

NCDC Newsletter

Quarterly Newsletter from National Centre for Disease Control (NCDC)



Director's Desk



Acute Respiratory infections account for more than two-third of communicable disease burden in India. There are numerous viruses contributing to this public health burden, and these infections remain a priority due to their potential to cause significant death and illness worldwide. The COVID-19 pandemic, in a short span claimed over 5.7 million lives. Even before the pandemic, three respiratory diseases were already among the top 10 causes of death globally. This issue of newsletter captures the respiratory virus landscape and comprehensive review of role of surveillance of respiratory viruses in early detection. This issue also presents diphtheria outbreak investigation conducted by NCDC

Epidemic Intelligence Surveillance Officers (EISOs). The other sections of this issue report various activities carried out by NCDC and its branches during the second quarter of the year like training of government medical colleges in conducting point prevalence survey on ambient use, field epidemiology training of paramedical staff and training on lymphatic filariasis elimination for medical officers. Laboratory section captures diagnostic utility of PCR in leptospirosis. In addition, this issue also captures global disease alerts. We hope that this newsletter has provided you with valuable insights, and updates. Inputs and ideas to improve it further are welcome.

Thematic Area: Respiratory Virus Landscape

Lead Story: Navigating the Respiratory Virus Landscape: What You Need to Know

Contributed by: Dr Simrita Singh¹, Dr. Nidhi Saini², Dr. Harshita Singh³

Peer reviewed by: Dr Purva Pankaj Sakarte², Dr Aarti Tewari²

¹Additional Director, NCDC; ²Joint Director, NCDC; ³DAD, NCDC

Respiratory viruses remain a significant health concern, causing a broad range of illnesses that impact millions globally each year particularly affecting children and vulnerable populations. These viruses, which include influenza, respiratory syncytial virus (RSV), rhinovirus, and newer threats like COVID-19 and avian influenza, cause a wide array of acute and chronic respiratory diseases. These viruses lead to both seasonal outbreaks, like influenza, and more severe public health crises, such as the ongoing COVID-19 pandemic. Additionally, viruses like avian influenza continue to pose emerging threats. In this evolving landscape, it is more critical than ever to understand the risks, transmission modes, and prevention strategies for these pathogens to protect ourselves, our families, and

File No. EpidemiologyDivision/NCDCNewsletter (Computer No. 8199162)

Highlights in this issue

Thematic Area: Respiratory Virus Landscape

Lead Story.....1

- Navigating the Respiratory Virus Landscape: What You Need to Know
- Respiratory Syncytial virus: A Critical Public Health Concern
- Avian Influenza (HPAI H5N1): Sustained Vigilance and Ongoing Monitoring Required

Surveillance Focus11

- Comprehensive Review: Surveillance of Respiratory Viruses and Their Role in Early Detection and Response

Outbreak Section.....15

- Diphtheria Outbreak Investigation in Odisha, June-July 2024

NCDC News.....18

- NCDC trains Government Medical Colleges of Kerala on Antibiotic Use Surveillance
- NCDC conducts Regional Training Programme for Prevention and Control of Communicable Diseases for the Paramedical Personnel of South East Asian region, 22nd April-17th May 2024

Laboratory Section.....20

- Diagnostic utility of PCR in Human Leptospirosis

NCDC Branches21

Global Disease Alert22

NCDC Buzz.....24

our communities. Persistent threats posed by seasonal influenza, newer COVID strains and the emerging danger of avian influenza emphasize the need for continued vigilance.

This article aims to shed light on the landscape of respiratory viruses and offer an overview of respiratory viruses in general with special emphasis on viruses of public health concern in the current context such as Avian Influenza and RSV. As we learn from the past and monitor new threats, understanding these viruses is a crucial step in reducing their impact on our health and well-being.

Respiratory Virus Pathogens

Acute respiratory diseases (ARDs), often caused by respiratory viruses, are among the leading causes of morbidity globally. Viruses like influenza (A and B), parainfluenza, respiratory syncytial virus (RSV), adenovirus, and rhinovirus contribute to the vast majority of ARDs. Influenza A and B are among the most common causes of viral respiratory infections, particularly during colder months. PIV (Parainfluenza Viruses) types 1-3 contribute to respiratory illnesses, especially in young children. Respiratory syncytial virus (RSV) is reported to be a leading cause of severe respiratory illness in infants and young children. Rhinovirus is known to be the main cause of the common cold, but also contributes to more severe respiratory infections. Adenovirus is known for causing both upper and lower respiratory infections.

In addition to these, newer and emerging pathogens such as the coronaviruses SARS-CoV

(2003) & SARS-CoV-2, H5N1 avian influenza, and human metapneumovirus have raised concerns due to their potential to cause widespread illness and hence pose ongoing public health challenges.

Respiratory infections often lead to more severe complications such as chronic obstructive pulmonary disease (COPD) exacerbations and pneumonia. These infections can also lead to complications like acute respiratory distress syndrome (ARDS) and contribute to significant health burdens in both the general population especially in elderly and children and those with underlying conditions such as diabetes, cardiovascular disease, and immunosuppression.

Transmission Modes and Challenges

The transmission of respiratory viruses occurs mainly through four routes: aerosol (fine particles less than 5 µm that can stay airborne and travel longer distances), droplet spray (Larger droplets more than 100 µm which travel short distances of typically less than 2 meters), direct contact, and indirect contact (fomites). Aerosolized particles, smaller than 5 microns, can linger in the air and spread over longer distances, making viruses like influenza, RSV, and SARS-CoV-2 particularly contagious.

The transmission period varies for different viruses, but infected individuals often shed the virus through activities like breathing, coughing, or sneezing. These particles can land on surfaces or linger in the air, making them highly contagious, particularly in enclosed spaces. The evidence for airborne

Virus	Incubation period (days)	Infection period	Mode of Transmission
Influenza Virus	1-4	7 days	Direct Contact, aerosolized droplets
PIV (Parainfluenza Virus)	1-7	1-3 weeks	Direct Contact or aerosolized droplets
RSV (Respiratory Syncytial Virus)	2-8	3-8 days, up to 3-4 weeks in infants	Direct Contact or aerosolized droplets
Adenovirus	2-13	Days to months	Direct Contact or aerosolized droplets
Rhinovirus	2-3	7-10 days	Direct Contact, aerosolized droplets
hMPV (human metapneumovirus)	4-6	Mean of 5 days	Droplets
CoV (non-SARS)	2-4	Not Known	Direct Contact or aerosolized droplets
SARS-CoV	2-10	Not Known	Aerosolized droplets

Table 1: Incubation period and mode of transmission for respiratory viruses

transmission of certain viruses underscores the importance of preventive measures such as masks, social distancing, and proper hygiene in minimizing transmission risk.

The incubation period for respiratory viruses varies from 1 to 10 days, with infection periods lasting from days to several weeks.

Host Factors and Vulnerability

Certain individuals are at a higher risk of severe outcomes from respiratory infections, including children, the elderly, and those with underlying health conditions. For instance, individuals with chronic pulmonary conditions like COPD, or immune impairments, such as those undergoing chemotherapy or with autoimmune diseases, are more susceptible to severe complications from respiratory viruses. Respiratory viruses are responsible for 10–20% of cases of adult community-acquired pneumonia (CAP) and 10–30% of hospital-acquired pneumonia (HAP). In COPD patients, viruses are responsible for approximately 50% of exacerbations, with rhinovirus and influenza being the most common causes.

In addition to aging, chronic conditions like obesity, hypertension, and cardiovascular diseases contribute to immune dysfunction, making individuals more vulnerable to infections and associated complications. These factors increase the risk of ICU admission, prolonged hospitalization, and even death.

Diagnostic and Sequencing Innovations

Accurate and timely diagnostics are vital in managing respiratory infections. Molecular diagnostic techniques, such as Nucleic Acid Amplification tests (NAATs), are now essential tools for identifying respiratory viruses, including emerging pathogens. These tests allow for the rapid and accurate detection of viruses, reducing unnecessary antibiotic use and guiding antiviral treatment.

Multiplex PCR testing, which can detect multiple viruses simultaneously, has further revolutionized diagnostic capabilities. As part of an integrated approach, sequencing respiratory viruses is critical for tracking viral mutations, understanding transmission dynamics, and improving vaccine

and treatment development.

High-throughput sequencing technologies are helping scientists monitor viral evolution, identify emerging strains, and respond to outbreaks. In the case of COVID-19, genomic surveillance of variants like Omicron and Delta has been key to predicting disease spread and assessing the impact on vaccine efficacy. Sequencing also provides valuable insights into virus-host interactions, helping to inform public health measures and the development of effective interventions.

Prevention Strategies: Vaccination and Hygiene

Vaccination remains the cornerstone of prevention against several respiratory viruses. Vaccines for influenza and COVID-19 have proven to be crucial in preventing severe disease, hospitalization, and death. Vaccines for emerging viruses like avian influenza are also important for mitigating potential threats along with close surveillance.

In addition to vaccination, hygiene measures such as hand washing, mask-wearing, and maintaining physical distance play vital roles in reducing transmission, particularly in crowded or healthcare settings.

Continuous surveillance of viral infections especially by adopting **One Health approach** with special emphasis on animal-human interface through molecular techniques and real-time data sharing ensures timely responses to outbreaks. International collaborations, such as those through Global Initiative on Sharing All Influenza Data (GISAID), facilitate global tracking of viral genomes, enabling quicker identification of variants of concern.

Conclusion

As respiratory viruses continue to evolve, staying informed about their characteristics, transmission methods, and prevention strategies is crucial. With global collaboration, advanced diagnostics, and vaccination efforts, we can mitigate the impact of these viruses on public health. Through ongoing research and monitoring, particularly with advancements in sequencing technologies, we are better equipped to respond to both current and emerging respiratory threats. Public health efforts, improved healthcare infrastructure, and individual protective measures will be essential in navigating

the complexities of the respiratory virus landscape to take proactive steps in safeguarding our health and protect ourselves and our communities from the continuing risks posed by these formidable pathogens.

Respiratory Syncytial virus: A Critical Public Health Concern

Contributed by: Dr Simrita Singh¹, Dr. Nidhi Saini², Dr. Harshita Singh³

¹Additional Director, NCDC; ²Joint Director, NCDC; ³DAD, NCDC

Respiratory Syncytial Virus (RSV) is a leading cause of hospitalization due to acute lower respiratory infections, particularly in infants and young children. Since its discovery in 1956, RSV has become a major cause of morbidity and mortality, especially in infants under six months. It is the leading cause of childhood acute respiratory infections and hospitalizations. In recent decades, it has been realized that it also afflicts various at-risk adults, including frail elderly and immunocompromised persons. Additionally, RSV is often underrecognized as a cause of severe acute respiratory infection (SARI) in older adults, who are more commonly diagnosed with influenza or COVID-19.

