecal or rectal swab samples (n = 250) collected from the field. The assay exhibited specific amplification for TGEV without cross-reactivity to PEDV, SIV, CSFV, PRRSV, or field samples. The one-step RT-qPCR assay proved to be both sensitive and specific for genomic detection of TGEV in pigs.

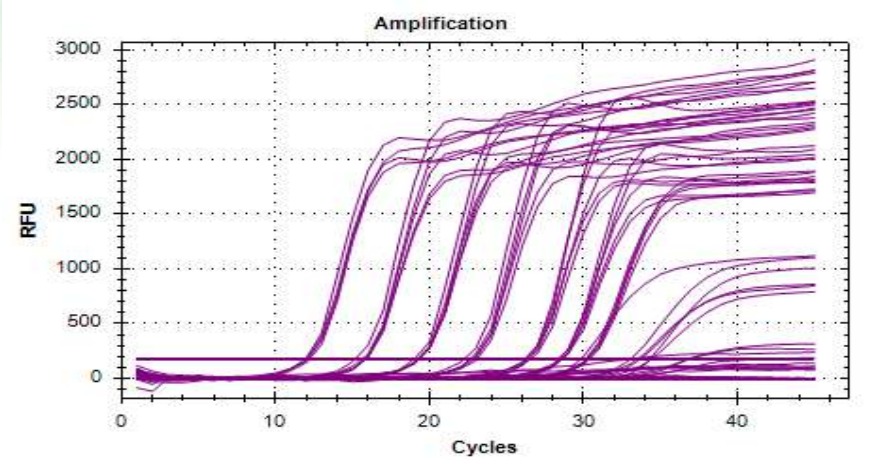


Figure: 14. *Amplification plot of PEDV RT-qPCR with 10-fold serial dilutions of IVT RNA*

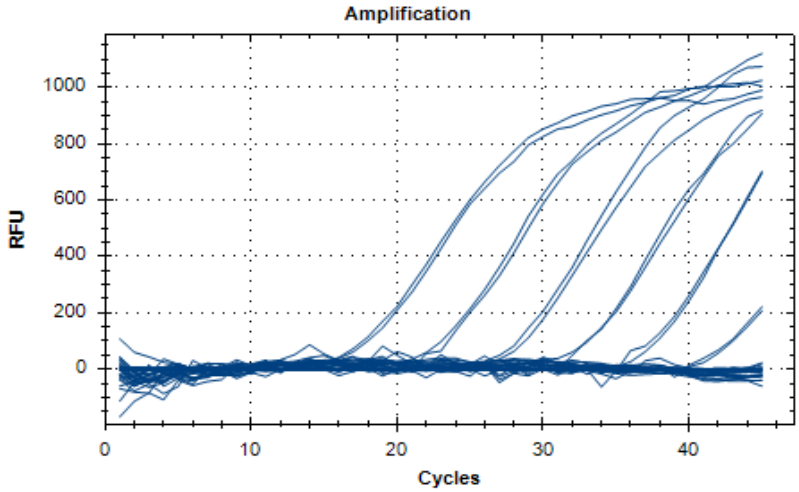


Figure: 15. *Amplification plot of TGEV RT-qPCR*

☞ Development of RPA-CRISPR/Cas9 based lateral flow assay for detection of ASFV genome

A recombinase polymerase amplification (RPA) assay was integrated with a CRISPR-Cas9–based lateral flow detection system. A specific sgRNA was designed using CRISPRscan and CHOPCHOP and synthesized with a tracrRNA. RPA primers with appropriate labels were optimized for amplification. The assay involved forming a labelled Cas9–sgRNA ribonucleoprotein complex that binds to the ASFV target DNA, with detection via streptavidin-coated lateral flow strips. Optimal conditions included 15 minutes at 37°C with varying concentrations of Cas9 and sgRNA. The assay showed high sensitivity without any cross-reactivity with other important swine viruses.

☞ CRISPR-Cas based-point-of-care diagnostic platform for animal diseases-MERS:

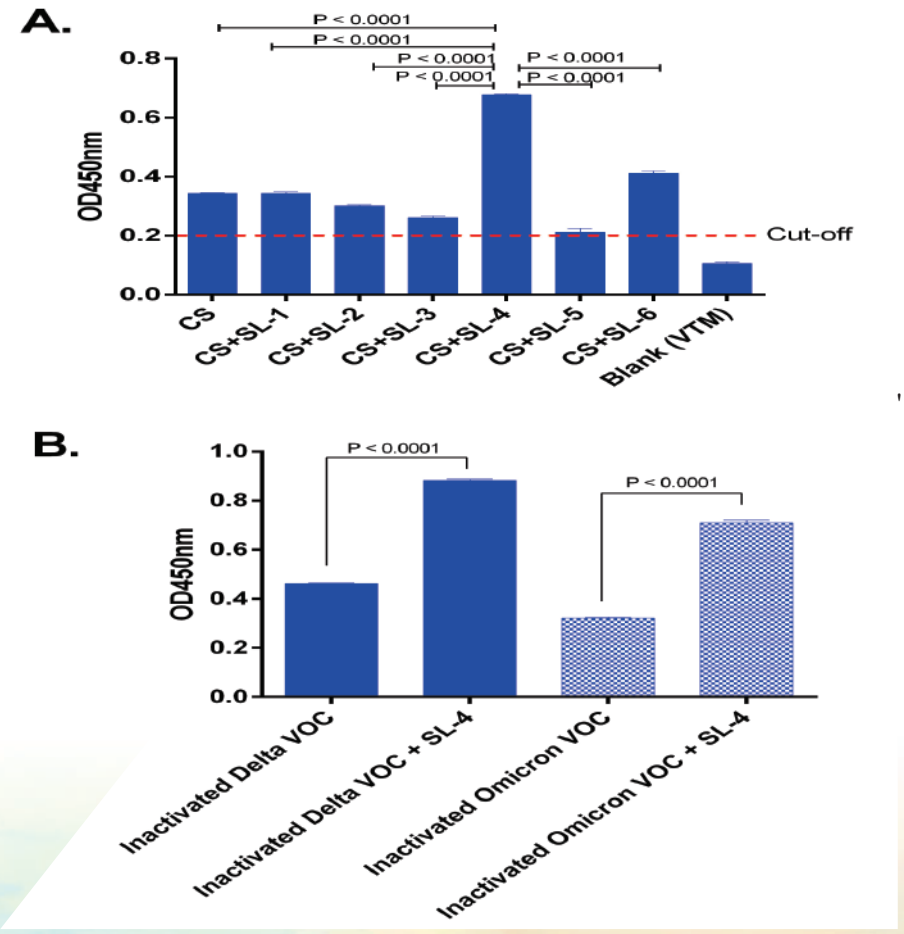
For In silico analysis of MERS CoV genes viz. Upstream of the envelope protein gene (*UpE*) and gene encoding the nucleocapsid protein gene (*N*), 30 representative sequences were retrieved from NCBI from different regions between 2015 and 2024 and aligned. Upon analysis the conserved region among both the genes were identified. These identified conserved *UpE & N* regions were commercially synthesized for generation of IVT RNA as positive control. Based on alignment, primers for Recombinase Polymerase Amplification (RPA) & one step RT-PCR were designed along with widely used published primers for genomic detection were synthesized. Two sgRNAs, one for the sense sequence and one for the antisense sequence of the *UpE & N genes with* a single-stranded DNA (ssDNA) reporter with FAM/Biotin label for respective genes were designed and synthesized.

☞ Development of One Step RT-PCR for Ganjam:

As in-house diagnostic assay for genomic detection of Ganjam virus, developed one step RT-PCR assay for detection of GANV genome in ticks using in-house developed primers targeting the conserved region of 'N' gene. To design the primers, nucleocapsid gene sequences were retrieved from the NCBI and aligned using MEGA software to identify the most conserved region. The reaction conditions like, annealing temperature, primer concentration and limit of detection was determined. The developed assay was used to screen the tick samples along with published assay.

☞ Development of Antigen capture ELISA for SARS-CoV-2:

Diagnostics employing multiple modalities have been essential for controlling and managing COVID-19, caused by SARS-CoV-2. However, scaling up Reverse Transcription–Quantitative Polymerase Chain Reaction (RT-qPCR), the gold standard for SARS-CoV-2 detection, remains challenging in low and middle-income countries. Cost-effective and high-throughput alternatives like enzyme-linked immunosorbent assay (ELISA) could address this issue. We developed an in-house SARS-CoV-2 nucleocapsid capture ELISA, and validated on 271 nasopharyngeal swab samples from humans (n = 252), bovines (n = 10), and dogs (n = 9). This ELISA has a detection limit of 195 pg/100 μL of nucleocapsid protein and does not cross-react with related coronaviruses, ensuring high specificity to SARS-CoV-2. Diagnostic performance was evaluated using receiver operating characteristic curve analysis, showing a diagnostic sensitivity of 67.78 % and specificity of 100 %. Sensitivity improved to 74.32 % when excluding positive clinical samples with RT-qPCR Ct values > 25. Furthermore, inter-rater reliability analysis demonstrated substantial agreement (κ values = 0.73–0.80) with the VIRALDTECT II Multiplex RT-qPCR kit and perfect agreement with the CoVeasy™ COVID-19 rapid antigen self-test (κ values = 0.89–0.93). Our findings demonstrated that the in-house nucleocapsid capture ELISA is suitable for SARS-CoV-2 testing in humans and animals, meeting the necessary sensitivity and specificity thresholds for cost-effective, large-scale screening (Figure: 16).



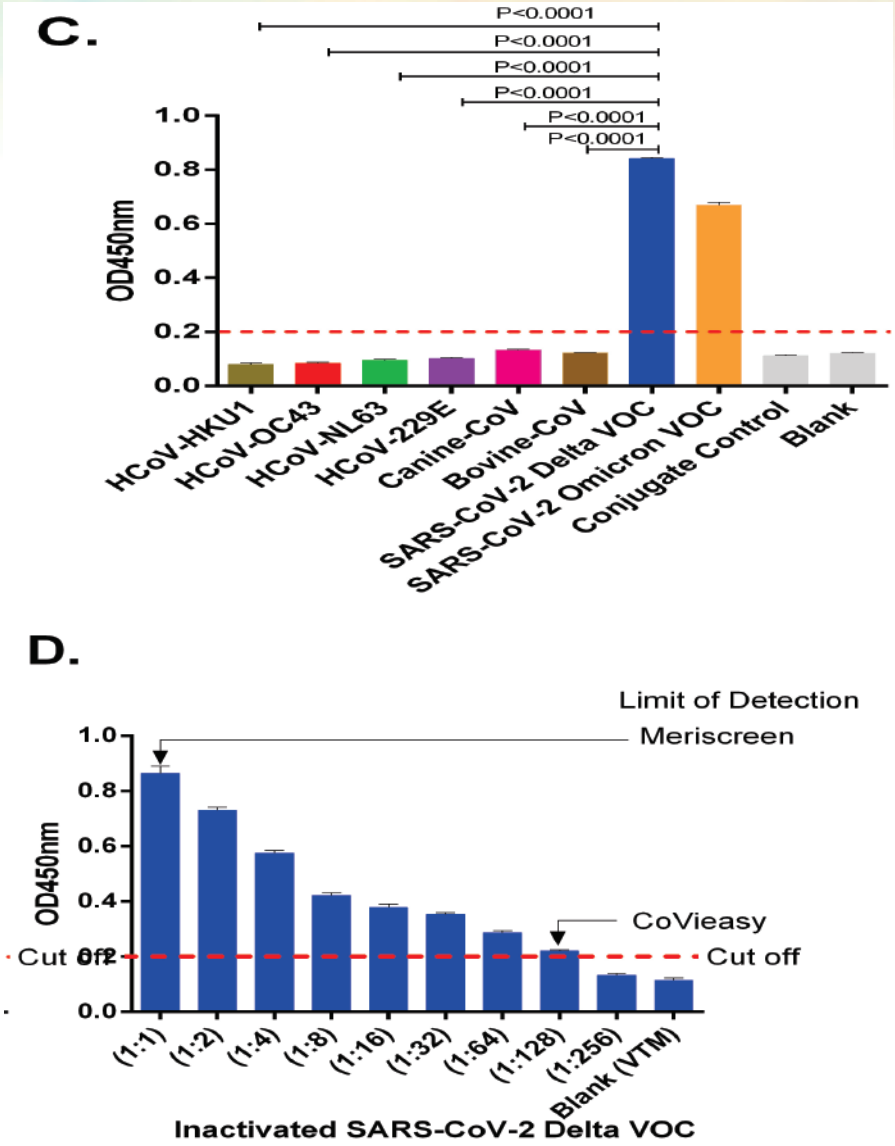


Figure: 16. *Development and validation of in-house antigen capture sandwich ELISA.*

(A.) *Assessment of six distinct sample lysis (SL-1 to -6) buffers for enhanced detection by capture and detector antibodies on a clinical sample (CS),* ***(B.)*** *Evaluation of analytical specificity (inclusivity) of optimized in-house ELISA for its ability to detect different variants of SARS-CoV-2 variants, such as delta and omicron VOC, as well as exclusivity* ***(C.)*** *for highly specific detection of SARS-CoV-2 only,* ***(D.)*** *Estimation of analytical sensitivity with 2-fold diluted inactivated SARS-CoV-2 delta VOC and its comparison with CoVeasyTM COVID-19 rapid antigen self-test, and Meriscreen COVID-19 antigen test kit. One-way analysis of variance (ANOVA) with the Turkey method for multiple comparisons was used to estimate the differences between more than two groups and $p < 0.01$ was considered statistically significant.*

☞ Label-free gold nanoparticles functionalized peptide dendrimer biosensor for visual detection of breakthrough infections in COVID-19 vaccinated patients

Given the global implementation of effective COVID-19 vaccines, which do not confer complete immunity, it is crucial to monitor the occurrence of breakthrough infections, particularly against newly emerging severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants. Hence, we developed a label-free colorimetric assay using gold nanoparticles (GNPs) functionalized with a peptide dendrimer incorporating highly reactive epitopes of the

nucleocapsid (N) protein. This assay relies on the tween-20 induced colorimetric changes caused by the aggregation of peptide dendrimer-coated GNPs in the absence of anti- SARS-CoV-2 N antibodies, and vice versa. Transmission electron microscopy, dynamic light scattering, and circular dichroism spectroscopy analyses all showed the formation of a uniform and highly stable coating of the peptide dendrimer over GNPs. Surface plasmon resonance experiments have demonstrated a strong binding affinity for the peptide dendrimer and anti- SARS-CoV-2 N antibodies, with a KD value of 525 nM. To validate the proof-of-concept, we have tested this assay on seventy human serum samples, and receiver operating characteristic curve analysis demonstrated high diagnostic sensitivity (88.89 %) and specificity (100 %). This approach opens up new avenues for the development of simple and rapid diagnostic assays for identifying antibodies against viral infections and other pathogens (Figure: 17).

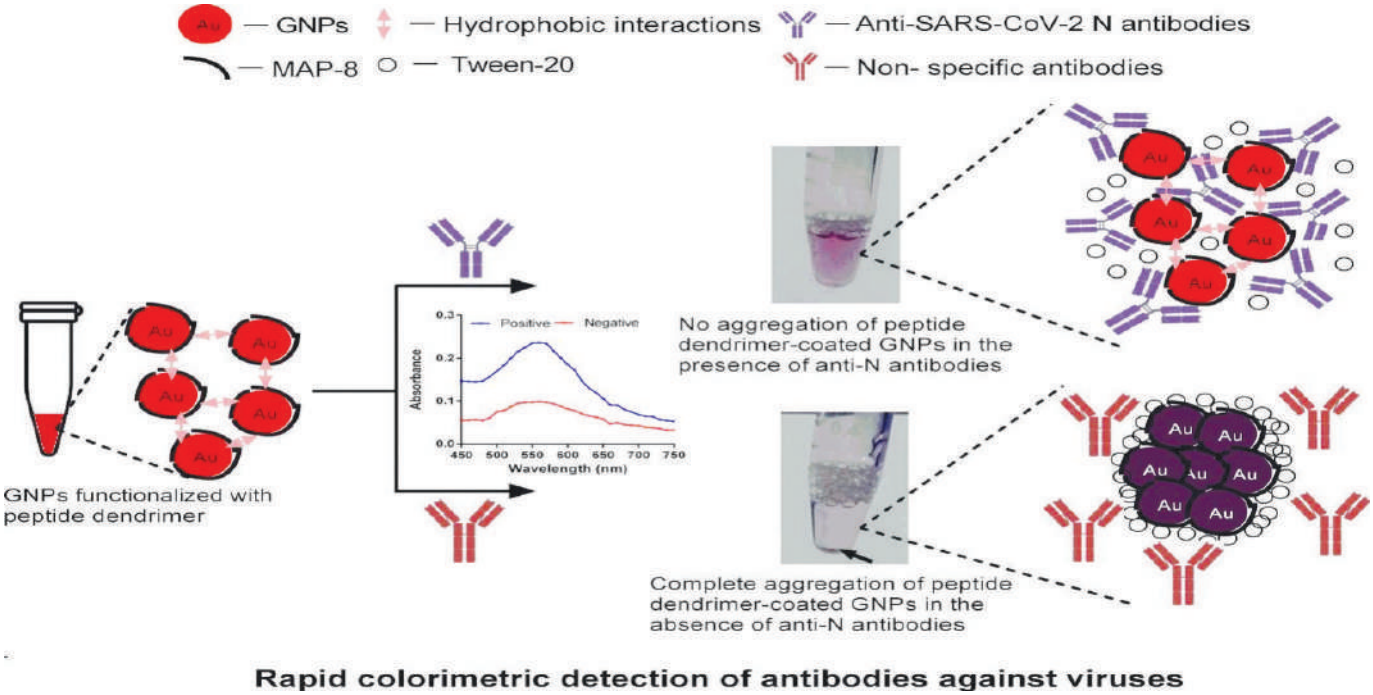


Figure: 17. *Schematic representation of working principle of peptide dendrimer for the detection of anti-SARS-CoV-2 N antibodies*

Disease Surveillance, Monitoring and Pathogen Characterization

☞ Avian Influenza

▸ Co-circulation of H5N1 clades 2.3.2.1a and 2.3.4.4b avian influenza viruses in India, 2024

Highly Pathogenic Avian Influenza (HPAI) H5N1 virus was detected in poultry in Andhra Pradesh, Jharkhand, and Odisha; domestic ducks and poultry in Kerala; poultry, tigers, and leopards in Maharashtra; and wild birds in Rajasthan during 2024. It is noted that the first-time detection of the H5N1 virus in wild mammals indicated an expanding host range of the virus. The viruses were isolated in chicken eggs, and the complete genome sequences were determined for comparison. Analysis of the HA gene cleavage region revealed the presence of multiple basic amino acid motifs (PQKERRRKR/G in Maharashtra, Jharkhand, and Odisha; PLREKRRKR/G in Kerala, Rajasthan, and PQRERRRKR/G in Andhra Pradesh), indicating HPAI to chickens. The viruses were clustered into two major clades (2.3.2.1a and 2.3.4.4b) (Figure: 18). The H5N1 viruses isolated from chicken, tiger, and leopard in Andhra Pradesh, Jharkhand, Maharashtra and Odisha belonged to clade 2.3.2.1a, and the H5N1 virus isolated from duck, chicken, quails and wild birds in Kerala and Rajasthan belonged to clade 2.3.4.4b, indicating co-circulation of both genetic clades in India during 2024. The conserved amino acids at HA positions Q222 and G224 (H5 numbering) indicated preferential binding to avian-like α2-3-linked sialic acid receptors. Two H5N1 clade 2.3.2.1a chicken isolates possessed a genetic mutation N295S (N1 numbering), indicating resistance to neuraminidase inhibitors.

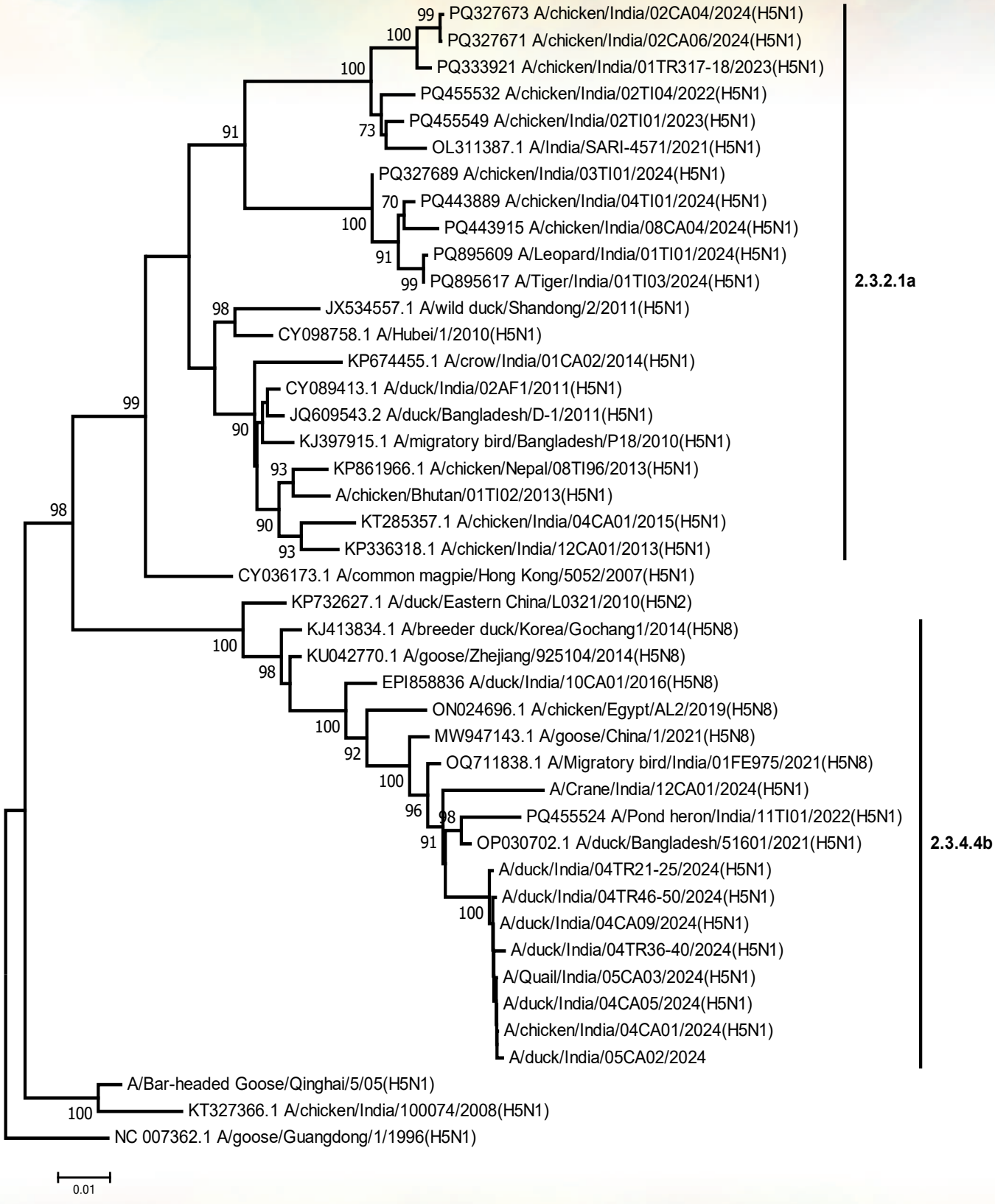


Figure: 18. *HA gene phylogeny of avian influenza H5 viruses. The tree is rooted with the A/goose/Guangdong/1/1996(H5N1) virus. Clades are shown to the right. Bootstrap values (≥ 70%, out of 1000 replicates) are shown near the nodes.*

☞ Disease monitoring for Avian Influenza:

A total of 66,702 samples (53,532 morbid materials and 13,170 sera) received from various parts of the country were tested as part of avian influenza virus surveillance during this year. The summary of results of active (Random and POSP) and passive (suspected) surveillance samples received during this year are given in Table 1 and Figure:19. The specimen-wise sample details and their results are given in Table 2 & 3 and Figure: 20 & 21 The species-wise samples received and their results are presented in Table 4 & 5 and Figure: … The States/Union Territories -wise morbid and sera samples tested and their results are presented in Table 6, 7 & 8 and Figure: 24, 25 & 26.

In the passive surveillance, out of 1192 suspected samples tested, a total of 487 samples from five States (Andhra Pradesh – 07, Jharkhand-02, Kerala- 392, Maharashtra – 01, Odisha - 81 and Rajasthan-04) have tested positive for H5N1 notifiable AIV and 3 sera samples from Kerala tested positive for H5 virus antibodies (Table 6 & 7 and Figure: and 24, 25 & 26). Twenty samples from Kerala were found positive for NDV.

In the active surveillance, out of the 48,125 morbid samples, 171 samples from ten States/UTs (Andhra Pradesh – 01, Bihar-04, Chhattisgarh -17, Himachal Pradesh-01, Jharkhand-10, Madhya Pradesh-35, Maharashtra-12, Odisha-62, Punjab-06 and Rajasthan-23) tested positive for H9N2 avian influenza virus and 109 samples from nine States (Andhra Pradesh – 03, Gujarat-30, Himachal Pradesh-04, Jammu-03, Kerala-20, Mahrashtra-12, Odisha-24, Punjab-08 and Rajasthan-05) tested positive for Newcastle disease virus. (Table: 7 and Figure: 25). Out of 11,170 sera samples tested, a total of 55 sera samples from six States (Andhra Pradesh-01, Gujarat-09, Kerala- 02, Odisha-36 and Rajasthan-07) were positive for H9 antibodies. A total of 124 sera from nine States/UTs (Andhra Pradesh-18, Chhattisgarh- 46, Gujarat-03, Jharkhand -03, Kerala- 02, New Delhi-04, Odisha-29 Rajasthan-06 and West Bengal-13) were positive against NDV antibodies. A total of six sera samples from Chhattisgarh were positive to both H9 and NDV antibodies (Table: 6 and Figure: 24). The state-wise details of POSP samples received and their results are given in Table 8 and Figure: 26. A total of 4315 swab samples received under POSP, 22 samples (Jharkhand-10 and Maharashtra-12) were tested positive for H9N2 avian influenza virus. A total of fifteen samples including 12 from Maharashtra and 03 from Odisha were found positive for NDV. Out of 1,900 sera samples received under POSP, 06 samples from Kerala were found positive against H9 virus antibodies and 03 samples from Jharkhand and 02 samples from Kerala were positive against NDV antibodies (Table 8).

Table 1: Summary of samples received for avian influenza surveillance

Nature of samples	No. of samples	Results						
		Morbid samples			Sera samples			
		H5N1	H9N2	NDV	H5N1	H9	NDV	H9+NDV
Passive Surveillance								
Emergency	1192	487	0	0	03	0	20	0
Active surveillance								
Random	59295	0	149	74	0	55	101	06
POSP	6215	0	22	15	0	10	23	0
Total Samples	**66702**	**487**	**171**	**89**	**03**	**65**	**144**	**06**

*- Includes all types of clinical samples. ** - Only swabs and tissues were tested for NDV.

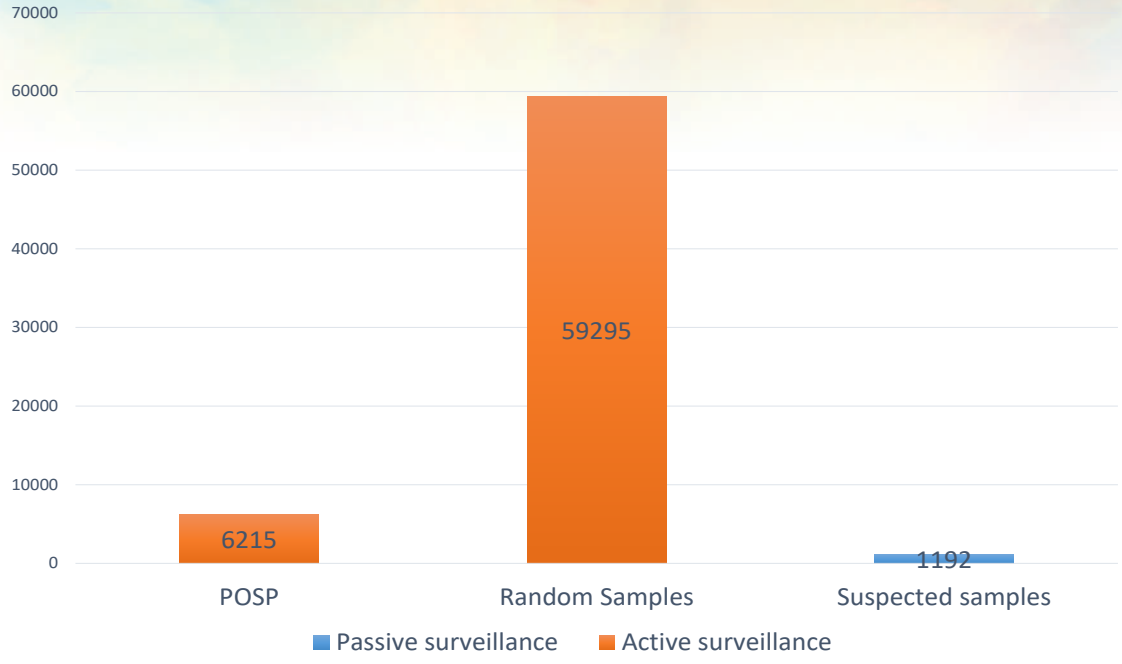


Figure: 19. *Summary of samples received for avian influenza surveillance*

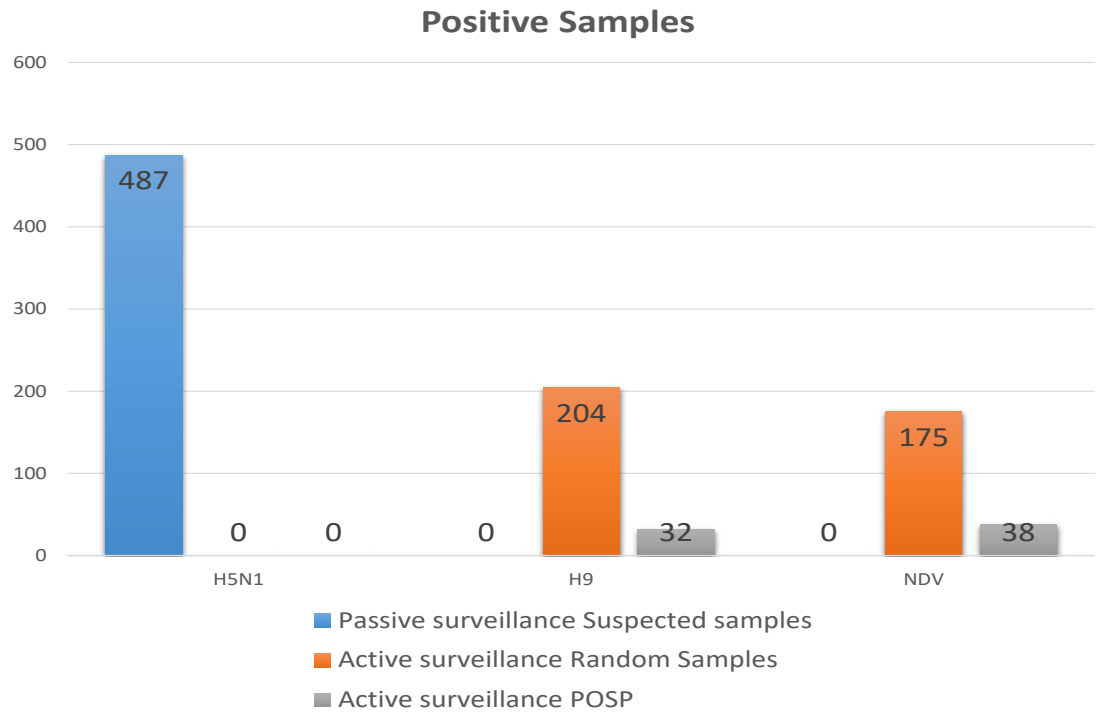


Table 2: Specimen-wise samples received for Passive surveillance of avian influenza

Specimen material	Samples Received	Positive samples				
		H5N1	H9N2	H9	H9+NDV	NDV
Cloacal swabs	298	158	0	0	0	20
Sera samples	100	03	0	0	0	0
Carcass/tissue	193	159	0	0	0	0
Oro-pharyngeal/Tracheal swabs	463	170	0	0	0	0
Environmental	138	0	0	0	0	0
Total	**1192**	**490**	**0**	**0**	**0**	**20**

