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# Editorial

# *Shamonda virus in Europe: an emerging threat, the potential role of Culicoides and the need for preparedness*

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The emergence of Shamonda virus (SHAV) in Europe during the summer of 2026 is a timely reminder that the epidemiological boundaries of vector-borne animal viruses are neither fixed nor readily predictable. Shamonda virus is an enveloped, negative-sense, single-stranded RNA virus with three genome segments (L, M and S), belonging to the genus *Orthobunyavirus*, family *Peribunyaviridae*, and the Simbu serogroup. Its segmented genome is epidemiologically important because related viruses infecting the same host or vector may exchange genome segments through reassortment, potentially altering antigenicity, host range or pathogenicity. Shamonda virus was first isolated from cattle in Ibadan, Nigeria, in 1965 and was subsequently detected in cattle and *Culicoides* biting midges in Japan. Its veterinary relevance became clearer after infection was associated with congenital disease in southern Japan: 15 calves exposed in utero during 2015-2016 showed arthrogryposis, torticollis, spinal curvature and central nervous system lesions, and six were stillborn (Hirashima et al., 2017). In South Africa, SHAV RNA was identified retrospectively in *Culicoides* pools collected between 2012 and 2017 and, in 2021, in the brain and lung of an aborted goat foetus (van der Walt et al., 2023). More recent genomic work also identified a Shuni/SHAV reassortant in a fatal neurological case in a horse, illustrating the biological relevance of segment exchange among co-circulating Simbu viruses (Rakaki et al., 2025). Europe entered this history abruptly in June 2026, when clusters of acute diarrhoea, transient fever, lethargy, anorexia and marked but generally reversible reductions in milk yield were reported in dairy herds in eastern France. In the initial investigation, herd bulk-milk production fell by 15-75%. Routine testing, including assays for Schmallenberg virus, did not identify a cause; untargeted Nanopore metagenomics instead recovered a previously unrecognised European SHAV lineage. Viral RNA was subsequently found in acutely affected cattle from several regions and in placental or foetal tissues from abortion cases, including foetal brain, supporting systemic and transplacental infection, although formal epidemiological and experimental studies are still required to establish the full causal spectrum (Kelleci et al., 2026). Within weeks, related detections were reported in Germany, Switzerland, The Netherlands, Austria, Belgium and Liechtenstein (Union of European Veterinary Practitioners, 2026). By late August, Switzerland had confirmed circulation in 22 cantons and had detected viral RNA in aborted bovine foetuses and in the brains of two horses with central nervous system disease. In those horses, blood and cerebrospinal fluid were negative, emphasising both the short viraemia and the limitations of ante-mortem molecular diagnosis (Institute of Virology and Immunology, 2026). European detections have since extended beyond cattle to sheep, goats, alpacas and horses (Friedrich-Loeffler-Institut, 2026a). Precise incidence and distribution remain difficult to quantify because the infection is not subject to harmonised mandatory notification. The genomic picture has also become more complex. On 1 September 2026, the Friedrich-Loeffler-Institut reported two genetically distinct variants, designated Shamonda virus Europe 1 (SHAV-EU1) and Shamonda virus Europe 2 (SHAV-EU2). SHAV-EU1 encompasses the variant initially recognised in Switzerland, France and southern Germany, whereas SHAV-EU2 has been identified in cattle from north-western and eastern Germany. All three genomic segments differ between the variants, indicating at least two independent introduction and spread events, which already overlap in some German landers. The concurrent circulation of SHAV-EU1, SHAV-EU2 and Schmallenberg virus creates opportunities for reassortment and makes complete three-segment genomic characterisation, rather than single-target detection alone, an essential component of surveillance (Friedrich-Loeffler-Institut, 2026b). Across Europe, the absence of a publicly reported detection in an individual country at the time of writing should not be interpreted as evidence of absence. The virus's rapid geographical expansion, widespread *Culicoides* populations and climatic suitability for prolonged midge activity create a credible risk of further spread or undetected circulation. *Culicoides* biting midges are currently considered the most likely vectors, based on the available epidemiological and virological evidence, including repeated detection of SHAV RNA in field-collected pools; however, their vector competence and role in transmission have not yet been formally



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demonstrated. Adult cattle usually experience a short, self-limiting disease, but herd-level production losses may be substantial. The more consequential effects may emerge later, when animals infected during susceptible stages of gestation abort or deliver stillborn or malformed offspring. The neurological findings in horses further broaden the syndromic surveillance required. No SHAV-specific vaccine or antiviral treatment is currently available. Measures aimed at reducing exposure to biting midges may be considered, although their effectiveness against SHAV transmission remains uncertain. Current evidence does not show that SHAV infects humans, and Simbu serogroup viruses are not generally regarded as major zoonotic agents. Nevertheless, the zoonotic potential of a newly introduced and incompletely characterised virus should be assessed rather than assumed. This is particularly appropriate because other orthobunyaviruses, including Shuni and Oropouche viruses, can cause human disease (Motlou & Venter, 2021; Zhang et al., 2024). A proportionate One Health response should therefore connect veterinary clinical intelligence, entomological surveillance, genomics and, where indicated, public-health vigilance without overstating the present human-health threat. European preparedness for SHAV should build on existing clinical, laboratory and entomological surveillance systems. Priority specimens for molecular testing should include samples collected from ruminants during the early febrile or milk-drop phase, particularly when routine tests for differential diagnoses, including bluetongue, are negative, as well as field-collected *Culicoides* pools, abortion material and specimens from animals with unexplained neurological disease, especially equids. Positive results should be confirmed and followed by sequencing of all three genome segments to support epidemiological investigations and genomic comparison with strains circulating in Europe. Retrospective testing of archived samples, combined with paired serology, may help establish whether silent circulation preceded clinical recognition; however, cross-reactivity with Schmallenberg virus and other Simbu serogroup viruses must be considered when interpreting serological results. The European SHAV episode illustrates the limitations of pathogen-specific monitoring and the value of combining syndromic approaches, broad-range assays, metagenomics and established vector-monitoring networks. Integration of these complementary tools would facilitate prompt recognition of new or previously unrecognised circulation, definition of its geographical and host distribution, and implementation of proportionate measures to limit further spread and mitigate its animal-health impact.

## Keywords

Shamonda virus, Culicoides, Simbu serogroup, reassortment, genomic surveillance

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