In resource-poor settings, it is an important cause of death due to lower respiratory tract infection, second only to pneumococcal pneumonia and H. influenzae type B. Resource-limited countries have more than twice the incidence severe disease seen in developed countries and, remarkably, 99% of the global deaths caused by RSV infection. Severe RSV infections can lead to long-term respiratory issues, such as wheezing and inflammatory airway disease. Advances in diagnostics, such as real-time PCR, enable early detection and better epidemiological tracking. Current prevention options, like Palivizumab, are limited to high-risk groups in wealthy settings. New vaccines and treatments could significantly reduce the global burden of RSV, particularly in areas with limited healthcare access by protecting the vulnerable population i.e young children, older adults, and pregnant women,

Recently, significant progress has been made in the

development of a range of RSV vaccine candidates, in particular for the protection of infants via maternal immunization. In addition, new longer acting monoclonal antibodies that can protect children for several months are in late-stage clinical development. Accurate estimates of RSV-related health burden including costs are needed to undertake economic evaluations comparing the cost-effectiveness of alternative interventions.

The World Health Organization (WHO) established an RSV surveillance pilot study in 2017 in fourteen countries from each WHO region, building on the Global Influenza Surveillance and Response System (GISRS). The WHO RSV surveillance project, based on GISRS and implemented in 25 countries across all six WHO regions from 2016 to 2023, aimed to generate evidence on RSV seasonality, risk factors, spread and evolution, along with basic hospitalization proportion estimates. The Global Vaccine Alliance (GAVI) prioritized conditional support for potential RSV vaccine products in its Vaccine Investment Strategy from 2018 to 2023. In light of ongoing efforts for the imminent licensure and availability of RSV vaccine products, it is crucial to generate country-level estimates of RSV disease burden based on surveillance in infants and young children. WHO recommends that countries must now develop sustainable surveillance strategies to monitor influenza, SARS-CoV-2, respiratory syncytial virus (RSV) and other respiratory viruses of epidemic and pandemic potential.

Epidemiology:

Respiratory Syncytial Virus (RSV) is a significant global health issue, particularly for infants, young children, and at-risk adults. It is the leading cause of pneumonia and bronchiolitis in infants. The global incidence of RSV-associated lower respiratory tract infections is estimated at over 30 million cases in children under the age of five, resulting in 3.2 million hospitalizations and over 60,000 deaths annually. By 18 months, 87% of children have antibodies to RSV, and nearly all children have been infected by age 3. In the USA, RSV accounts for 20% of ARI hospitalizations in children under 5, with the highest mortality risk in those under 6

months.

RSV epidemics are seasonal in temperate regions, peaking in winter, while tropical areas experience year-round outbreaks, especially during the rainy season. Cold weather increases viral transmission due to indoor crowding and greater viral stability. Children at higher risk for severe RSV include those with low birth weight, prematurity, and underlying health conditions. Environmental factors, such as tobacco smoke and low socioeconomic status, also contribute to vulnerability.

Adults, especially the elderly and those with chronic diseases or immunocompromised states, are more likely to suffer severe illness. According to Centers for Disease Control and Prevention, RSV is responsible for an estimated 60,000 - 160,000 hospitalizations and 6,000 - 10,000 deaths annually among US adults aged ≥ 65 years.

Immunocompromised individuals, such as HIV-infected children and those who have undergone stem cell transplants, are especially prone to severe RSV infection, with HSCT patients experiencing high mortality rates (up to 83% in severe cases). Key factors affecting severity include age, gender, and graft-related issues.

RSV presents a major health burden globally, emphasizing the need for preventive measures and early intervention, particularly for vulnerable populations.

Virology of Respiratory Syncytial Virus (RSV):

RSV is a negative-sense, single-stranded RNA virus belonging to the Pneumoviridae family, genus Orthopneumovirus. It has a 15.2 kb genome encoding 11 proteins, with two major surface glycoproteins: G (attachment protein) and F (fusion protein), which are crucial for viral attachment and entry into host cells.

RSV is classified into two antigenic subgroups, RSV-A and RSV-B, based on the reactivity of the G and F proteins to monoclonal antibodies. These subgroups further diverge into 16 genotypes for RSV-A and 22 genotypes for RSV-B, with variability mainly in the G protein's hypervariable region (HVR2). Subgroup A viruses tend to be more virulent, replicating to higher titers than

subgroup B.

Viral Structure and Replication: RSV particles are pleomorphic, with both spherical and filamentous forms. The virion surface proteins F, G, and SH are involved in viral attachment and fusion. The G protein binds to host glycosaminoglycans (GAGs), and the F protein facilitates fusion with the host cell. After fusion, the viral nucleocapsid is released into the host cytoplasm, where RNA replication occurs. The L protein, an RNA-dependent RNA polymerase, facilitates transcription and replication. The M protein coordinates the assembly of new virions, and M2 proteins are involved in regulating transcription.

RSV can generate both spherical and filamentous virions, with filamentous forms exhibiting a helical assembly of matrix (M) proteins, crucial for infectious particle formation.

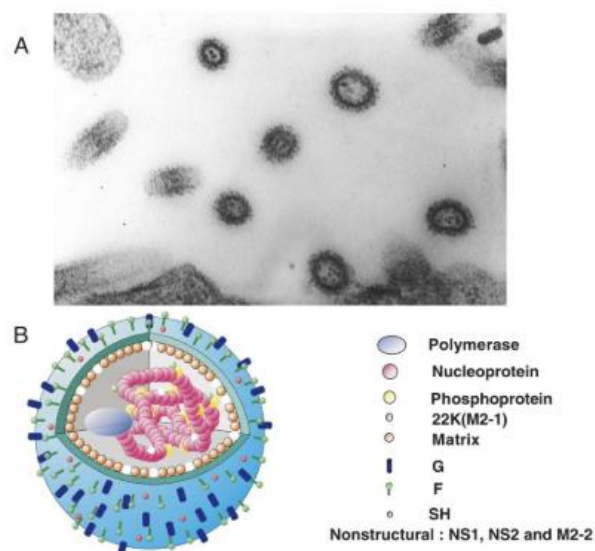


Fig 1: (A) Electron Microscope (B) Schematic Diagram of RSV virion

Reference: Respiratory Syncytial Virus (RSV) by Patricia Cane

Genetic Diversity: RSV has only one serotype, but is divided into 45 genotypes based on genetic differences in the G protein. Genotypes like ON1 (RSV-A) and BA9 (RSV-B) have dominated recent outbreaks, including in China. Different RSV genotypes exhibit varying levels of pathogenicity, and during epidemics, one genotype typically predominates, although multiple genotypes can co-circulate.

F protein variability affects disease severity and may impact monoclonal drugs and vaccine efficacy. Genetic changes in the G protein of RSV-A and

RSV-B have enabled immune evasion, leading to the dominance of RSV-A ON1 and RSV-B BA genotypes.

Clinical features and pathogenesis:

RSV is highly contagious and spreads through direct contact or inhalation, with an incubation period of 2–8 days. It survives on surfaces, aiding transmission. The virus infects ciliated epithelial cells in the upper and lower respiratory tract, especially in the bronchioles, and can also affect basal cells, influencing airway development.

Infection causes inflammation, epithelial damage, mucus overproduction and airway obstruction due to epithelial sloughing and immune cell buildup. Syncytia may form, particularly in immunocompromised patients. Severe disease likely results from a specific viral strain interacting with a host's adverse immune response, though this is not fully understood.

RSV infection ranges from mild upper respiratory illness to severe lower respiratory tract involvement like bronchiolitis, pneumonia, and croup. 15-50% of infants develop LRTI, with 1-3% needing hospitalization, especially infants 2-6 months old. Reinfections are common, occurring in 30-75% of children under 2, and are usually less severe with subsequent exposures.

Diagnosis is primarily clinical, with chest X-rays used when needed. RT-PCR is increasingly used for virus detection, improving identification of RSV and other viruses like hMPV. Genomic surveillance tracks RSV genetic and antigenic variability, which impacts seasonality, outbreaks, and vaccine development. Variations in the F protein affect disease severity, while changes in the G protein enable immune escape, leading to dominant new RSV genotypes like ON1 and BA9.

Treatment of RSV:

For severe bronchiolitis, treatment mainly involves supportive care (nasal suction, fluids, oxygen, feeding). Ribavirin is used for severe cases, especially in immunocompromised patients such as lung transplant patients and others with hematological diseases, but not recommended for healthy children.

Palivizumab, approved for RSV prevention in high-risk infants, has been studied for treatment, but its role in acute infection is still being explored.

Role of surveillance and lab testing:

Global genomic surveillance of hRSV helps understand its variability, seasonality, outbreaks, and helps in obtaining accurate RSV disease burden estimates which are crucial for policy-making and evaluating new vaccines or monoclonal antibodies. The WHO RSV Surveillance strategy aims to test the feasibility of leveraging the Global Influenza Surveillance and Response System platform for RSV surveillance without adversely affecting the well-established ILI and SARI surveillance of influenza

NAATs (like rRT-PCR) are highly sensitive for detection, while antigen tests offer quicker but less sensitive results. Genomic surveillance of the hRSV at the global level is important to improve the understanding of; antigenic and genetic variability of circulating strains, implications on seasonality and outbreaks, transmission dynamics, monoclonal therapies and vaccine development. The development of RSV vaccines and drugs is based on the understanding of RSV epidemic genotypes and their sequence variation. Several vaccines and drugs related to RSV are being studied, mainly targeting the G and F proteins, and a few involving other proteins.

Conclusion:

RSV remains a significant cause of illness and death in children, with potential long-term consequences. Its impact on the elderly is often overlooked, as clinicians tend to focus on influenza or COVID-19, especially in regions where RSV research is limited. The absence of effective treatments or vaccines, with Palivizumab being the only approved immunoprophylaxis for high-risk children, is a major concern. Nevertheless, global efforts to include RSV in broader respiratory virus surveillance, along with progress in understanding its epidemiology, diagnostics, and antiviral development, offer optimism. Continued research, clinical trials, and exploration of combined antiviral therapies are essential to enhance treatment effectiveness and reduce resistance.