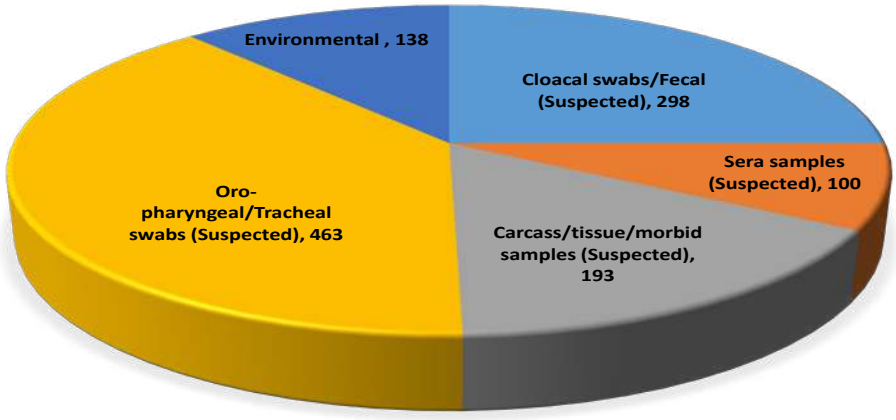


Figure: 20. *Specimen wise samples received for Passive surveillance of avian influenza*

Table 3: Specimen-wise samples received for Active surveillance of avian influenza

Specimen material	Samples Received	Positive samples				
		H5N1	H9N2	H9	H9+NDV	NDV
Sera samples (Random)	11170	0	0	55	06	101
Cloacal swabs/Fecal (Random)	21821	0	36	0	0	32
Oro-pharyngeal/Tracheal swabs (Random)	16551	0	82	0	0	42
Tissue/Morbid samples (Random)	28	0	0	0	0	0
Environmental (water/soil/knife)	9725	0	31	0	0	0
Sera samples (POSP)	1900	0	0	10	0	23
Cloacal swabs/Fecal (POSP)	1925	0	12	0	0	15
Oro-pharyngeal/Tracheal swabs (POSP)	2390	0	10	0	0	0
Total	**65,510**	**0**	**171**	**65**	**06**	**213**

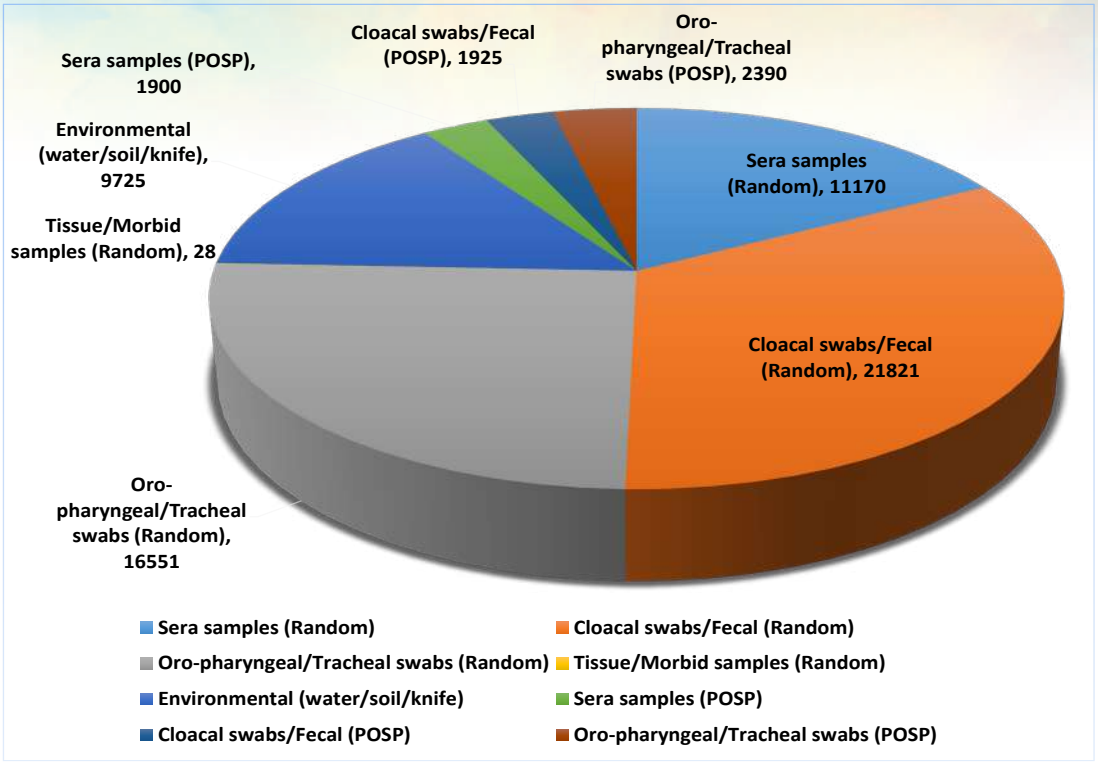


Figure: 21. *Specimen-wise samples received for Active surveillance of avian influenza*

Table 4: Species-wise morbid samples received for avian influenza

Species-wise	Samples received	Positive samples		
		H5N1	H9N2	NDV
Chicken				
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	13784	0	82	42
Cloacal swabs/Fecal (Random)	18709	0	36	32
Carcass/tissue/morbid samples (Random)	04	0	0	0
Environmental Samples (Random)	3511	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	168	105	0	0
Cloacal swabs/Fecal (Emergency)	168	115	0	0
Carcass/tissue/morbid samples (Emergency)	87	78	0	0
Oro-pharyngeal swabs/ Tracheal (POSP)	2340	0	10	0
Cloacal swabs/Fecal (POSP)	1778	0	12	15
Duck				
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	284	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	100	50	0	0

Cloacal swabs/Fecal (POSP)	120	0	0	0
Cloacal swabs/Fecal (Random)	466	0	0	0
Cloacal swabs/Fecal (Emergency)	102	35	0	20
Carcass/tissue/morbid samples (Random)	50	0	0	0
Carcass/tissue/morbid samples (Emergency)	57	46	0	0
Migratory Bird				
Cloacal swabs/Fecal (Random)	298	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	03	0	0	0
Carcass/tissue/morbid samples (Random)	11	0	0	0
Dropping Sample (Random)	1121	0	0	0
Carcass/tissue/morbid samples (Emergency)	01	0	0	0
Crow				
Carcass/tissue/morbid samples (Emergency/ Random)	03	13	0	0
Cloacal swabs/Fecal (Random)	04	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	04	0	0	0
Carcass/tissue/morbid samples (Emergency)	13	0	0	0
Environmental samples (Emergency)	01	0	0	0
Peacock				
(Carcass/tissue/morbid samples- Emergency)	1	1	0	0
Cloacal swabs/Fecal (Emergency)	1	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	1	0	0	0
Peahen				
Carcass/tissue/morbid samples – (Random)	2	0	0	0
Carcass/tissue/morbid samples – (Emergency)	1	1	0	0
Pigeon				
Cloacal swabs/Fecal (Random)	163	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal/Dropping (Random)	16	0	0	0
Cloacal swabs/Fecal (Emergency)	2	0	0	0
Carcass/tissue/morbid samples (Emergency)	8	1	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal/Dropping (Emergency)	3	0	0	0
Wild Bird				
Cloacal swabs/Fecal (Random)	326	0	0	0

Carcass/tissue/morbid samples (Random)	01	0	0	0
Dropping (Random)	217	0	0	0
Cloacal swabs/Fecal (Emergency)	10	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	10	0	0	0
Carcass/tissue/morbid samples (Emergency)	05	4	0	0
Dropping Samples (Emergency)	57	0	0	0
Environmental Samples (water/soil/knife/table)	18	0	0	0
Bat				
Carcass/tissue/morbid/dropping samples (Random/Emergency)	06	0	0	0
Buffalo				
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	03	0	0	0
Cattle				
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	614	0	0	0
Environmental Samples (Random)	236	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	113	0	0	0
Environmental Samples (Emergency)	50	0	0	0
Crane				
Carcass/tissue/morbid samples (Emergency)	04	04	0	0
Environmental Samples (Random)	24	0	0	0
Goat				
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	212	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	43	0	0	0
Environmental Samples (Emergency)	07	0	0	0
Mollusc				
Carcass/tissue/morbid samples (Emergency)	8	0	0	0
Quail				
Cloacal swabs/Fecal (Emergency)	15	8	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	15	15	0	0
Carcass/tissue/morbid samples (Emergency)	11	11	0	0
Pig/Swine				

Oro-pharyngeal swabs/ Tracheal/Nasal (Emergency)	23	0	0	0
Sheep				
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	41	0	0	0
Turkey				
Cloacal swabs/Fecal (Random)	06	0	0	0
Vulture				
Carcass/tissue/morbid samples (Random)	01	0	0	0
Environmental Sample				
Environmental Samples (Random)	4203	0	31	0
Environmental Samples (Emergency)	18	0	0	0
Species Not Known				
Oro-pharyngeal swabs/ Tracheal/Nasal (Random)	1593	0	0	0
Dropping Sample (Random)	145	0	0	0
Dropping Sample (Emergency)	3	0	0	0
Cloacal swabs/Fecal (POSP)	27	0	0	0
Cloacal swabs/Fecal (Random)	1849	0	0	0
Environmental Samples (Random)	183	0	0	0
Oro-pharyngeal swabs/ Tracheal/Nasal (POSP)	50	0	0	0
Total	**53532**	**487**	**171**	**109**

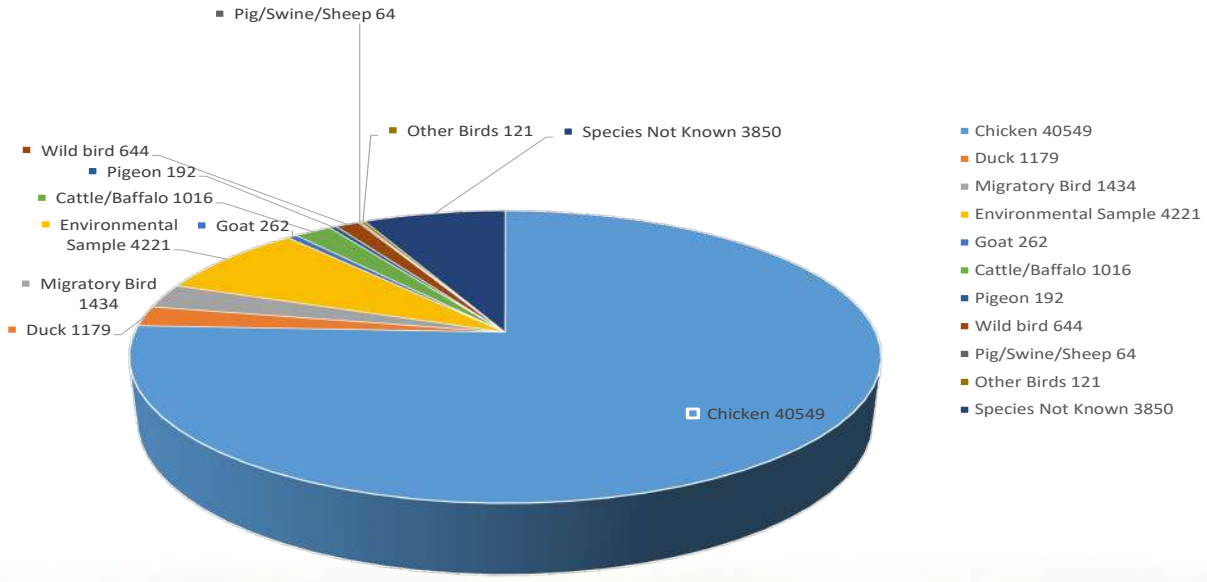


Figure: 22. *Species-wise morbid samples received for avian influenza*

Table 5: Species-wise Sera samples received for avian influenza

Species-wise	Samples received	Positive samples			
		H5N1	H9	H9+NDV	NDV
Chicken					
Blood/Sera samples (POSP)	1611	0	10	0	23
Blood/Sera samples (Random)	9374	0	55	06	101
Blood/Sera samples (Emergency)	24	0	0	0	0
Duck					
Blood/Sera samples (POSP)	264	0	0	0	0
Blood/Sera samples (Random)	487	0	0	0	0
Blood/Sera samples (Emergency)	73	03	0	0	0
Pigeon					
Blood/Sera samples (Emergency)	3	0	0	0	0
Turkey					
Blood/Sera samples (Random)	3	0	0	0	0
Species Not Known					
Blood/Sera samples (POSP)	25	0	0	0	0
Blood/Sera samples (Random)	1306	0	0	0	0
Total	**13170**	**03**	**65**	**06**	**124**

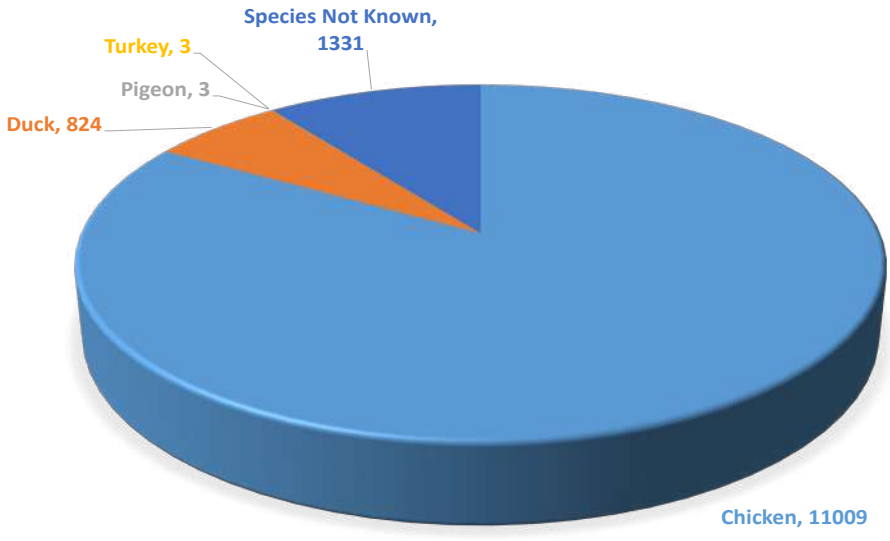


Figure: 23. *Species-wise Sera samples received for avian influenza*

Table 6: State-wise distribution and results of sera samples received

State	Samples tested	Sub typing by HI test
Andhra Pradesh	756	05 (H9), 18 (NDV)
Bihar	1023	0
Chhattisgarh	761	06 (H9+NDV), 46 (NDV)
Gujarat	234	09 (H9), 3 (NDV)
Haryana	123	0
Himachal Pradesh	120	0
Jammu	11	0
Jharkhand	377	3 (NDV)
Karnataka	544	0
Kerala	2707	03 (H5N1), 08 (H9), 02 (NDV)
Madhya Pradesh	155	0
Maharashtra	741	0
New Delhi	32	04 (NDV)
Odisha	3116	36 (H9), 29 (NDV)
Rajasthan	437	07 (H9), 06 (NDV)
Sikkim	126	0
Uttarakhand	760	0
West Bengal	1147	13 (NDV)
Total	**13,170**	**03 (H5N1), 65 (H9), 124 (NDV), 06 (H9+NDV)**

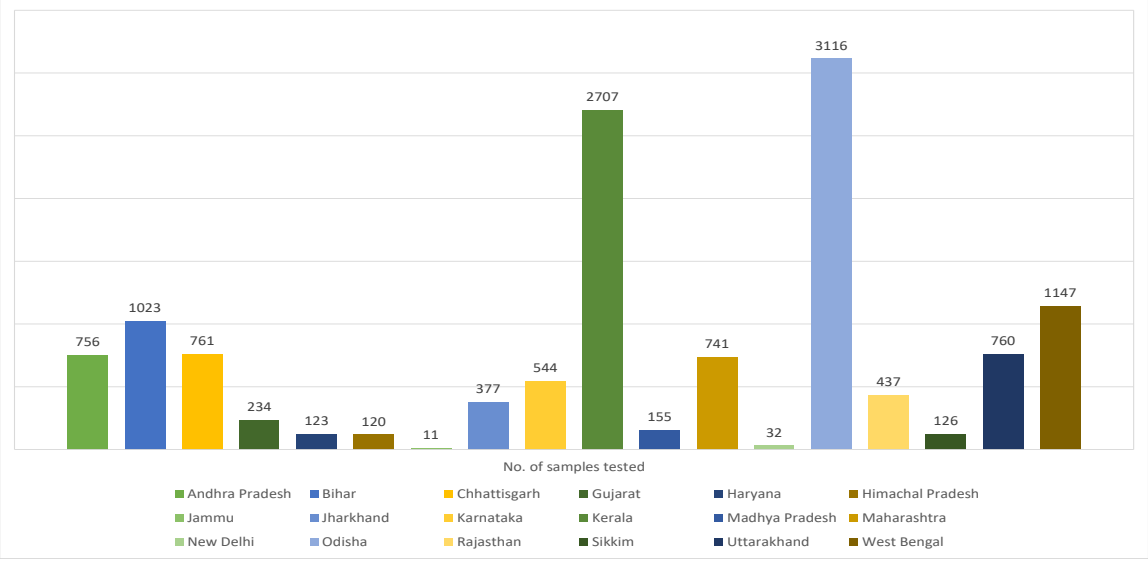


Figure: 24. *State wise distribution and results of sera samples received*

Table 7: State-wise distribution and results of tissue/swab samples received and their results

State	Samples tested	Positive samples (AIV and NDV)
Andhra Pradesh	1660	07 (H5N1), 01 (H9), 03 (NDV)
Assam	55	0
Bihar	2402	04 (H9)
Chandigarh	24	0
Chhattisgarh	805	17 (H9)
Goa	758	0

Gujarat	3181	30 (NDV)
Haryana	1140	0
Himachal Pradesh	918	01 (H9), 04 (NDV)
Jammu	504	03 (NDV)
Jharkhand	1263	02 (H5N1), 10 (H9)
Karnataka	607	0
Kerala	3030	392 (H5N1), 20 (NDV)
Madhya Pradesh	7633	35 (H9)
Maharashtra	1217	01 (H5N1), 12 (H9), 12 (NDV)
New Delhi	68	0
Odisha	14943	81 (H5N1), 62 (H9), 24 (NDV)
Punjab	1785	06 (H9), 08 (NDV)
Rajasthan	7715	04 (H5N1), 23 (H9), 05 (NDV)
Sikkim	53	0
Uttar Pradesh	866	0
Uttarakhand	17	0
West Bengal	2888	0
Total	**53532**	**487 (H5N1), 171 (H9N2), 109 (NDV)**

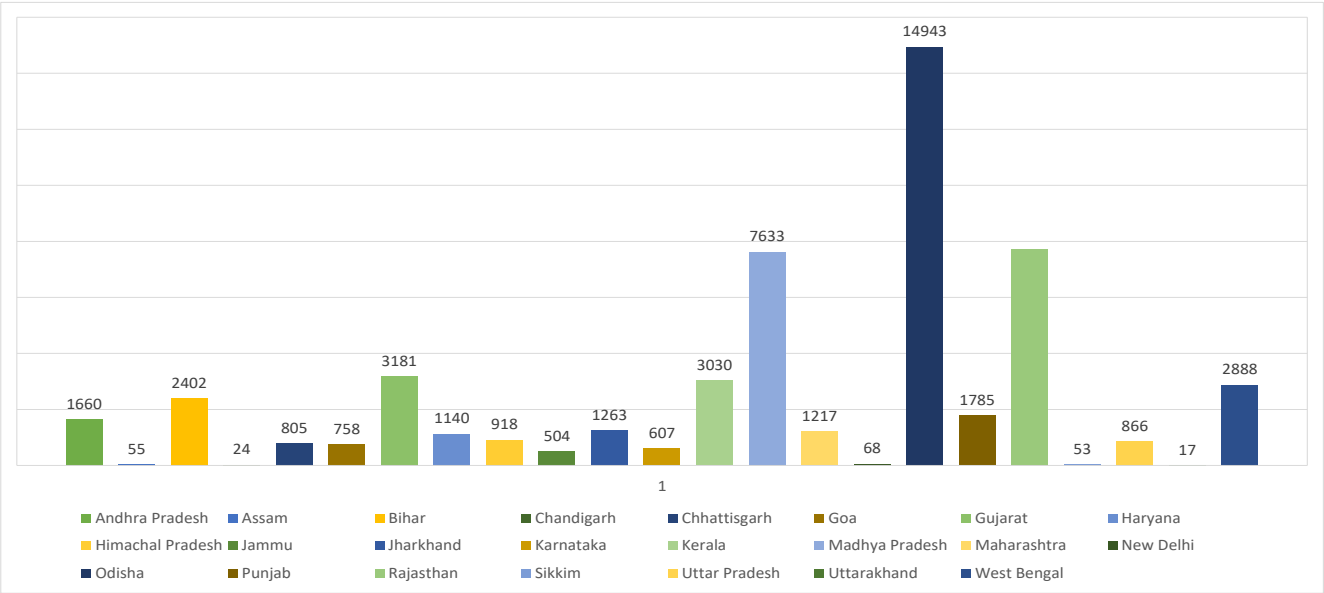


Figure: 25. *State wise distribution and results of tissue/swab samples received and their results*

Table 8: State-wise distribution of POSP samples received

State	Serum			Morbid			Total
	Received	AGID positive	Subtyping by HI test	Received	Positive*	Subtype	
Andhra Pradesh	354	-	-	354	-	-	708
Jharkhand	51	03	03 (NDV)	207	10	10 (H9N2)	258
Kerala	696	08	02 (NDV), 06 (H9)	624	-	-	1320
Maharashtra	52	-	-	112	24	12 (NDV), 12 (H9N2)	164
Odisha	747	-	-	3018	03	03 (NDV)	3765
Total	**1900**	**11**	**6 (H9), 5 (NDV)**	**4315**	**37**	**22 (H9N2), 15 (NDV)**	**6215**

* - Positive by real time RT-qPCR, RT-PCR and virus isolation.

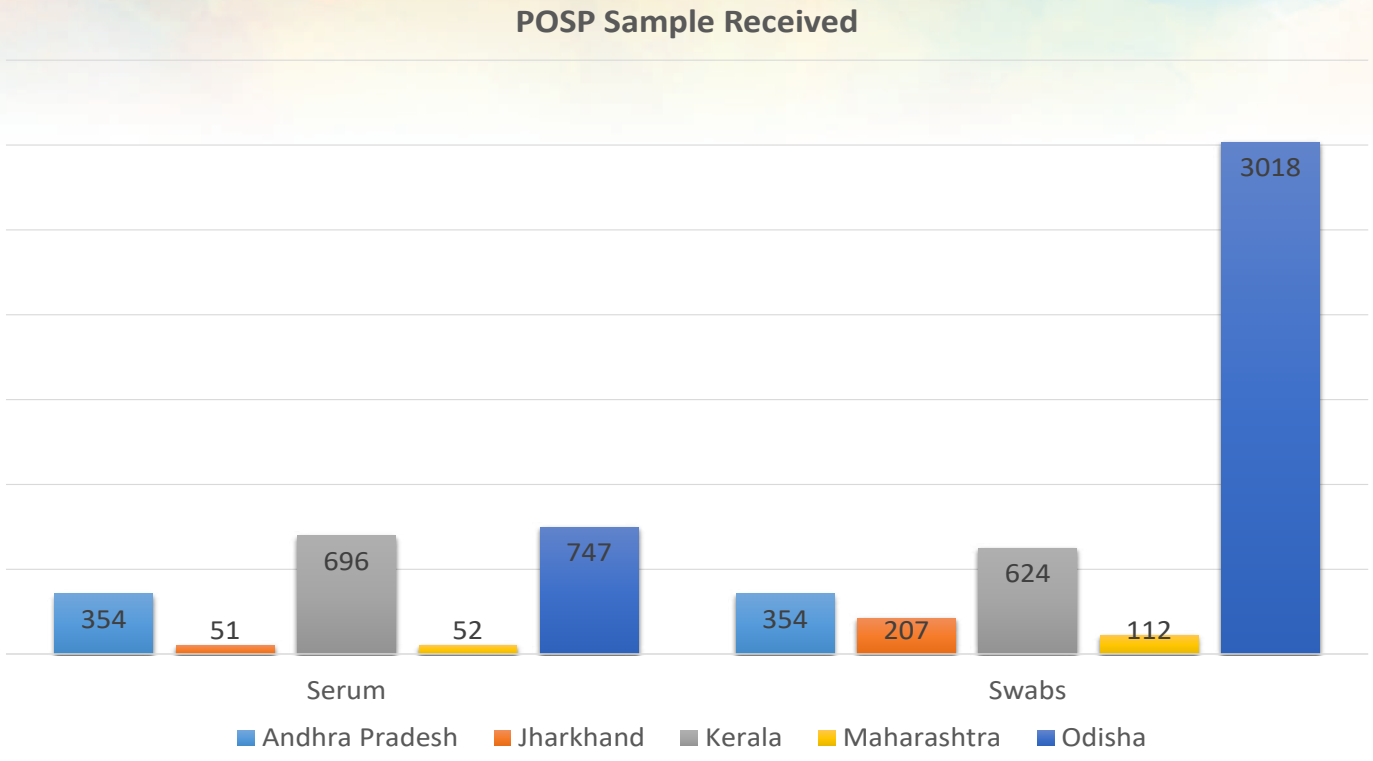


Figure: 26. *POSP State-wise (Sera/Swab) Samples*

Table 9: Avian influenza virus repository available at NIHSAD

S. No.	Subtype	Number
1	H5N1	506
2	H9N2	254
3	H5N8	215
4	H4N6	01
5	H3N8	05
6	H2N3	01
7	H11N9	01
8	H6N2	01

☞ Ruminant Diseases

▸ Emergence of lumpy skin disease in domestic water buffaloes in India provides evidence of a broadening LSDV host range

Lumpy skin disease (LSD) has emerged as a threat to cattle production in Asia, and India has been facing LSD epidemics since 2019. Although it was initially thought that LSDV has a restricted host range, emerging evidence suggests broadening of host range, with reports of natural LSDV infection in several domestic and wild life species in Asia and Africa. However, confirmed cases of natural LSDV infection in water buffalo (Bubalus bubalis) have so far been reported only from Egypt and Nepal. Therefore, global reports of LSDV infection in water buffalo still remain limited and there is yet no confirmed report of LSDV infection in water buffaloes from India. Hence, we investigated suspected cases of LSD in water buffaloes from 12 Indian states and one union territory during 2020-2023.

Investigated buffaloes showed mild to moderate clinical disease with fever and nodular skin lesions (Figure: 27), but most remained asymptomatic, indicating challenges in monitoring the skin lesions in LSD affected buffaloes.

A total of 18 out of 177 (10.18%) buffaloes in 12 districts in three states tested positive for LSDV by real-time PCR, providing the first molecular evidence of LSDV infection in water buffaloes in India (Figure: 28). The LSDV positive buffaloes belonged to 12 different districts spread across three states, Maharashtra, Rajasthan and Andhra Pradesh (Figure: 28). Maximum number of LSDV positive buffaloes (n=12) were found in Maharashtra State involving eight districts (Beed, Hingoli, Jalgaon, Latur, Nanded, Pune, Osmanabad and Palghar), followed by five in Rajasthan involving three districts (Jhalawar, Nagaur and Rajsamand) and one in Andhra Pradesh involving Kurnool district. VNT results showed that out of the total 57 buffaloes from eight States tested, LSDV neutralizing antibodies were detected in sera of 22 (38.59%) buffaloes from six States (Andhra Pradesh, Haryana, Maharashtra, Madhya Pradesh, Punjab and Rajasthan) involving nine districts, providing first serological evidence of LSDV infection in buffaloes in India (Figure:28). However, the LSDV neutralizing antibody titers in buffaloes ranged between 1:2 and 1:8, indicating presence of low to moderate level of antibodies against LSDV. Comparative evaluation of 19 sera (from 12 buffaloes) of a LSD affected buffalo unit by VNT and commercial ELISA showed that anti-LSDV antibodies were detected in 12 (63.1%) sera by VNT, but all 19 tested antibody negative by commercial ELISA indicating that the sensitivity of VNT and ELISA may differ depending on the animal host. Successful virus isolation and nucleotide sequencing confirmed natural LSDV infection in buffaloes. This is the first confirmed report of natural LSDV infection in water buffaloes in India. The study demonstrated that Indian water buffaloes are susceptible to natural LSDV infection, underscoring the need to identify all potential hosts to better understand the LSD epidemiology.

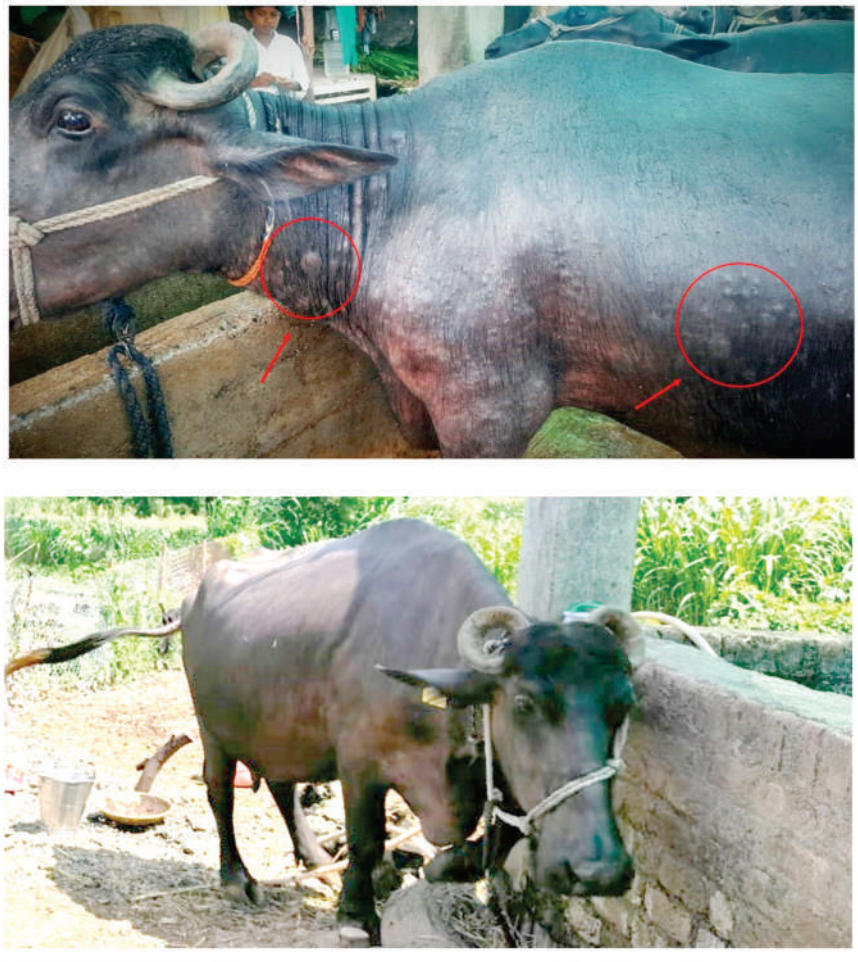


Figure:1. *Clinical signs in LSD affected water buffalo in a small-holder unit, Nanded, Maharashtra.*

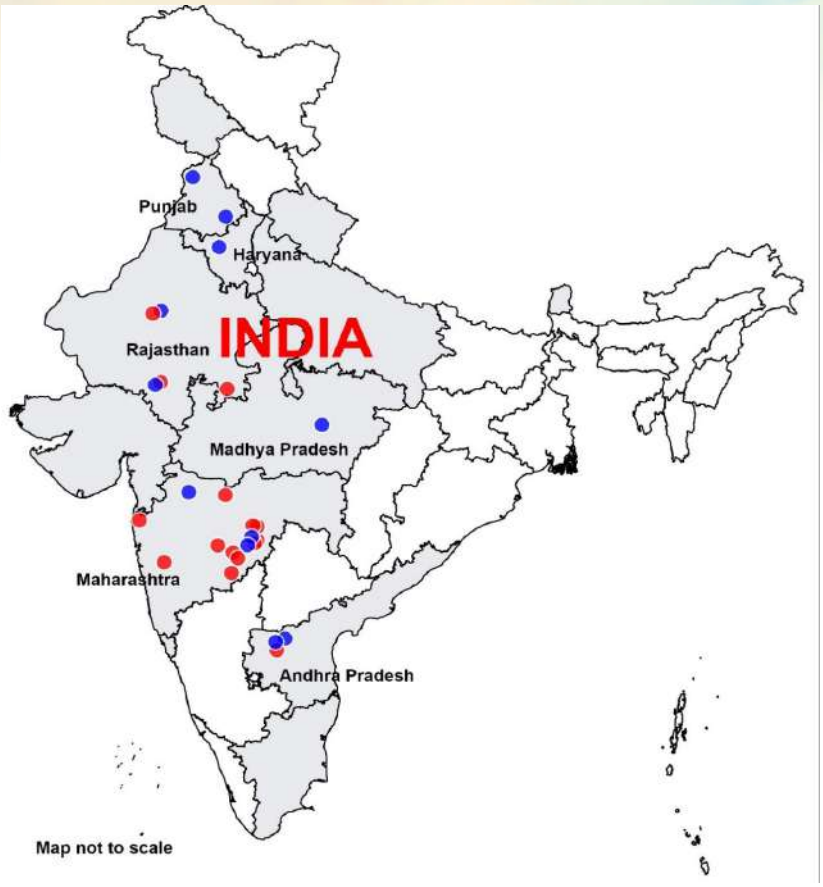


Figure: 28. *Map of India showing locations of sampling sites and sites with prevalence of LSDV infection in water buffaloes (Bubalus bubalis), during 2020-23. Sampled States/UTs are shaded in grey. Sites with molecular evidence of LSDV infection in buffaloes are indicated with circles in red, while those with serological evidence of infection are indicated with circles in blue.*

Genetic characterization of LSDVs infecting water buffaloes during 2020-2023 revealed co-circulation of wild-type strains of two divergent LSDV lineages (1.2.1 and 1.2.2) in Indian buffaloes.

