THE SCIENCE WORLD
A Monthly e Magazine
ISSN:2583-2212
Popular Article
Oct, 2026 Vol.6(10), 3365-3368

Shamonda virus: The Hidden world of an emerging orthobunyavirus

A. Pravalika[1] and M. Sangavi Priya[2]
[1] PhD. Scholar, Department of Veterinary Microbiology, Indian Veterinary Research Institute, Hebbal, Bengaluru
[2]MVSc. Scholar, Department of Veterinary Microbiology, Indian Veterinary Research Institute, Hebbal, Bengaluru
doi.org/10.5281/ScienceWorld.23943728

Introduction

Shamonda virus (SHAV) is an enveloped, negative-sense, single-stranded RNA virus belonging to the genus *Orthobunyavirus* within the family *Peribunyaviridae* and the Simbu serogroup. Its genome consists of three segments—large (L), medium (M), and small (S)—a feature of significant epidemiological importance because co-infecting viruses can exchange genome segments through reassortment, potentially altering antigenicity, host range, or pathogenicity.

Primarily a midge-borne pathogen, SHAV affects ruminants and livestock such as cattle, sheep, goats, horses, and alpacas. In dairy cattle, clinical manifestations include fever, diarrhea, and marked reductions in milk production.

Epidemiology and Emergence

The virus was first isolated in 1965 from bovine blood sample at the University of Ibadan in Nigeria, deriving its name from the surrounding Samonda neighborhoodShamonda virus (SHAV) has been also detected in Culicoides biting midges in Japan, expanding the evidence of its circulation in the region. Its veterinary significance became more apparent during an outbreak of congenital abnormalities in southern Japan in 2015–2016. Among 15 calves exposed to the virus in utero, reported clinical and pathological findings included arthrogryposis, torticollis, spinal curvature and central nervous system lesions; six calves were stillborn (1). Evidence of SHAV circulation has also emerged from South Africa, where retrospective molecular investigations detected viral RNA in Culicoides pools collected between 2012 and 2017.

Furthermore, SHAV RNA was identified in the brain and lungs of an aborted goat foetus in 2021, suggesting a possible association with reproductive disease in small ruminants. More recently, genomic analysis revealed a reassortant virus involving Shuni virus and SHAV in a horse that died following neurological disease. This finding highlights the potential for genetic reassortment among co-circulating Simbu serogroup viruses and its possible implications for viral diversity and disease emergence (2).

However, the epidemiological landscape shifted on July 31, 2026, when a new variant designated Shamonda-Europe emerged following disease investigations on cattle farms in Germany and Switzerland, subsequently spreading to France, Spain, Portugal, and other European nations. Two distinct European sub-variants currently circulate:

- SHAV-EU1: Initially detected in Switzerland, France, and southern Germany.
- SHAV-EU2: Identified in northwestern Germany.

Human Transmission

In October 2026, France reported the first documented human infection of SHAV. A severely immunocompromised patient hospitalized in Lyon acquired the virus—likely via a *Culicoides* midge bite in eastern France—and subsequently died from virus-induced neurological complications (3). Public health officials emphasized that this was an exceptional incident restricted to an immunocompromised individual, posing no generalized risk to the general public.

Etiology and Pathology

As a member of the Simbu serogroup, SHAV shares close phylogenetic ties with other veterinary pathogens, such as the Akabane virus and the Schmallenberg virus (which is well-documented for causing congenital malformations and stillbirths in domestic ruminants).
In infected livestock, primary signs include:

- Acute fever
- lethargy
- Reduced milk yield
- Gastrointestinal distress including severe diarrhea and abdominal discomfort
- Reproductive disorders and fetal abnormalities

Laboratory Diagnosis:

Because symptoms mirror other arboviral or livestock diseases, confirmation relies on pan-Simbu PCR or RT-PCR assays targeted at the viral segments. Next-generation sequencing is utilized to track clades.

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Published 30/10/2026

Prevention and Control

There are currently no commercially available vaccines or specific antiviral therapies for either humans or animals. Containment focuses heavily on controlling the *Culicoides* insect vectors. The World Organisation for Animal Health (WOAH) recommends several biosecurity and management strategies to reduce transmission rates:

- Physical Barriers: Installing fine mesh screens on housing facilities and implementing double-door entry-exit systems.
- Environmental Management: Reducing or eliminating vector-breeding sites around farming infrastructure.
- Surveillance and Control: Conducting active vector surveillance and targeted control measures around agricultural buildings.
- Transport Precautions: Utilizing insect repellents during the transit of animals and scheduling transport during periods of low vector activity.

Conclusion

The recent detection of the Shamonda virus in a human patient in Europe marks a fascinating yet sobering turning point for a pathogen that was once strictly the domain of veterinary medicine. For decades, this insect-borne orthobunyavirus—spread primarily by *Culicoides* midges—was known only to cause economic and reproductive headaches for livestock farmers in parts of Africa, Asia, and more recently, parts of Europe.

However, this first documented human case serves as a reminder of how porous the boundary between animal and human health truly is. While public health authorities emphasize that the risk to the general public remains low and that the virus does not spread from person to person, the event highlights the unpredictable nature of emerging zoonotic diseases.

Ultimately, there is no cause for widespread alarm or drastic lifestyle changes. Scientists and international health agencies are closely monitoring the situation to determine whether this human infection was a rare, isolated event tied to unique underlying vulnerabilities, or part of a broader trend. Until research provides clearer answers, the best approach is one of calm awareness: supporting ongoing veterinary and public health surveillance, practicing sensible protection against insect bites if you live near livestock areas, and letting science—rather than speculation—guide our understanding of the Shamonda virus's next moves.

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Published 30/10/2026

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