Avian Influenza (HPAI H5N1): Sustained Vigilance and Ongoing Monitoring Required

Contributed by: Dr Simrita Singh¹, Dr. Nidhi Saini², Dr. Harshita Singh³

¹Additional Director, NCDC; ²Joint Director, NCDC; ³DAD, NCDC

Introduction: The Highly Pathogenic Avian Influenza (HPAI) H5N1 virus remains a significant concern for both animal and human health. Since its emergence in 1996, the virus has spread globally, causing devastating outbreaks in poultry, with widespread economic consequences, particularly in developing nations.. Although its potential for causing a human pandemic is uncertain, the virus poses a serious risk given its ability to evolve and hence its control remains a global priority. While its impact on wildlife and ecological balance remains understudied, it is an important aspect that needs requires attention due to its far-reaching consequences.

The H5N1 virus is a segmented RNA virus that exhibits considerable morphological variability, ranging from spherical particles approximately 80–120 nm in diameter to long, filamentous forms extending several microns in length. This variability plays a role in the virus's ability to infect different species and adapt to various environments.

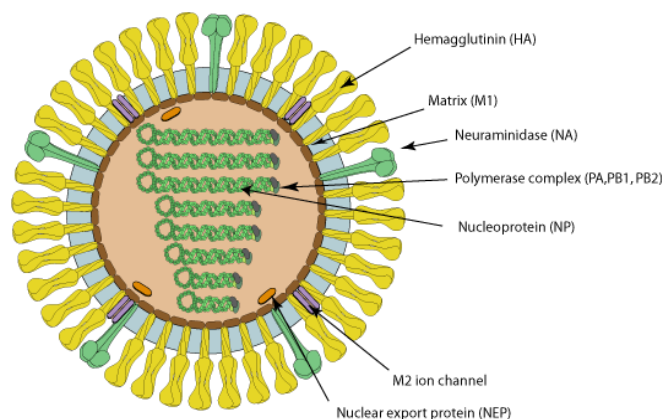


Fig 1: Morphology of H5N1 subtype of Influenza A

Current Scenario: HPAI H5N1 is a subtype of influenza A that primarily infects birds but can occasionally infect mammals, including humans. Since its first emergence in 1996, H5N1 has caused severe outbreaks in poultry and has been transmitted to mammals, including humans. So far, more than 950 cases of H5N1 bird flu have been reported to the [World Health Organization](https://www.who.int/); about half of those have resulted in death. The H5N1 avian influenza virus has undergone genetic diversification since 2005, forming several

genotypes. In 2020, HPAI A(H5N1) clade 2.3.4.4b viruses emerged from A(H5Nx) strains, spreading via migratory birds across Africa, Asia, and Europe, causing significant wild bird deaths and poultry outbreaks. The virus reached North America in 2021 and South America by 2022. Since then, A(H5N1) has been detected in wild and domestic mammals, including recent cases in U.S. livestock. Most cases involve clade 2.3.4.4b, though regional variants exist. Although human infections remain rare, they tend to be severe, with a high fatality rate. The virus is not easily transmitted between humans, with infections typically linked to close contact with infected animals or contaminated environments. The global public health risk remains low, but the potential for future human-to-human transmission cannot be ruled out, especially if the virus mutates into a more transmissible form. Studies on strains from mammalian hosts have shown genetic mutations changes in the PB2 gene (e.g., Q591K and D701N) associated with increased adaptability and better replication in mammals.

Animal Infections: In recent years, H5N1 has expanded its host range, infecting a broader spectrum of animals, including wild mammals, domestic pets such as cats and dogs, marine mammals, and even cattle. Mass die-offs in wild bird populations and infections in carnivorous mammals have raised ecological concerns. Analyses of sequence data of viruses from infected dairy cows has suggested a bird-to-dairy cow transmission event of a B3.13 genotype A(H5N1) virus that occurred in late 2023 or early 2024. Transmission in cattle, particularly through contaminated milking equipment and shared farming tools, is currently being studied.

Human Infections: Human cases of H5N1 remain sporadic, with infections typically linked to direct contact with infected poultry or other animals. From 2021 to 2024, the World Health Organization (WHO) has reported around 100 confirmed human cases of H5N1 infection, with 17 linked to clade 2.3.4.4b and detected in countries including China, Chile, Ecuador, Spain, the UK, and the USA.

Cambodia reported 13 infections in 2023, primarily linked to clade 2.3.2.1c, with one fatality in Vietnam in 2024. Australia reported a travel-associated case in early 2024 with clade 2.3.2.1a. Most human cases in Europe and North America were asymptomatic or mild, except one in China, one in Canada, and one fatal case in Louisiana, US which had symptoms ranging from fatigue and mild respiratory issues to severe pneumonia and death. Exposure to infected animals was common, either through direct contact or outbreak response. Partial viral genome data indicates that the virus belongs to the D1.1 genotype related to highly pathogenic H5N1 viruses recently detected in wild birds and poultry in the United States. This avian influenza A(H5N1) virus genotype is different from the B3.13 genotype spreading widely and causing outbreaks in dairy cows, poultry, and other animals, with sporadic human cases in the United States.

Transmission of Avian Influenza (H5N1)

Avian Influenza (H5N1) primarily spreads through direct contact with infected birds or contaminated environments. Early studies suggested that the virus persists in waterfowl through transmission from adult to juvenile birds at lakes. Infected ducks shed large amounts of the virus in their faeces, contaminating water sources like lakes and ponds, where the virus can remain infectious for up to 4 days at 22°C and over 30 days at 0°C. The epidemiology of H5N1 has evolved, with transmission shifting from primarily faecal/oral routes to respiratory transmission, particularly in land birds, increasing the risk of spread to mammals, including humans.

Vaccine Development and challenges: While vaccines against HPAI exist, they provide partial immunity and do not guarantee complete protection from infection. Vaccinated birds can still carry and transmit the virus, which complicates surveillance and detection. Furthermore, vaccination programs can contribute to the emergence of vaccine-resistant strains. Given these challenges, current strategies prioritize surveillance, culling, and movement control, with vaccination seen as a secondary tool.

However, there is ongoing research into developing more effective vaccines.

The WHO, in collaboration with organizations like the FAO and WOA, continues to assess candidate vaccine viruses for H5N1. In India, ICAR-NIHSAD has made progress in developing an indigenous vaccine for HPAI, and ICMR is exploring cell-culture-based vaccines for human use.

Salient Actions for Prevention and Control

Countries should take several measures to mitigate the spread of H5 influenza viruses:

- **Enhance Surveillance:** Increase monitoring of both domestic and wild bird populations for early detection of A(H5) viruses. Surveillance should include non-avian species, especially those in high-risk environments such as livestock, and must be integrated into both national and global health networks. :
- **Surveillance at human-animal interface:** Countries should continue surveillance for human and animal health, using a standardized case definition and conducting active case finding, particularly in regions with known outbreaks of H5N1. Information sharing between animal and human health sectors is essential for rapid joint risk assessments.
- **Reporting and Data Sharing:** Promptly report outbreaks of HPAI in all species to international organizations such as WOA, FAO, and others. Genetic sequences of avian influenza viruses and associated data should be shared through public databases to aid global surveillance efforts.
- **Biosecurity Measures:** Implement strict biosecurity protocols at all levels of the animal production chain to prevent the introduction and spread of AI. This includes good hygiene practices when handling animal products and ensuring proper protection for personnel working with animals by wearing appropriate personal protective equipment (PPE).
- **One Health Approach:** Apply a One Health strategy that integrates human, animal, and environmental health. Increased vigilance through serological studies and epidemiological investigations in high-risk populations will help assess the zoonotic risk. National Influenza Centres (NICs) and other

influenza laboratories should work collaboratively to monitor zoonotic infections and provide timely risk assessments.

National Preparedness: India's Strategy

India's approach to Avian Influenza includes several key components reference The National Action Plan for Prevention, Control, and Containment of Avian Influenza in India.

- *Surveillance: Routine and targeted surveillance systems are in place to detect outbreaks early, including in migratory birds and poultry populations. These efforts are aimed at preventing the spread of AI and minimizing its impact.*
- *Response Actions: Immediate measures include culling infected poultry, restricting movement, and destroying contaminated materials to contain outbreaks.*
- *Laboratory support: Diagnostic support is provided by regional and national laboratories, including NIHSAD, CDDL, and others, which assist in confirming outbreaks and guiding control efforts.*
- *Public awareness: Information Education Communication (IEC) activities are conducted through various media channels to raise public awareness about Avian Influenza and the necessary precautions.*
- *Human Health Preparedness: The human health sub-component is focused on pandemic*

preparedness, with continuous monitoring through passive and active surveillance

- *systems led by ICMR and IDSP. Real-time data is available through the IHIP portal for quick response.*

India's government has also organized high-level discussions, such as those led by the Department of Animal Husbandry & Dairying, to coordinate efforts across sectors. The One Health approach is at the core of these discussions, emphasizing the importance of cross-sector collaboration between animal health, human health, and environmental experts to better control and prevent Avian Influenza outbreaks. India also has its own pandemic preparedness plan for respiratory pathogens and contingency plan for management of human cases of Avian influenza.

The Role of Surveillance in Avian Influenza Control

India's poultry sector is vital for both food and nutritional security. However, recurrent outbreaks of HPAI, especially those caused by the evolving H5N1 virus, present significant challenges to the sector's growth and its export potential. The One Health approach stresses the importance of integrated surveillance systems at the human-animal-environment interface. Migratory bird flyways in India further necessitate robust surveillance efforts, particularly during the winter season when the risk of AI introduction is high.