Studies on genetic characterization of LSDV from cattle are extensive, but little is known about genetic characteristics of LSDV from buffaloes. On the basis of whole-genome sequence based phylogenetic analysis, globally circulating LSDV classical strains have been classified into two monophyletic clusters (clades), cluster 1.1 and cluster 1.2, while LSDV recombinant strains are classified into six separate clades (2.1 - 2.6). Furthermore, LSDV cluster 1.2 wild-type strains has been divided into three sub-clusters, 1.2.1, 1.2.2 and 1.2.3. The dominant circulating strain of LSDV in cattle in India since its emergence in 2019, belongs to sub-cluster 1.2.2, resembling the ancestral Kenyan wild-type strains. Subsequent studies revealed emergence of LSDV 1.2.1 wild-type strains since the 2022 LSD outbreaks. However, the genetic profile of LSDV strains circulating in Indian buffaloes has not yet been determined.

In this study, to determine the genetic profile of the LSDV strains in buffaloes, sequence analysis was carried out on the complete LSDV GPCR (1134 nt), RPO30 (606 nt), and EEV (546 nt) gene sequences, together with representative sequences of LSDV, SPPV, and GTPV strains obtained from GenBank database. Genetic and phylogenetic analyses of LSDV sequences of three complete genes (GPCR, RPO30 and EEV), and the concatenated datasets (GPCR-RPO30-EEV) revealed that LSDV wild-type strains of two sub-clusters (1.2.1 and 1.2.2) are circulating in water buffaloes in India (Figure: 29). LSDVs from buffaloes in Rajasthan and Andhra Pradesh belonged to 1.2.2 sub-cluster with highest genomic similarity to LSDV 1.2.2 strains circulating in South Asia. On the contrary, LSDVs from buffaloes in Maharashtra belonged to both 1.2.1 and 1.2.2 sub-clusters, indicating co-circulation of multiple LSDV sub-clusters in the same region (Figure: 30). The discovery of the co-existence of multiple LSDV lineages in

buffaloes in the same region warrants continuous monitoring of circulating LSDVs to better understand the dynamics of interspecies transmission. The results also showed that although the LSDV 1.2.1 strains from buffaloes clustered with 1.2.1 strains from Africa, Middle East, Europe and Russia, they were grouped separately and found identical with the recently reported 1.2.1 variants in multiple hosts, such as cattle, Indian gazelle and yaks from India (Figure: 3, Figure: 4). Detection of LSDV 1.2.1 strain in buffaloes in this study suggests that strains of at least two LSDV lineages (1.2.1 and 1.2.2) are now circulating in both cattle and buffaloes, confirming multiple introductions of LSDV into India. Nevertheless, they are distinct from the Neethling derived vaccine strains and virulent LSDV recombinant strains. Additionally, the comparative sequence analysis showed that the LSDVs from the water buffaloes and local cattle were identical, substantiating the previous hypothesis that susceptible domestic and wildlife hosts can become infected with LSDV circulating in cattle in the region. The study provides the first evidence of co-circulation of multiple LSDV sub-clusters in the same area and highlight the importance of LSDV surveillance and genetic analysis in understanding the role of buffalo in LSD epidemiology.

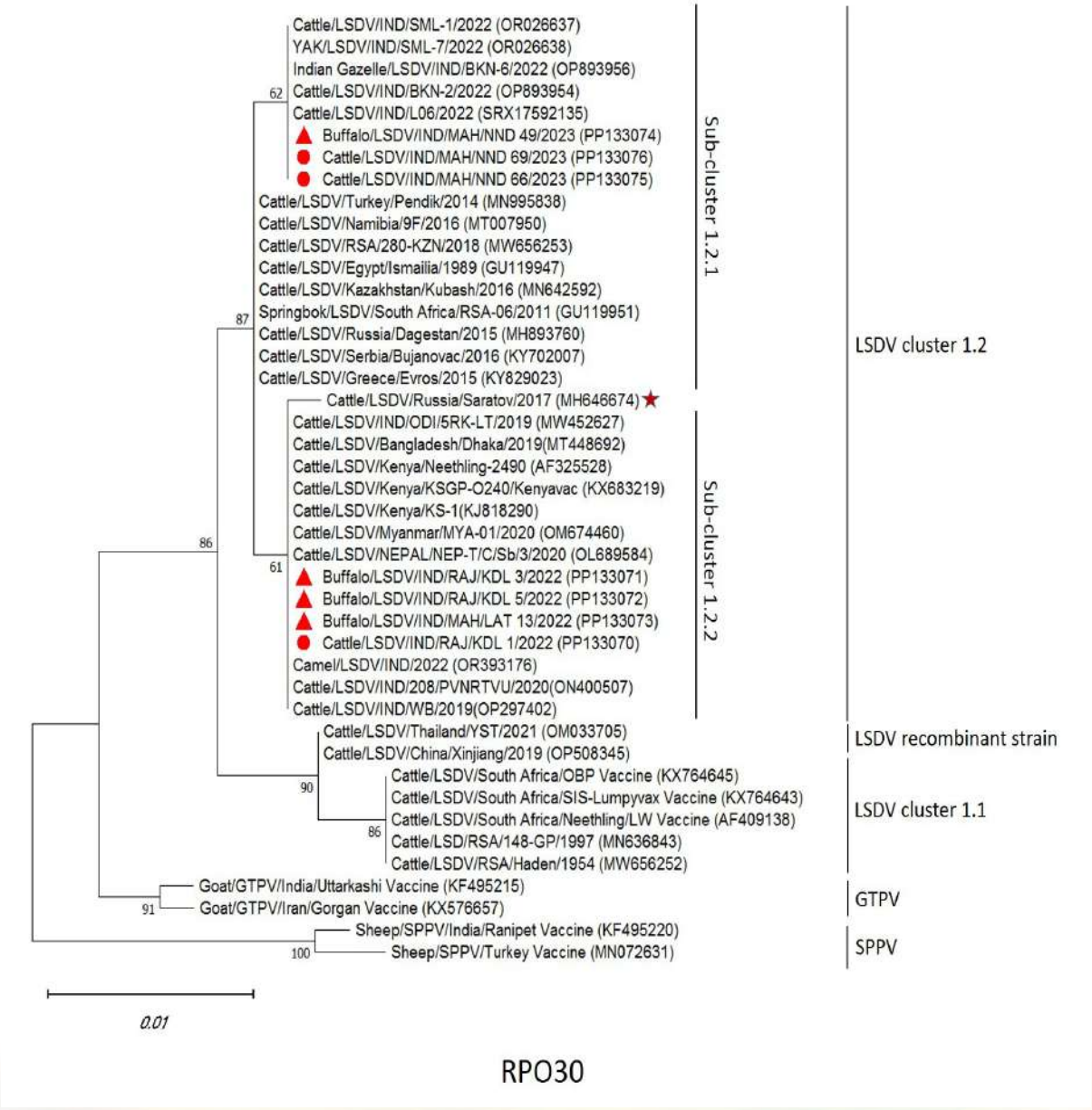


Figure: 29. *Maximum likelihood (ML) phylogenetic tree based on LSDV RPO30 gene sequences from Indian buffaloes (2020-23).*

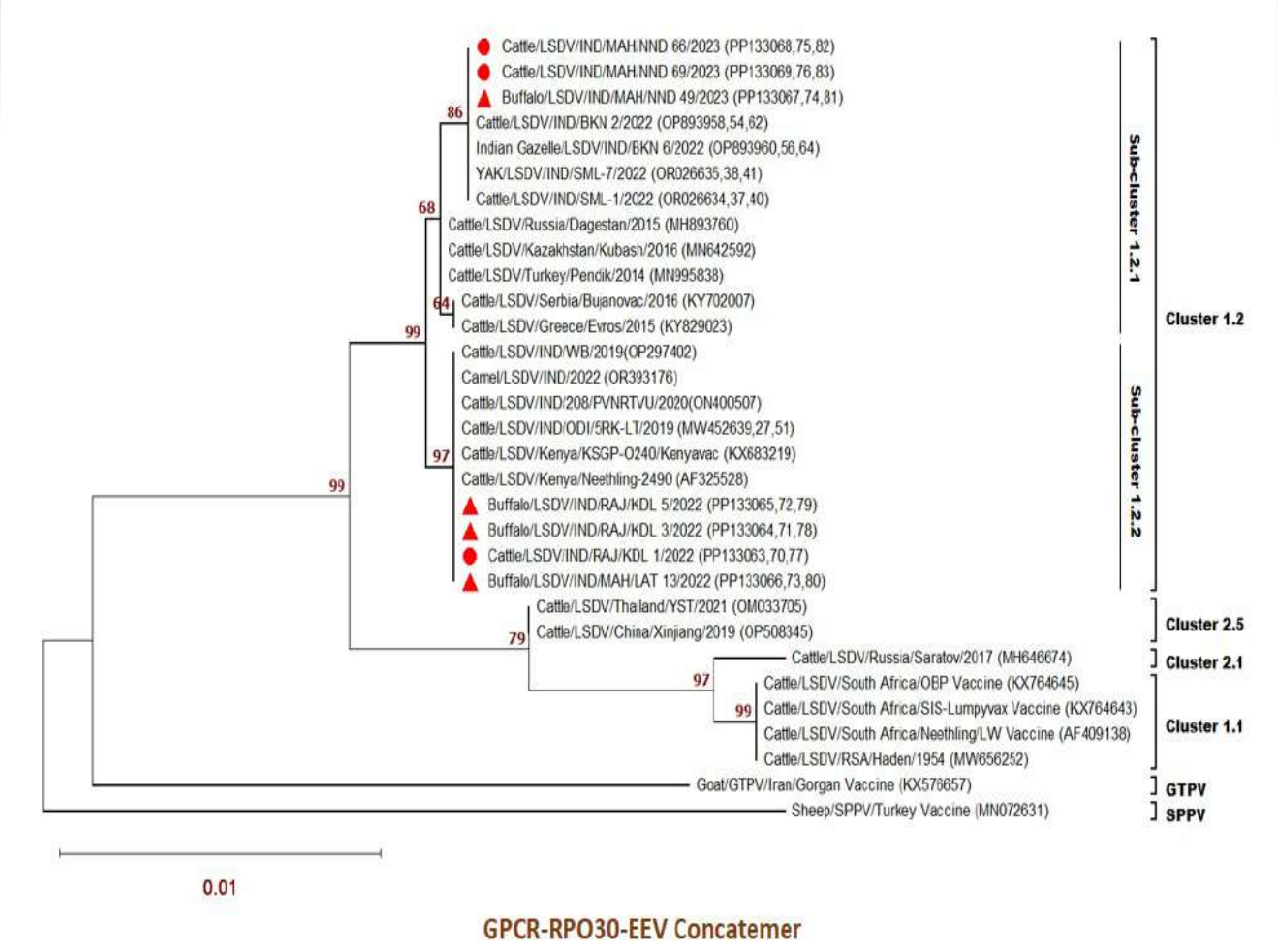


Figure: 30. *Maximum likelihood (ML) phylogenetic tree based on concatenated GPCR-RPO30-EEV sequences from Indian buffaloes.*

Genetic characterization of border disease virus originating from persistently infected migratory sheep reveals high genetic diversity of BDV-3 strains circulating in India.

Border disease (BD), caused by border disease virus (BDV) inflicts significant economic losses in sheep farming worldwide. The genetic diversity of BDV is greater than that of most other pestivirus species and BDV strains thus far have been classified into eight genotypes (BDV-1 to BDV-8). In India, the first confirmed case of BDV infection was reported in sheep showing respiratory and reproductive disorders in Jammu and Kashmir in 2010. Although BDV has been identified and characterized in farmed sheep, BDV has not yet been studied in sheep migrating for summer pasturing in India. Screening of blood and serum samples from 90 lambs of a migratory sheep flock (600) in Central India by qRT-PCR, VNT and virus isolation revealed detection of BDV in two lambs and one apparently healthy lamb was found persistently infected with BDV. Genetic characterization of BDV isolate (Ind 293299/12) from the PI sheep was conducted in 5'-UTR and Npro genes.

Phylogenetic analysis of 5'-UTR sequences showed that the BDV isolate, Ind 293299/12 belonged to BDV-3 genotype, but was more closely related to the BDV-3 strains from China (AH12-01, JS12/04), Slovakia (297) and Tajikistan (N3f) than the previously reported BDV-3 strain (Ind 830-09) from India. It showed only 88.0% sequence homology with the previously reported BDV-3 strain (Ind 830-09) from India. Phylogenetic analysis of Npro sequences and the concatenated sequences of 5'-UTR-Npro confirmed that the BDV isolate Ind 293299/12 belonged to BDV-3 genotype but it was placed in a branch clearly separated from the previously reported Indian BDV-3 strain

Ind 830-09 (Figure: 31). When compared with other BDV-3 strains, Ind 293299/12 was found more closely related to the BDV-3 strains circulating in goats (AH12-01, JS12/04) and sheep (JSLS12-01) from China, while BDV-3 strains from Germany and France grouped together. There was only 78.6% nucleotide and 86.9% amino acid sequence homology in Npro between the Indian BDV-3 strains indicating considerable genetic variability among them. Previous studies have shown that BDV-3 is the most prevalent genotype in Europe. In Asia, BDV-3 has been detected in sheep and goats in China and in sheep in India, while BDV-1 has been detected in pigs in Japan. Detection of BDV-3 in migratory sheep from a different geographical region in India provides evidence that this genotype may be the most prevalent BDV genotype also in Asia. It is also noteworthy to find that BDV-3 strains from India are more closely related with BDV-3 strains from China, than those found in other countries, indicating a probable common origin. The study provides insights on epidemiology and genetic diversity of BDV strains, highlighting the need for surveillance of BDV covering major sheep rearing regions of India to optimize the control measures.

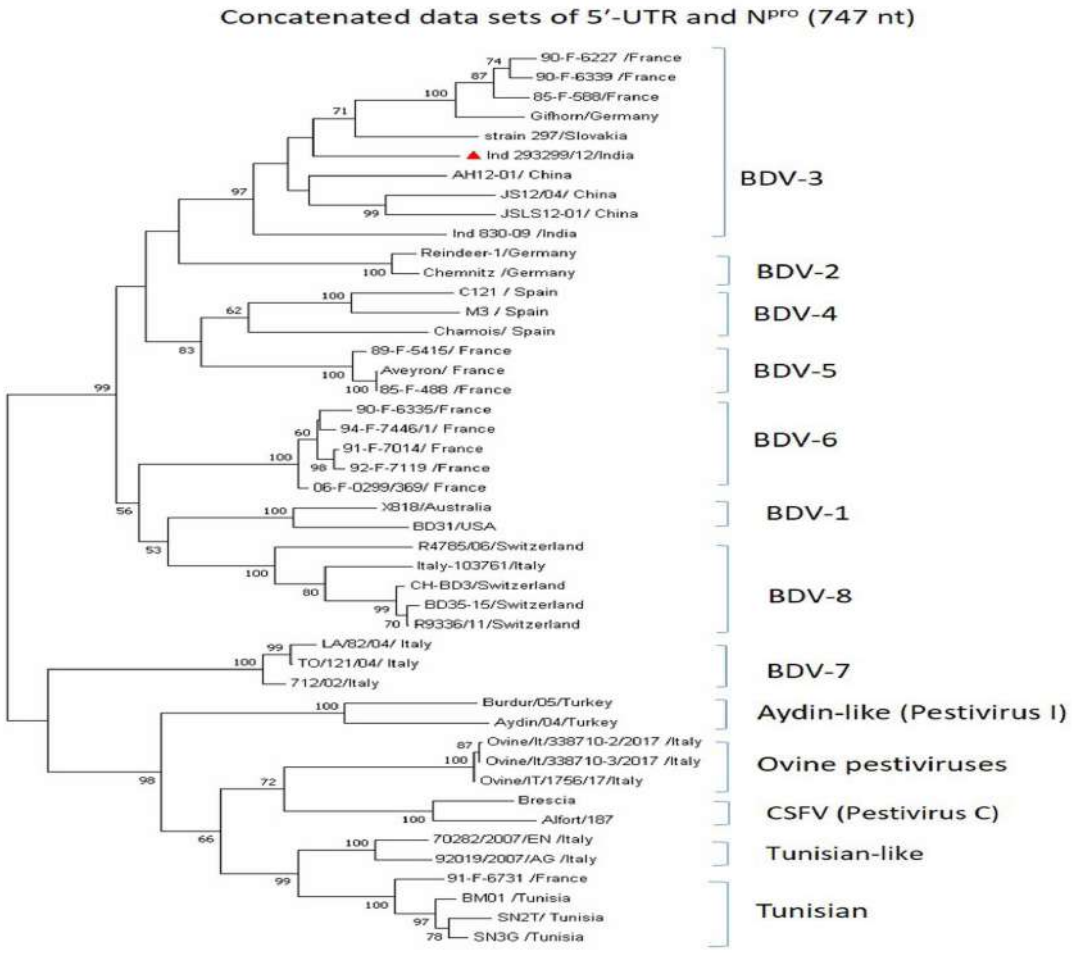


Figure: 31. *ML phylogenetic tree based on concatenated 5'-UTR-Npro sequences of border disease virus infecting migratory sheep.*

Disease monitoring for Lumpy skin disease (LSD):

A total of 81 samples from cattle from five states have been tested for lumpy skin disease, of which 40 samples from four states (Tamil Nadu, Punjab, West Bengal and Madhya Pradesh) have been found positive for LSDV. Laboratory confirmed cases of LSD were reported from cattle in the states of Tamil Nadu, Punjab, West Bengal and Madhya Pradesh. Emergence of LSD in domestic water buffaloes was reported for the first time in India, indicating susceptibility of Indian buffaloes to natural LSDV infection. Laboratory confirmed cases (n=3) of buffalopox have been detected in LSD-negative buffaloes in Maharashtra.

Swine Diseases

Complete genome analysis of African swine fever viruses revealed unique mutations in MGF-360-21R gene indicating its susceptibility to genetic changes during evolutionary adaptation in wild boars

Thirty eight out of the 41 samples collected from suspected outbreaks of ASF in Mizoram state in 2021, severely affecting both domestic pigs and wild boars with high mortality rates, were positive for ASFV genome by qPCR. Samples tested from various districts of Mizoram state during this outbreak is presented in Figure: 32. ASFV could be isolated from 16 out of the 38 positive samples by inoculating into porcine pulmonary alveolar macrophages (PAM), which exhibited hemadsorption (HAD) starting from the second passage.

One ASFV isolate from a domestic pig (MZ/21/PO-314) and another from a wild boar (MZ/21/PO-324) were further propagated in PAM cultures to obtain high-titer virus stocks for viral enrichment and next-generation sequencing (NGS). The assembled genome of the ASF virus of wild boar origin (IND/MZ/324/2021) comprised 190,489 base pairs, with inverted terminal repeats (ITR) of 1,597 bp at the 5' end and 1,122 bp at the 3' end. The genome of the ASF virus of domestic pig origin (IND/MZ/314/2021) consisted of 189,390 base pairs, with ITR of 422 bp at the 5' end and 1,150 bp at the 3' end. The average coverage depths were 121× and 105×.

Comparative genomic analysis of ASF virus isolated from wild boar revealed nucleotide identity of 99.93% with ASFV isolated from domestic pig from Mizoram (IND/MZ/314/2021), Arunachal Pradesh (IND/AR/SD-61/2020), Assam (IND/AS/SD-02/2020) and Meghalaya (OM481275 ABTCVSCK, OM481276 ABTCVSCK). Alignment of the complete genome sequence of ASFV isolated from wild boar with the reference strain Georgia/2007 revealed notable nucleotide variations. Seven single-nucleotide insertions (1G, 1T, 2C, 3A), a double nucleotide insertion (TA) at position 74327, two triple nucleotide insertions (GGG) at 17837 and 21796, a six-nucleotide insertion (TAAAAT) at 17936, and a ten-nucleotide insertion (TATATAGGAA) at 173381 were identified in the wild boar ASFV genome. Five single-nucleotide deletions (2A, 3T) were observed at positions (with respect to Georgia/2007) 2958, 6774, 12568, 21786, and 176021. Other deletions included a two-nucleotide deletion at 19791, a twelve-nucleotide deletion at 11933, four-nucleotide deletions at 14224 and 15665, a three-nucleotide deletion at 19998, and a nine-nucleotide deletion at 100436. These insertions and deletions resulted in frame shift mutations affecting amino acid expression in DP60R and ASFV-GACD 190 genes.

Truncations could be predicted in proteins encoded by MGF 110-7L gene (due to insertion of one extra G at position 133), MGF 110-10L & MGF 110-14L fusion gene (due to a four-nucleotide deletion at position 343) and MGF 110-13Lb gene (due to a four-nucleotide deletion at position 363). Protein truncations observed in these genes may affect immune-modulatory functions (Zhong et al., 2022). The nine-nucleotide deletion in the B475L gene led to the loss of three amino acids in its amino-terminal region, while a single nucleotide deletion at position 586 of I196L gene caused protein truncation, potentially impacting its immune evasion function (Huang et al., 2024).

A 50-nucleotide deletion (from positions 972 to 1021) observed in the MGF 360-21R gene (Figure: 33) resulted in a truncation with a 30-amino-acid reduction in the carboxyl terminus of the protein. Interestingly, this deletion was not observed in the ASFV isolate of domestic pig origin and was unique to the wild boar isolate reported in this study. Further analyses and multiple sequence alignment of the MGF-360-21R gene of ASFV isolates obtained from wild boar, warthog, and domestic pigs across different countries revealed that this gene is particularly susceptible to deletions during replication in species other than domestic pigs, especially causing truncations at the carboxy terminus of the encoded protein (Figure: 33). These observations reflect the possible role of MGF-360-21R gene in evolutionary adaptations of the ASFV in wild boar populations.

The sequence variations identified in this study highlight structural diversity within the ASFV genome, particularly in genes associated with immune modulation, such as B475L and members of the MGF family. Frame shifts, deletions, and truncations observed in these genes suggest possible impacts on viral functions that contribute to immune evasion. Given that ASFV is known to exploit immune modulation strategies, these changes may influence the virus's ability to evade the host immune system effectively. Further studies are necessary to determine the effects of these variations, both individually and in combination, on ASFV pathogenesis and immune evasion.

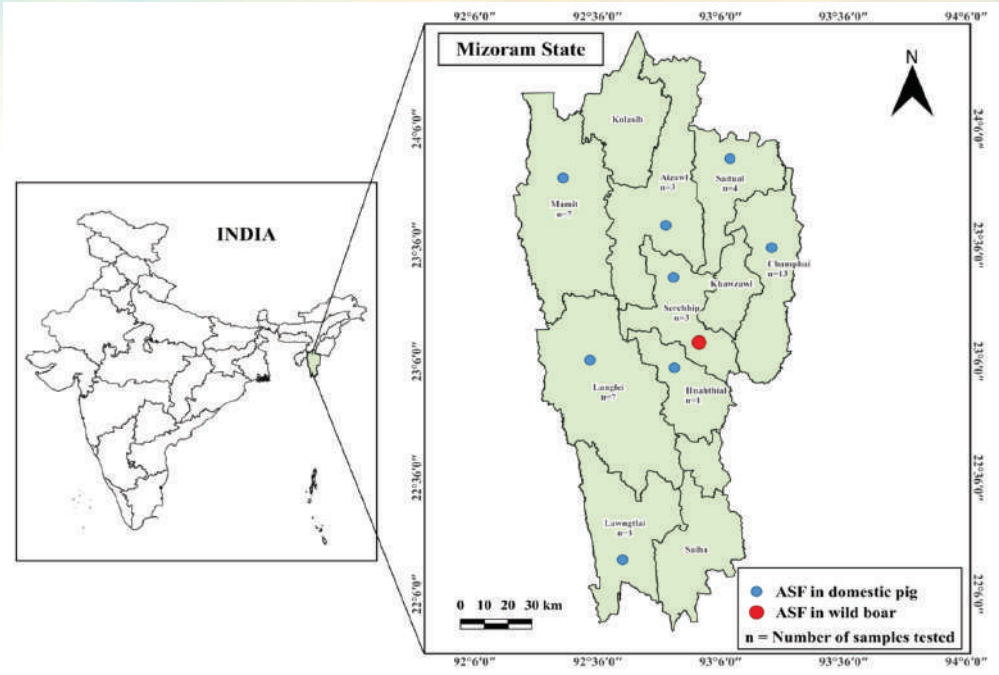


Figure: 32. *Map of Mizoram state highlighting the districts sampled during the African swine fever outbreak, along with the number of samples tested for ASFV detection in this study.*

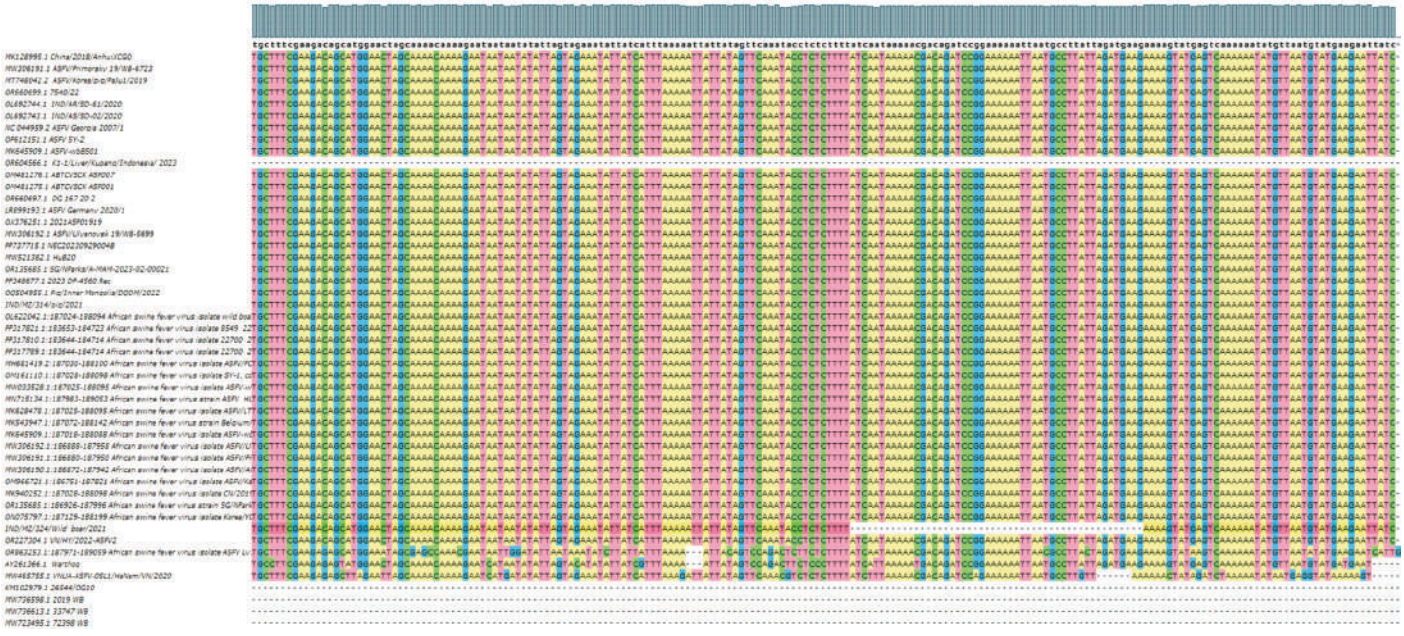


Figure: 33. *50-nucleotide deletion is observed in the MGF-360-21R gene of the ASFV isolate obtained from a wild boar in Mizoram, India, as compared to ASFV isolates derived from domestic pigs in India.*

Faecal Metavirome analyses revealed high viral diversity in pigs

Faecal metavirome sequencing and analysis of the pooled faecal samples, from Madhya Pradesh (n=13) and Assam (n=18), revealed high viral diversity including *Picornaviridae* (*Posavirus, Kobuvirus, Porcine enterovirus, Porcine sapelovirus, Porcine teschovirus, Swine pasivirus 1*), *Astroviridae* (*Porcine astrovirus/Mamastrovirus, Bastrovirus*), *Parvoviridae* (*Bocavirus, Avian adeno-associated virus*), *Paramyxoviridae* (*Parainfluenza virus 5*), *Spinareoviridae (Mammalian orthoreovirus 3*), *Picobirnaviridae* (*Picobirnavirus*), *Circoviridae* (*Porcine circovirus 1/2*), *Adenoviridae*

(*Porcine adenovirus 3*), *Herpesviridae* (*Papiine herpesvirus 2*), *Smacoviridae* (*Porcine-associated porprismacovirus*), *Anelloviridae* (*Gyrovirus 4*) and Porcine serum-associated circular DNA virus 2. Among these viruses, complete genomes have been assembled for *Posavirus*, *Kobuvirus*, and Porcine serum-associated circular DNA virus 2, while the nearly-complete genomes could be assembled for porcine enterovirus G, porcine sapelovirus, and porcine astrovirus.

The enteric viruses, including porcine bocavirus and *Rotavirus C*, identified earlier from West Bengal swine samples, were characterised at the genomic level. NS1 gene-based phylogeny of porcine bocavirus revealed that the Indian porcine bocavirus strain clustered within clade 3, exhibiting the highest nucleotide identity (94.98%) with those strains reported earlier from the United States (Figure: 34c). Eight segments of Rotavirus C could be assembled.

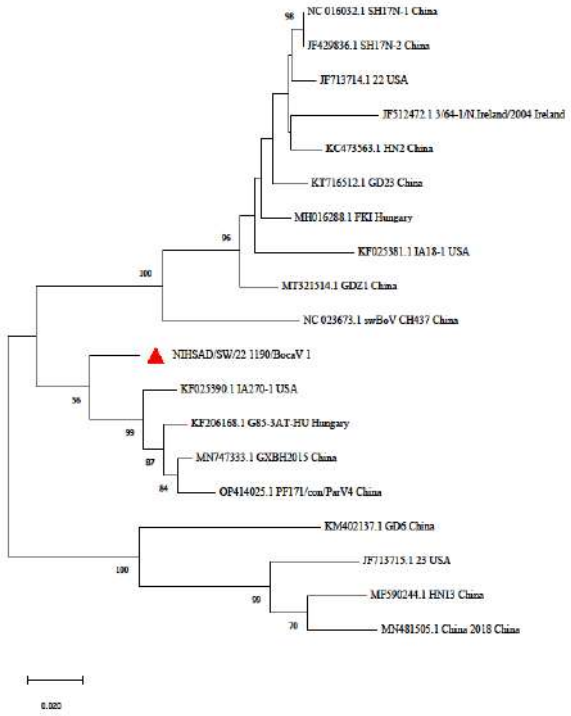


Figure: 34. *Phylogenetic analysis of porcine bocavirus strains. The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model, with bootstrap value 1000.*

Disease monitoring for swine diseases:

Table 10: African swine fever (ASF)

S. No.	State/Source	Samples tested	ASFV positive
1	Andhra Pradesh	2	2
2	Chhattisgarh	54	0
3	Haryana	6	6
4	Karnataka	7	6
5	Kerala	22	15
6	Madhya Pradesh	38	7
7	Maharashtra	31	15
8	Rajasthan	19	11
9	Sikkim	25	6
	Total	**204**	**68**

Table 11: Porcine Reproductive and Respiratory Syndrome (PRRS)

S. No.	State/Source	Samples tested	PRRSV positive
1	Chhattisgarh	54	0
2	Madhya Pradesh	38	0
3	Maharashtra	31	0
4	Sikkim	25	0
	Total	**148**	**0**

Porcine Epidemic Diarrhea (PED) and Transmissible Gastroenteritis (TGE)

A total of 160 faecal samples, collected from Assam (n=80), Meghalaya (n=22), Chhattisgarh (n=35) and Kerala (n=23), were tested for the genome of PED virus (PEDV) and TGE virus (TGEV) by RT-qPCR and found to be negative.

