



A Monthly e Magazine
ISSN:2583-2212

June, 2026 Vol.6(6), 1620-1623

Popular Article

From Farm to Laboratory: Tracking the Spread of Classical Swine Fever in Assam

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doi.org/10.5281/ScienceWorld.20630197

In many regions of Assam, pig farming is not just a livelihood but it is a way of life. Pig provides income, nutritional security and financial support for thousands of families during economic crisis. However, this vital sector still continues to face a persistent threat from a highly contagious viral disease known as Classical Swine Fever (CSF) (WOAH, 2026).

Classical swine fever often called as hog cholera is one of the devastating disease of pigs occurring worldwide. The disease spreads rapidly, causing high mortality, which can lead to severe economic losses for the farmers (WOAH, 2026). In a state like Assam, where pig farming contributes significantly to the rural economy, the impact of such outbreaks can be particularly severe.

A Disease That Continues to Challenge Farmers

The early signs of CSF often go unnoticed. The affected animals appear dull, loss of appetite, and there is high fever. As the disease progresses affected animals may develop diarrhoea, respiratory distress, skin haemorrhages, weakness and occasionally neurological



signs (Malik *et al.*, 2020). Pregnant sows may have reproductive failures such as abortions, stillbirths and mummified foetuses.

For small-scale farmers even, the loss of a few animals can cause financial hardship. During an outbreak entire herds may get effected in a short period of time and result in significant economic loss and emotional distress for farming families. Several outbreaks have been reported from different parts of Assam and North-east India over the years which shows the need for continuous disease surveillance and control measures (Patil *et al.*, 2018).

Following the Virus from the Field

The understanding of how the disease spreads starts far from the laboratories. It begins on farms, in villages and at local markets, where veterinarians and researchers investigate outbreaks of disease. When pigs develop clinical signs suggestive of CSF, Samples such as blood, serum, spleen, lymph nodes, tonsils and other tissues are collected for laboratory examination. The samples are then taken to diagnostic laboratories where it is the processed to identify the causative agent. An important scientific investigation what appears to be a sudden disease outbreak to farmers. Researchers tries to identify the virus, if it is there, mode of transmission, and whether new variants of the virus are developing in the region.

The utilization of Molecular Diagnostics

Modern veterinary science has changed the way we identify diseases. The traditional diagnosis based on clinical signs and post-mortem findings is often inadequate, as most of the viral disease of swine can produce similar signs and symptoms.

Molecular techniques like Reverse Transcription Polymerase Chain Reaction (RT-PCR) today enables detection of the genetic material of Classical Swine Fever Virus (CSFV) with remarkable accuracy (Malik *et al.*, 2020). These methods allow to quickly confirm the infection and help veterinarians to take preventive measures in time.

Molecular diagnostics have been widely used in India for disease surveillance and outbreak investigations and have provided reliable detection of CSFV even during the early stages of infection (Malik *et al.*, 2020).

Reading the Genetic Fingerprint of the Virus

One of the most fascinating aspects of modern disease investigation is molecular characterisation. All viruses have a distinctive genetic make-up that can provide important information as to the source and evolution of the virus.



Scientists compare field strains circulating in different geographic regions by looking at specific viral genes such as E2 and NS5B. Researchers build phylogenetic trees by looking at these genetic sequences, which can be used to trace the relationships between viral isolates (Khatoon *et al.*, 2017).

The existence of various sub-genotypes of CSFV has been shown in Assam and other areas of North-east India (Khatoon *et al.*, 2017; Ahuja *et al.*, 2015] with subgroups 1.1 and 2.2 being the most predominant. These results provide useful information on viral evolution and transmission patterns and help researchers to track changes occurring in the virus over time.

Why Assam Matters in CSF Research

North-east India has one of the largest pig populations in the country with its porous borders and hence the region is of high importance for swine disease research and surveillance. Animals are often moved and backyard farming practices are common, with variable vaccination rates, all of which can affect disease transmission dynamics (Malik *et al.*, 2020).

Recent molecular epidemiological studies from Assam have greatly contributed in understanding the diversity of CSFV circulating in India (Khatoon *et al.*, 2017; Ahuja *et al.*, 2015). These studies are critical for strategies for disease control, vaccine development and future surveillance programs.

Beyond the Microscope: Protecting Livelihoods

Research on CSF is not just about viruses, genes and lab tests. It is to help economically weaker section of the people which includes small scale farmers and woman's and sustaining rural livelihoods.

The early diagnosis allows veterinarians and authorities to better implement disease control measures. The main tools to prevent outbreaks and reduce disease burden are still vaccination, improved farm hygiene, movement restrictions and regular disease surveillance and awareness among the farmers (WOAH, 2026; Malik *et al.*, 2020).

As scientists further examine the virus at the molecular level, the results help improve pig health and disease control strategies throughout the region. Every field sample is a part of a larger mosaic to protect the future of pig farming in Assam.



Looking Ahead

The path of a disease sample from an outbreak farm to a lab that analyses viral genes is the intersection point of veterinary medicine, molecular biology and public service. It represents how science can be used to solve real-world issues faced by farming communities.

Classical Swine Fever continues to be a major threat for pig production in Assam and across the globe, but advances in molecular diagnostics and epidemiological research are keeping scientists one step ahead of the disease (Malik *et al.*, 2020; Khatoon *et al.*, 2017). Laboratory-based analysis and field investigations are giving researchers valuable insights into the spread and evolution of the virus.

Every outbreak investigated, every sample analysed and every genetic sequence studied brings us a step closer to better understanding of disease control and a safer future for pig farmers across the region in the fight against Classical Swine Fever.

References

- World Organisation for Animal Health (WOAH). Classical Swine Fever (CSF) (2026). Available at: <https://rr-asia.woah.org>
- Malik, Y.S., Bhat, S., Kumar, O.V., Yadav, A.K., Sircar, S., Ansari, M.I., Sarma, D.K., Rajkhowa, T.K., Ghosh, S. and Dhama, K. (2020). Classical swine fever virus biology, clinicopathology, diagnosis, vaccines and a meta-analysis of prevalence: a review from the Indian perspective. *Pathogens*, **9**(6): p.500.
- Patil, S.S., Suresh, K.P., Saha, S., Prajapati, A., Hemadri, D. and Roy, P. (2018). Meta-analysis of classical swine fever prevalence in pigs in India: A 5-year study. *Veterinary world*, **11**(3): p.297.
- Khatoon, E., Barman, N.N., Deka, M., Rajbongshi, G., Baruah, K., Deka, N., Bora, D.P. and Kumar, S. (2017). Molecular characterization of classical swine fever virus isolates from India during 2012–14. *Acta tropica*, **170**: pp.184-189.
- Ahuja, A., Bhattacharjee, U., Chakraborty, A.K., Karam, A., Ghatak, S., Puro, K., Das, S., Shakuntala, I., Srivastava, N., Ngachan, S.V. and Sen, A. (2015). Complete genome sequence of classical swine fever virus subgenogroup 2.1 from Assam, India. *Genome Announcements*, **3**(1): pp.e01437-14.