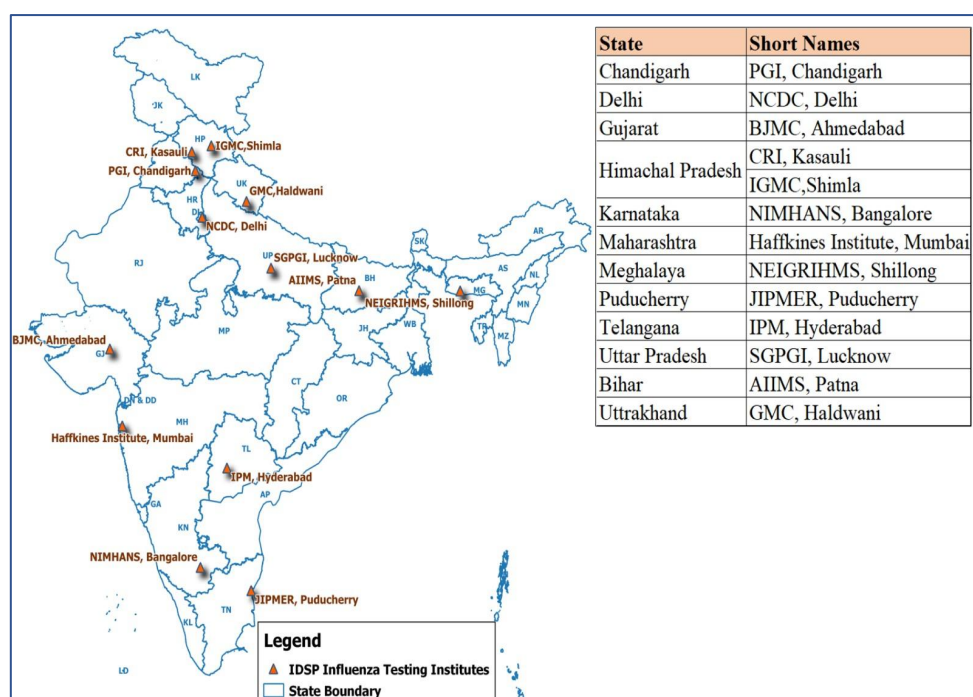
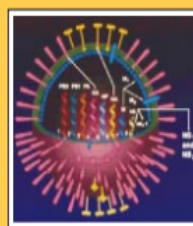


Figure 2: IDSP Lab network for influenza surveillance in India

Environmental surveillance is gaining prominence as an effective early detection strategy. Research initiatives by ICMR, NIV, and CCMB are exploring low-cost methods for monitoring AI in water bodies, wastewater, wet markets, slaughterhouses, and poultry farms. Early detection through environmental sampling, including wastewater screening, has shown promise in identifying the virus before it spreads widely. The currently existing human surveillance laboratory networks under ICMR-VRDLs and IDSP-IHIP and NIC ensure continuous vigil on any possibility of avian Influenza human cases via passive and active surveillance (including laboratory based) and in real time basis on the IHIP portal. Laboratory technique used for diagnosis of H5N1 is Realtime PCR method and sequencing of the full genomes of viruses detected in human and animal cases.

Conclusion: While the immediate global health

risk of H5N1 remains low, the virus's ability to spread among animals, particularly migratory birds and mammals, and its potential for mutation into a more transmissible form makes ongoing surveillance and vigilance essential. The virus's spread into new animal populations and the recent cases in humans underscore the need for continued research and preparedness. A "One Health" approach, integrating human, animal, and environmental health efforts in a comprehensive and coordinated manner is crucial for effectively managing the risks posed by H5N1 and preventing future outbreaks. India's National Action Plan outlines key strategies such as enhanced surveillance, prompt outbreak response, and biosecurity measures. Continued research into vaccines and environmental surveillance and enhanced global cooperation, including the sharing of surveillance data and research findings, remains critical in addressing the evolving threat of Avian Influenza to cause widespread outbreaks / pandemic.



Contingency plan for management of human cases of Avian Influenza

Model Agency
National Institute of Communicable Diseases
(NICD)
22 Shom Nath Marg, Delhi 110054



Directorate General of Health Services
Ministry of Health and Family Welfare
Govt. of India
Nirman Bhavan, New Delhi



December 2005

Directorate General of Health Services
Ministry of Health and Family Welfare
Govt. of India
Nirman Bhavan, New Delhi

Surveillance Focus

Comprehensive Review: Surveillance of Respiratory Viruses and Their Role in Early Detection and Response

Contributed by: Dr. Simrita Singh¹, Dr. Nidhi Saini², Dr. Harshita Singh³, Mrs. Suman Gupta⁴

¹Additional Director, NCDC; ²Joint Director, NCDC; ³DAD, NCDC; ⁴ARO, NCDC

Introduction

Respiratory viruses, including influenza, coronaviruses, respiratory syncytial virus (RSV), and rhinoviruses, pose significant threats to global public health, particularly among vulnerable populations such as children, the elderly, and immunocompromised individuals. Surveillance of these viruses plays a crucial role in early detection, guiding timely public health responses, and preventing widespread outbreaks. Effective surveillance systems can mitigate the risks associated with respiratory viruses, inform vaccination strategies, and enhance healthcare preparedness. This review discusses the key aspects of respiratory virus surveillance, its role in early detection and response, the challenges faced, and the importance of global collaboration.

Background

Respiratory infections, particularly lower respiratory infections (LRI), remain the leading cause of death due to communicable diseases globally. According to the World Health Organization (WHO), acute lower respiratory infections (ALRI) contribute to approximately 6.1% of all global deaths. Viral infections, such as influenza and respiratory syncytial virus (RSV), are major contributors to ALRI, especially among children and the elderly. Influenza alone affects 5-10% of the global population annually, causing an estimated 650,000 deaths. The increasing burden of respiratory viral infections underscores the need for robust surveillance systems to detect and respond to these threats.

Role of Lab Networks in Surveillance of Respiratory Viruses

The integration of laboratory networks in respiratory virus surveillance is essential for timely detection and control. In India, the laboratory network initially established for avian influenza surveillance has evolved to tackle pandemic

influenza (H1N1), RSV, and other respiratory viruses.

The Early Response to Avian Influenza and Pandemic Influenza

India's laboratory network was first utilized for surveillance of avian influenza (AI) following global outbreaks, particularly after the H5N1 strain was detected in 2006. The network became crucial in monitoring the potential for human infection, particularly after the H1N1 pandemic in 2009, when the Integrated Disease Surveillance Program (IDSP) and the National Institute of Virology (NIV) were activated to conduct nationwide surveillance for influenza and other emerging respiratory viruses. **H1N1 Influenza Surveillance:** The first H1N1 case in India was reported in May 2009, a month after the outbreak in Mexico. India's laboratory network was promptly mobilized to conduct diagnostic testing and confirm cases. In addition to monitoring human cases, the network extended its surveillance to detect any new viral strains circulating in poultry and wild birds, preventing wider transmission to humans.

Current Role of Laboratory Networks in India

India has a well-established three-tiered laboratory network under the Integrated Disease Surveillance Program (IDSP) that supports the surveillance of over 40 epidemic-prone diseases. It includes the Central Surveillance Unit (CSU), State Surveillance Units (SSU), and District Surveillance Units (DSU). Surveillance is further strengthened through the Integrated Health Information Platform (IHIP), which facilitates near-real-time reporting of data on disease cases, including influenza-like illness (ILI) and severe acute respiratory infections (SARI).

- The ICMR, through its Virus Research and Diagnostic Laboratories (VRDLs), actively monitors influenza viruses, using PCR testing and genome sequencing to detect viral strains in human and animal cases.