Swine Influenza

A total of 265 porcine serum samples and 234 nasal swabs were either received or collected from different states. 28 serum samples were found positive for presence of H1 antibodies by haemagglutination inhibition test. All the nasal swabs were negative for presence of SIV genome by RT-qPCR test.

Table 12: Testing of Field samples for H1N1 SIV

S. No	States	Nature of samples	No of samples tested	HI Positive (For Serum)	RT-qPCR Positive (For swabs)
1	Sikkim	Serum	8	NIL	Not applicable
2	Bihar		8	02	
3	Jharkhand		8	01	
4	Assam		10	01	
5	MP		17	NIL	
6	Kerala		55	02	
7	Chhattisgarh		159	22	
8	MP	Nasal Swabs	17	Not applicable	NIL
9	Assam		42		NIL
10	Kerala		51		NIL
11	Chhattisgarh		124		NIL

Zoonotic Diseases

Sero-prevalence of Crimean-Congo Haemorrhagic Fever virus in livestock population of Wayanad, Kerala

The Wayanad district falls under the Western Ghat region and has blooming flora and fauna including wild and domestic animal species that provide an ideal ecological niche for the ticks. Even though the tick-borne KFDV is endemic in Wayanad, the data on prevalence of other significant zoonotic tick-borne viruses such as CCHFV and GANV are scanty. Therefore CCHFV Sero-prevalence study consisting of 300 serum samples comprising of cattle (n=198), goats (n=98) and buffaloes (n=04) collected from the forest fringe areas of 10 villages from three taluks of Wayanad district viz., Vythiri (n=138), Sulthan Bathery (n=88) and Mananthavady (n=74) was conducted. The study revealed overall CCHFV seroprevalence of 2.34 with species-wise seropositivity of 1.01% and 5.10% in cattle and goats, respectively. Despite the CCHFV seroprevalence, CCHFV could not be detected in ticks. Even though ticks were negative for the CCHFV genome, seroprevalence indicates the local virus circulation (Figure:1). Moreover, we reported the presence of ticks belonging to 03 genera viz. *Rhipicephalus, Amblyomma,* and *Haemaphysalis*. The segregated and classified 59 tick pools comprised of the genera *Rhipicephalus* spp (n=46, 77.9%), *Haemaphysalis* spp. (n=06, 10.1%) and *Amblyomma* spp. (n=07, 11.86%). (Figure: 36).

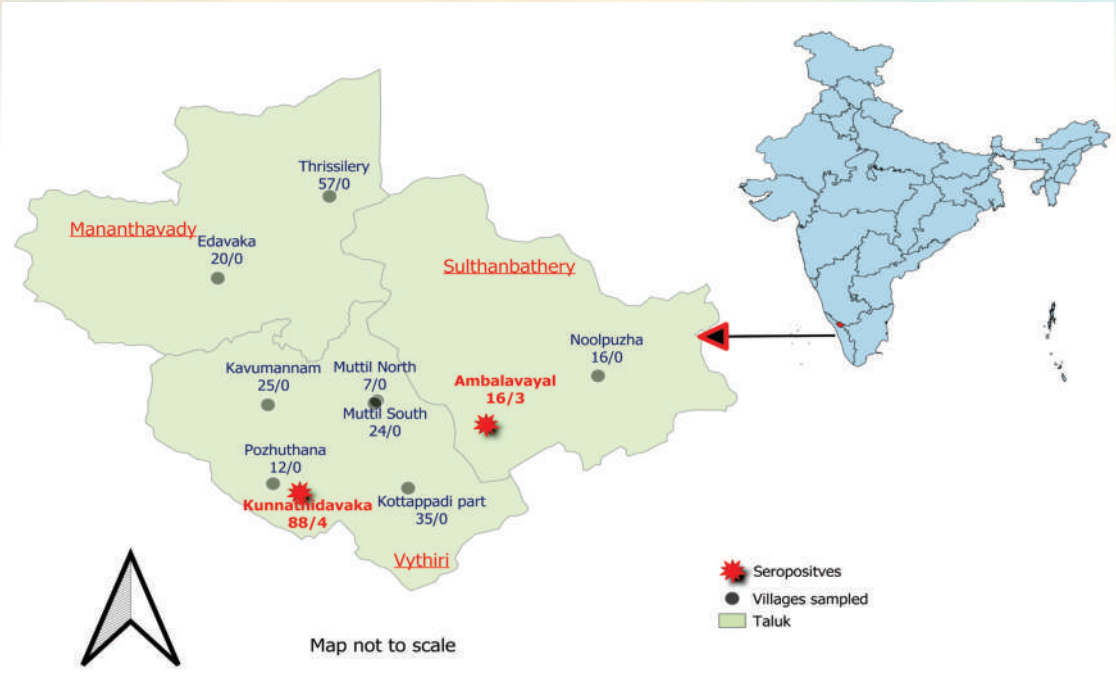


Figure: 35. *GIS mapping depicting sampling locations and seropositivity*

Figure: 36. *Morphological identification of tick species:*
a. Haemaphysalis species,
b. Amblyomma species, and c. Rhipicephalus (Boophilus) species

Exploring the Therapeutic Potential of *Cordyceps militaris* against SARS-CoV-2 through In-silico and in-vitro approach

The Molecular docking analysis revealed that the Cordycepin, a bioactive compound in *Cordyceps militaris*, has the highest binding affinity to the SARS-CoV-2 spike protein. The in-vitro analysis of antiviral potential of crude aqueous extract of *C. militaris* at 100 μg/mL in Vero E6 cells could reduce the viral copy numbers to 149638 copies/mL from 297839 copies/mL compared to the virus-only control, equating to a 50.24% reduction in viral particles. These findings suggest that *C. militaris* has promising anti-SARS-CoV-2 activity and may be explored as traditional medicine for other viruses of public/animal health importance. (Figure: 37 & 38).

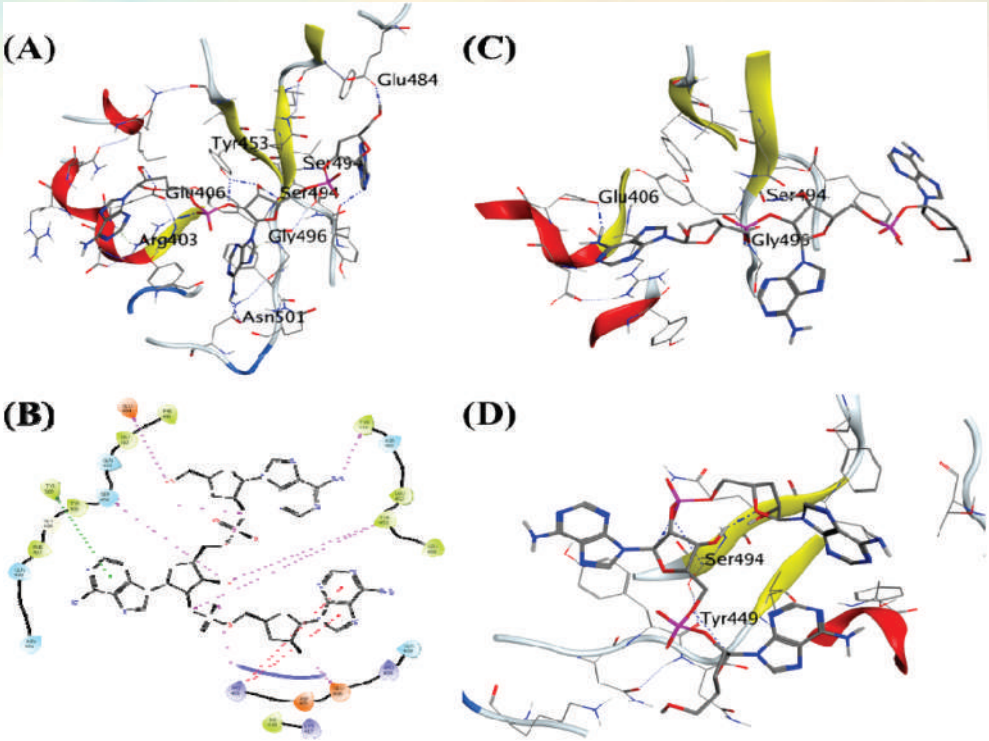


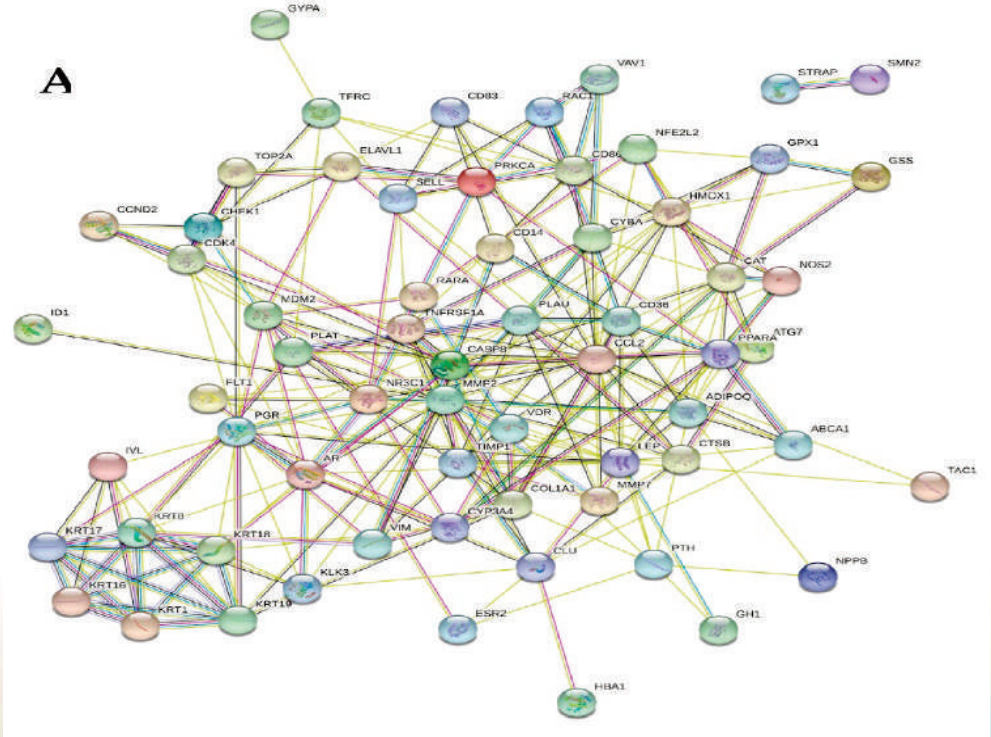
Figure: 37. *Ligand-protein interactions.*

A. MD of Cordycepin on the interface of the SARS-CoV-2 receptor binding domain and ACE2 receptor,

B. Two-dimensional interaction map for the Cordycepin with the interface residues.

C. Initial frame of the production phase for the MDS of the docked ligand-receptor complex.

D. The final frame of the production phase for the 100 ns MDS of the docked ligand-receptor complex.



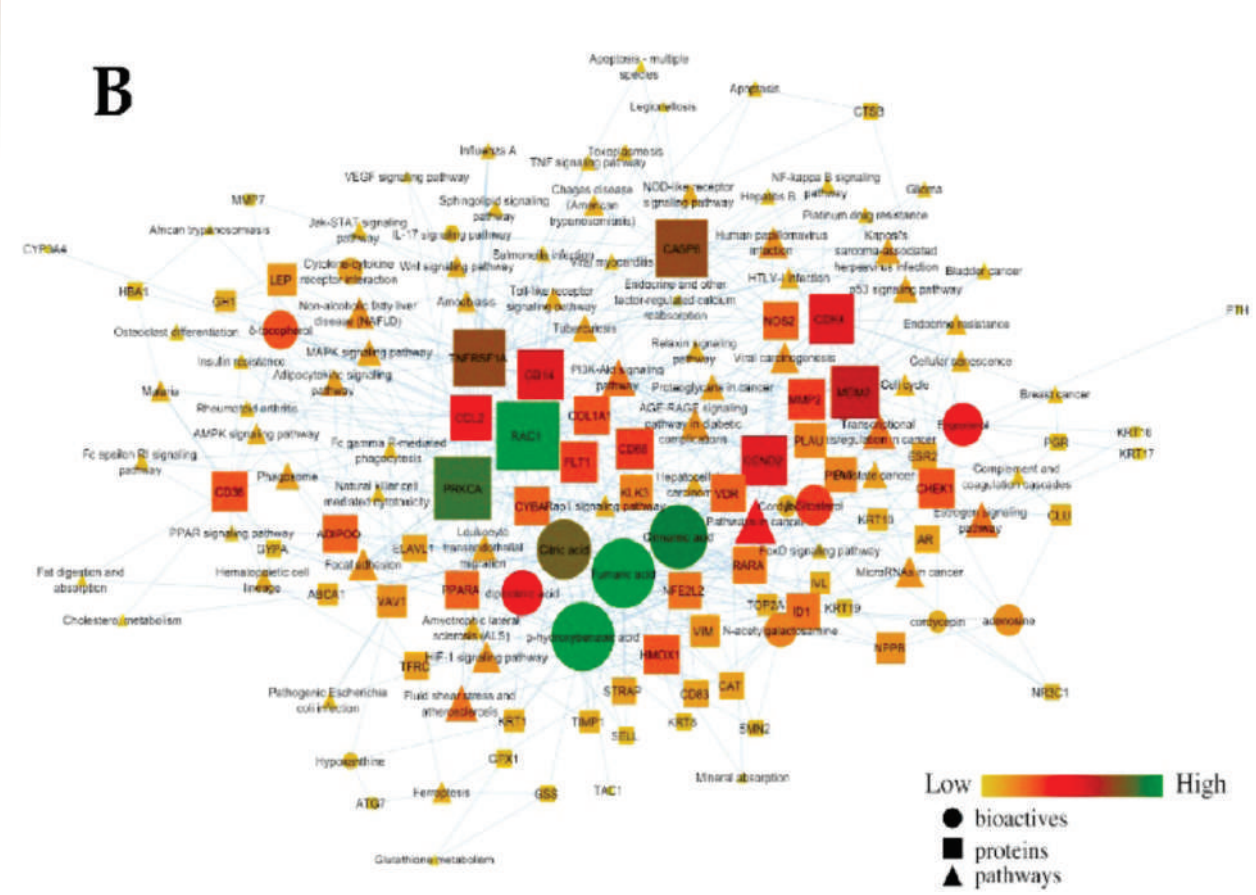


Figure: 38. (A) *Protein-protein interaction of the bioactive-targeted proteins. Node color; coloured nodes: query proteins and first shell of interactors; from curated databases, experimentally determined, Predicted Interactions; gene neighbourhood, gene fusions, gene co-occurrence and Others; text mining, co-expression, protein homology.*

(B) *Compounds-proteins-pathways interaction. Circular, square and triangle nodes represent the compounds, proteins and pathways, respectively. The size of the node is directly proportional to the edge count.*

Viral diversity in ticks collected from the Madhya Pradesh:

Developed automated NGS data analysis pipeline for seamless analysis of NGS data to extract blast ready viral sequence using different bioinformatics analysis tools viz. Fast QC, Multi QC, Trim Galore, Kraken 2, Kraken-biom-csv,Python Script,CAP3. Total of 16 representative tick pools of Rhipicephalus/ Hyalomaa were sent for NGS. Paired end library was sequenced and generated ≈10GB of data for each sample with ≈15.3 million forward and reverse reads.Reads were analysed through automated NGS data analysis pipeline Even though virome analysis revealed genetic evidence of important viruses, only short contigs ranging from 125 - 357 bases could be obtained. However, upon blast at NCBI, contigs could be designated into virus family belonging to *Phenuiviridae, Rhabdoviridae, Flaviviridae, Orthomyxoviridae, Reoviridae, Nairoviridae, Parvoviridae, Papillomaviridae, Retroviridae, Poxviridae, Hepeviridae, Phlebovirus, Arenaviridae, Peribunyaviridae, herpesviridae* and *simbu* serogroup viruses were identified. Though whole virus/viral gene could not be assembled, obtained contigs indicated that closely related virus from that families are circulating in tick population.

Surveillance of zoonotic pathogens in rodent population:

74 Rodent samples from different regions of Maharashtra were subjected to a comprehensive panel of diagnostic tests to screen for multiple zoonotic rodent borne pathogens of public health significance post verification and optimization of assays (Table 13.). The sample details have been elaborated in Table 14. All samples were tested negative for all the targets.

Table 13: Diagnostic Assays optimized for screening of rodent pathogens

S. No.	Pathogen	Assay Ref.
1	Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV)	Genes2Me Viral Detect-II kit
2	Mpox virus	Zhao et al 2010
3	Hantaan virus	Pang et al 2014
4	Crimean-Congo Hemorrhagic Fever (CCHF)	Wolfel et al 2007
5	Hepatitis E virus (HEV)	Jyothikumar et al 2006
6	Kyasanur Forest Disease (KFD) virus	Mourya et al 2012
7	Influenza virus	Kamboj et al 2014
8	Coxiellaburnetii (Q fever)	De bruin et al 2011
9	Orientiatsutsugamushi (Scrub typhus)	Tantibhedhyangkul et al 2017
10	Rickettsia	Kato et al 2013
11	Yersinia pestis	Bai et al 2020

Table 14: Rodent sample collection, location and pathogen screening details

Details of Rodent Samples Tested					
	Location	**Udgir, Maharashtra**	**Nagpur, Maharashtra**		**Total Rodent Tested**
	Type of sample	**Intestinal loop**	**Intestinal loop**	**Organ Pools (Brain, Heart, Kidney)**	
	Period Collection Pathogens Tested	Nov, 2023	Jan, 2024	April, 2024	
1	Mpox	12	50	12	74
2	CCHF	12	50	12	74
3	Hepatitis E Virus	12	50	12	74
4	SARS-CoV2	12	50	12	74
5	KFDV	12	50	12	74
6	Hantaan virus	12	50	12	74
7	Yersinia pestis	12	50	12	74
8	Coxiella burnetti	12	50	12	74
9	Rickettsia spp.	12	50	12	74
10	Scurb typhus	12	50	12	74
	ALL SAMPLES TESTED NEGATIVE				

Genomic surveillance by metaviromics profiling

Metavirome profiling of a pool of bat faecal samples and a pool of organ samples from a shrew from urban location in Bhopal was carried out. Metavirome data was generated using in-house protocols on Oxford Nanopore. Approximately 3.2 Gb and 1.6 Gb of data was generated from total nucleic acid extracted from the bat faecal sample and Shrew organ pool respectively.

In case of the bat fecal samples, 10% of the reads have viral hits. Kaiju classified data in 1388 unique hits. Approx. 75%, 12% and 11% data was classified by Kaiju as phage families, large DNA virus families and unclassified data. Hits for RNA viruses are roughly 1% and comprise of some plant and unclassified viruses (Figure 39).

On the other hand the data from the Shrew organ pool, 67% of the data was of the host genome. 1475 unique hits were obtained from the remaining dataset. 57%, 37% and 4% data was classified by Kaiju as large DNA virus families, retroviral element families and phage families while 2% was unclassified data. A high proportion of RNA viral hits are of retro elements from the genome (Figure :40).

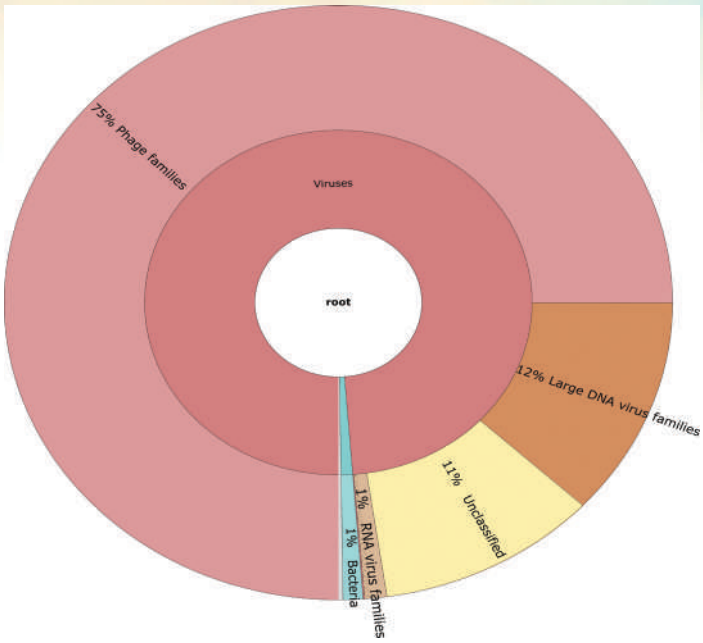


Figure :39. *Krona chart showing the distribution of bat fecal metavirome data*

2. Shrew tissue samples were homogenized and clear supernatant filtered using using 0.45 um syringe filter and nucleic acids were extracted. cDNA conversion without DNAse digestion was performed and sequencing was performed using Oxford Nanopore technologies MinION flow cell. Roughly 1.6 Gbases of data was generated which was basecalled and quality controlled before subjecting to BLASTx and Kaiju classification against viral Refseq database. 67% of the data was of the host genome. 1475 unique hits were obtained from the remaining dataset. 57%, 37% and 4% data was classified by Kaiju as large DNA virus families, retroviral element families and phage families while 2% was unclassified data. A high proportion of RNA viral hits are of retro elements from the genome.

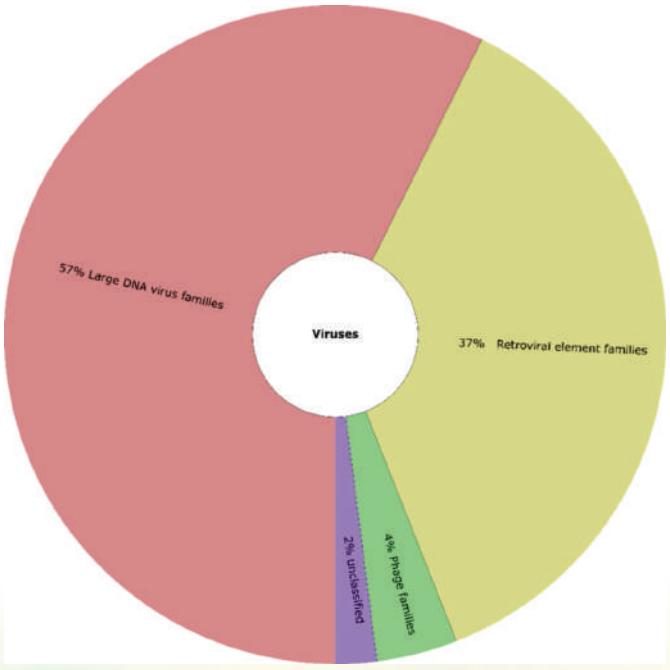


Figure : 40. *Krona chart showing the distribution of shrew tissue metavirome data*

Monitoring of Zoonotic Diseases

Animal samples referred from different state department screened for emerging diseases including COVID-19 (SARS-CoV-2), Nipah, West Nile Virus, Monkey pox, Kyasanur Forest Disease etc. The details of samples tested are as given in Table 15.

Table 15 : Details of samples screened for emerging zoonotic diseases

S. No.	Disease Tested	State	Species (No of Animals)	No of samples tested
1	COVID-19	Kerala	Bat(5)	16
		MP	Bat(1)	1
		Kerala	Monkey(2)	8
		Assam	Wild Rhesus macaque(1)	3
		Kerala7	Wild Pig(5)	5
Subtotal of number of samples tested for COVID-19				33
2	West Nile Virus	Kerala	Wetland bird(1)	1
		Kerala	Crow(2)	4
		Kerala	Cormorant(1)	2
Subtotal of number of samples tested for West Nile Virus				7
3	Monkeypox	Kerala	Monkey(2)	8
		Assam	Wild Rhesus macaque(1	3
Subtotal of number of samples tested for Monkeypox				11
4	Kysanur Forest Disease	Kerala	Monkey(2)	8
		Assam	Wild Rhesus macaque(1	3
Subtotal of number of samples tested for Kysanur Forest Disease				11
5	Hepatitis E	Kerala	Monkey(2)	8
		Assam	Wild Rhesus macaque(1	3
Subtotal of number of samples tested for Kysanur Forest Disease				11
Total samples tested				**73**

Outbreak Investigation

Avian Influenza Outbreak Investigation:

In 2024 an outbreak of H5N1 avian influenza virus was reported in Nellore District of Andhra Pradesh. The Department of Animal Husbandry & Dairying constituted a Central team to investigate the outbreak and oversee the control and containment operations as per the extant National Action Plan on avian Influenza. The Central team visited the Surveillance zone of two epicentres of Nellore district for collection of samples. The swab samples from poultry and environmental samples from the Pulicat Lake were collected to assess the persistence of virus in poultry/ environment.

All the samples collected during investigation were tested for detection of Avian Influenza virus using RT-qPCR as per the protocol approved under ISO17025:2017 certification of Avian Influenza Testing Laboratory of ICAR-NIHSAD. All the samples were found negative for avian influenza virus. The State Animal Husbandry Department of Andhra Pradesh was advised to adhere to implementation of Action Plan for Prevention, Control & Containment of Avian Influenza (Revised – 2021) at all times and in all areas including commercial poultry farms. The state Animal Husbandry Department should have more proactive approaches with active and targeted surveillance and monitoring in the high-risk areas and high-risk periods with regular awareness programmes to local animal/bird owners related to biosecure management practices and veterinary care.

Nipah Outbreak Investigations in Kerala

In 2024, two laboratory-confirmed human cases of Nipah virus were reported in Malappuram district, Kerala, one each in July and September. The National Joint Outbreak Response Team (NJORT) conducted a comprehensive investigation, involving an interdepartmental team comprising experts from the human, livestock, and wildlife sectors. During the investigation, samples were collected from the epicenter (location of the index case) and its surrounding areas, targeting reservoir host bats (*Pteropus giganteus*) and amplifier host pigs. Additionally, samples were obtained from other animals, including cattle, cats, horses, goats, dogs, and bat-eaten fruits, as well as environmental samples, to assess the potential sources and transmission dynamics of the outbreak.

All samples collected during the investigation were tested for Nipah virus using the World Health Organization (WHO) and World Organisation for Animal Health (WOAH) recommended reverse transcription quantitative polymerase chain reaction (RT-qPCR) method, as outlined by Guillaume et al. (2004) and Mungall et al. (2006). All tested samples yielded negative results for Nipah virus. Following the investigation, an Emergency Surveillance Plan and a Long-term Surveillance Plan were developed and provided to the State Animal Husbandry Department (SAHD), Kerala, under the guidance of the Department of Animal Husbandry and Dairying (DAHD), Government of India. Additionally, Standard Operating Procedures (SOPs), instructions for the collection, storage, and transport of samples, and an advisory for outbreak management were prepared and submitted to the relevant authorities.

Table: 16 Details of the animal samples tested from Malppuram, Kerala

Animal Samples from Malppuram, Kerala tested following the human cases of Nipah					
S.No.	**Species**	**Animal Samples Tested in July 2024**		**Animal Samples Tested in Sept 2024**	
		No. of Animal	**No. of Sample**	**No. of Animal**	**No. of Sample**
1	Cattle	12	23	6	12
2	Buffalo	2	4	1	2
3	Goat	14	24	3	6
4	Dog	1	1	3	4
5	Cat	5	5	1	2
6	Poultry	4	4	-	-
7	Wild Pig	1	7	-	-
8	Pig	10	30	5	10
	Total	**49**	**98**	**19**	**39**

Table: 17 Details of the environmental samples tested from Malppuram, Kerala

Environmental Samples from Malppuram, Kerala tested following human cases of Nipah		
S. No	**Sample**	**No. of samples tested**
1	Fruit	6
2	Spitted fruit pulp under bat roost	5
3	Bat dropping	9
4	Water mixed with bat dropping	2
5	Water under Bat roost	4
	Total	**26**

Host-Pathogen Interaction Studies

H5 transmission in Guinea pigs

The novel reassortant H5Nx avian influenza viruses of the 2.3.4.4 clade have caused global concern due to their rapid evolution and global spread in recent years. Infections in mammals have been reported due to clade 2.3.4.4b H5N1 viruses in wild or captive mammals as well as in humans. Herein, we assessed the in-contact transmission potential of A/duck/India/11TR05/2021 (H5N1) clade 2.3.4.4b virus in guinea pigs. Six guinea pigs were inoculated with 10 6.0 EID 50 of virus and six in-contact guinea pigs were introduced 24h later. Nasal washings in PBS were collected daily till 14 dpi from infected and in-contact guinea pigs to assess the virus transmission. None of the guinea pigs in infected and in-contact group show any overt signs of illness. Viral RNA was detected by RT-qPCR in nasal washings of infected guinea pigs. In infected group genome was consistently detected in all the infected animals till 7 dpi. In in-contact group Cq <30 was detected in only two animals 6-9 days post contact. Sera was collected on 14 dpi from all the animals to ascertain the seroconversion against H5N1 virus. All the infected guinea pigs seroconverted against H5N1 virus. However, only one in-contact showed seroconversion against the virus (Figure: 41). Hence, this study highlights that H5N1 clade 2.3.4.4b virus could transmit from infected to in-contact guinea pigs without prior adaptation in mammalian host.

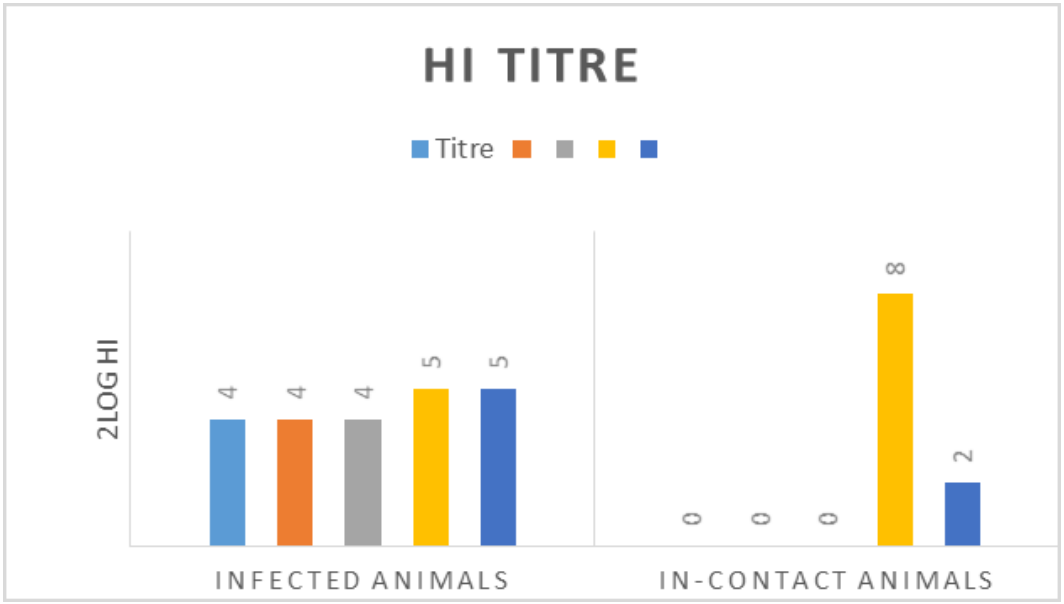


Figure : 41

Identification of critical metabolites involved in the pathogenesis of H5N1 infection in chicken lungs

Owing to its high prevalence and mortality rates in poultry and recent expansion of host range, unravelling the metabolomics underlying of HPAI H5N1 pathogenesis and host-pathogen interactions is critical for developing effective control strategies. LC-MS/MS data on QTRAP 6500 mass spectrometer (AB Sciex) was generated from H5N1 infected and mock-infected chicken lungs in biological and technical triplicate both in positive and negative ionization mode. Pronounced metabolite changes were observed in the lungs . Total of 31 +ve ionization and 26 –ve ionization metabolites were identified to be differentially expressed in AIV infected chicken lung as compared to control (Figure: 42). Significant enrichment in sphingolipid metabolism, tryptophan metabolism, and arginine-proline metabolism were found in lungs (Figure: 43). Influenza virus possibly exploits sphingolipid metabolism to facilitate critical interactions such as plasma membrane fusion, viral endocytosis, cell signaling, & viral budding. Tryptophan metabolism associates with inflammation and central nervous system (CNS) pathology seen in H5N1 infection.These findings provide new insights into the chicken host's response to H5N1 infection and sheds light on virus-host interactions, potentially elucidating the infection mechanisms of HPAI H5N1.