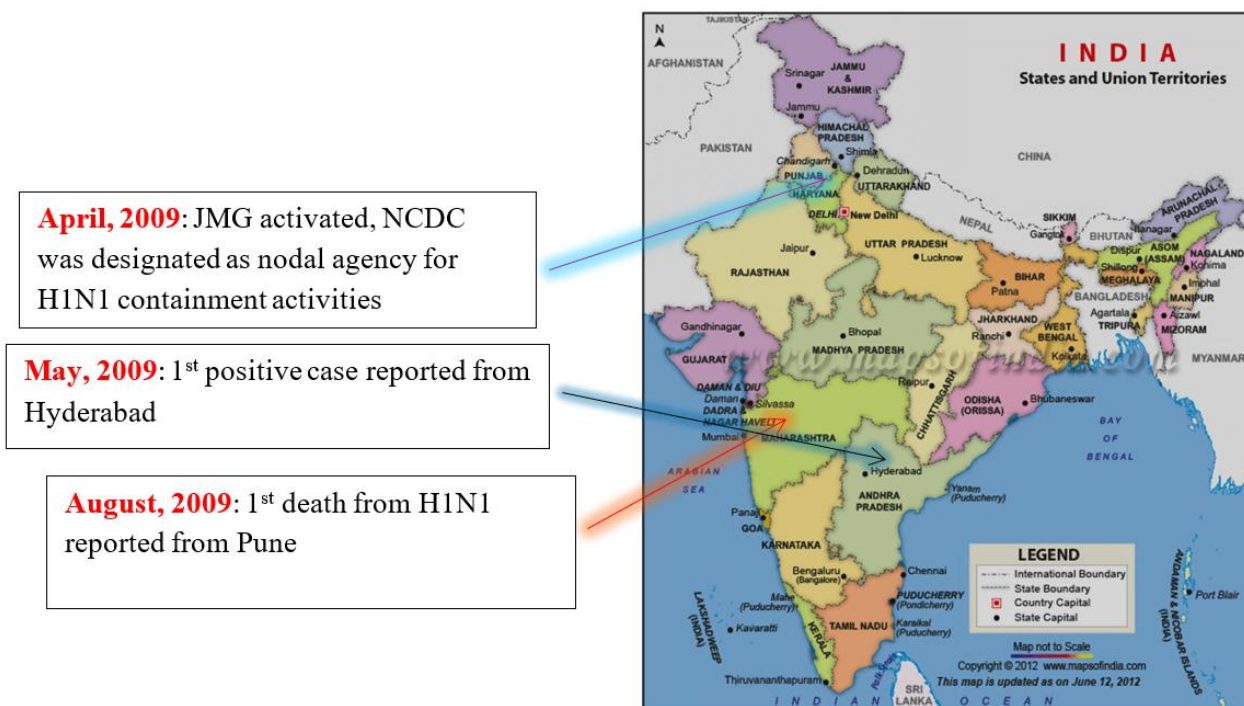


Figure 1: Effect of Influenza H1N1pdm 2009 in India

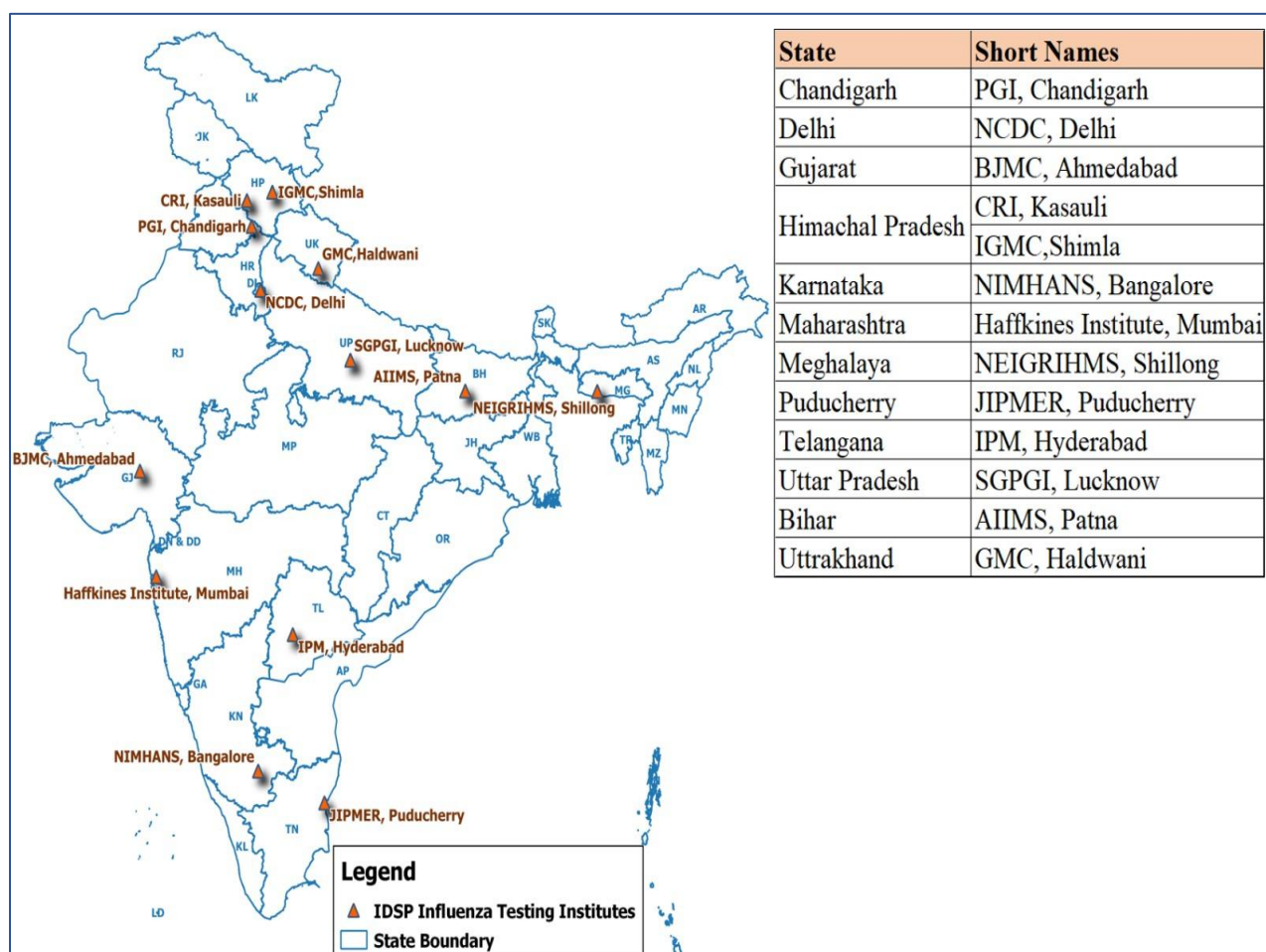


Figure 2: IDSP Lab network for influenza surveillance in India

- Under IDSP lab network for influenza surveillance in India, NCDC lab carries out surveillance testing of suspected cases of Influenza from designated sentinel sites as

Nodal lab under the Influenza Surveillance network program of IDSP and co-ordinates with the 12 network labs spread across India for influenza surveillance tests. The lab network is under process

for expansion of surveillance to other important respiratory viruses including RSV, Adenoviruses and human metapneumovirus. The laboratory network uses Realtime PCR to diagnose avian influenza and influenza strains such as H1N1 and H3N2. Additionally, the sequencing of viral genomes provides insights into mutations, helping to track the virus's evolution and informing vaccine development. Preliminary results of sequencing studies carried out with the assistance of Biotechnology division on samples received and tested by Respiratory viruses laboratory NCDC suggest that these strains are similar to the circulating vaccine strains.

- **Environmental Surveillance:** Environmental surveillance has become an important tool in early detection of respiratory viruses, particularly in monitoring water bodies, wastewater, and poultry farms. The One Health approach integrates animal, human, and environmental health data to prevent the spread of avian influenza and other viruses. Environmental sampling, including wastewater screening, has proven effective in detecting viral infections before they spread widely among humans.

Surveillance of Respiratory Syncytial Virus (RSV)

Human respiratory syncytial virus (hRSV) is a significant pathogen, particularly in infants, young children, and the elderly. RSV is a leading cause of hospitalization for respiratory infections in young children and can lead to severe illness in older adults. Genomic surveillance of RSV is crucial for understanding its variability, seasonality, and patterns of outbreaks, all of which are vital for guiding vaccine and antiviral therapy development.

Diagnostic Methods for RSV: NAATs (Nucleic Acid Amplification Tests), particularly rRT-PCR, are the most sensitive diagnostic tests for RSV. Antigen-based rapid tests provide quicker results but are less sensitive than PCR. Some tests can differentiate between RSV subtypes, although the clinical significance of these differences remains unclear.

Challenges in RSV Surveillance

RSV surveillance presents several challenges due to the variability in clinical presentation, especially in infants and the elderly. Infants under six months of age may present with apnea or sepsis, while many infected individuals, particularly older adults, may not present with fever, making it difficult to standardize definitions for RSV cases. Additionally, some RSV subtypes (A and B) show variability in their ability to cause disease, which complicates the interpretation of surveillance data.

Strengthening Surveillance Systems: India's Preparedness

India has made significant strides in strengthening its surveillance systems for respiratory viruses, particularly through the integration of laboratory networks and public health initiatives. India is committed for Integrated surveillance with aim for expanding the existing ongoing surveillance activity for COVID-19 and Influenza to include other crucial respiratory viruses of public health importance like RSV and Adenovirus in line with the Global e-GISRS initiative.

- **National Pandemic Preparedness Plan:** The Indian government has developed a National Pandemic Preparedness Plan for respiratory viruses. This plan aligns with the PRET Framework (Preparedness, Response, and Emergency Training) and the 5Cs (Collaboration, Communication, Coordination, Capacity Building, and Contingency Planning). The plan provides a roadmap for preparedness during different phases, including pre-pandemic surveillance, outbreak detection, and post-pandemic recovery.
- **Epidemiological and Virological Surveillance:** The IDSP Influenza Surveillance network and the ICMR-VRDL network (Virus Research and Diagnostic Laboratories) contains laboratories spread across India. IDSP lab network lab is linked to 3 sentinel sites (OPD for ILI cases and IPD for SARI cases) for influenza surveillance. These sites collect samples from individuals presenting with ILI and SARI. The three-tiered laboratory network ensures quality control, mentoring, and technical support.

- **Real-time Surveillance:** The IDSP-IHIP portal has allowed India to transition from paper-based reporting to near-real-time surveillance. This system integrates data from 179,423 reporting units, providing an overview of ILI and SARI cases, helping public health authorities track outbreaks and allocate resources efficiently.

Nevertheless, there are many challenges faced in surveillance like in data sharing and co-ordination, reporting issues, resource limitations, and acquiring optimal quality data etc.

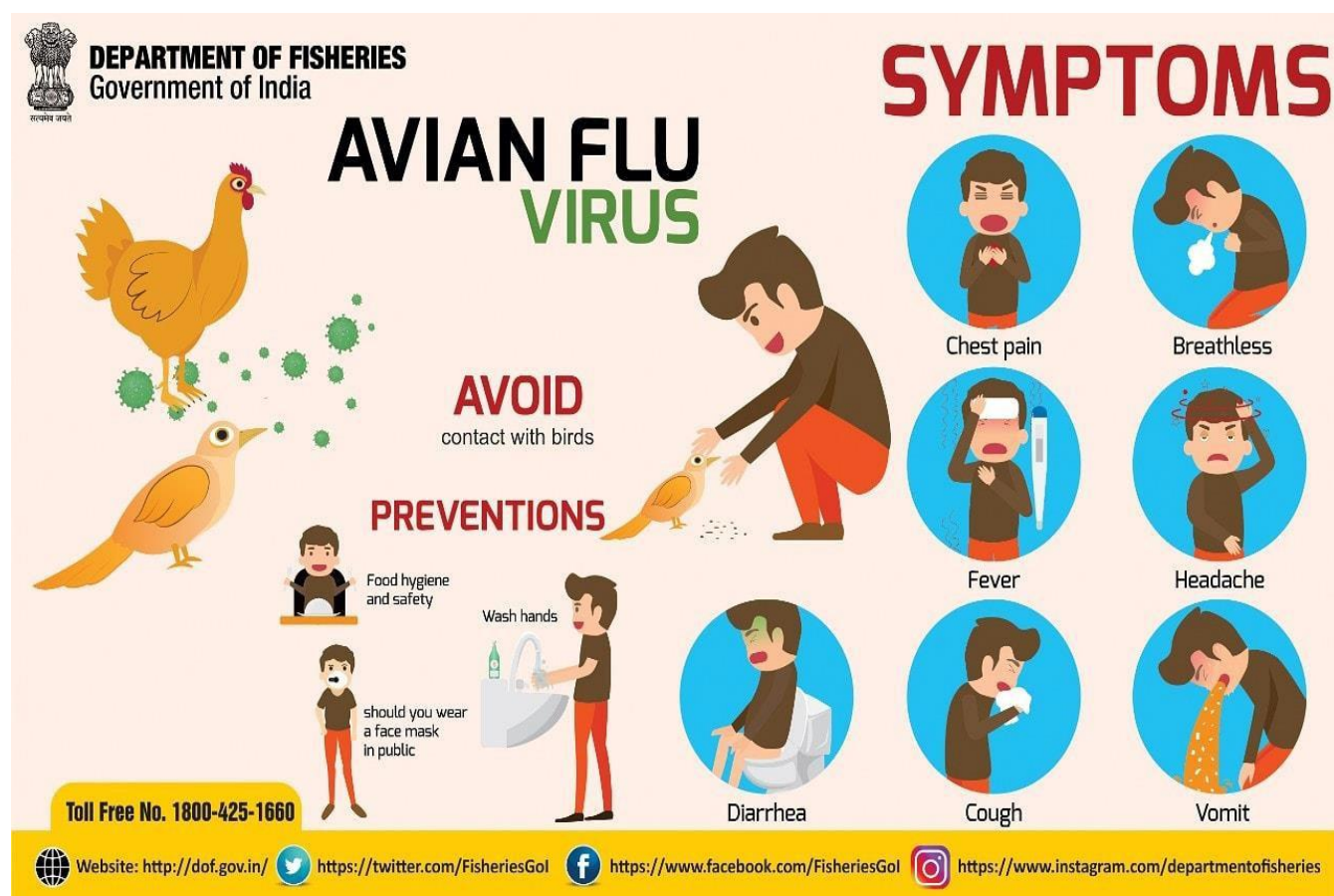
Global Collaboration

Surveillance of respiratory viruses is most effective when integrated into global networks. Global Influenza Surveillance and Response System (GISRS) and GISAID play crucial roles in sharing viral samples, genomic sequences, and

epidemiological data. These networks enable coordinated efforts to monitor and control the spread of respiratory viruses, facilitating early detection and rapid responses.

Conclusion

Surveillance of respiratory viruses is essential for global health security. It facilitates the early detection of outbreaks, informs public health responses, and helps mitigate the impact of infectious diseases. Strengthening surveillance systems, enhancing global collaboration, and adopting innovative diagnostic technologies will improve our ability to detect and control respiratory viruses. As demonstrated by India's robust response to respiratory viruses through its integrated surveillance systems, preparedness, and laboratory networks, countries can build resilience to future pandemics, saving lives and reducing the social and economic impacts of infectious diseases.



Outbreak Section

Diphtheria Outbreak Investigation in Odisha, June-July 2024

Contributed by: Dr Arushi Ghai¹, Dr Arti Nareda², Dr Satyajit¹, Dr Sushma Choudhary³, Dr Debdutta Bhattacharya⁴, Dr Ashish Chakraborty⁵, Dr Ramesh Chandra⁶

¹EIS Officer, NCDC, ²Consultant Epidemiologist, IDSP, NCDC, ³SAFETYNET India, ⁴Scientist E, ICMR-RMRC, Bhubaneswar, ⁵Public Health Specialist Grade 1 Immunization Div, MoHFW, ⁶Joint Director, NCDC

Introduction

Diphtheria, is a vaccine-preventable disease caused by toxigenic strains of *Corynebacterium diphtheriae* and primarily causes acute infectious disease of upper respiratory system. It was a significant cause of morbidity and mortality in children in the pre-vaccination era. Although global vaccination efforts have significantly reduced its incidence, diphtheria remains a public health concern, particularly in populations with suboptimal vaccination coverage. Diphtheria is characterized by the formation of a thick, greyish pseudo membrane in the throat and/or nose, which can obstruct the airway and cause respiratory distress. Vaccination is highly effective in preventing diphtheria, but multiple doses and booster doses are required to establish and maintain long-term immunity.

Following multiple event alerts regarding child deaths due to diphtheria and cases being reported from a village in Kashipur block in Rayagada district, a central multidisciplinary team was deployed for epidemiological investigation including public health experts from Immunization division, MoHFW, Epidemiology division and IDSP, NCDC.

Methods

We described the outbreak epidemiology. Data for diphtheria cases and deaths was collected by conducting interviews with cases and verbal autopsies for death cases. Data was collected from diphtheria suspects, confirmed cases and deaths. In Rayagada and Koraput districts, data was captured using VPD Case Investigation Form (CIF) as per MoHFW Field guide for Diphtheria Pertussis and Neonatal Tetanus Surveillance, and record review of hospital case files. Details were captured on village, district, date of illness onset, age in years and months, sex, full immunization status, clinical features like presence of sore throat, fever, greyish white membrane in throat,

bloody nasal discharge, hoarseness of voice, neck swelling, nasal regurgitation, difficulty in swallowing, sample collection, laboratory results and date of death. Following case definitions were formed. Suspect case- a suspect case was defined as any person with fever and upper respiratory tract illness or neck swelling, between May residing in district Rayagada or Koraput, Odisha. Probable case- a suspect case with epidemiological linkage to lab confirmed diphtheria case. Confirmed case- a suspect case with laboratory confirmation for diphtheria by isolation of *Corynebacterium* sp by culture or positive Elek test. Data analysis included descriptive statistics of demographic characteristics, clinical presentation, vaccination status, and outcomes.

Results

The number of reported cases of diphtheria on P form in IDSP-IHIP in 2024 exceeded the number of cases reported in 2022 and 2023 in both Rayagada and Koraput district (Fig 1). A total of 24 cases of diphtheria were identified during the outbreak period, seven suspect cases, 10 probable and seven lab confirmed diphtheria cases were identified in the two districts of Rayagada and Koraput in Odisha. Out of the 17 confirmed and probable cases, seven cases, (4 probable and 3 lab confirmed cases) had died, (table 1) and case fatality rate was 41%. Of these, interviews were conducted for all recovered and under treatment cases and verbal autopsies were conducted for all deaths. After the suspect cases from Koraput came negative on diphtheria testing, they were excluded from further analysis.

Among the probable and confirmed cases, median age was 10 years with an interquartile range (IQR) of 6-11 years. Among the 17 cases reported, including 7 lab confirmed and 10 probable cases, 53% were males. Among these, 53% were in the age group 10-18 years, 29% were in age group 5-9-year and 12% were under 5 years of age. Among the 10 probable cases, 3 were immunized for pentavalent (1,2,3) and DPT B1, while the immunization status of the rest

was unknown. Among these 10 cases, 70% were in the age group 10-18 years with 2 cases having history of vaccination against diphtheria, and 20% were under 5 years of age with 1 case having history of vaccination against diphtheria. (table 2). Among the 7 lab confirmed cases, 2 were immunized for pentavalent (1,2,3) and DPT B1, while the immunization status of the rest was unknown. Among these, 57% (4) were between 5-9 years of age with 1 having history of diphtheria vaccination, and 29% (2) were in the age group 10-18 years, with 1 having history of diphtheria vaccination.

Out of the total 17 cases in Rayagada and Koraput, 100% had sore throat, 96% had fever, and difficulty swallowing (71%), bloody nasal discharge (71%), pseudo-membrane (67%), difficulty breathing (67%), neck swelling (63%), hoarseness (63%) were the other symptoms reported. Among the eight children with weight data, 75% (6/8) were underweight.

Among the seven death cases, 71% (5/7) were between the age 10-18 years, and 43% (3/7) were lab confirmed. Among the seven deaths, 43% (3/7) were hospitalised and were given Diphtheria anti toxin (DAT). Median interval from onset to hospital admission and DAT administration among death cases was 4 days with range 3-4 days.

The affected village in Rayagada district, i.e.,

Manuspadar village is classified as a hard-to-reach village and has all tribal residents. It is situated in the Devgiri Hills of the Eastern Ghat is not connected by motorable road, has no piped water supply, electricity or mobile connectivity. It is about 6 km away from the nearest motorable point and the RI (routine immunisation) site in D.murka village (which takes approximately 2 hours walk through the hills). Nearest health facility- PHC Dongasil was about 10km from the village, most of which is non motorable and hilly area. There was a hesitance among the community members towards accepting health services especially for severe illnesses requiring hospital admission.

• **Public health actions** taken by the district included:

- Administering post exposure prophylaxis to all village residents and conducting special vaccination drive to vaccinate (Td) all residents (including healthy), as well as health care workers involved in field activities in Manuspadar village of Rayagada district.
- Post exposure prophylaxis (Tab Azithromycin as per dosage) and contact doses of vaccination were given to household and close contacts of cases from villages in Narayanpatna and Bandhugaon blocks Koraput district.

Age groups	Male (n)	Female (n)	Total
<5	2	0	2
5-9	5	0	5
10-18	1	8	9
>18	1	0	1
Total	9	8	17

Table 1: Age distribution of cases (probable and confirmed) in Rayagada and Koraput districts, Odisha, June 2024 (N=17)

Age groups	Vaccinated/ Probable (n/N)	Total	Vaccinated / confirmed (n/N)	Total Lab	Deaths n
<5	1/2		0		01
5-9	0/1		1/4		01
10-18	2/7		1/2		05
>18	00		0/1		00
Total vaccinated	3/10		2/7		07

Table 2: Vaccination status of Probable and Confirmed cases, Odisha, June 2024 (N=17)

- Catch up vaccination for all due children (Penta, DPT boosters, or Td boosters) in affected villages was done in both districts.

Conclusions

This was a laboratory confirmed outbreak of Diphtheria in Rayagada and Koraput districts with high case fatality and cases predominantly occurring in hard-to-reach villages. Majority of death cases were adolescents, with low coverage of booster

doses in this age group. Delay in presenting to health facility and reporting of death cases could be due to difficult accessibility to health care in hard-to-reach areas and hesitancy among the community towards facility-based healthcare services. Active case searches, post-exposure prophylaxis, and special vaccination drives were implemented by the district in response to the outbreak.

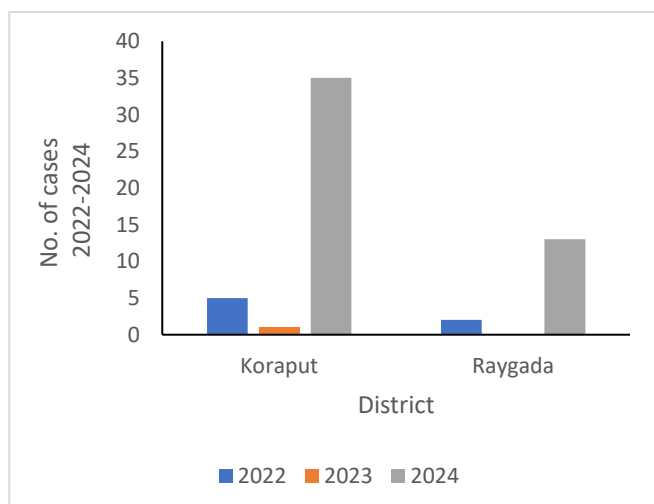


Figure 1: Diphtheria cases reported in Rayagada and Koraput districts on IDSP-IHIP (P form), 2022-2024

Recommendations

- Re-sensitization of Medical Officers and Health care workers for VPD Surveillance.
- Regular sensitization of field workers carrying out routine immunization and special vaccination drives in hard-to-reach areas for AEFI management.
- Routinely monitoring the designated hard-to-reach areas for any vaccine preventable disease outbreak.
- Improving utilization of healthcare services by the tribal population in hard-to-reach areas through appropriate health education (IEC and BCC) activities

Strengthening out of school vaccination in 5-16 years age group in hard-to-reach areas through integrated VHN data and conducting RI session in these villages.