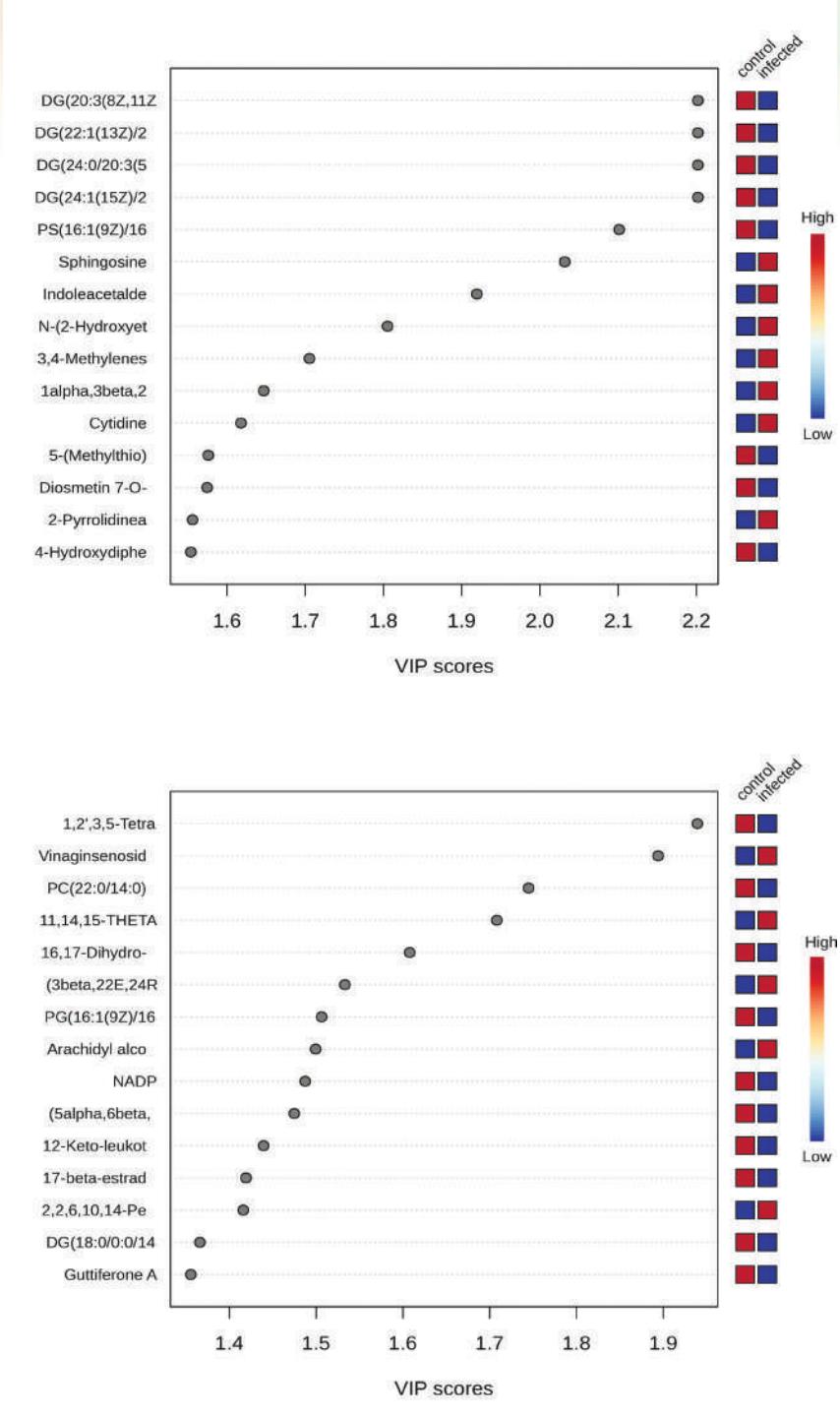


Figure: 42. *Variable Importance Projection (VIP) plot of significantly differentially expressed metabolites identified in H5N1 infected chicken lungs (a)Positive ionization mode and (b) Negative ionization mode*

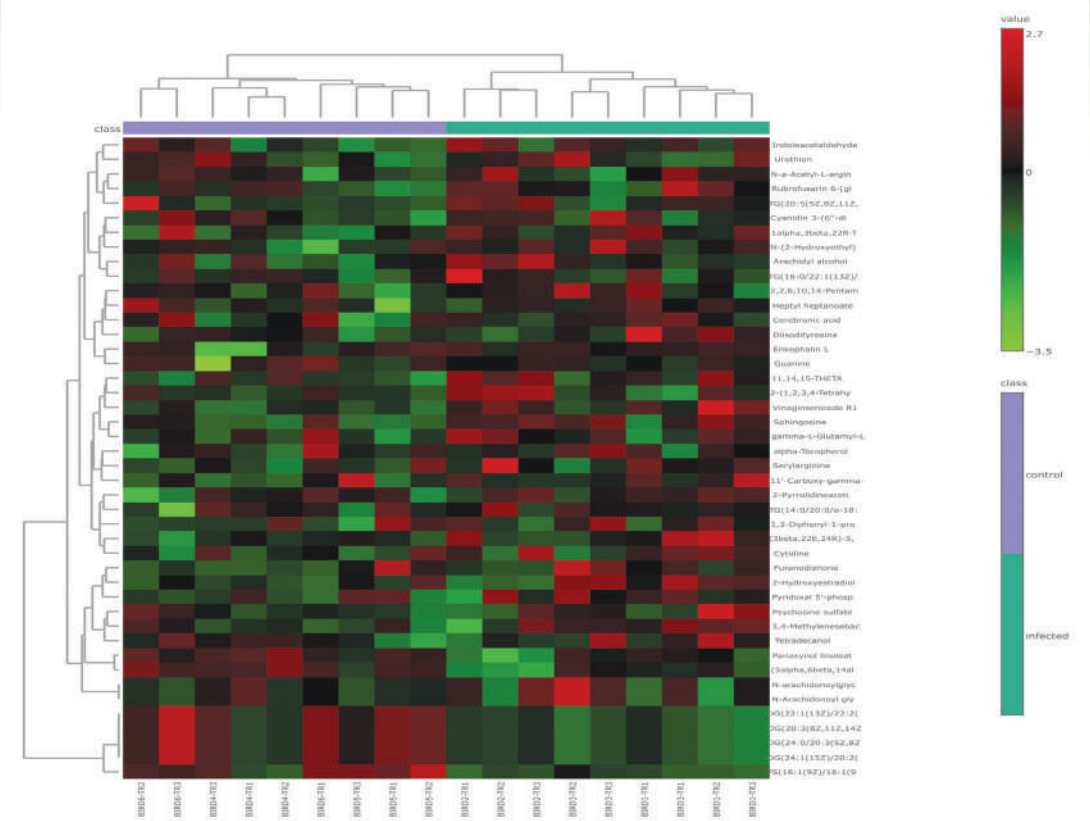
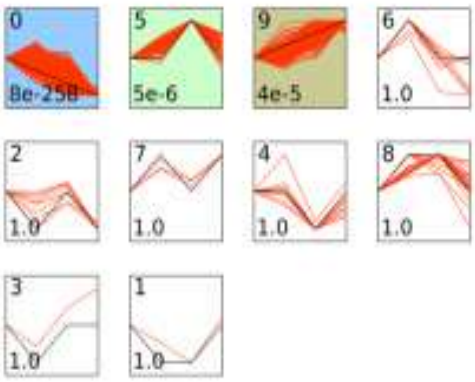
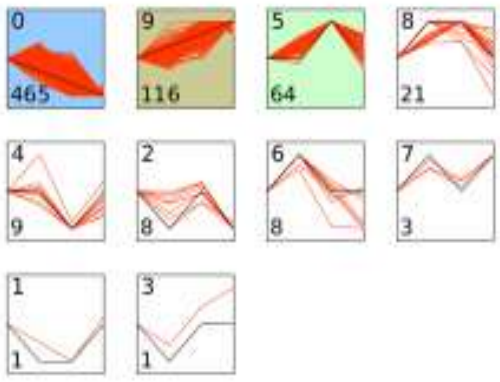


Figure: 43. *Heat map of metabolites differentially expressed in H5N1 infected chicken lungs*

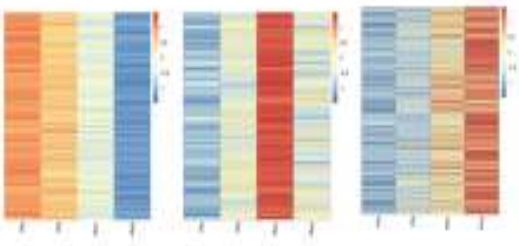
Transcriptome analysis of SARS CoV-2 infected cat and dog lung explant cultures

The emergence of SARS-CoV-2 variants, notably Delta (B.1.617.2) and Omicron (B.1.1.529), created new public health challenges due to their high transmissibility and diverse clinical impacts. Given the close human-animal interactions and potential for animals to act as viral reservoirs, investigating SARS-CoV-2's molecular dynamics in pet animals is crucial. Lung explant culture from domestic cats and dogs, infected *ex-vivo*, with Delta and Omicron SARS CoV-2 was used to assess their transcriptional response to infections. Transcriptomic profiling at multiple post-infection time points revealed disruptions in key biological processes, including extracellular matrix (ECM) organization, surfactant homeostasis, angiogenesis, and immune responses in both species. In cats, Delta variant infection triggered early activation of tissue damage-associated genes by 12 hours post-infection (hpi). By 24 hpi, both Delta and Omicron variants led to significant gene activation in cats and dogs, with Delta inducing a more pronounced inflammatory response and increased tissue damage (Figure: 44-45). Notably, dogs displayed activation of reparative response genes at 24 hpi, suggesting potential for tissue recovery, whereas cats did not show similar activation, indicating a potentially higher susceptibility to lung injury. Hub gene analysis identified significant biomarkers for infection severity, particularly in cats, with genes involved in focal adhesion, PI3K-Akt signaling, and TNF signaling pathways showing diagnostic potential. Dogs infected with Omicron showed upregulation of genes associated with mitochondrial and ribosomal functions, likely contributing to lung injury and altered metabolism, while keratin gene upregulation suggested active epithelial repair in response to lung damage (Figure: 46-47). Integrins, essential for immune cell trafficking and tissue repair, were consistently downregulated in both variants, indicating impaired immune cell migration. The findings underscore the utility of the *ex-vivo* lung explant model in studying viral infections under near-physiological conditions, providing valuable insights into SARS-CoV-2 pathogenesis across species. These insights can help in monitoring cross-species transmission and support public health efforts to mitigate future zoonotic outbreaks.





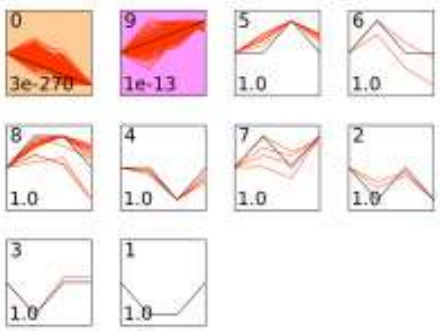
Delta infected cat profile ordered by significance level

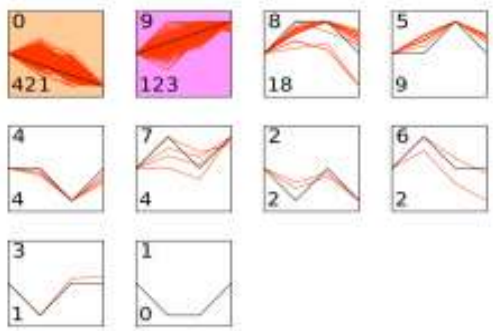


Delta infected cat profile ordered by number of genes

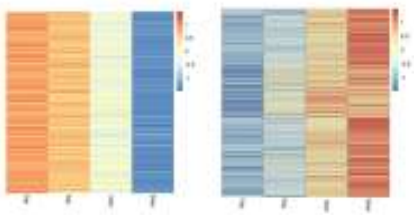
Profile	Number of genes assigned
0	465
5	64
9	116

Figure: 44. *Short Time-series Expression Miner (STEM) analysis for cat lungs explant culture infected with SARS CoV-2 Delta variant infection*





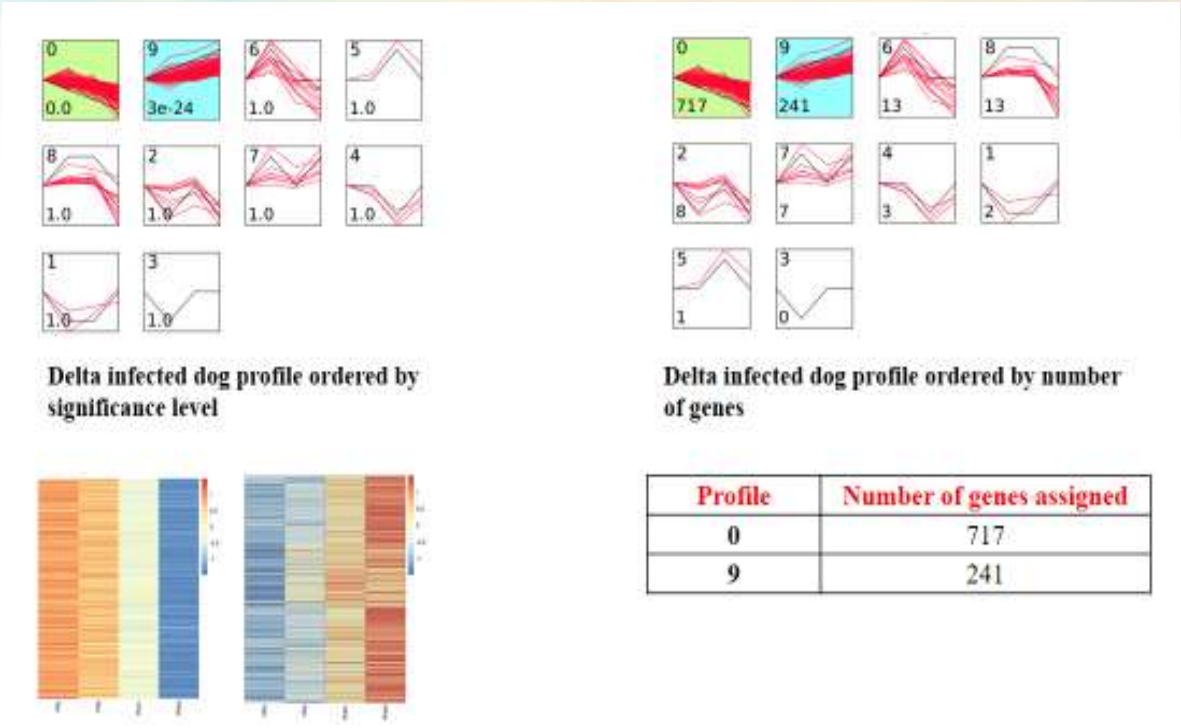
Omicron infected cat profile ordered by significance level



Omicron infected cat profile ordered by number of genes

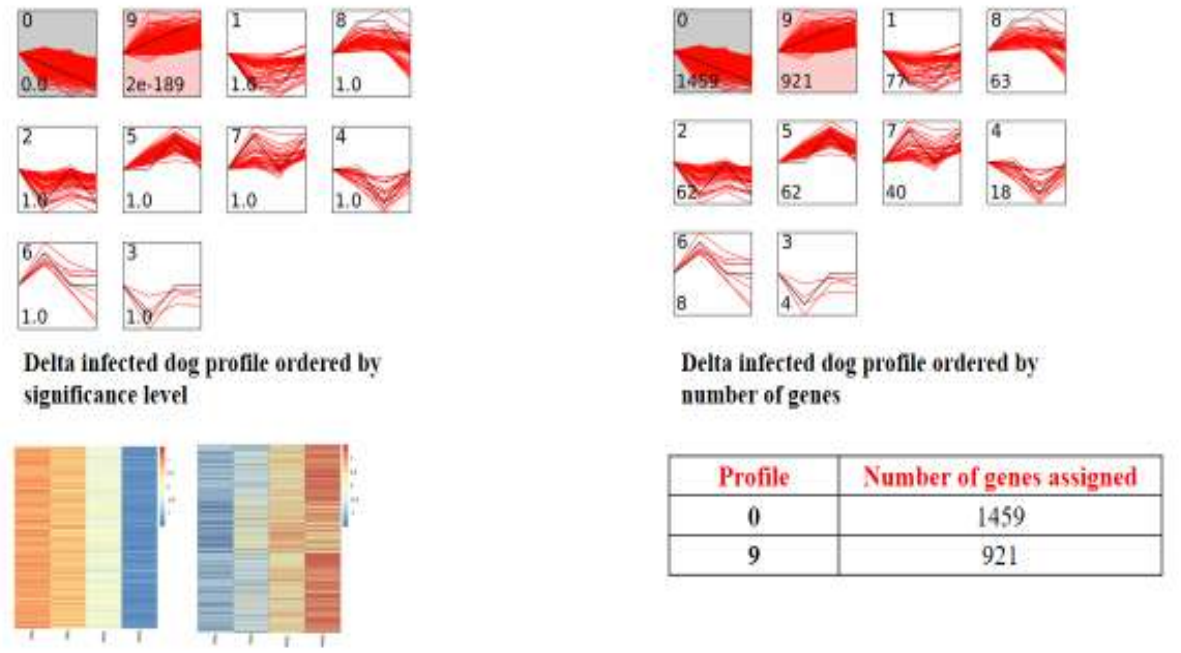
Profile	Number of genes assigned
0	421
9	123

Figure: 45. *Short Time-series Expression Miner (STEM) analysis for cat lungs explant culture infected with SARS CoV-2 Omicron variant infection*



Profile	Number of genes assigned
0	717
9	241

Figure: 46. *Short Time-series Expression Miner (STEM) analysis for dog lungs explant culture infected with SARS CoV-2 Delta variant infection*



Profile	Number of genes assigned
0	1459
9	921

Figure: 47. *Short Time-series Expression Miner (STEM) analysis for dogt lungs explant culture infected with SARS CoV-2 Omicron variant infection*

DIAGNOSTIC SERVICES

Diagnostic Services to Animal quarantine and Certification offices, DAHD, MoFAHD, GoI for various exotic and emerging diseases

A total of 8890 imported samples of imported biological, poultry & livestock and related products from AQCS office (New Delhi, Mumbai, Chennai, Kolkata, Hyderabad) including SPF eggs, pet foods/supplements, pig bristles, pork meat/powder, cloacal swab, tracheal swab, poultry meat, turkey meat, duck meat, duck/hen feather, shuttlecock feather, poultry serum, bovine semen, bovine leather, bovine serum, bovine embryo, bovine cells, pig semen were tested negative for various exotic and emerging diseases listed in (Table 18). The distribution of samples received from different AQCS offices is presented in Figure: 48.

Table 18: Disease and Specimen-wise testing of samples for AQCS Offices

S. No	AQCS Office	AIV	PRRS	ASF	MCF	NSD	RVF	CAE	BVD	SI	AJD	PED	TGE	RHD	LSD	Total
1	New Delhi	1326	2	27	1	1	0	0	60	21	1	0	0	0	3	1442
2	Chennai	170	0	0	4	4	4	4	107	0	0	0	0	0	1	294
3	Mumbai	5359	130	130	47	47	36	47	41	50	50	50	50	1	1	6039
4	Kolkata	46	0	0	0	0	0	0	0	0	0	0	0	0	0	46
5	Bangalore	16	0	0	1	1	1	1	49	0	0	0	0	0	1	70
6	Hyderabad	3	166	166	0	0	0	0	0	166	166	166	166	0	0	999
Total		**6920**	**298**	**323**	**53**	**53**	**41**	**52**	**257**	**237**	**217**	**216**	**216**	**1**	**6**	**8890**

AI- Avian Influenza, BVD – Bovine Viral Diarrhea, MCF- Malignant catarrhal fever, NSD- Nairobi Sheep Disease, RVF- Rift Valley Fever, CAE- Caprine Arthritis and Encephalitis, PRRS- Porcine Reproductive & Respiratory Syndrome, ASF- African Swine Fever, SI- Swine Influenza, AJD- Aujeszky's Disease, PED -Porcine Epidemic Diarrhea, TGE - Transmissible Gastroenteritis, RHD - Rabbit Haemorrhagic Disease, LSD – Lumpy Skin Disease.

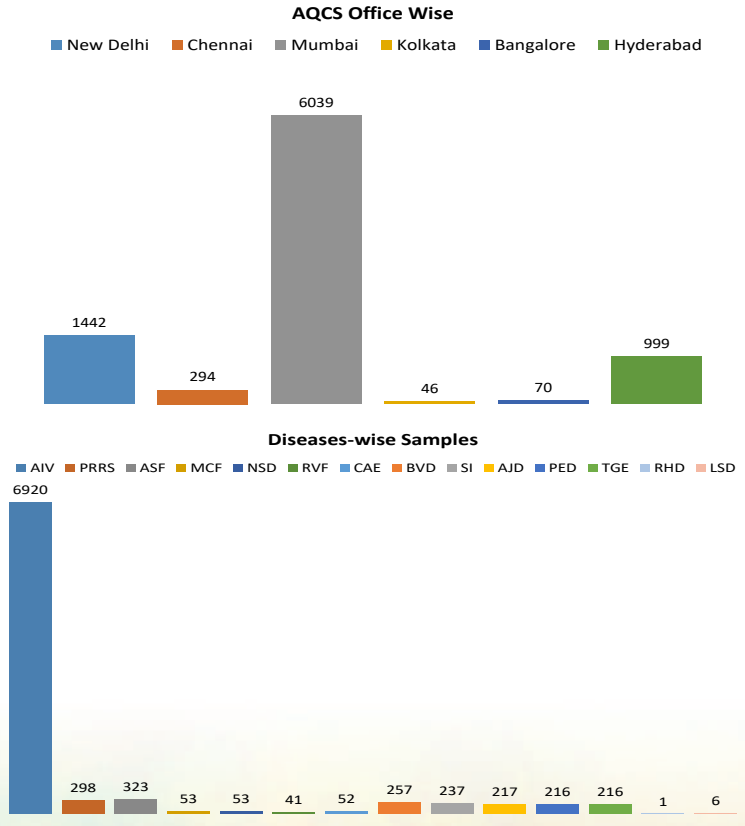


Figure: 48. *AQCS Office and Disease-wise Samples*

TECHNOLOGIES

Release of Inactivated Bovine Viral Diarrhea Virus (BVDV-1) Vaccine for cattle by Shri Shivraj Singh Chouhan, Hon'able Union Minister of Agriculture and Farmers Welfare

Bovine viral diarrohea (BVD) is an economically important viral disease of cattle and widely prevalent in India. BVD causes significant economic losses to the dairy farmers/industry due to reproductive disease (abortion, congenital malformation, infertility and birth of weak calves), respiratory disease, gastrointestinal disease, losses in milk yield and neonatal mortality. However, vaccine against BVD is not yet available in India. To overcome the gap, the first indigenous BVD (BVDV-1) vaccine for cattle has been developed by ICAR-NIHSAD, Bhopal. The newly developed inactivated whole virus BVD (BVDV-1) vaccine using a field isolate (BVDV-1) from India, is intended for prevention and control of BVDV infections in cattle that can reduce the economic losses of dairy farmers/industry. The BVD vaccine has passed the sterility, safety, immunogenicity and efficacy testing in experimental cattle under laboratory conditions, and safety and immunogenicity testing in field cattle. It provides protective immunity against BVDV-1 in cattle from day 35 of vaccination till 12 months, under experimental conditions and covers all the BVDV-1 strains circulating in India. Additionally, it has shown protective immune response in field cattle up to the study period of 6 months post vaccination and partial protective immune response against infections with BVDV-2 and HoBiPeV. This advancement marks a significant step towards safeguarding India's dairy sector, reducing economic losses, increasing milk production and reinforcing the country's capabilities in the field of animal health and disease control. This technology was released by Shri Shivraj Singh Chouhan, Hon'able Union Minister of Agriculture and Farmers Welfare on 96th ICAR Foundation day (16th July 2024) at New Delhi.

PUBLICATIONS

Research Publications

1. Chingtham, S., Kulkarni, D.D., Sivaraman, S. Mishra,A., Pateriya,A.K ., Singh,V. P.& Raut, A. A. (2024). Novel triplex nucleic acid lateral flow immunoassay for rapid detection of Nipah virus, Middle East respiratory syndrome coronavirus and Reston ebolavirus. Anim. Dis. 4, 21.

2. Dixit, B., Murugkar, H. V., Nagarajan, S., Tosh, C., Kumar, M., Pathak, A., Panickan, S., Shrivastav, N., Mishra, A. K., & Dixit, M. (2024). Prevalence and risk factor for H9N2 avian influenza virus in poultry retail shops of Madhya Pradesh. Virusdisease, 35(2), 321–328.

3. Duragkar, N., Chikhale, R., Piechota, M., Danta, C. C., Gandhale, P., Itankar, P., Chikhale, S., Gurav, N., Khan, M. S., Pokrzywa, W., Thapa, P., Bryce, R., & Gurav, S. (2024). SARS-CoV-2 inhibitory potential of fish oil-derived 2-pyrone compounds by acquiring linoleic acid binding site on the spike protein. Int. J. Biol. Macromol., 275(Pt 1), 133634.

4. Gandhale, P., Chikhale, R., Khanal, P., Biswa, V., Ali, R., Khan, M. S., Gurav, N., Ayyanar, M., Das, S., & Gurav, S. (2024). Quest for Anti-SARS-CoV-2 antiviral therapeutics: in-silico and in-vitro analysis of edible mushroom- Cordyceps militaris. J. Ayurveda Integr. Med., 15(3), 100979.

5. Gupta,M.K., Kumar, S., Lakra, P.P., Senthilkumar, Rajukumar,K., Kumar, B., Pamia, J., Kumar, R., Kumar, A., Mahtha, B.B & Prasad, S. (2024). Study on the mortality pattern of African Swine Fever in pigs during an outbreak in Ranchi, Jharkhand. Indian J. Vet. Pathol., 48 (1), 18-25

6. Kalaiyarasu, S., Rajukumar, K., Mishra, N., Sudhakar, S. B., & Singh, V. P. (2024). Detection and Genetic Characterization of Border Disease Virus (BDV) Isolated from a Persistently Infected Sheep in a Migratory Flock from Rajasthan State, Northwestern India. Viruses, 16(9), 1390.

7. Kant, R., Kumar, N., Malik, Y. S., Everett, D., Saluja, D., Launey, T., & Kaushik, R. (2024). Critical insights from recent outbreaks of Mycoplasma pneumoniae: decoding the challenges and effective interventions strategies. Int. J. Infect. Dis, 107200.

8. Kaushik, R., Kumar, N., Yadav, P., Sircar, S., Shete-Aich, A., Singh, A., Tomar, S., Launey, T., & Malik, Y. S. (2024). Comprehensive Genomics Investigation of Neboviruses Reveals Distinct Codon Usage Patterns and Host Specificity. Microorg, 12(4), 696.

9. Krishna Kumar, S., Palanivel, K., Mishra, N. (2024). Bovine Viral Diarrhoea Genotype-Based Pathogenicity in Dairy Cattle of Tamil Nadu. Indian Vet J., 101(7): 38 – 41.

10. Kulkarni, P. M., Basagoudanavar, S. H., Gopinath, S., Patangia, H., Gupta, P. K., Sreenivasa, B. P., Senthilkumar, D., Sharma, R., Bhatia, S., Sharma, G. K., Bhanuprakash, V., Saikumar, G., Yadav, P., Singh, R. K., Sanyal, A., & Hosamani, M. (2024). Characterization of monoclonal antibodies targeting SARS-CoV-2 spike glycoprotein: Reactivity against Delta and Omicron BA.1 variants. J. Virol. Methods., 330, 115027.

11. Kumar, N., Kaushik, R., Yadav, P., Sircar, S., Shete-Aich, A., Singh, A., & Malik, Y. S. (2024). A highly divergent enteric calicivirus in a bovine calf in India. Arch. Virol., 169(5), 102.

12. Panwar A, Sehgal P, Bhatia S, Jangir A, Kumar P, Raut AA, Mishra A. **(2024).** Establishment of an ex vivo lung explant culture model for dogs and cats to study SARS-CoV-2 infection. Int. J. Adv. Biochem. Res,8(10S):1009-1016.

13. Pateriya, A. K., Nagarajan, S., Khandia, R., Dixit, R., Bhatia, S., Murugkar, H., Kumar, M., & Singh, F. (2024). Adapting the Eurasian H5 TaqMan RT-qPCR assay for the detection of avian influenza strains circulating in India.Asian J. Microbiol. Biotechnol. Environ. Sci.,26(4), 523–530.

14. Pateriya, A. K., Nagarajan, S., Khandia, R., Dixit, R., Bhatia, S., Murugkar, H., Kumar, M., & Singh, F. (2024). Prokaryotic expression of non-structural 1 protein (NS1) of avian influenza (H5N1) virus and evaluation of its immunogenicity in chicken. Asian Asian J. Microbiol. Biotechnol. Environ. Sci., 26(4), 531–537.

15. Singh, A., Sahu, U., Kulkarni, P. M., Yadav, R., Bhatia, S., Murugkar, H. V., Hosamani, M., Basagoudanavar, S., Sharma, G. K., Gupta, P. K., Kumar, N., Sanyal, A., & Kumar, N. (2024). A safe, cost-effective, and high-throughput SARS-CoV-2 antigen capture ELISA suitable for large-scale screening in low-resource settings. J. Virol. Methods, 329, 114995.

16. Singh, F., Rajukumar, K., Senthilkumar, D., Venkatesh, G., Sudhakar, S. B., Singh, V. P., & Sanyal, A. (2024). Development of one-step reverse transcription PCR assay for detection of porcine epidemic diarrhoea virus in pigs. The Indian J. Anim. Sci., 94(5), 401–405.

17. Sruthy, S., Asha, K., Prejit, N., Das, G., Verma, R., Sunanda, C., Vinod, V. K., Vergis, J., Rajasekhar, R., Milton, A. A. P., Das, S., Murugkar, H., Sanyal, A., & Gandhale, P. N. (2024). Prevalence of Crimean-Congo Haemorrhagic Fever virus and Ganjam virus among livestock & ticks in Wayanad, Kerala. Vet. Res. Commun., 49(1), 13.

18. Sudhakar, S. B., Mishra, N., Kalaiyarasu, S., Puri, R., Ghule, P., Agarwal, F., Mustare, A., Pawar, S. J., Pathan, Y. K., & Sanyal, A. (2024). Evidence of natural lumpy skin disease virus (LSDV) infection and genetic characterization of LSDV strains from water buffaloes (Bubalus bubalis) in India. Arch. Virol., 170(1), 11.

19. Sudhakar, S. B., Mishra, N., Kalaiyarasu, S., Sharma, R. K., Ahirwar, K., Vashist, V. S., Agarwal, S., & Sanyal, A. (2024). Emergence of lumpy skin disease virus (LSDV) infection in domestic Himalayan yaks (Bos grunniens) in Himachal Pradesh, India. Arch. Virol., 169(3), 51.

20. Vijayakumar, P.; Mishra, A.; Deka, R.P.; Pinto, S.M.; Subbannayya, Y.; Sood, R.; Prasad, T.S.K.; Raut, A.A. **(2024).** Proteomics Analysis of Duck Lung Tissues in Response to Highly Pathogenic Avian Influenza Virus. Microorg, 12, 1288.

Copyright

- Bhatia, S., Mishra, N., Tosh, C., Raut, A.A., Rajukumar, K., Murugkar, H. V., Nagarajan, S., Venkatesh,G., Mishra, Kumar, M., A., Pateriya, A. K., Sudhakar, S .B., Singh, F., Kalaiyarasu, S., Senthil Kumar, D., Gandhale, P. N., Kumar, N., Pathak, A. & Sanyal, A. (2024). Copyright: L-156911/2024 (STATUS OF EMERGING VIRAL DISEASES OF ANIMALS IN INDIA).

INTELLECTUAL PROPERTY INDIA
PATENTS | DESIGNS | TRADE MARKS | GEOGRAPHICAL INDICATIONS

सत्यमेव जयते

Extracts from the Register of Copyrights

प्रतिलिप्यधिकार कार्यालय, भारत सरकार | Copyright Office, Government Of India

दिनांक/Dated:20/11/2024

1.	पंजीकरण संख्या/Registration Number	:	**L-156911/2024**
2.	आवेदक का नाम, पता तथा राष्ट्रीयता Name, address and nationality of the applicant	:	DIRECTOR ICAR-NATIONAL INSTITUTE OF HIGH SECURITY ANIMAL DISEASES , DIRECTOR, ICAR-NATIONAL INSTITUTE OF HIGH SECURITY ANIMAL DISEASES, ANAND NAGAR, BHOPAL, MADHYA PRADESH-462022 INDIAN
3.	कृति के प्रतिलिप्यधिकार में आवेदक के हित की प्रकृति Nature of the applicant's interest in the copyright of the work	:	PUBLISHER
4.	कृति का वर्ग और वर्णन Class and description of the work	:	LITERARY/ DRAMATIC WORK ORIGINAL SCIENTIFIC LITERARY WORK
5.	कृति का शीर्षक Title of the work	:	STATUS OF EMERGING VIRAL DISEASES OF ANIMALS IN INDIA
6.	कृति की भाषा Language of the work	:	ENGLISH

रजिस्ट्रार ऑफ कॉपीराइट
Registrar of Copyrights

Abstracts/posters in Conferences/Symposia

1. Althaf Mohammed, K.T., Panwar, A., Shrungeswara, T.A.H., Keshava Prasad, S., Raut, A.A. and Mishra, A. (2024). Identification of Potential Biomarkers of Highly Pathogenic Avian Influenza (H5N1) Infection Through Metabolomic Profiling in Chickens. In: Book of Abstracts, 39th Annual Conference and National Symposium of Indian Poultry Science Association, October 16-18, 2024, MAFSU, Nagpur.

2. Bhawana, R., Gandhale, P.N., Nagarajan, S., Murugkar, H.V. and Sanyal, A. (2024). Snapshot of Viral diversity in ticks collected off the Cattle from Madhya Pradesh. Oral presentation in XXth Annual conference of Indian Association of Veterinary Public Health Specialists (IAVPHS) and National Symposium on "Integrated One Health: Bridging the Gap at Human-Animal-Environment Interfaces" during November, 14-15, 2024 at KNPCVS, MAFSU, Shirval.

3. Borah, R., Kalaiyarasu, S., Mishra, N., Sudhakar, S.B., Patidar, D.K., Punwani, T., Awasthi, S., Richariya S. and Sanyal A. (2024). BVDV induced immunomodulation in immune and naïve cattle: An experimental investigation. Presented in International conference on Emerging viruses: Pandemic and Biosecurity Perspectives (VIROCON-2024) at DRDO-DRDE, Gwalior, 11-13 Nov. 2024.

4. Das, S., Milton A.A.P. and Gandhale, P. N. (2024). Understanding Bovine Tuberculosis in India: A Zoonotic Perspective. Abstract in 1st National Veterinary Summit, Agrivision-2024 on "Role and Contribution of Veterinary and Allied Sciences towards making Viksit Bharat @ 2024" during August, 24-25, 2024 at NDVSU, Jabalpur.

5. Kalaiyarasu, S., Mishra, N., Borah, R., Sudhakar, S.B., Patidar, D.K., Punwani, T., Awasthi, S., Richariya, S. and Sanyal, A. (2024). Comparison of VNT and BVDV antibody ELISAs in cattle experimentally infected with BVDV-1. Presented in International conference on Emerging viruses: Pandemic and Biosecurity Perspectives (VIROCON-2024) at DRDO-DRDE, Gwalior, 11-13 Nov. 2024.

6. Kumar, N., Tomar, S., Kumar, R., Kumar, M., Bhatia, S. and Sanyal, A. (2024). Chimeric stabilized neuraminidase tetramers as the potential candidates for universal influenza vaccine. Poster presentation titled in ASM Microbe 2024 held at Atlanta, USA (June 13-17, 2024).

7. Milton, A.A.P., Srinivas, K., Das, S., Ghatak, S., Bhuvana Priya, G., Puro K. and Gandhale P.N. (2024). Transboundary Animal Diseases in Northeastern India: Enhancing Veterinary and Laboratory Infrastructure, Surveillance and Regional Cooperation. Abstract in 1st National Veterinary Summit, Agrivision-2024 on "Role and Contribution of Veterinary and Allied Sciences towards making Viksit Bharat @ 2024" during August, 24-25, 2024 at NDVSU, Jabalpur.

8. Milton, A.A.P., Srinivas, K., Momin, A.G., Gandhale, P.N., Samir Das, Bhuvana Priya, G., Ghatak, S., Firake, D.M., Zakir Hussain, Azhahianambi P. and Arnab Sen (2024). Rodents and shrews of Meghalaya as reservoirs of emerging zoonotic pathogens: A One Health study. Oral presentation in XXth Annual conference of Indian Association of Veterinary Public Health Specialists (IAVPHS) and National Symposium on "Integrated One Health: Bridging the Gap at Human-Animal-Environment Interfaces" during November, 14-15, 2024 at KNPCVS, MAFSU, Shirval.

9. Pateriya, A. K., Bhatia, S. and Sanyal, A. (2024). Prokaryotic expression of Non Structural 1 protein (NS1) of Avian Influenza (H5N1) virus and evaluation of its immunogenicity in Chicken. Presented in IXth International Conference on Global Research Initiatives for Sustainable Agriculture & Allied Sciences (GRISAAS-2024) 10-12th December 2024.

10. Pateriya, A.K., Nagarajan, S., Khandia, R., Bhatia, S., Murugkar, H.V., Kumar, M. and Singh, F. (2024). Adapting the Eurasian H5 Taqman RT-qPCR Assay for the detection of Avian Influenza strains circulating in India. Abstract presented in International conference on Animal Science & Veterinary Medicine (IVASVM 2024) on 30-Nov-2024.

11. Pathak, A., Bera, B.C., Bishnoi, G., Choudhary, S., Mittal P. and Gulati, B.R., (2024). Complete Genome Sequencing reveals Equine and Bubaline Rotaviruses with zoonotic potential from India. Abstract presented in XXth Annual Conference of the Indian Association of Veterinary Public Health Specialists (IAVPHS) and the National Symposium on "Integrating One Health: Bridging the Gap at Human-Animal-Environment Interfaces" Held On: 14-15 November 2024 held at Krantisinh Nana Patil College of Veterinary Science, Shirwal, Maharashtra, India.

12. Senthilkumar, D., Rajukumar, K., Venkatesh, G., Singh, F. and Sanyal, A. (2024). Complete genome analysis of African swine fever virus isolated from domestic pig in Mizoram, India: A First report. In the IXth International Conference on GRISAAS-2024 during 10-12 December 2024 at SKNAU-RARI, Durgapura, Jaipur, Rajasthan, India.

13. Senthilkumar, D., Rajukumar, K., Venkatesh, G., Singh, F., Tosh, C. , Sarkar, G., Patel, J., Mishra, S., Sahu, R., Singh, V.P. and Sanyal, A. (2024). Complete genome analysis of African swine fever virus isolated from wild boar in Mizoram, India. In International Conference on Impact of Climate change on Biodiversity- A global perspective held during 11-13, July 2024 at Madras Veterinary College, Chennai, Tamil Nadu, India.

14. Singh, F., Rajukumar, K., Venkatesh, G., Senthilkumar, D., Sarkar, G., Mondal, S., Sahu, R., Mishra, S., Khan, N., Patel, J., Singh, V.P. and Sanyal, A. (2024). Genomic characterisation of Porcine Picornaviruses (Enteroviruses) causing enteric co-infections and diarrhoea in piglets. Poster in Proceedings of the International Conference of the International Virological Society (VIROCON-2024) on "Emerging Viruses: Pandemic & Biosecurity Perspectives" organised by DRDO-DRDE, Gwalior from 11- 13th Nov. 2024.

15. Singh, F., Rajukumar, K., Venkatesh, G., Senthilkumar, D., Pateriya, A.K., Sarkar, G., Sahu, R., Patel, J., Singh, V.P. and Sanyal, A. (2024). Metatranscriptomic analyses indicates a high viral diversity in faecal specimens of domestic pigs in India. Oral Presentation in International Conference on Biotechnology and Bioengineering (ICBB-2024), virtually organised by BrainyMeet (ICBB-2024) from May 20-21, 2024.

16. Singh, F., Rajukumar, K., Venkatesh, G., Senthilkumar, D., Pateriya, A.K., Mondal, S., Sarkar, G., Sahu, R., Patel, J., Singh, V.P. and Sanyal, A. (2024). Isolation and genetic characterization of emerging swine enteric viruses from domestic pigs. Oral presentation in XXXVI Annual Conference of the Indian Association of Microbiologists, Immunologists & Specialists in Infectious (IAVMICON-2024) organised by College of Veterinary and Animal Sciences, RAJUVAS, Udaipur form June 6-7, 2024.

17. Sudhakar, S.B., Mishra, N., Kalaiyarasu, S. and Sanyal, A. (2024). Molecular Characterization of Lumpy Skin Disease Virus Isolates from Domestic Yaks in Himachal Pradesh, India. In the IXth International Conference on GRISAAS-2024 during 10-12 December 2024 at SKNAU-RARI, Durgapura, Jaipur, Rajasthan, India.

Book chapters/Technical papers/review articles/Popular articles:

1. Bhatia, S. and Kalaiyarasu, S. Malignant Catarrhal Fever. In Manoranjan Rout, Raj Pal Diwakar (Eds.). Introduction to Infectious Viral Diseases of Animals, pp (333-341), Daya Publishing house, New Delhi.

2. Bhatia, S., Pateriya, A.K., Kumar, N. Malignant Catarrhal Fever (MCF). In: Status of Emerging Viral Diseases of Animals in India.2024. p. 24–29. Copyright No.: L-156911/2024.

3. Gandhale, P. (2024). Crimean-Congo Haemorrhagic Fever virusIn: Status of Emerging Viral Diseases of Animals in India. 2024, pp70-75.

4. Ghoke, S.S., Sood, R., Kumar, N., Bhatia, S. (2024). *In Ovo*-Based Antiviral Assay for Screening of Herbal Formulations Against Influenza Viruses. In: Kumar, N., Malik, Y.S., Tomar, S., Ezzikouri, S. (eds) Advances in Antiviral Research. Livestock Diseases and Management. Springer, Singapore. https://doi.org/10.1007/978-981-99-9195-2_15

5. Kalaiyarasu, S., Mishra, N. and Sudhakar, S.B. (2024). Border Disease. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 14-17.

6. Kalaiyarasu, S., Mishra, N. and Sudhakar, S.B. (2024). West Nile Fever. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 94-98.
7. Kaushik, R., Kumar, N., Launey, T. (2024). A High-Throughput Computational Pipeline for Selection of Effective Antibody Therapeutics against Viruses. In: Kumar, N., Malik, Y.S., Tomar, S., Ezzikouri, S. (eds) Advances in Antiviral Research. Livestock Diseases and Management. Springer, Singapore.
8. Kumar, N., Singh A., Sahu U., Desai D., Kumar M., Bhatia, S. & Sanyal, A. (2024). Epigenetic- and Epitranscriptomic-Targeted Reprogramming: Novel Targets for the Development of Broad-Spectrum Antivirals. In: Kumar, N., Malik, Y.S., Tomar, S., Ezzikouri, S. (eds) Advances in Antiviral Research. Livestock Diseases and Management. Springer, Singapore.
9. Mishra, A., Kaur I., Sharma, A., Manu, M., De, U.K., Kumar, N. and Malik, Y.P.S. (2024). Antivirals: Approaches and the Way Forward. In: Kumar, N., Malik, Y.S., Tomar, S., Ezzikouri, S. (eds) Advances in Antiviral Research. Livestock Diseases and Management. Springer, Singapore.
10. Mishra, N., Kalaiyarasu, S. and Sudhakar, S.B. (2024). Bovine Viral Diarrhea. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 10-13.
11. Mishra, N., Kalaiyarasu, S. and Sudhakar, S.B. Bovine Viral Diarrhea - Mucosal Disease (BVD-MD). In Manoranjan Rout, Raj Pal Diwakar (Eds.). Introduction to Infectious Viral Diseases of Animals, pp (197-225), Daya Publishing house, New Delhi.
12. Murugkar, H.V., Gandhale, P.N. and Pathak, A. (2024). Rift Valley Fever. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp76-80.
13. Pateriya, A.K., Bhatia, S., Kumar, N., Singh, F. Aujeszky's Disease. In: Status of Emerging Viral Diseases of Animals in India. 2024. p.38–42.
14. Rajukumar, K., Senthilkumar D., Singh, F. and Venkatesh, G. (2024). Porcine Reproductive and Respiratory SyndromeIn: Status of Emerging Viral Diseases of Animals in India. 2024. pp43-51.
15. Raut, A.A., Mishra, A. and Pathak, A. Ebola Virus. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp. 87– 93. 3.
16. Raut, A.A., Mishra, A. and Pathak, A. Middle East Respiratory Syndrome Coronavirus. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp. 103–107.
17. Senthilkumar, D., Rajukumar, K. Venkatesh, G. and Singh, F. (2024). African Swine Fever. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 31-37.
18. Singh, A., Fazal, R., Sahu, U., Kumar, M., Bhatia, S., Sanyal, A., Kumar, N. (2024). Zoonotic Origin, Genomic Organization, Transmission, and Mutation of SARS-CoV-2. In: Chavda VP, Uversky VN (eds) SARS-CoV-2 Variants and Global Population Vulnerability, Apple Academic Press, New York.
19. Singh, A., Kumar N., Desai D., Sahu, U., Bhatia, S., Kumar, M., Tripathi, B.N. and Sanyal, A. (2024). Organoids in Antiviral Research: Potential and Challenges. In: Kumar, N., Malik, Y.S., Tomar, S., Ezzikouri, S. (eds) Advances in Antiviral Research. Livestock Diseases and Management. Springer, Singapore.
20. Singh, F., Rajukumar, K. and Pateriya, A.K. (2024). Transmissible Gastroenteritis. In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 52-56.
21. Singh, F., Venkatesh, G., Senthilkumar, D. and Bhatia, S. (2024). Porcine Epidemic Diarrohea, In S Bhatia, C Tosh, N Mishra, AA Raut, K Rajukumar& A Sanyal (Eds.), Status Paper on Exotic and Emerging Animal Diseases in India, pp 52-56.
22. Sudhakar, S.B., Mishra, N. and Kalaiyarasu, S. (2024). Lumpy Skin Disease (LSD). In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 18-23.
23. Venkatesh, G., Senthilkumar, D., Singh F. and Rajukumar, K. (2024). Swine Influenza, In: Status of Emerging Viral Diseases of Animals in India. 2024. pp 61-65.

Invited lead lectures in conference/symposia

1. Gandhale,P.N., Murugkar, H.V. and Sanyal, A. (2024). Lead paper on "Introduction to One Health concept" in 1st National Veterinary Summit, Agrivision-2024 on "Role and Contribution of Veterinary and Allied Sciences towards making Viksit Bharat @ 2024" during August, 24-25 at NDVSU, Jabalpur.
2. Kumar, M. (2024).Invited lecture on 'Perspectives of One Health and Wildlife'. Organized by Ela Foundation and Indian Medical Association, Pune the first CME Program Symposium on 'One Health' including Zoonotic Diseases. 15th December; IMA Hall, Tilak Road, Pune.
3. Kumar, N. (2024).Invited lead talk 'Global evolution and spread of avian influenza in climate change scenario: need for proactive mitigation strategies' in the International Conference on Climate Change and Environmental Sustainability in Mountainous and Hilly Landscapes held at Assam University, Silchar, Assam (September 30-October 1.).
4. Mishra, N., Sudhakar, S.B. and Kalaiyarasu, S. (2024). Invited Lead talk on "LSD in India: Perspectives of changing host range and genetic profile of circulating strains" in International conference on Emerging viruses: Pandemic and Biosecurity Perspectives (VIROCON-2024) at DRDO-DRDE, Gwalior, 11-13 Nov.
5. Murugkar, H.V. (2024). Lead paper on, "Laboratory biosafety under one health paradigm" during the XX Annual Conference of the Indian Association of Veterinary Public Health Specialists (IAVPHS) and the National Symposium on "Integrating One Health: Bridging the Gap at Human-Animal-Environment Interfaces" 14-15 November at the Krantisinh Nana Patil College of Veterinary Science, Shirwal, Maharashtra..
6. Murugkar, H.V. (2024). National Consultation on Legal Framework for One Health Implementation on 27th – 28th June,organised by PSA, ICMR and NCDC
7. Nagarajan, S. (2024). Activities update by laboratory experts HPAI - ICAR, India. Presented at Regional Workshop on Avian Disease Prevention and Control in Asia and the Pacific 2024 held at Seoul, Republic of Korea from August 27 – 29.
8. Nagarajan, S., Kumar, M., Tosh, C. and Sanyal, A. (2024). Expanding host horizon of clade 2.3.4.4b H5N1 highly pathogenic avian influenza virus and its implications for control. A symposium organized by NIAB aimed at bringing together researchers and industrial stakeholders to discuss strategies to combat economically important porcine and poultry viruses in India. BRIC-NIAB, Gachibowli, Hyderabad, Telengana, 3rd-4th October.
9. Nagarajan, S., Manoj Kumar, Murugkar, H.V., Tosh, C. and Sanyal, A. (2024). Highly pathogenic avian influenza- Indian perspective. Presented In: 5th Biennial pouty health conference and national symposium on "Poultry Health: Current challenges and future strategies" AAHP 2024. 23-24 February, Hyderabad, India (pp 49-51)
10. Pankaj,DK., Kumar, M., Tosh,C., Nagarajan,S., Murugkar,H.V., Gaurav,K., Bajaj,S. and Sanyal, A.(2024). Evaluation of in-contact transmissibility of clade 2.3.4.4b H5N1 avian influenza virus in mammalian model. VIROCON -2024, International Conference on Emerging Viruses: Pandemic & Biosecurity Perspectives, November 11-13, pp 209 at DRDO (DRDE), Gwalior.
11. Rajukumar, K., Senthilkumar, D., Singh, F., Sarkar, G.,Patel,J., Venkatesh,G. and Sanyal,A (2024) "Recent approaches for development of diagnostics and vaccine for African swine fever" invited lecture delivered in in 41st Annual Conference of Indian Association of Veterinary Pathologists and National Symposium on 'Exploring Veterinary Pathology and Diagnostic Innovations in Animal and Poultry Diseases Amidst Climatic Challenges' organized at SKUAST- Jammu., 28 – 30 November.
12. Rajukumar, K., Senthilkumar, D., Teotia,V.K. and Sanyal,A (2024) "African Swine Fever – Risk communication and community engagement in India" talk presented in "9th meeting of the Standing Group Experts (SGE) on African swine fever (ASF) for Asia and the Pacific" organized by FAO and WOAH in Manila, Philippines, 25th to 27th June.

13. Rajukumar,K., Senthilkumar, D., Singh,F., Venkatesh,G. and Sanyal, A. (2024) "Vaccine approaches and the challenges for African swine fever" invited lecture delivered in Symposium on 'Strategies to combat economically important Porcine and Poultry viruses in India', organized by NIAB, Hyderabad between 3rd -4th October.

14. Singh, F., Rajukumar, K., Senthilkumar, D., Venkatesh, G., & Sanyal, A. (2024). *Emerging swine enteric coronaviruses: Current status and future implications*. Invited paper/ Lead paper in XXXVI Annual Conference of the Indian Association of Microbiologists, Immunologists & Specialists in Infectious (IAVMICON-2024) organised by College of Veterinary and Animal Sciences, RAJUVAS, Udaipur form June 6-7.

15. Tosh, C. (2024) Avian influenza - Control and Containment, presented in Training program on "Shaping Animal Health Sector with Modern & Precision Diagnostics under ASCAD" VOTI, Bhubaneswar, Animal Husbandry & Veterinary Services, Government of Odisha, India, 31st May 2024 (virtual)

16. Tosh, C. (2024). Laboratory diagnosis of avian influenza. Presented in Sensitization workshop on Avian Influenza, SMS Medical College, Jaipur, 24th December 2024. (virtual)

17. Tosh, C., Kumar, M., Nagarajan, S., Murugkar, H.V. and Sanyal, A.(2024) Wild bid surveillance: An early warning system for avian influenza control. Presented in VIROCON-2024, International Conference on Emerging Viruses: Pandemic & Biosecurity Perspective, Organized (DRDE), Gwalior, India, 11th-13th November.

18. Venkatesh,G., Rajukumar,K., Fateh Singh, Senthil Kumar,D., Murugkar, H.V and Sanyal,A (2024). Presented an invited paper titled "Laboratory Biosafety and Biosecurity for handling emerging zoonotic viruses" delivered online in the Kerala Veterinary Science Congress 2024 & International Seminar conducted at College of veterinary & animal sciences, Mannuthy, Thrissur, Kerala from 8-10th Nov 2024.

Participation (Talk, Oral presentation etc) Other presentations/talks/lectures

1. Gandhale, P. Delivered talk on Practical solutions and best practices for maintaining cleanliness in agricultural settings during the Kisan Diwas celebration on 23.12.2024 to the farmers gathered on the occasion.

2. Gandhale, P. Delivered talk on Improved animal husbandry practices and animal disease control to the farmers during Workshop organised for the Scheduled Caste farmers in Umraoganj block of the district Raisen under the SCSP scheme on 9th October 2024.

3. Gandhale, P. Delivered talk on Business opportunities in Poultry rearing and management of diseases to the poultry farmers in a Workshop and Field-day organised for the Scheduled Caste farmers in Gudawal village at Umraoganj block of the district Raisen under the SCSP scheme on 10th October 2024.

4. Gandhale, P. Delivered talk on entrepreneurial opportunities in animal husbandry sector to the farmers in a Farmers-Scientists interaction meet organised for the Scheduled Caste farmers in Hatiyakheda village of the district Raisen under the SCSP scheme on 20th June 2024.

5. Gandhale, P. Lecture cum demonstration on "Processing of Animal and Vector samples for NAATs and Virus Isolation" Training cum Workshop on Biosafety for handling and diagnosis of high risk animal pathogens in ABSL-3 and BSL-3 laboratory' for 'National Network of BSL3/4 Laboratories' under National One Health Mission (NOHM) component of PM-ABHIM during First Batch: 19th to 23rd August & Second Batch: 26th to 30th August, 2024.

6. Gandhale, P. Lecture cum demonstration on "Virus isolation in embryonated eggs & laboratory animals & harvesting of allantoic fluids" Training cum Workshop on Biosafety for handling and diagnosis of high risk animal pathogens in ABSL-3 and BSL-3 laboratory' for 'National Network of BSL3/4 Laboratories' under National One Health Mission (NOHM) component of PM-ABHIM during First Batch: 19th to 23rd August &Second Batch: 26th to 30th August, 2024.

7. Kalaiyarasu, S., Mishra, N., Borah, R., Sudhakar, S.B., Patidar, D.K., Punwani, T., Shalini, A., Richariya, S., Sanyal, A. Comparison of VNT and BVDV antibody ELISAs in assessing the humoral immune response in cattle experimentally infected with BVDV-1. International conference on Emerging viruses: Pandemic and Biosecurity Perspectives (VIROCON-2024) at DRDO-DRDE, Gwalior, 11-13 Nov. 2024.

8. Singh, F. A lecture on Important Animal Diseases, their Prevention and Control to the farmers in a Farmers-Scientists interaction meet organised for the Scheduled Caste farmers in Hatiyakheda village of the district Raisen under the SCSP scheme on 20th June 2024.

9. Singh, F. A lecture on Important Animal Diseases, their Prevention and Control to the farmers in a Workshop organised for the Scheduled Caste farmers in Umraoganj block of the district Raisen under the SCSP scheme on 9th October 2024.

10. Singh, F. A lecture on Poultry diseases and their Prevention and Control to the poultry farmers in a Workshop and Field-day organised for the Scheduled Caste farmers in Gudawal village at Umraoganj block of the district Raisen under the SCSP scheme on 10th October 2024.

11. Singh, F. A lecture on the topic "Economically important diseases of goats and their management" delivered in a training on 'Advanced Management and Health Practices in Livestock and Poultry & Distribution of Inputs to the Farmers of Meghalaya State ' organised by ICAR-NIHSAD, Bhopal in collaboration with CoA, CAU (Imphal), Kyrdemkulai on Feb 22, 2024.

12. Tosh, C. (2024) Avian influenza surveillance in poultry and beyond poultry. Presented in "Brainstorming Session on Avian Influenza with special reference to surveillance and vaccination", DAHD, MoFAH&D, GOI, KrishiBhawan, New Delhi, 16 July 2024.

13. Tosh, C. (2024) Vaccination of poultry for H5N1. Presented in "Brainstorming Session on Avian Influenza with special reference to surveillance and vaccination", DAHD, MoFAH&D, GOI, KrishiBhawan, New Delhi, 16 July 2024.

14. Tosh, C. (2024). Avian influenza current situation- animal health sector, Presented at: Avian influenza outbreak and response simulation exercise, DAHD, MoFAH&D, GOI, 19th and 20th June 2024, Bhopal, Madhya Pradesh

Submissions in NCBI: GenBank Database

1. Accession No. PQ638341-PQ638352. Singh, F., Sarkar, G., Rajukumar, K., Senthilkumar, D., Venkatesh, G., Mondal, S., Sahu, R., Patel, J., Mishra, S., Khan, N., Singh, V.P. and Sanyal, A. Rotavirus A, strain NIHSAD/SW/22_1191-1201/RotaV_A, Segment 1-11. Faecal virome of domestic pigs. NCBI GenBank.

2. Accession No. PQ638339-PQ638340.Singh, F., Sarkar, G., Rajukumar, K., Senthilkumar, D., Venkatesh, G., Mondal, S. and Sanyal, A. Porcine astrovirus 4 NIHSAD/SW/22_1191-1201/PoAstroV4, Porcine astrovirus 2 NIHSAD/SW/22_1191-1201/PoAstroV2, partial genomic sequence. Faecal virome of domestic pigs. NCBI GenBank.

3. Accession No. PQ807171-PQ807172. Singh, F., Rajukumar, K., Sarkar, G., Senthilkumar, D., Venkatesh, G.,Pateriya, A.K., Mondal, S., Sahu, R., Khan, N., Mishra, S., Patel, J.,Singh, V.P. and Sanyal, A. (2024). Porcine bocavirus strain NIHSAD/SW/22_1190/BocaV_1 NP1 gene,complete cds, NIHSAD/SW/22_1190/BocaV_2 VP1 and VP2genes, partial cds..

4. Accession No. PV023909. Senthilkumar D, K. Rajukumar, G. Venkatesh, F. Singh, Gopal Sarkar, Jaswant Patel, Suman Mishra, Rohit Sahu, Nourin Khan, C. Neihthangpuii, Esther Lalzoliani, Vijendra Pal Singh, Aniket Sanyal (2024).Complete genome analysis of African swine fever virus isolated from a Wild boar in India -A first report. NCBI GenBank.

5. Accession No. PV023910. Senthilkumar D, K. Rajukumar, G. Venkatesh, F. Singh, Gopal Sarkar, Jaswant Patel, Suman Mishra, Rohit Sahu, Nourin Khan, C. Neihthangpuii, Esther Lalzoliani, Vijendra Pal Singh, Aniket Sanyal (2024).Complete genome analysis of African swine fever virus isolated from a domestic pig in Mizoram. NCBI GenBank.

6. GenBank Acc. No. PQ443886- PQ443915. Kumar,M., Nagarajan,S., Murugkar,H.V., Agarwal,S., Gaurav,K., Namdeo,P.K., Bajaj,S., Ansari,K., Sanyal,A. and Tosh,C. 2024. Characterization of Influenza A/H5N1 viruses isolated in India, 2024.

7. GenBank Acc. No. PQ226231 - PQ226245. Kumar,M., Nagarajan,S., Murugkar,H.V., Agarwal,S., Gaurav,K., Namdeo,P.K., Bajaj,S., Ansari,K., Sanyal,A. and Tosh,C. 2024. Characterization of Influenza A/H5N1 viruses isolated in India, 2024.

8. GenBank Acc. No. PQ443894 - PQ443914. Kumar,M., Nagarajan,S., Murugkar,H.V., Agarwal,S., Gaurav,K., Namdeo,P.K., Bajaj,S., Ansari,K., Sanyal,A. and Tosh,C. 2024. Characterization of Influenza A/H5N1 viruses isolated in India, 2024.

9. GenBank Acc. No. PQ327670- PQ327693. Kumar,M., Nagarajan,S., Murugkar,H.V., Agarwal,S., Gaurav,K., Namdeo,P.K., Bajaj,S., Ansari,K., Sanyal,A. and Tosh,C. 2024. Characterization of Influenza A/H5N1 viruses isolated in India, 2024.

10. GenBank Acc. No. PQ333918 - PQ333925. Kumar,M., Nagarajan,S., Murugkar,H.V., Agarwal,S., Gaurav,K., Namdeo,P.K., Bajaj,S., Ansari,K., Sanyal,A. and Tosh,C. 2024. Characterization of Influenza A/H5N1 viruses isolated in India, 2024.

✓ **MassIVE database submission:**

LC MS/MS raw data submitted to MassIVE database, Massive study ID: MSV000097417. Serum and tissue metabolomics data of H5N1 influenza infected chicken. [doi:10.25345/C5JM23T89] [dataset license: CC0 1.0 Universal (CC0 1.0)]. https://massive.ucsd.edu/ProteoSAFe/dataset.jsp?task=3afef197172545bdb49069838848e704

☞ Training Manual:

Manual for 'Training cum Workshop on Biosafety for handling and diagnosis of high risk animal pathogens in ABSL-3 and BSL-3 laboratory' for 'National Network of BSL3/4 Laboratories' under National One Health Mission (NOHM) component of PM-ABHIM (In 2 batches; 19th to 23rd August and 26th to 30th August, 2024).

HONORS, AWARDS & PEER RECOGNITIONS

Awards

1. Bhawana Rani, Gandhale, P.N., Nagarajan,S., Murugkar, H.V. and A. Sanyal (2024).Best oral presentation award for "Snapshot of Viral diversity in ticks collected off the Cattle from Madhya Pradesh" in XXth Annual conference of Indian Association of Veterinary Public Health Specialists (IAVPHS) and National Symposium on "Integrated One Health: Bridging the Gap at Human-Animal-Environment Interfaces" during November, 14-15th, 2024 at KNPCVS, MAFSU, Shirval.

2. Borah,R., Kalaiyarasu,S., Mishra,N., Sudhakar,S.B., Patidar,D.K., Punwani, T., Awasthi,S., Richariya, S and A. Sanyal, (2024).Best Poster award for BVDV induced immunomodulation in immune and naïve cattle: An experimental investigation presented in International conference on Emerging viruses: Pandemic and Biosecurity Perspectives (VIROCON-2024) at DRDO-DRDE, Gwalior, 11-13th Nov. 2024.

3. Kalaiyarasu,S. (2024). SADHNA All India Best Research Award at Doctorate Level 2023 for for his Ph.D thesis research awarded by SOCIETY FOR ADVANCEMENT OF HUMAN AND NATURE on Feb, 2015.