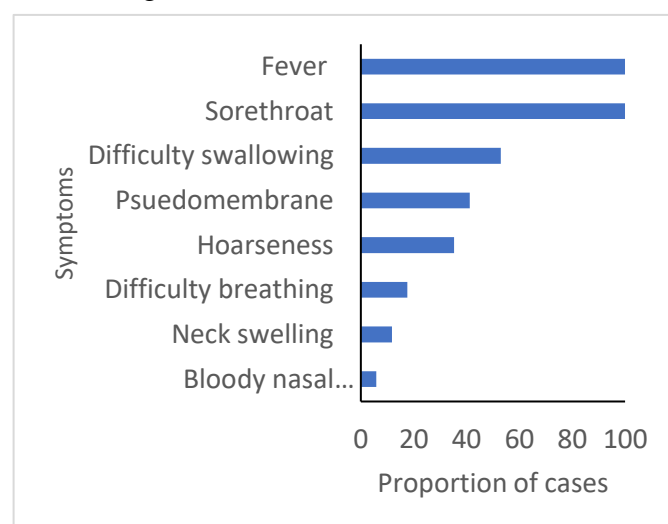


Figure 2: Clinical symptomatology, Diphtheria probable and confirmed cases, June 2024 (N=17)

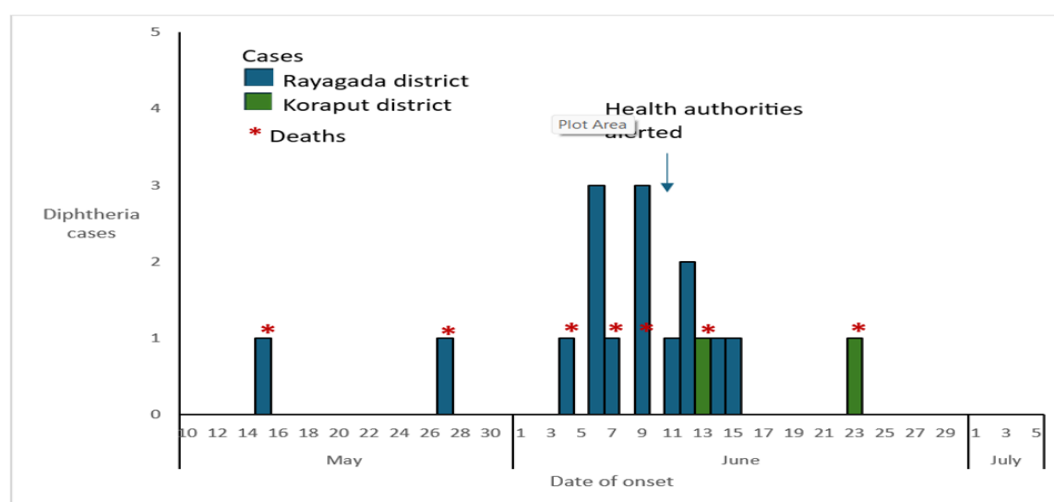


Figure 3: Time distribution of diphtheria cases (probable and confirmed) in Rayagada and Koraput districts, Odisha, June 2024

NCDC News

NCDC trains Government Medical Colleges of Kerala on Antibiotic Use Surveillance

Contributed by: Dr Suneet Kaur¹, Dr Arti Bahl²

¹Joint Director, ²Additional Director

A two-day training of trainers workshop on Point Prevalence Survey (PPS) on antibiotic use for Government Medical Colleges of Kerala was organised by GMC Thiruvananthapuram on 12th-13th June, 2024 with the objective to train the hospitals in conducting the Point Prevalence Survey on antibiotic use, data handling and analysis. NCDC provided technical support and hands on training.

On 12th June 2024, the session was attended by 29 participants which included faculty and residents of department of Pharmacology and Head of Department of Microbiology who is also the nodal officer for KARSAP. On 13th June 2024, 27

faculty members from Departments of Pharmacology from 10 medical colleges of Kerala attended the workshop and hands on training. The faculty and residents of department of Pharmacology also attended the training (Overall 55 participants)

During the workshop, the trainees were apprised about the importance of conducting antibiotic use studies, planning the study across all the 11 medical colleges. They were also given Hands-On training using dummy case sheets on conducting PPS. NCDC will provide technical support to the medical colleges in data handling and analysis.



Glimpses of training

NCDC conducts Regional Training Programme for Prevention and Control of Communicable Diseases for the Paramedical Personnel of South East Asian region, 22nd April-17th May 2024

Contributed by: Dr Anubhav Srivastava¹

¹Joint Director

The National Centre for Disease Control (NCDC), Delhi is a WHO Collaborating Centre for Epidemiology and Training. The one Regional Training Programme for Prevention and Control of Communicable Diseases for the Paramedical Personnel of South East Asian region countries of the South East Asia Region was started in 1999. The objective of the FETP is to provide the knowledge and skills for the field application of Epidemiology in the prevention and control of communicable diseases. The course is open to paramedical officers working in the field of public health in the countries of the South East Asia Region. This is one of the prestigious courses of the Region. The other activities of the collaborating centers are outbreak investigation and applied research in the field of communicable disease area.

About the training:

- This training is conducted in NCDC every year since 1999. 251 participants from Bangladesh, Bhutan, Maldives, Myanmar, Nepal, Sri Lanka, India and Timor Leste have successfully completed the previous courses in 21 batches.
- It is a tailor-made training programme for participants from countries of South East Asia Region to strengthen their epidemiological skills.
- Course is designed to augment the capacity to understand disease dynamics in community and intervention for its prevention and control.

Objectives: The objective of the course is to strengthen the technical capabilities and skills of paramedical personnel of the SEARO region by providing practical training in prevention & control of communicable diseases and application of computer for surveillance purposes

Course contents:

- Principles and methods for prevention & control of diseases of public health importance
- Epidemiology of selected epidemic-prone communicable diseases

- Disease surveillance
- Data analysis, presentation & interpretation of data
- Outbreak investigation and control
- Public health response in emergencies
- Use of computers in data analysis and presentation
- Field studies and report writing

The course is of four weeks duration:

- 3 weeks- classroom sessions including lecture, group-discussions, modular exercises, group presentations, 'hands-on-training' in laboratory procedures, protocol preparation and computer usage including Ms Power point, Excel and Epi-Info software
- 1 week: for field practice including community survey, data collection, compilation, analysis, report writing and presentation

For the 21st Paramed FETP, this year there were 20 candidates (14 candidates from India (Delhi, Punjab, Uttar Pradesh), and 6 participants were from RoHFWs.

Senior faculty of the NCDC, WHO, CBHI, and CHEB participated in the Programme. The methodology of FETP involved a variety of teaching/learning approaches such as lectures, discussions, modular exercises, demonstration and fieldwork. The trainees acquired basic skills for use of computers and EPI INFO at computer workstations in the computer laboratory.

Field Survey: During the field posting, all the participants were posted at Alwar branch of NCDC from 6th-10th May. The participants were placed under supervision of Dr. Naveen Chharang, Joint Director and Branch officer in- charge of the NCDC branch who supervised the groups and field visit arrangements.

Assessment: The training programme was evaluated through comparing the performance of the participants before the course through assessment questionnaire. The post training assessment was done on 17th May 2024 before the valedictory session and feedback of the training was also taken. Expectations from the training programme was also sought.

Valedictory programme was held on 17th May'2024 in the presence of Director, NCDC, HoDs, Faculty of Epidemiology and other invited officials.

Laboratory Section

Diagnostic utility of PCR in Human Leptospirosis

Contributed by: Ms. Preeti Khatri¹, Mr. Vinay Singh², Dr. Pravin Panditrao Kalyankar³, Dr. Cordelia⁴, Dr. Monil Singha⁵

¹Technician, ²Research Assistant, ³DNB Student, ⁴Deputy Assistant Director, ⁵Joint Director

Leptospirosis is a zoonotic disease caused by spirochetes from the genus *Leptospira*. *Leptospira* is phenotypically classified into two species namely, *L. interrogans* (pathogenic) and *L. biflexa* (non-pathogenic). Antigenically *L. interrogans* is classified into Approximately 30 serogroups which are subclassified into more than 250 serovars.

The symptoms of leptospirosis usually present after 5-14 days and appears like mild disease with flu-type illness-fever, chills, cough, and headache, most people recover within a week. However, in about 10% of cases severe disease develops where multiple organ failure causes fatal outcomes. Leptospirosis should be considered as an emerging infectious disease spreading in urban areas specially slums with rat infections from the rural to the urban centers. The incidence of leptospirosis with hemorrhagic pneumonitis & ARDS is on the rise. Human Leptospirosis cannot be diagnosed based on clinical grounds alone due to the variability in clinical manifestations, similarity of signs and symptoms with those of other infections and frequent occurrence of the disease in atypical forms.

The laboratory diagnosis of Leptospirosis includes direct methods such as direct microscopy, culture and molecular assays and indirect method such as serological assays ELISA and the Microscopic Agglutination Test (MAT) assay.

Serological assays such as ELISA and MAT are useful tool for diagnosis easy to perform but have some limitations due to background prevalence and non-availability of standardized cut-offs for various geographic areas when performed on a

single sample. The dilemma in diagnosing such cases can be addressed by performing paired sample testing/ seroconversion from IgM to IgG to some extent. MAT is considered a reference test for epidemiological surveillance and mapping of prevalent serovars in different geographical areas. Molecular assays in suspected leptospirosis in the early stage of illness also have clinical and diagnostic utility. There are various targets identified to diagnose pathogenic leptospirosis by molecular methods. However, these methods do not have ability to identify and distinguish the serovars. We conducted a surveillance on 159 samples of Acute Febrile Illness to better understand the diagnostic utility of PCR. The mean age of our AFI cases was 27.7 yrs with a range of age 1-85 years. The range of fever was 1-9 days. We found that out of 159 Samples; 7(11.13%) samples turned out positive. The samples that turned out positive were those that were having fever as early as 2-3 days and those who had not taken any antibiotics.

In cases with pyrexia of unknown origin, the timely intervention with molecular methods can be life-saving as initial symptoms of leptospirosis often overlap with dengue, rickettsia, and other AFI, implicating dilemma in the early diagnosis of leptospirosis and potentially leading to delayed treatment.