4. Kumar, N (2024). Bill & Melinda Gates Foundation Travel Award for presentation of research work entitled "Chimeric stabilized neuraminidase tetramers as the potential candidates for universal influenza vaccine" in ASM Microbe-2024 held at Atlanta, USA (June 13-17th, 2024),

5. Milton, A.A.P., Srinivas,K., Momin,A.G., Gandhale,P.N., Samir Das,Bhuvana Priya,g., Ghatak,S., Firake,D.M., Hussain,Z., Azhahianambi, P and Arnab Sen (2024).Best oral presentation award for "Rodents and shrews of Meghalaya as reservoirs of emerging zoonotic pathogens: A One Health study" in XXth Annual conference of Indian Association of Veterinary Public Health Specialists (IAVPHS) and National Symposium on "Integrated One Health: Bridging the Gap at Human-Animal-Environment Interfaces" during November, 14-15th, 2024 at KNPCVS, MAFSU, Shirval

6. Murugkar, H.V. (2024). Awarded Dr. A.T. Sherikar Outstanding Public Health Veterinarian Award by the Indian Association of Veterinary Public Health Specialists on 14th Novemver, 2024 At Shirwal, Pune.

7. Nagarajan,S : Invited as laboratory expert by WOAH Regional Representation for Asia and the Pacific (WOAH RRAP), Japan) and MAFRA, South Korea and nominated by ICAR for attending Regional Workshop on Avian Disease Prevention and Control in Asia and the Pacific 2024 held at Seoul, Republic of Korea from August 27 – 29th, 2024.

8. Pateriya, A.K. (2024). Conferred with "Outstanding Scientist in Animal Biotechnology Award" in the International Conference on Animal Science and Veterinary Medicine held on 30th November 2024 Organized by SciConfex.

9. Raut, A.A. and Mishra, A (2024). Best poster presentation award for Identification of Potential Biomarkers of Highly Pathogenic Avian Influenza (H5N1) Infection Through Metabolomic Profiling in Chicken. in Indian Poultry Science Association Conference (IPSACON – 2024) and National Symposium on "Shaping the Indian Poultry Sector for Sustainable Growth" held at MAFSU-Nagpur Veterinary College, on 16-18th October 2024.

10. Senthilkumar D., Rajukumar, K., Venkatesh, G., Singh, F., Tosh,C., Sarkar,G., Patel,J., Mishra,S., Sahu,R., Singh,V.P. and Sanyal, A (2024). Best oral paper presentation award for"Complete genome analysis of African swine fever virus isolated from wild boar in Mizoram, India"- International Conference on Impact of Climate change on Biodiversity- A global perspective held during 11-13th, July 2024 at Madras Veterinary College, Chennai, Tamil Nadu, India.

11. Singh,Fateh., Rajukumar,K., Venkatesh,G.,Senthilkumar, D., Pateriya,A.K.,Sarkar,G., Sahu,R.,Patel,J.,Singh, V.P and A. Sanyal, (2024). Research Excellence Award for Metatranscriptomic analyses indicates a high viral

diversity in faecal specimens of domestic pigs in India. In the International Conference on Biotechnology and Bioengineering (ICBB-2024), organised by VDGOOD Professional Association, India, on May 20th, 2024

12. Singh,Fateh., Rajukumar,K., Venkatesh,G., Senthilkumar,D.,Pateriya,A.K., Mondal, S., Sarkar,G., Sahu,R., Patel,J., Singh, V.P and A. Sanyal, (2024). Best Oral Presentation Award for Isolation and genetic characterization of emerging swine enteric viruses from domestic pigs. In the XXXVI Annual Conference of the Indian Association of Microbiologists, Immunologists & Specialists in Infectious (IAVMICON-2024) organised by the College of Veterinary and Animal Sciences, RAJUVAS, Udaipur from June 6-7th, 2024.

13. Sudhakar,S.B., Mishra,N., Kalaiyarasu,S. and Sanyal, A (2024). Best oral paper presentation award for the paper entitled "Molecular Characterization of Lumpy Skin Disease Virus Isolates from Domestic Yaks in Himachal Pradesh, India" in the IXth International Conference on GRISAAS-2024 during 10-12th December 2024 at SKNAU-RARI, Durgapura, Jaipur, Rajasthan, India.

☞ Peer Recognitions

C. Tosh:

- ✓ Co-Chairperson, Scientific Session: Veterinary Virology- Emerging and Re-emerging viruses. VIROCON-2024, International Conference on Emerging Viruses: Pandemic & Biosecurity Perspective, Organized by Defence Research & Development Establishment (DRDE), Gwalior, India, 11-13th November 2024.
- ✓ Member, Central team of Animal Health Sector for mock drill under One Health Mission. Vishanu Yudh Abhyas –Avian influenza mock drill carried out at Ajmer, Rajasthan, 27th to 31stAugust 2024.
- ✓ Member, Central Team for control and containment of avian influenza (H5N1) outbreak in Puri District, Odisha. 4th to 5th September 2024.
- ✓ Member, Empowered Committee on Animal Health (ECAH) Subcommittee regarding application in Form-44 for grant of permission for New Drug for Manufacture of Low Pathogenic Influenza (H9N2) Vaccine, Inactivated by M/s Venkateshwara Hatcheries Private Limited, DAHD, MoFAH&D, GOI, 12th July 2024 (virtual mode)
- ✓ Contributed for development of Poultry Action Plan, 2024, DAHD, MoFAH&D, Government of India.

N. Mishra:

- ✓ Expert comments on WOAH Terrestrial Code: Revised Chapter on infection with bovine pestiviruses (BVD), 2024.
- ✓ Expert opinion on import of bovine skin and hides (raw/wet salted/dried), and leather (raw/wet blue) into India.

K. Rajukumar:

- ✓ Nominated by DAHD, GoI to attend "Ninth meeting of the Standing Group Experts (SGE) on African swine fever (ASF) for Asia and the Pacific" organized by FAO and WOAH in Manila, Philippines.
- ✓ Reviewed and provided comments for Empowered Committee on Animal Health (ECAH) Subcommittee regarding application in Form-44 for grant of permission on import and marketing of African swine fever vaccine by Indian vaccine manufacturer

S. Nagarajan:

- ✓ Technical assessor for evaluating Cali-Labs Pvt. Ltd., Bhopal by NABL.for assessment for ISO170025 : 2017 accreditation on 13th May, 2024.
- ✓ Member of expert committee constituted for evaluation of State Institute for Animal Diseases (SIAD), Pallode,

Kerala for testing against avian influenza vide letter No. K - 11053 /48/ 2024 - LH of Department of Animal Husbandry and Dairying, Government of India dated 18thJuly, 2024. The committee in consultation with the SIAD authorities, evaluated the laboratory on 12.08.2024 and submitted its report to DAHD, GoI.

- ✓ Contributed for development of Poultry Action Plan, 2024, DAHD, MoFAH&D, Government of India.
- ✓ Chairman of expert team for "Epidemiological Investigation of H5N1 avian influenza in Cats in Chhindwara, Madhya Pradesh". The investigation was conducted on 31.01.25 in collaboration with SADIL, Bhopal.

A. A. Raut:

- ✓ Member, Technical Expert Committee, Livestock and Animal Biotechnology, Department of Biotechnology, GOI.
- ✓ Member, Project Review and Monitoring Committee under Office of Principal Scientific Advisor to GOI.
- ✓ Member, Expert Committee for BSL4 Laboratory, ICMR-National Institute of Virology, Pune.
- ✓ Technical Expert, Drafting of National Wildlife Health Policy, Central Zoo Authority, MoEFCC, GOI.
- ✓ Expert Member, ICMR Mobile BSL3 Laboratory Specifications Committee, DHR, GOI.
- ✓ Expert Member, ICMR-DBT Joint Group on Drafting of Guidelines for Establishment of BSL3 Laboratories' ICMR, MoHFW, GOI.

M. Kumar:

- ✓ Member of Central Team constituted for overseeing the control and containment operations for control of Avian Influenza (H5N1) in Andhra Pradesh constituted by Department of Animal Husbandry and Dairying, GoI. Visited the Epicenters during 11th-14th March, 2024.

P.N. Gandhale:

- ✓ Member, International Network for Governmental Science Advice (INGSA)
- ✓ Member, National Organizing Committee, 1st National Veterinary Summit, Agrivision-2024 on "Role and Contribution of Veterinary and Allied Sciences towards making Viksit Bharat @ 2024" during August, 24-25th, 2024 at NDVSU, Jabalpur.

S.B. Sudhakar:

- ✓ Expert opinion on import of bovine skin and hides (raw/wet salted/dried), and leather (raw/wet blue) into India.

☞ Journal Editorial Board chairperson/member, Reviewer for Research Paper etc.

C. Tosh	✓ Member, Editorial Board, Indian Journal of Comparative Microbiology Immunology and Infectious Diseases (IJCMID) ✓ Editor (Veterinary Virology), VirusDisease, Springer ✓ Reviewer for Indian Journal of Medical Virology
N. Mishra	✓ Sectional editor (Animal Virology) of Editorial Board, VirusDisease (published by Springer) ✓ Reviewer of International scientific journals: J. Virol. Meth; Vet. Microbiol; Archives of Virology, Infection, Genetics and Evolution; Transboundary and Emerging
K. Rajukumar	✓ Reviewer: Transboundary and emerging diseases
S. Nagarajan	✓ Reviewer: VirusDisease, BMC Veterinary Research; International Journal of Veterinary Science and Research, Infectious Disorders – Drug Targets journals
S. Kalaiyarasu	✓ Review Editor: Frontiers in Molecular Innate Immunity, Frontiers in Veterinary Infectious Diseases, Frontiers in Veterinary Infectious Diseases,Frontiers in Antimicrobials, Resistance and Chemotherapy ✓ Reviewer: Veterinary Research Communications
Fateh Singh	✓ Reviewer:Current Microbiology
Pradeep Gandhale	✓ Review Editor for Fundamental Virology, ✓ Editorial Board of Discover Epidemics, ✓ Reviewer for Microbial Pathogenesis, Acta Virologica, South African Journal of Botany, Biochemical and Biophysical Research Communications, International Journal of Biological Macromolecules, VirusDisease,BMC Veterinary Research.
Naveen Kumar	✓ Associate Editor: Frontiers in Microbiology (Virology), ✓ Editorial Board Member: BMC Genomics, BMC Microbiology, PLOS ONE, and The Journal of Immunology and Immunopathology, ✓ Review Editor: Frontiers in Veterinary Sciences.
Anubha Pathak	✓ Review Editor: The Haryana Veterinarian

☞ International/National collaboration/MOU signed:

✓ MOU signed between ICAR-NIHSAD, Bhopal and NCBS-TIFR, Bengaluru on 16th October 2024 for collaboration for the Research project on "BMGF-Environmental surveillance and early warning system for animal pathogen surveillance".

✓ Contribution to WHO zoonotic influenza pandemic preparedness: NIHSAD shared genome sequences of eleven avian influenza viruses (09 H5N1 and 02 H9N2 subtypes) to WHO, coordinated by the OFFLU Network.

✓ Participation in Proficiency Testing: ICAR-NIHSAD participated in the following PT programs:

- Asia-Pacific Terrestrial PT Program on avian diseases PCR (Test period 14th May 2024 to 11th June 2024). The program was conducted by CSIRO-ACDP, Australia.
- OFFLU PT Program- Influenza A virus PCR (Test Period 11th March 2024 to 11th June 2024). The program was conducted by CSIRO-ACDP, Australia.

Participation of Scientists In Conferences, Workshops, Symposia, Trainings Etc. In India and Abroad

S. No.	Name of conference/workshop/ symposia/ training/meeting	Date	Venue	Participating scientist
	INTERNATIONAL			
1	International Conference on Biotechnology and Bioengineering (ICBB-2024).	20-21 May, 2024	Virtually organised by Brainy Meet	Fateh Singh
2	ASM Microbe 2024	13-17 June, 2024	Atlanta, USA	N. Kumar
3	Ninth meeting of the Standing Group Experts (SGE) on African swine fever (ASF) for Asia and the Pacific organized by FAO and WOAH	25-27 June, 2024	Manila, Philippines	K. Rajukumar
4	OFFLU Global Technical Meeting	2-4 July 2024	FAO Headquarters, Rome, Italy	C. Tosh
5	International Conference on Impact of Climate change on Biodiversity- A global perspective	11-13 July, 2024.	Madras Veterinary College, TANUVAS, Chennai	Senthil Kumar D.
6	WOAH Regional Workshop on Avian Disease Prevention and Control in Asia and the Pacific 2024	27–29 August, 2024	Seoul, Republic of Korea	S. Nagarajan
7	Webinar on Synthetic Biology: Technological Developments and Policy Discussions organized by the Korea Institute for Promoting Asia Biosafety Cooperation and United Nations Environment Programme	13 September, 2024	Virtual mode	Pradeep Gandhale
8	Webinar on Risk Assessment and Risk Management"organized by the Korea Institute for Promoting Asia Biosafety Cooperation and United Nations Environment Programme	23 September, 2024	Virtual mode	Pradeep Gandhale
9	International Conference on Climate Change and Environmental Sustainability in Mountainous and Hilly Landscapes	30 September - 1 October, 2024	Assam University, Silchar, Assam	N. Kumar
10	VIROCON-2024, International Conference on Emerging Viruses: Pandemic & Biosecurity Perspective.	11-13 November, 2024	DRDE, Gwalior	C. Tosh, N. Mishra, S. Kalaiyarasu, M. Kumar & Fateh Singh,
11	International Conference on One Health and Emerging Infections organized by the Institute of Advanced Virology, Kerala	20 November, 2024	Virtual mode	S. Kalaiyarasu

12	AMR conclave 2024 "Addressing Antimicrobial Resistance: A One Health Action Plan" organised by CVAS, Mannuthy, School of Zoonoses, Public Health and Pathobiology, ReAct Asia Pacific and INGSA-Asia.	November, 20, 2024	Virtual mode	Pradeep Gandhale
13	International conference on Animal Science & Veterinary Medicine (IVASVM 2024) on 30-Nov-2024.	30 November, 2024	Virtual mode	Atul Kumar Pateriya
14	IXth International Conference on Global Research Initiatives for Sustainable Agriculture & Allied Sciences (GRISAAS-2024) 10-12th December 2024.	10-12 December, 2024	Virtual mode	Atul Kumar Pateriya
	NATIONAL			
15	AgrIP 2024, Online short course on Patents in Agriculture 'AgriIP' jointly organized by IP&TM, New Delhi, and ICAR-CIFT, Kochi.	15 January to 15 February, 2024	Virtual mode	S. Kalaiyarasu & Senthil Kumar D
16	ICMR one health webinar on Avian Influenza: A looming threat	2 February, 2024	Virtual mode	Pradeep Gandhale
17	3rd Contact Session for batch of SectorConnect Field Epidemiology Programme in One Health (FEP OH) at Surat organized by the National Centre for Disease Control (NCDC) and the Department of Animal Husbandry (DAHD)	12-14 February, 2024	Virtual mode	Pradeep Gandhale
18	ICAR-CGIAR Annual Review Meeting held under the Chairmanship of DG ICAR	17 February, 2024	NASC, New Delhi	K. Rajukumar
19	5th Biennial pouty health conference and national symposium on "Poultry Health: Current challenges and future strategies" AAHP 2024.	23-24 February, 2024	Hyderabad,	S. Nagarajan
20	Webinar on Inter-country Knowledge Sharing Webinar on the Biosafety related Target 17 of the Global Biodiversity Framework (GBF) organized by theKorea Institute for Promoting Asia Biosafety Cooperation (KIPABiC) and Biotech Consortium India Limited (BCIL),	22 March, 2024	Virtual mode	Pradeep Gandhale
21	Training on Biosafety and Biosecurity for handling high-risk pathogens in BSL-3 laboratory	15-19 April, 2024	ICMR-National Institute of Virology (NIV), Pune	H.V. Murugkar
22	Meeting on Surveillance of Non-poultry species for Avian Influenza	19 April, 2024	Virtual Mode	A. Sanyal, C. Tosh, S. Nagarajan

23	**Training on ARMS 2.0 for Nodal Officers**	**22 April, 2024**	Virtual mode	Pradeep Gandhale
24	**Meeting on The expert and stakeholders consultation on development of poultry action plan organized by DAHD.**	29-30 April, 2024	DAHD, MoFAH&D, GOI, New Delhi	A. Sanyal, C. Tosh, & S. Nagarajan
25	4th Stakeholder Engagement Workshop for SectorConnect: Fellowship in One Health organized by the National Centre for Disease Control (NCDC) and the Department of Animal Husbandry (DAHD)	14 May, 2024	National Centre for Disease Control, Delhi	Pradeep Gandhale
26	XXXVI Annual Conference of the Indian Association of Microbiologists, Immunologists & Specialists in Infectious (IAVMICON-2024).	6-7 June, 2024	CVASc, RAJUVAS, Udaipur	Fateh Singh
27	World accreditation day and QualMacon,(Quality Managers of NABL accredited Labs) organized by NABL	10 June, 2024	Bhopal, Madhya Pradesh	C. Tosh
28	Webinar on 'How to Get Your Research Paper to the Finish Line: AI Writing Tips	13 June, 2024	Virtual mode	Pradeep Gandhale
29	Ethical principles and practices for research involving human participants with environmental associated ailments	14 June, 2024	ICMR-National Institute for Research in Environmental Health (NIREH), Bhopal	H.V. Murugkar
30	Assessors training program on ISO: 20387:2018 Standards was attended and successfully passed.	15-18 June, 2024	NABL, QCI, India.	A. A. Raut
31	"One Health for Pandemic Preparedness and Avian Influenza Simulation Exercise." Organized by Department of Animal Husbandry & Dairying, Government of India, in collaboration with the World Bank	19-20 June, 2024	Marriot Hotel, Bhopal	A. Sanyal, C. Tosh, S. Nagarajan & M. Kumar
32	Vaccine Stewardship in Prevention and control of High Pathogenicity Avian influenza for Asia and Pacific	25 June-18 July, 2024	Virtual Learning Centres, FAO	M. Kumar
33	National Consultation on Legal Framework for One Health Implementation at Udaipur, Rajasthan organized by NCDC, MoH&FW, GOI & UNDP.	27-28 June, 2024	Udaipur, Rajasthan	A. A. Raut
34	Industry-Scientist Meet on ICAR Technologies for commercialization.	15 July, 2024	NASC, New Delhi	N. Mishra
35	Interaction of the SMDs and the Directors of ICAR Institutes and Concurrent Industry-Institute Interaction	15 July, 2024		A. Sanyal, S. Nagarajan

36	Brainstorming Session on Avian Influenza with special reference to surveillance and vaccination organized by DAHD, MoFAH&D, GOI.	16 July, 2024	Delhi	A. Sanyal, C. Tosh, S. Nagarajan
37	Webinar on Advancing Antibody Discovery and Vaccine Development with Lipoparticles and Reporter Viruses	31 July, 2024.	Virtual mode	Pradeep Gandhale
38	IP Awareness/Training program under National Intellectual Property Awareness Mission organized by Intellectual Property Office, India	9 August, 2024	Virtual mode	S. Kalaiyarasu
39	1st National Veterinary Summit, Agrivision - 2024 on "Role and Contribution of Veterinary and Allied Sciences towards making Viksit Bharat @ 2024"	24-25, August 2024	NDVSU, Jabalpur	Pradeep Gandhale
40	OFFLU Zoom call to update avian and swine influenza data contributions to Sept 2024 WHO VCM	18 September, 2024	Virtual mode	C. Tosh
41	Editor's Workshop- Enabling A Research Ecosystem organized by the Elsevier Researcher Academy and ICAR	24 September, 2024	Virtual mode	Pradeep Gandhale
42	Technical session on the topic "Biosafety and Biosecurity" during 2nd Contact Session of Sector Connect FEP OH, Bengaluru	25-27 September, 2024	NIVEDI	G. Venkatesh
43	Symposium on 'Strategies to combat economically important Porcine and Poultry viruses in India'	3-4 October, 2024	NIAB, Hyderabad	K. Rajukumar
44	Meeting for strengthening the surveillance for avian influenza in wild and migratory birds at Ramsar/wetland sites, Uttar Pradesh	10 October, 2024	Virtual Mode	C. Tosh
45	Webinar on Understanding IP: Encouraging creativity and innovation.	18 October, 2024	CAZRI, Jodhpur	N. Mishra
46	Meetings on Expert consultation for revision of National Action Plan for Prevention Control and Containment of avian influenza	17-18 October, 2024	DAHD, MoFAH&D, GoI, at Bangalore, Karnataka,	A. Sanyal, C. Tosh, S. Nagarajan
47	Webinar on 'IPR awareness' conducted by the Office of Controller General of Patents, Designs and Trade Marks (CGPDTM), New Delhi	18 October, 2024	Virtual mode	N. Kumar
48	National Intellectual Property Awareness Mission (NIPAM) (NIPAM 2.0) organized by the Office of Controller General of Patents, Designs and Trade Marks	18 October, 2024	Virtual mode	Pradeep Gandhale
49	Meeting for finalization of Pandemic Fund Project and to attend the official launch of Pandemic Fund Project	24-25, October 2024	DAHD, MoFAHD, GoI in New Delhi	A. Sanyal, S. Nagarajan

50	Symposium aimed at bringing together researchers and industrial stakeholders to discuss strategies to combat economically important porcine and poultry viruses in India	3-4 October, 2024	BRIC, NIAB, Hyderabad.	S. Nagarajan & K. Rajukumar
51	Policy Workshop on "Organisational Livestock Research and Development Priorities for India"	14 November, 2024	ILRI, NASC Complex, New Delhi	K. Rajukumar
52	XX Annual Conference of the Indian Association of Veterinary Public Health Specialists (IAVPHS) and the National Symposium on "Integrating One Health: Bridging the Gap at Human-Animal-Environment Interfaces"	14-15 November, 2024	Krantisinh Nana Patil College of Veterinary Science, Shirwal, Maharashtra, India.	H.V. Murugkar, Pradeep Gandhale & Anubha Pathak
53	41st Annual Conference of Indian Association of Veterinary Pathologists and National Symposium on 'Exploring Veterinary Pathology and Diagnostic Innovations in Animal and Poultry Diseases Amidst Climatic Challenges'	28-30 November, 2024	SKUAST- Jammu	K. Rajukumar
54	Consultation Workshop on guidelines for Integrated Community Outreach Program for One Health (ICOP-OH) at New Delhi, by NCDC, MoH&FW, GOI & WHO	12-13 December, 2024	NCDC, New Delhi	A. A. Raut
55	Six-monthly meeting of Nagar Rajbhasha Karyanvayan Samiti (NARAKAS)	24 December, 2024.	NITTTR, Bhopal	Fateh Singh

EXTENSION ACTIVITIES

Webcast of Hon'ble PM's programme

✓ The farmers meet on occasion of release of climate resilient and bio-fortified 109 Crop varieties was organised on 11thAugust, 2024. Dr. Aniket Sanyal, Director, briefed about ICAR's role and achievements indeveloping the climate resilient and bio-fortified crop varieties to the more than 75 farmers attending the event. He also emphasized the role of ICAR and urged the scientist of NIHSAD to work tirelessly in achieving the goal of "Viksit Bharat @ 2047" as envisioned by honorable PM Shri. Narendra Modi ji. During the event, Dr. Pradeep Gandhale, Sr. Scientist, apprised the farmers about need and significance of climate resilient and bio-fortified crop varieties in food security.

Plantation drive

✓ The plantation drive as part of the Global Campaign "Ek Ped Maa ke Naam" launched by the Hon'ble Prime Minister of India on the occasion of World Environment Day 2024, was organised at ICAR-NIHSAD, Bhopal on September, 17, 2024. As trees are essential for halting and reversing land degradation, building drought resilience and preventing desertification, various types of trees including fruit and medicinal plants were planted. All the scientists, staff and students enthusiastically participated in the drive.

Hands-on demonstration of effective use of Fire extinguishers

✓ Hands-on demonstration & awareness drive on fire exigency preparedness was organized at the institute for section incharges, security personnel & contractual staff. Dr. Pradeep N. Gandhale, Sr.Scientist & I/c. Fire Section and Mr. Asanna Badge, Technical Officer, based on working of the laboratory, explained the possible fire hazards and accordingly, the best suitable extinguishers for dousing these various fire hazards were demonstrated in detail. The classification of fire based on combustion materials which have or could be ignited was also explained to all the staff.The hands-on demonstration of proper & safe use of different type of fire extinguishers such asABC type, Carbon dioxide,Foam and clean agent based extinguishers were done.

Activities under Scheduled Caste Sub Plan

✓ Goat and Feed distribution programme and a Farmers-Scientists interaction meet for the Scheduled Caste beneficiaries in Hatiyakheda village of Umraoganj block in the district of Raisen was organized on 20th June 2024. A total of 100 goats and 1.25 tons of goat feed were distributed equally to 25 SC beneficiaries. A total of 170 farmers/ animal owners participating in the events were awakened to follow good health practices and profitable goat rearing and management. Dr. Fateh Singh, Senior Scientist & Nodal Officer, SCSP, and Dr. Pradeep Gandhale, Senior Scientist, coordinated and executed the program.

✓ In continuation of the activities under the SCSP, organised an Advanced Goat Rearing Workshop and a Farmers-Scientists interaction meet for the Scheduled Caste beneficiaries in Umraoganj block of the district Raisen, on 9th Oct. 2024. During the programme distributed 60 goats, 750 kilograms of goat feed, and 375 kilograms of mineral mixture equally to15 SC beneficiaries. More than 50 48 farmers/ animal owners participated in the programme. The lectures on profitable animal husbandry practices and animal disease control were delivered to the farmers. Dr. Fateh Singh, Senior Scientist & Nodal Officer, SCSP, and Dr. Pradeep Gandhale, Senior Scientist, coordinated and executed the program.

✓ An Advanced Poultry Rearing Workshop and a Field Day for Scheduled Caste beneficiaries were organised in Gudawal village of Umraoganj block in the Raisen district on 10th October 2024. The 700 poultry birds and 1.4 tons of poultry feed, were distributed to 28 beneficiaries (25 birds and 50 kilograms of feed per beneficiary) of the Scheduled Caste. More than 60 farmers/ poultry owners participating in the workshop were briefed about profitable poultry rearing and management by Dr. Fateh Singh, Senior Scientist & Nodal Officer, SCSP, and Dr. Pradeep Gandhale, Senior Scientist.

Kisan Diwas

✓ The Scientist-Farmers interaction Workshop was organized at ICAR-NIHSAD, Bhopal on the occasion of Kisan Diwas on 23.12.2024. More than 90 farmers from Bhopal (villages Kanhasaiya, Kalua, Chhoti Khajuri), Vidisha (Gyaraspur) and Raisen (Bilkhiriya, Gudawal, Silwani) including 15 Mahila Kisan and Sitaram Swa-Sahayata Uhar Mahila Samuh, kotra, Gyaraspur attended the workshop. The farmers informed that several Swachhata initiatives have been taken by Panchayats, Schools and Swa-Sahayata Samuh in their villages and these initiatives have created mass awareness in public about cleanliness. To show gratitude towards their hardwork and contribution in food seurity the farmers were felicitated with Gamcha and flowers. The kit containing mineral mixture, anthelmintic medicines and disease leaflets were also distributed to the farmers.

The experts from the State Animal Disease Investigation Laboaratory, Bhopal and ICAR-Indian Institute of Soil Science, Bhopal were invited to the workshop to interact with farmers. During the workshop to sensitize the farmers on animal health as well as Parali management, interactive lecture emphasizing the environmental health was delivered. The discussion session to brief the farmers about various schemes of the Central & Madhya Pradesh governments for livestock owners/farmers was conducted and leaflets were distributed amongst the farmers. Soil is integral part of the animal husbandry and soil health plays significant role in animals as well as human health. Therefore, to explain therole of healthy soil and balanced nutrition in improved animal husbandry, awareness lecture was delivered. Moreover Scientist-Farmers interaction session was also conducted during the workshop to discuss the farmer's problems and to provide the solution.

Extension cum Training Programme on "Advanced Management and Health Practices in Livestock and Poultry & Distribution of Inputs to Farmers of Meghalaya State"

✓ An Extension cum Training Programme on "Advanced Management and Health Practices in Livestock and Poultry & Distribution of Inputs to Farmers of Meghalaya State" was successfully organized in collaboration with the College of Agriculture (CoA), Central Agricultural University (CAU), Imphal, Kyrdemkulai campusunder NEH funds. The initiative aimed to enhance the knowledge base and practical skills of local farmers in scientific livestock and poultry management, while also providing them with essential farm inputs to strengthen their livelihood support systems.The programme featured a series of focused technical interactions and expert-led sessions on key topics of relevance to livestock and poultry health. Notable sessions included:"Important Zoonotic Diseases of Pigs and Their Preventive Measures" by Dr. Ashwin A. Raut, which addressed crucial pig-borne zoonoses, their transmission risks, and effective preventive strategies to safeguard both animal and human health, "Economically Important Diseases of Goats and Their Management" by Dr. Fateh Singh, highlighting major diseases affecting goat productivity, early detection signs, and management practices to reduce economic losses, "Avian Influenza: An Introduction and Strategies to Prevent and Control Outbreaks" by Dr. Atul Kumar Pateriya, which covered the nature of avian flu, its zoonotic potential, and essential biosecurity and control measures to prevent outbreaks.

In addition to the training sessions, the programme incorporated a distribution of essential livestock and poultry inputs aimed at empowering farmers to apply improved practices and increase productivity. The distributed inputs included: 666 poultry birds (4 weeks old), distributed across 15 units (each unit comprising 44–45 birds),20 goats, divided into 10 units (2 goats per unit),40 packets of goat feed, allocated as 10 units (4 packets per unit).

These inputs directly benefited 25 farmers—15 farmers received poultry units, while 10 farmers received goats along with feed support. The event witnessed enthusiastic participation, with a total of 40 farmers attending the programme. This initiative not only facilitated the dissemination of scientific knowledge and best practices in animal husbandry but also served as a practical step toward strengthening the rural agrarian economy in Meghalaya through targeted support and capacity building.

CAPACITY BUILDING

Training cum Workshop on Biosafety for handling and diagnosis of high risk animal pathogens in ABSL-3 and BSL-3 laboratories

A training titled 'Training cum Workshop on Biosafety for handling and diagnosis of high risk animal pathogens in ABSL-3 and BSL-3 laboratories' was conducted under the project titled 'Creation of a national network of existing and upcoming high risk pathogens laboratories (BSL-3/4) labs across departments and keeping their interlinkages' funded under the National One Health Mission (NOHM) component of PM-ABHIM. The training was conducted in coordination with Office of the Principal Scientific Advisor, GOI and Indian Council of Medical Research (ICMR), DHR, GOI. The objectives of the training have been detailed below:

- Sensitization of participants towards Animal Biosafety Level 3 laboratories design, establishment and maintenance.
- Capacity building for animal experimentation, collection and processing of animal samples with high risk pathogen and their disposal following proper ABSL3 and BSL3 standards.
- Capacity development of participants on basic animal diseases diagnostic techniques and work practices.

The training targeted to enhance biosafety and biosecurity knowledge, raise awareness about animal disease diagnostic techniques, and foster a culture of responsibility and mutual collaboration across the different sectors. Additionally, it sought to improve inter-organizational coordination among the BSL3 labs under the network, enabling them to share workloads during emergencies. The training program was designed to ensure both personal and environmental safety from the infectious pathogens handled by these laboratories of the country.