In conclusion, the leptospiremia phase precedes the immune response phase and molecular methods like NAAT (Nucleic Acid Amplification Test) can help to identify leptospirosis in the early stage, provided the correct sample is collected at the right time.

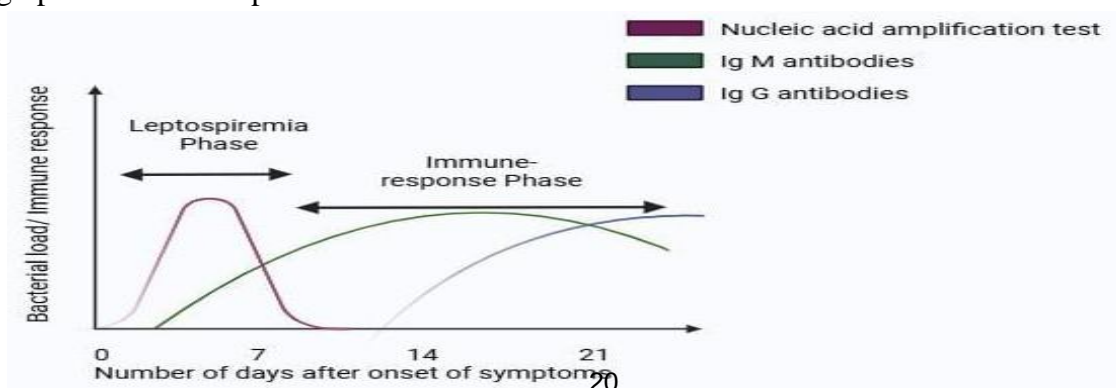


Figure 1: Utility of Diagnostic test (NAAT, IgM & IgG) in different clinical phases of Leptospira Infections.

NCDC Branches

NCDC Varanasi conducts trainings on Lymphatic Filariasis

Contributed by: Dr. Prateek Kumar Singh¹, Dr. Awanindra Dwivedi², Sh. Anukesh Singh³

¹Medical Officer & OIC, ²Research Assistant, ³Technician

NCDC Varanasi branch conducted one “three working days Lymphatic Filariasis Elimination training programme for MOs/Biologists/DPOs” from 03.04.2024 to 05.04.2024 and one “five working days Lymphatic Filariasis Elimination (LFE) training programme for Filaria Inspectors/Technicians” from 03.06.2024 to 07.06.2024. Total 05 participants (01 from Tamil Nadu, 01 from Telangana and 03 from UP) and total 16 participants (Karnataka – 14, Maharashtra – 01 and Gujarat – 01) respectively, attended the trainings. The key objective of these trainings was

to develop skilled manpower in the field of lymphatic filariasis particularly to support the National Filariasis Elimination Programme.

Didactic classroom lectures were delivered along with entomological field training session. Methodology of Night Blood Survey, Transmission Assessment Survey and preparation of Night Blood Smear, staining and microscopic examination for mf detection were discussed and demonstrated. Morbidity Management and Disability Prevention (MMDP) practices were also discussed and demonstrated to trainees.



MMDP washing technique being demonstrated to trainees



Mosquito collection by trainees during field visit



NBS slides staining being demonstrated to trainees



Demonstration of entomological techniques during LF training

Global Disease Alert

Contributed by: NFP IHR Secretariat, Division of Public Health Preparedness & NCD

1. Avian Influenza A(H5N1) - Viet Nam

2 April 2024

On 25 March 2024, Viet Nam's national authorities reported a human infection with influenza A(H5N1) to the World Health Organization (WHO). The patient, without underlying health conditions, developed symptoms on 11 March and died on 23 March, with likely exposure to birds in February. This marks Viet Nam's first reported human case of A(H5N1) since 2022. Epidemiological investigations, disinfection of the patient's residence, and contact tracing were conducted. Samples from close contacts and nearby birds tested negative for the virus. The Provincial Department of Health in Khanh Hoa province was advised to ensure readiness of drugs like Oseltamivir and other resources to support hospitals in managing potential outbreaks.

2. Avian Influenza A(H5N1) - United States of America

9 April 2024

On 1 April 2024, the United States IHR National Focal Point reported a laboratory-confirmed case of human infection with influenza A(H5N1) to the World Health Organization (WHO). The patient developed symptoms on 27 March following exposure to dairy cattle suspected of being infected with the virus. This is the second confirmed human case of A(H5N1) in the United States and the first believed to result from contact with an infected mammal. No additional cases have been identified. Public health officials are conducting surveillance in Texas, and the US CDC is monitoring and testing workers exposed to potentially infected animals. The CDC has issued guidelines to avoid unprotected contact with sick or dead animals and their droppings, as well as to refrain from consuming raw or undercooked animal products from potentially infected sources.

3. Rabies - Timor-Leste

10 April 2024

On 22 March 2024, Timor-Leste reported its first fatal human rabies case to WHO. The patient, from Oecusse's Pasabe Sub-Region, died following a dog bite on 26 December 2023. As of 24 April 2024, 95 dog exposure cases and 10 rabid dogs have been reported in Oecusse, with seven people bitten by confirmed rabid dogs. Public health measures include dog vaccination, risk communication, healthcare worker training, active surveillance, and ensuring access to rabies vaccines and immunoglobulin.

4. Avian Influenza A(H9N2) - Viet Nam

19 April 2024

On 9 April 2024, Viet Nam reported its first human infection with avian influenza A(H9N2) to WHO. The patient, with underlying conditions, was hospitalized in severe condition on 21 March, and testing confirmed A(H9N2) on 8 April. The patient resided near a busy poultry market, but no additional cases or community outbreaks have been reported as of 15 April. Public health and animal health authorities conducted investigations, contact tracing, disinfection, and testing to identify potential further cases or outbreaks. On 5 April, the Ministry of Health issued a press release with details of the case and preventive public health guidance.

5. Hepatitis E – Chad

8 May 2024

Between 2 January and 28 April 2024, 2092 suspected hepatitis E cases, including seven deaths (CFR 0.3%), were reported in Ouaddai province, Chad, primarily from refugee camps (95%) in Adré and Hadjer-Hadid health

districts. The most affected groups were individuals aged 6-17 years (53.2%) and 18-59 years (23.9%), with 27 pregnant women among the cases. Diagnosis was confirmed using rapid diagnostic tests and PCR. In response, the national Public Health Emergency Operations Centre was activated, and WHO deployed a team to support ongoing interventions with partners. Key measures include providing safe drinking water, promoting hygiene, ensuring quality public water supplies, and managing sanitation services to reduce transmission.

6. Middle East respiratory syndrome coronavirus-Kingdom of Saudi Arabia

8 May 2024

Between 10 and 17 April 2024, Saudi Arabia reported three MERS-CoV cases, including one death, to WHO. The cases, males aged 56-60 with underlying conditions, were linked to a healthcare facility in Riyadh. Since January, the country has reported four cases and two deaths. In response, the Ministry of Health initiated contact tracing with daily monitoring and testing for high-risk contacts, implemented respiratory disease triage in emergency departments, and provided refresher training for healthcare workers on case detection, infection prevention, and control (IPC). IPC measures, including PPE and hand sanitizers, have been reinforced to prevent further transmission.

7. Avian Influenza A(H5N2) - Mexico

5 June 2024

On 23 May 2024, Mexico reported the first globally confirmed human case of avian influenza A(H5N2) to PAHO/WHO, a fatal infection in a resident of the State of Mexico. The source of exposure remains unknown, though A(H5N2) has been detected in poultry in Mexico. Public health measures include epidemiological investigations, contact monitoring, enhanced surveillance for respiratory illnesses in nearby areas, and risk factor analysis. Training on outbreak preparedness and coordination with animal health authorities was initiated to strengthen poultry and wild bird surveillance. PAHO/WHO is enhancing surveillance at the human-animal interface, improving molecular diagnostics, supporting sample shipment for analysis, updating influenza response guidelines, and bolstering risk communication and clinical management capacities. Intersectoral collaboration and lessons from prior zoonotic influenza outbreaks are being utilized to guide the response.

8. Avian Influenza A (H5N1) - Australia

7 June 2024

On 22 May 2024, Australia reported its first human case of avian influenza A(H5N1) (clade 2.3.2.1a) to WHO, likely acquired during the patient's travel to India, where this clade has been detected in birds. Australia activated its National Incident Centre, convened a Monitoring and Investigation Team, and issued health advisories and public health guidance, emphasizing seasonal influenza vaccination to prevent virus mixing and mutation. India, upon notification, launched an epidemiological investigation involving multiple sectors. Both countries are closely monitoring the situation, with Australia providing regular updates and risk assessments regarding avian influenza outbreaks.

9. Avian Influenza A (H9N2) – India

11 June 2024

On 22 May 2024, India reported its second human case of avian influenza A(H9N2) to WHO, involving a child from West Bengal who has since recovered and been discharged. In response, a multidisciplinary team, including public health, veterinary, and pediatric experts, was deployed to investigate influenza-like illness (ILI) in local poultry. Surveillance of ILI in humans and animals was intensified in the affected district and neighboring areas to monitor and mitigate potential risks.

Source: WHO



Editorial Board

Advisor Editorial board

Prof. (Dr.) Atul Goel

Chief Editor:

Dr. Anil Kumar

Executive Editor

Dr. Sandhya Kabra

Assistant Executive Editor

Dr. Meera Dhuria

Editorial Panel

Drs. Arti Bahl, Aakash Shrivastava, Simrita Singh, Tanzin Dikid, Himanshu Chauhan, Simmi Tiwari, Vinay Garg, Monil Singhai, Purva Sarkate

Editorial Coordinator:

Dr. Suneet Kaur

Design and Layout:

Abhishek Saini

For comments and inputs, e-mail ncdcnewsletter21@gmail.com

Digital Library section. Address: National Centre for Disease Control, 22-Sham Nath Marg, Delhi — 110054. India the editorial board does not hold any responsibility for the materials contained in this publication which is based on information available from various sources. Reproduction of material from the NCDC Newsletter, in part or in whole, is encouraged, as long as credits and acknowledgement are given. The article/s may be cited as **Author, Year, Article Title, NCDC Newsletter, Volume (), Issue () Quarter, Page**

Online version of NCDC Newsletter is available at NCDC website www.ncdc.gov.in under Resource/Digital Library Section