The details of duration and participants and their participating institutes have been detailed below:

Details of the batches, duration and number of trainees

Batch No	Duration (5 Days)	No of Trainees
Batch I	19th to 23rd Aug 2024	9
Batch II	26th to 30th Aug 2024	12
	Total Participants Trained	21

Details of the participating institutes

Institutes (Batch-I)	Institutes (Batch-II)
PGIMER, Chandigarh	JIPMER, Puducherry
ICMR-NIV, Pune	RMRC, Dibrugarh
ICMR-NARI, Pune	ICMR-NIV, Kerala Unit
ICGEB, Delhi	THSTI, Faridabad
InSTEM, Bangalore	ILS, Bhubaneshwar
RGCB, Kerala	CSIR-IMTECH, Chandigarh
NRCE, Hisar	CSIR-CCMB, Hyderabad
CCS, Baghpat	ICAR-IVRI, CADRAD, Izatnagar
AIIMS, Bhopal	AIIMS, Jodhpur
Mobile BSL3, Pune	Mobile BSL3, Gorakhpur
	ICAR-NIFMD, Bhubaneshwar

Glimpses of on Training cum Workshop on Biosafety for handling and diagnosis of high risk animal pathogens in ABSL-3 and BSL-3 laboratories

Thesis Research Guidance

Discipline	Name of the Scientist	MVSc	PhD
Animal Genetics	Anamika Mishra	01	01
Veterinary Microbiology	C. Tosh	-	01
	S. Bhatia	01	-
	S.B. Sudhakar	01	
	S. Kalaiyarasu	01	-
	Pradeep Gandhale	02	02
Veterinary Public Health	H.V. Murugkar	02	-
Veterinary Pathology	K. Rajukumar	-	01
	Manoj Kumar	-	01
Total		**08**	**06**

MEETINGS & VISITS

☞ Research Advisory Committee (RAC) Meeting

The 10th Research Advisory Committee (RAC) meeting of ICAR-NIHSAD was held on 12th March 2024 at the institute under the chairmanship of Prof. K.M.L. Pathak, Former Vice-Chancellor, DUVASU, and Ex-DDG (Animal Science), ICAR. The meeting was attended by RAC members, including Dr. Ashok Kumar, ADG (Animal Health), ICAR; Dr. A. Sanyal, Director, ICAR-NIHSAD; Dr. R. Somvanshi, Former Head, Division of Pathology, IVRI; Dr. (Mrs.) Madhu Swamy, Professor, Department of Veterinary Pathology, NDVSU, Jabalpur; Dr. Debasis Biswas, Head, Department of Microbiology, AIIMS, Bhopal; Dr. B.R. Gulati, Director, ICAR-NIVEDI, Bengaluru (attended online); Dr. Sandeep Bhatia, Principal Scientist, ICAR-NIHSAD; Dr. S. Nagarajan, Principal Scientist and In-charge, PME Cell, ICAR-NIHSAD. All scientists of the institute also participated in the meeting.Dr. A. Sanyal, Director, presented the major achievements of the institute, followed by the presentation of the Action Taken Report on the previous RAC recommendations by Dr. S. Nagarajan, Member Secretary, RAC. Research accomplishments were shared by respective group leaders across the thematic areas of Avian Diseases, Ruminant Diseases, Swine Diseases, and Zoonotic Diseases. The committee engaged in detailed discussions on the institute's research priorities, development of diagnostics and vaccines, and the scientific services rendered to the country and neighboring nations. The RAC provided several valuable recommendations to strengthen the institute's research programs.The meeting concluded with closing remarks from the RAC members and Chairman, followed by a vote of thanks delivered by Dr. S. Nagarajan, In-charge, PME Cell, ICAR-NIHSAD.

☞ World Intellectual Property Day

The World IP day was celebrated by NIHSAD, Bhopal under the Chairmanship of Director, on 26 April 2024 to highlight the role that IP rights, such as, patents, copyrights, designs, trademarks, plant variety, technology licensing, IP auditing, IP litigation play and to explore how IP encourages and can amplify the innovative and creative solutions that are so crucial to building our common future. The theme was "IP and the SDGs: Building our common future with innovation and creativity". Mrs. Vidisha Garg, IPR Specialist at Anand & Anand, NOIDAdelivered a lecture onPatent filing procedure and drafting of patent specifications. A total of 35 participants including scientists, staff, SRF/young professionals and students attended the event.

Institute Technology Management Committee Meeting

Three ITMC meetings were held during the year on 31st May, 3rd July and 29th November to consider various Institute technologies for release, technology transfer, technology certification and IPR (Patent, Copyright and Trade mark) filing.

Institute Research Committee (IRC) Meeting

The Institute Research Committee (IRC) meeting was held on 2nd August 2024 under the chairmanship of the Director, ICAR-NIHSAD. The In-charge of the PME Cell briefed the committee on newly proposed projects recommended by the Research Management Committee (RMC) for IRC presentation, as well as ongoing institute and externally funded projects. All scientists of the institute participated in the meeting, during which each project and the institute's research priorities were thoroughly discussed. Constructive suggestions were provided to enhance the outcomes of individual projects. The Director emphasized the need to focus on the development of diagnostics and vaccines for various exotic and emerging animal diseases. He also underscored the importance of adhering to RAC recommendations while formulating new projects.

Institutional Biosafety Committee (IBSC) meeting

Institute Animal Ethics Committee meeting was held on 24th September, 2024 under the chairmanship of Dr. Aniket Sanyal, Director, ICAR-NIHSAD. The meeting was attended by Dr. Debasis Biswas, Dean (Research), AIIMS, Bhopal & DBT Main nominee along with other committee members.

☞ Institute Animal Ethics Committee (IAEC) meeting

Institute Animal Ethics Committee meeting was held on 5th November, 2024 under the chairmanship of Dr. Aniket Sanyal, Director, ICAR-NIHSAD. Presentations of new projects was made and Dr. Sarman Singh, CPCSEA main nominee along with the committee members approved all new projects. Progress report of the ongoing projects was presented by member secretary Dr. G. Venkatesh.

CELEBRATIONS & EVENTS

☞ Republic Day Celebrations:

The staff members of ICAR-NIHSAD celebrated Republic Day and Independence Day with great enthusiasm and joy on 26th January 2024. The event saw the hoisting of the national flag by the Director, Dr. Aniket Sanyal. The staff members, along with their family members, attended the function and participated in various activities organized on the occasion. The celebrations reflected the institute's commitment towards honoring and celebrating the country's rich cultural heritage and values.

Foundation day celebrations

Foundation day of the institute was celebrated on 8th Aug 2024. Dr. R.N. Tiwari. Director, ICMR-NIREH, Bhopal presided the function as the chief guest and Dr. S.C. Dubey, former Joint Director, HSADL, Bhopal as guest of honour. The event was graced by Dr. C.R. Mehta, Director, ICAR-CAIE, Bhopal and Dr.S.P.Datta, Director, ICAR-IISS, Bhopal and Officials from the state animal husbandry departments. The celebrations started with the plantation drive by the dignitaries. Dr.Aniket Sanyal, Director, ICAR-NIHSAD briefed the gathering about milestones and accomplishments of the institute and future endeavours. The foundation day lecture was delivered by Dr. S.C. Dubey and appraised the gathering about the contributions made by the visionaries in veterinary sciences for planning and commissioning the first bio-containment laboratory of India leading to the genesis of the institute. All staff, students and research staff enthusiastically participated in the celebration.

Independence Day

The ICAR-NIHSAD celebrated Independence Day with great enthusiasm and joy on 15th August 2024, respectively. The Director, Dr. Aniket Sanyal event has hoisted the national flag. The staff members, along with their families attended the function and participated in various activities organized on the occasion. The celebrations of this important event at ICAR-NIHSAD reflect the institute's commitment towards honoring and celebrating the country's rich cultural heritage and values.

Flag hoisting by the Director on 15th August, 2024

☞ Hindi Week Celebration

ICAR-NIHSAD, Bhopal, has organized the Hindi Week at the Institute from 13th to 20th September 2024, including the Hindi Day on 14th September 2024. A range of activities were conducted for the Institute staff, including self-composed Hindi poetry recitation, dictation, essay writing, noting and drafting, idioms and proverbs, and extempore/ elocution competitions to promote Hindi work culture in the offices. All the events were systematically performed and adjudged through a panel of jurors. The Hindi week concluded on 20th September 2024 with a closing ceremony, during which the winners of the various events were honoured and felicitated by the Director of the Institute. All the programmes related to Hindi Week were planned and coordinated by Dr. Fateh Singh, Senior Scientist & I/c, Hindi Rajbhasha.

☞ Observance of Vigilance Awareness Week

On 30th October 2024, Dr. Aniket Sanyal, Director, ICAR-NIHSAD, administered the integrity pledge in presence of vigilance officer to all the scientists, administrative & technical staff, research fellows, students and contractual staffs of the institute. He further briefed everyone present about its significance and highlighted the activities to be undertaken by the institute as a part of "Vigilance Awareness Week" from 28th October 2024 to 3rd November 2024.

Swachh Bharat Abhiyan

✓ **Swachhata Pakhawada:** "Swachhta Hi Sewa campaign with the theme of 'Swabhav Swachhata - Sanskaar Swachhata' was organised from 15th September-2nd October 2024 at ICAR-NIHSAD, Bhopal. The campaign was started on 17th September with the administration of pledge by secretary DARE & DG, ICAR virtually. Swachhta Hi Sewa campaign was coordinated by Dr. PN Gandhale, Sr.Scientist/Nodal officer and Mr. S Barange, ACTO/co-Nodal officer under the able guidance of Dr. Aniket Sanyal, Director.To spread awareness about cleanliness, various activities such as Swachhata Samvad with school children and cleanliness campaign at nearby villages, schools, Factory Workers Colony, Anganwadi were organised. Swachhata Abhiyan was also organised in two very sacred and ancient religious places of Madhya Pradesh, Kankali Mata Mandir and Bhojpur Mandir educating school children, villagers, devotees, visitors, shopkeepers and explained the importance of cleanliness and its potential impact on both environment and human health. Swachhata Abhiyan was also conducted in the institute premises wherein identified black spots around the boundary of the institute and collected and disposed of biodegradable and non-biodegradable waste including plastic, glass and scrap material, etc. For sanitation workers, health check-up camp was organized in the institute and sugar, BP, oxygen level and fever were tested and medicines were distributed. Moreover, to protect cleaning and contractual workers from occupational hazards, PPE kits and safety equipments were also distributed.

✓ **Swachhata Pakhawada:** Swachhata Pakhawadawas celebrated with fervor at ICAR-NIHSAD, Bhopal during December, 16-31, 2024. Swachhata Pakhawada was started with administration of Swachhata pledge by Dr. Aniket Sanyal, Director and all activities were coordinated by Dr. PN Gandhale, Sr.Scientist/Nodal officer and Mr. S Barange, ACTO/co-Nodal officer. During the pakhwada various activities like Swachhta Awareness Drive, Swachhata Seminar, Mass awareness activities, cleanliness & sanitation drives, community outreach, cleanliness of public places, swachhata runs and plantation drive were organised at nearby villages, schools and public places to create the awareness on Swachhata, importance of personal hygiene &segregation of waste among the masses.

COMMITTEES

Research Advisory Committee (RAC)

S. No.	Name	Designation
1	Prof. (Dr.) Col. A.K. Gahlot, Ex. Vice Chancellor, Rajasthan University of Veterinary & Animal Sciences, Bikaner.	Chairman
2	Dr. J.M. Kataria, Ex-Director, ICAR-Central Avian Research lnstitute (CARI), lzatnagar, UP	Member
3	Dr. A.K. Tiwari, Director, ICAR-Central Avian Research lnstitute (CARI), lzatnagar, UP.	Member
4	Dr R.C. Ghosh, Professor and Head, Department of Veterinary Pathology, Dau Shri Vasudev Chandrakar Kamdhenu Vishwavidyalaya, Aniora, Durg, GE Road, Chattisgarh	Member
5	Dr. Y.N. Reddy, Retd. Professor, Department of Microbiology, PVNRTVU, Hvderabad	Member
6	Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	Member
7	Dr. Divakar Hemadri, ADG (AH), Indian Council of Agricultural Research, New Delhi	Member
8	Prof (Dr). Avadh Bihari Shrivastav Founder Director (Rtd.), School of Wildlife Forensic and Health, NDVSU, Jabalpur - 482001, M P	Member
9	Shri Dinesh Kumar Patidar, Village- Dassanga, Post-Dongargaon Distt. Tahsil-Khargaone-451442.	Member
10	Dr. S. Nagarajan, Principal Scientist and Incharge, PME Cell, NIHSAD, Bhopal	Member Secretary

Institute Management Committee (IMC)W

S. No.	Name	Designation
1	Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	Chairman
2	Dr. Ashok Kumar, ADG(Animal Health), ICAR, New Delhi	Member
3	Dr. R.K. Mahiya, Director, Veterinary Services and Animal Husbandry, Govt of M.P., Bhopal	Member
4	Dr. Bhawani Singh Rathore, Director of Veterinary Services and Animal Husbandry, Govt of Rajasthan, Jaipur, Rajasthan	Member
5	Prof (Dr.) S.P. Tiwari, Vice Chancellor, NDVSU, Jabalpur	Member
6	Dr. Shiv Chandra Dubey, Ex Joint Director, HSADL, Bhopal (Upto Oct 2023)	Member
7	Shri Sandeep Kumar Sharma, Ex. President, Chhattisgarh State Kisan Morcha, Raipur (Upto Oct 2023)	Member
8	Dr. H.V. Murugkar, Principal Scientst & Bio safety Officer, ICAR-NIHSAD, Bhopal	Member
9	Dr. G. Sai Kumar, Principal Scientist, IVRI, Izatnagar	Member
10	Dr. A.K. Shukla, PC, IISS, Bhopal	Member
11	Dr. T.K. Bhattacharya, PS, DPR, Hyderabad	Member
12	Mr. Kunal Kalia, Senior Finance & Accounts Officer, ICAR, New Delhi	Member
13	Admin. Officer, ICAR-NIHSAD, Bhopal	Member Secretary

Institute Animal Ethics Committee (IAEC)

S. No.	Name	Designation
1	Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	Chairmen
2	Dr. Sarman Singh, Director, Medical Research and Institutional Collaboration, AVME, Pondicherry	CCSEA Main nominee & member
3	Dr. Gayatri Dewangan Mishra, CVSAH, Mhow, Indore	CCSEA Link nominee & member.
4	Dr. Neeraj Upamanyu, Professor & Pro-Vice Chancellor, SAGE, Bhopal	CCSEA nominee & member
5	Shri. Har Govind Garg, Professor, LNCT, Bhopal	CCSEA nominee & member
6	Dr. Anamika Mishra, Principal Scientist, ICAR-NIHSAD, Bhopal	Member
7	Dr. Manoj Kumar, Senior Scientist, ICAR-NIHSAD, Bhopal	Member
8	Dr. Kalaiyarasu S., Senior Scientist, ICAR-NIHSAD, Bhopal	Member
9	Dr. G. Venkatesh, Principal Scientist & ABSO, ICAR-NIHSAD, Bhopal	Member -Secretary

Institute Technology Management Committee (ITMC)

S. No.	Name	Designation
1	Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	Chairman
2	Dr. H.V. Murugkar, Principal Scientist, ICAR-NIHSAD, Bhopal	Member
3	Dr. Sandeep Bhatia, Principal Scientist, ICAR-NIHSAD, Bhopal	Member
4	Dr. S. Nagarajan, Principal Scientist I/c PME Cell, ICAR-NIHSAD, Bhopal	Member
5	Dr. Sanjay Shrivastava, Principal Scientist & I/c ITMU, ICAR-IISS, Bhopal	External Member
6	Dr. N. Mishra, Principal Scientist & I/c ITMU, ICAR-NIHSAD, Bhopal	Member Secretary

Institutional Biosafety Committee (IBSC)

S. No.	Name	Designation
1	Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	Chairman
2	Dr.Debasis Biswas, Dean (Research), AIIMS, Bhopal	DBT Nominee
3	Dr. Atul Gupta, AMA, NIHSAD, Bhopal	Member
4	Dr. P.K. Mishra, Scientist F & Head, ICMR-NIREH, Bhopal	Member
5	Dr. R.K. Garg, Professor, Barkatullah University, Bhopal	Member
6	Dr. H.V. Murugkar, Biosafety officer & Principal Scientist, NIHSAD, Bhopal	Member
7	Dr. A.A. Raut, Principal Scientist, NIHSAD, Bhopal	Member
8	Dr. S.Nagarajan, Principal Scientist, NIHSAD, Bhopal	Member
9	Dr. G. Venkatesh, Principal Scientist, NIHSAD, Bhopal	Member Secretary

Quinquennial Review Team Committee (QRT)

S.No.	Name	Designation
1	Dr. RNS Gowda, Former Vice Chancellor, KVAFSU, Bengaluru	Chairman

2	Dr. S. Yathiraj, Former Dean, Veterinary College, Bengaluru	Member
3	Dr. Mohinder S. Oberoi Oberoi Former Manager, ECTAD RAP, FAO, Rajguru Nagar	Member
4	Dr Manmahon Parida, Director, DRDE, College of Vety. Sciences, Assam Agricultural University, Guwahati	Member
5	Dr. Nagendra Nath Barman, Professor & Head	Member
6	Dr. Jyoti Misri, Epidemiology, AMR and Zoonosis Specialist, FAO of the UN, New Delhi.	Member
7	Dr. P. Swain, Vice President, Q-Line Biotech Pvt. Limited	Member
8	Dr. Divakar Hemadri, ADG (AH), ICAR Hqrs.	Member
9	Dr. S. Nagarajan	Member
	Principal Scientist & I/C PME Cell	Secretary

Institute Joint Staff Council (IJSC) and Central Joint Staff Council (CJSC)

S.No.	Name	Designation
	(A) Official Side	
1.	Dr. Aniket Sanyal, Director, ICAR-NIHSAD, Bhopal	Chairman
2.	Dr. H.V. Murugkar, Principal Scientist	Member
4.	Dr. (Mrs.) Anamika Mishra, PrincipalScientist	Member
5.	Dr. Fateh Singh, Senior Scientist	Member
6.	F & AO	Member
7.	AO	Member Secretary
	(B) STAFF SIDE	
1.	Shri B.K. Singh, AAO	Member/Member Secy.
2.	Mrs. MehjabinBilgrami, Assistant	Member
3.	Shri R.K. Shukla, Technical Officer	Member, CJSC
4.	Shri S.B. Somkuwar, Technical Officer	Member
5.	Shri Sita Ram Imne, SSS	Member

RESEARCH PROJECTS AT ICAR-NIHSAD

S.No.	Project Title	Duration	PI and Co-PI
	Service Project		
1.	Surveillance of Exotic and Emerging Animal Diseases in Indian and ImportedLivestock & Poultry and their Products.	Continuous activity	PI: Aniket Sanyal, Co-PIs: H.V. Murugkar, C. Tosh, N. Mishra, Sandeep Bhatia, Ashwin Ashok Raut, K. Rajukumar, S. Nagarajan, G. Venkatesh, Anamika Mishra, Manoj Kumar, S.B. Sudhakar, A.K. Pateriya, P.N. Gandhale, S. Kalaiyarasu, Fateh Singh, D. Senthil Kumar, Naveen Kumar and Anubha Pathak
	Avian Diseases		
	Institute Funded projects		
2.	Environmental surveillance for influenza A virus in wetlands and live bird markets	Apr, 24 – Mar, 26	PI: C. Tosh Co-PIs: Manoj Kumar, S Nagarajan, HV Murugkar
3.	Investigation of HPAIV (H5N1) Pathogenesis in chicken by metabolomics approach	Apr, 24 – Mar, 26	PI: Anamika Mishra Co-PIs: Ashwin Ashok Raut, H. V. Murugkar
4.	Development of Herpes Virus of Turkey Virus Vector expressing HA gene(s) of H5 Avian Influenza Virus	Apr, 23 - Mar, 25	PI: S. Nagarajan; Co-PIs: C. Tosh, Manoj Kumar, Senthilkumar, D. Naveen Kumar
5.	Adaptation and transmission of clade 2.3.4.4.b highly pathogenic avian influenza virus (H5N1) in mammals	Apr, 23 - Mar, 25	PI: Manoj Kumar; Co-PIs: S. Nagarajan, C. Tosh, H.V.Murugkar, Naveen Kumar
6.	Multiplex Real Time Reverse Transcriptase PCR (MP RT-qPCR) Kit for Avian Influenza A typing and detection of highly pathogenic H5 and H7 subtypes	Apr, 24 – Mar, 26	PI: Atul K Pateriya Co-PIs: S. Nagarajan, Manoj Kumar, S Bhatia, C Tosh, AA Raut
7.	Designing and Assessment of PCR amplicon based reverse genetics system for rescue of Avian Influenza virus	Apr, 24 – Mar, 26	PI: Atul K Pateriya Co-PIs: S. Nagarajan, Manoj Kumar, S Bhatia, C Tosh CCPI: Rekha Khandia, BU, Bhopal

8.	Exploring the epigenetic landscape during highly pathogenic avian influenza (HPAI) H5N1 2.3.4.4b virus infection in chickens	Apr, 24 – Mar, 26	PI: Naveen Kumar Co-PIs: Manoj Kumar, S Nagarajan, C Tosh, HV Murugkar
9.	Lipid nanoparticles as adjuvant-cum- vaccine or drug delivery platform: synthesis and their efficacy testing in BALB/c mice	Apr, 24 – Mar, 26	PI: Naveen Kumar Co-PIs: Manoj Kumar, S Nagarajan, C Tosh, HV Murugkar CCPI: R. S. Tomar, IISER, Bhopal
	ICAR Funded Scheme		
10.	ICAR - CRP on Vaccine & Diagnostics funded project entitled: Development of Lateral Flow Assay for detection of Avian Influenza infection.	Dec, 22 – Jan, 26	PI: Atul Kumar Pateriya , Co-PIs: S. Bhatia, Naveen Kumar
11.	Network Program on Gene Editing Technology: Establishment of a herpes virus vector platform and identification of vaccine candidates by gene editing for emerging and exotic diseases of livestock and poultry	Aug. 24 – Mar, 26	PI: S Nagarajan (PI) Co-PIs: C Tosh, Manoj Kumar, Senthilkumar D, Naveen Kumar, K Rajukumar, G Venkatesh, Fateh Singh
12.	Network Program on Gene Editing Technology: CRISPR-Cas based point- of-care diagnostic platform for animal diseases – Avian Influenza (H9):	Aug. 24 – Mar, 26	Leader: Manoj Kumar, Co-PIs: Senthil Kumar,D, C Tosh, G. Venkatesh, S Nagarajan
	Externally Funded Schemes		
13.	BMGF- Environmental surveillance and early warning system for animal pathogen surveillance	Oct, 24 – Mar, 27	PI: C. Tosh Co-PIs: Manoj Kumar, S Nagarajan, HV Murugkar
	Ruminant Diseases		
	Institute Funded projects		
15.	Development of an indigenous inactivated lumpy skin disease virus vaccine for cattle	Oct, 23 - Sep, 25	PI : S B Sudhakar; Co-PIs: S Kalaiyarasu, N Mishra
16.	Surveillance of farmed ruminant species for influenza A viruses and viruses associated with bovine respiratory disease complex	Apr, 24 – Mar, 26	PI: S. Kalaiyarasu Co-PIs: Niranjan Mishra, S. Nagarajan, Manoj Kumar, S. B. Sudhakar

	ICAR Funded Scheme		
17.	ILRI-ICAR Collaborative Proposal - Development of vaccines for prioritized exotic and emerging Diseases - RVF	Apr 23 – December, 26	PI : Niranjan Mishra; Co-PI: S. Kalaiyarasu
	Swine Diseases		
	Institute Funded projects		
18.	Development of CRISPR-Cas9 expressing African swine fever virus (ASFV) permissive cell line for rapid generation of ASFV mutants.	Apr, 23-Mar, 25	PI: Senthilkumar D; Co-PIs: K. Rajukumar, G. Venkatesh, Fateh Singh
19.	Evaluation of virulence, immunogenicity of ASFV mutant(s) generated by passaging in a heterologous cell line.	Apr, 24 – Mar, 26	PI: Senthilkumar D; Co-PIs: K. Rajukumar, G. Venkatesh, Fateh Singh
	ICAR Funded Schemes		
20.	ICAR NASF Project: Development and evaluation of genetically engineered vaccine candidates for African swine fever, Equine Herpes virus-1 and Equine Influenza (clade 1 & 2)	July, 22 - June, 25	PI - K. Rajukumar; Co-PIs: Senthilkumar D, G. Venkatesh, Fateh Singh
21.	ICAR - CRP on Vaccine & Diagnostics funded project entitled: Development of recombinant HA based indirect ELISA for detection of antibodies against H1N1 swine influenza virus in pigs.	Dec, 22 - Jan, 26	PI - G. Venkatesh; Co-PI's: K. Rajukumar, Fateh Singh, Senthilkumar D.
22.	ICAR - CRP on Vaccine & Diagnostics funded project entitled: Development of an indirect ELISA for detection of ASFV antibodies in Pigs	Apr. 24 – Mar, 27	PI - G. Venkatesh; Co-PI's: K. Rajukumar, Fateh Singh, Senthilkumar D., Juwar Doley (NRC PIG)
23.	Network Program on Gene Editing Technology: CRISPR-Cas based point- of-care diagnostic platform for animal diseases – Swine influenza	Aug. 24 – Mar, 26	CCPI - G. Venkatesh; Co-PI's: K. Rajukumar, Fateh Singh, Senthilkumar D.
24.	ILRI-ICAR Collaborative Proposal - Development of vaccines for prioritized exotic and emerging Diseases (ASF)	Apr. 23 – December 26	PI : K. Rajukumar; Co-PI: Senthilkumar D.
25.	ICAR-All India Network project on Challenging and Emerging Diseases of Animals (ASF component)	Sep. 24 – March 26	PI - Senthilkumar D, Co-PIs: K. Rajukumar; G. Venkatesh

	Zoonotic Diseases		
	Institute Funded projects		
26.	Investigation of HPAIV (H5NI) Pathogenesis in chicken by metabolomics approach	Apr, 24-Mar, 26	PI: Anamika Mishra ; Co-PIs: A. A.Raut, H.V. Murugkar
27.	Metaviromic profiling of tick population & risk mapping for Ganjam Virus in Madhya Pradesh.	Apr, 23 Mar, 25	PI: P. N. Gandhale; Co-PIs: H.V. Murugkar, K. Rajukumar CCPI: Giridhari Das CC-Co-PI: Rupesh Verma C. Vet. Sci.& A. Hus. NDVSU, Jabalpur
	ICAR Funded Schemes		
28.	Studies on host pathogen interactions and development of vaccine for zoonotic coronaviruses. (ICAR-NASF funded)	June, 21 - May, 24	PI- S. Bhatia; Co-PI's: Richa Sood, Anamika Mishra, D. Senthilkumar, Fateh Singh, Manoj Kumar, AK Pateriya, Naveen Kumar
29.	Network Program on Gene Editing Technology: CRISPR-Cas based point- of-care diagnostic platform for animal diseases – MERS virus	Aug. 24 – Mar, 26	Leader: Pradeep Gandhale, Co-PIs: Senthil Kumar D, Fateh Singh
30.	Network Program on Gene Editing Technology: Development of gene edited chicken with enhanced resilience to avian influenza (H5N1)	Aug. 24 – Mar, 26	CCPI - Anamika Mishra Co-PI's: Ashwin A Raut, Anubha Pathak
31.	Epidemiological studies and development of antiviral therapeutics against Coronaviruses (ICAR-NASF funded)	June, 21 - May, 24	PI- A. A. Raut, Co-PIs: Anamika Mishra, Atul K. Pateriya
32.	ILRI-ICAR Collaborative Proposal - Development of vaccines for prioritized exotic and emerging Diseases - Middle East Respiratory Syndrome (MERS)	Apr 23 – Mar 26	PI : Ashwin A. Raut; Co-PI: Pradeep Gandhale
33.	All India Network Project on ONE HEALTH (AINP-OH)	Aug. 24 – Mar, 26	PI : Ashwin A. Raut; Co-PI: HV Murugkar, Anamika Mishra, PN Gandhale, Naveen Kumar, Anubha Pathak
	Externally Funded Schemes		
34.	NOHM-National network of BSL3/4 Laboratories – Funded by ICMR	Apr, 24 – Mar, 29	PI - Aniket Sanyal; Co-PI's: Ashwin Ashok Rout, H. V. Murugkar

35.	Training cum Workshop on Biosafety for handling and diagnosis of highrisks animal pathogens in ABSL3/BSL3 Laboratories – Funded by NOHM	Aug, 24 – Mar, 25	Course Dir.: Aniket Sanyal Course Coordinators: H V Murugkar, Ashwin A Raut Co-PI's: Anamika Mishra, Manoj Kumar, Atul Pateriya, Anubha Pathak
	Non-division based projects		
	Institute Funded projects		
36.	Subproject I under SCSP: Socio- economic upliftment of the Scheduled Caste farmers by benefiting with substantial inputs and technical support for profitable livestock rearing and animal diseases management	Apr, 24 – Mar, 26	PI - Fateh Singh; Co-PI's: Atul Kumar Pateriya, P.N. Gandhate, S. Kalaiyarasu
37.	Subproject 2 under SCSP: Surveillance of rodent-borne pathogens in synanthropic rats associated with Musahari community of North India	Apr, 24 – Mar, 26	PI - Anubha Pathak; Co-PI's: Ashwin Ashok Rout, H, V, Murugkar, Anamika Mishra

PERSONNEL

Administration		
S.No.	**Name**	**Designation**
1	Dr. Aniket Sanyal	Director
2	Shri Ashish Chobey	Administrative Officer
3	Shri Maithile Sharan Hedau	Finance & Account Officer
4	Shri B.K. Singh	Assistant Administrative Officer
5	Shri Mansing Hansda	Assistant Administrative Officer
6	Shri Ashok Kumar Malviya	Private Secretary
7	Mrs. M. Bilgrami	Assistant (w.e.f: 24th July 2024)

Scientist			
S.No.	**Name**	**Designation**	**Discipline**
1	Dr. H.V. Murugkar	Principal Scientist	Veterinary Public Health
2	Dr. C. Tosh	Principal Scientist	Veterinary Microbiology
3	Dr. N. Mishra	Principal Scientist	Veterinary Microbiology
4	Dr. Sandeep Bhatia	Principal Scientist	Veterinary Microbiology
5	Dr. Ashwin Ashok Raut	Principal Scientist	Animal Biotechnology
6	Dr. K. Rajukumar	Principal Scientist	Veterinary Pathology
7	Dr. S. Nagarajan	Principal Scientist	Animal Biotechnology
8	Dr. G. Venkatesh	Principal Scientist	Animal Biotechnology
9	Dr. (Mrs.) Anamika Mishra	Principal Scientist	Animal Genetics and Breeding
10	Dr. Manoj Kumar	Senior Scientist	Veterinary Pathology
11	Dr. S.B. Sudhakar	Senior Scientist	Veterinary Microbiology
12	Dr. Atul Kumar Pateriya	Senior Scientist	Animal Biotechnology
13	Dr. Pradeep N Gandhale	Senior Scientist	Veterinary Microbiology
14	Dr. S. Kalaiyarasu	Senior Scientist	Veterinary Microbiology
15	Dr. Fateh Singh	Senior Scientist	Veterinary Microbiology
16	Dr. D. Senthil Kumar	SeniorScientist	Veterinary Pathology
17	Dr. Naveen Kumar	Scientist	Veterinary Microbiology
18	Anubha Pathak	Scientist	Veterinary Public Health (w.e.f.22.01.2024)

Technical Staff		
S.No.	**Name**	**Designation**
1.	Shri Sunil Barange	Asst. Chief Technical Officer
2.	Shri R.K. Shukla	Senior Technical Officer
3.	Shri Asanna Badge	Senior Technical Officer
4.	Shri Som Kuwar	Technical Officer
5.	Shri Mahesh Kumar	Technical Officer
6.	Shri Malkhan Singh	Senior TechnicalAssistant
7.	Shri Ram Lakhan	TechnicalAssistant (upto: 31st August 2024)
8.	Shri J.N. Meena	TechnicalAssistant

Supporting Staff		
S.N.	**Name**	**Designation**
1.	Shri Ram Prasad	Skilled Supporting Staff
2.	Shri S.R. Imne	Skilled Supporting Staff
3.	Shri Sitai Prasad	Skilled Supporting Staff
4.	Shri Sita Ram	Skilled Supporting Staff
5.	Shri R.K. Tiwari	Skilled Supporting Staff

PROMOTIONS/TRANSFERS/JOINING/SUPERANNUATION

Promotions

- Mrs. Mehjabeen Bilgrami, Upper Division Clerk, has been promoted as Assistant w.e.f.24th July 2024.

Superannuation

- Shri Ram Lakhan, Technical Assistant, has been superannuated from gracious service on 31st August 2024.

Joining

- Dr. Anubha Pathak, Scientist joined the ICAR-NIHSAD, Bhopal on 22nd January, 2024.
- Shri Veer Singh, Technical-1 has been Joined the ICAR-NIHSAD, Bhopal on 29th April 2024.
- Shri Nasim, Technical-1 has been Joined theICAR-NIHSAD, Bhopal on 8th May 2024.
- Shri Vikram Grewal, Assistant has been Joined theICAR-NIHSAD, Bhopal on 2nd September 2024.
- Shri Himanshu Choudhary, Assistant has been Joined theICAR-NIHSAD, Bhopal on6th September 2024.
- Shri Parvesh Mathur, Assistant has been Joined theICAR-NIHSAD, Bhopal on 22nd October 2024.

Notes

Director
ICAR-National Institute of High Security Animal Diseases
Anand Nagar, Bhopal – 462022 Madhya Pradesh, India
Ph: +91-755-2759204, Fax: +91-755-2758842
Email:director.nihsad@icar.gov.in
Website: www.nihsad.nic.in