

Incursion of European Shamonda virus clade II in dairy cattle on Jersey, Channel Islands

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Short Report

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Abstract

Outbreaks of reduced milk yield and diarrhoea were investigated in four Jersey dairy herds on Jersey, Channel Islands, in July 2026. Faeces and sera from two farms tested positive by pan-Simbu RT-qPCR but negative for Schmallenberg virus. Next-generation sequencing identified a Shamonda virus, with L, M and S genome segments clustering within European clade II. Detection of SHAV clade II in Jersey, indicates wider distribution of this clade in western Europe, with implications for surveillance, and preparedness in north-west Europe.

FullText

In early July 2026, disease outbreaks occurred in four pedigree Jersey dairy herds in Jersey, Channel Island. Affected animals were lactating cows and clinical signs included abrupt reductions in milk yield, reduced rumination, foul-smelling diarrhoea and, in severe cases, recumbency. In the most severely affected herd, 47/120 (39.2%) milking cows developed clinical signs, including 34 (28%) that became recumbent during the outbreak. The outbreak evolved over approximately three weeks, with new cases occurring daily. Similar but less severe syndromes were observed on other holdings. No significant disease was observed in youngstock, heifers or bulls.

Farmers and veterinarians observed increased incidence of reproductive problems, including returns to service, abortions and stillbirths, although causality could not be established. Most affected animals remained normothermic. Oral electrolytes and non-steroidal anti-inflammatory drugs appeared to reduce progression to recumbency.

The outbreak was unusual in the context of Jersey's historically high animal health status [1], prompting investigation for emerging infectious causes. The combination of diarrhoea, sudden reductions in milk production and reproductive losses led to consideration of orthobunyaviruses recently detected elsewhere in Europe. Here we describe the investigations leading to the identification of Shamonda virus (SHAV) strain 0209/2026 and its genomic characterisation.

Respiratory swabs, faeces and blood samples were submitted from four dairy farms. Initial differential diagnoses included heat stress, dietary changes, mycotoxin exposure and infectious causes of diarrhoea in adult cattle, including *Salmonella* spp., Johne's disease and liver fluke infestation. However, investigations for these infectious diseases returned negative results.

Viral RNA was extracted from the clinical samples using the Qiagen QIAamp Viral RNA mini kit and tested using two pan-Simbu RT-qPCRs [2,3], together with a Schmallenberg virus (SBV) RT-qPCR assay (virotype SBV 2.0 RT-qPCR Kit, Indical Bioscience). Sera and faeces from two of the four farms tested positive in both pan-Simbu RT-qPCRs, with a lowest C_q value of 19, but were negative in the commercial SBV assay.

Two SHAV-positive serum samples (0209 and 0221) and two pooled respiratory swab samples from affected farms underwent Illumina MiSeq sequencing. Near complete L, M and S genome segment sequences were obtained from combined next-generation sequencing (NGS) data of the two sera. Reads were mapped to recently described German SHAV sequences (GenBank accession numbers OZ502471.1, OZ502472.1, OZ502473.1 for the L, M and S genome segments, respectively) to assemble this SHAV segments' sequences. Serum 0209 generated 13,098,122 sequence reads, of which 3,457, 2,263, and 280 mapped to the assembled L, M, and S genome segments, respectively. Similarly, serum 0221 generated 11,428,012 sequence reads, with 58, 24, and 6 reads mapping to the L, M, and S genome segments, respectively. No additional viral pathogens were detected in either the serum samples or the pooled respiratory swab samples.

No evidence of SHAV infection was identified on the two PCR-negative holdings, where heat stress and management-related factors were considered the most likely explanation for the observed clinical signs.

Phylogenetic analysis of near-complete L, M and S genome segments was conducted using MegAlign software of the DNASTAR Lasergene 17 package and MEGA X [4]. The analysis placed SHAV 0209/2026 within European clade II [5], clustering with German strains detected in 2026 (Fig. 1). Sequence identity was also the highest with contemporary European clade II viruses (99.7-99.9% across all three genome segments) (Table 1). Similar phylogenetic placement across all three genome segments provided no evidence of recent reassortment. Compared with SBV, the virus showed high conservation of the S segment but marked divergence within the M segment, confirming its classification as SHAV.

The clinical syndrome, observed in Jersey, shared several features with recent SHAV outbreaks described elsewhere in Europe, including reductions in milk yield and diarrhoea [6]. Recumbency was also a prominent feature of Jersey outbreak. Although recumbency has not been widely described in recent European SHAV outbreaks, Jersey breed cattle are recognised as being more susceptible than many other dairy breeds to conditions associated with recumbency, particularly those linked to hypocalcaemia [7]. Nevertheless, the high morbidity observed in the most severely affected herd (47/120 milking cows affected, including 34 recumbent animals) indicates a substantial impact on animal welfare and productivity. Reproductive problems, including returns to service, abortions and stillbirths, were also observed, although their association with SHAV infection remains uncertain. In contrast, investigation of the remaining affected farms suggested heat stress as the most likely cause of the observed clinical signs.

The route of introduction remains uncertain. However, the close genetic relationship to European clade II viruses is consistent with introduction from mainland Europe. As orthobunyaviruses are primarily transmitted by *Culicoides* spp., windborne dispersal of infected midges represents a plausible mechanism of introduction. Additional sequence data from animals and vector populations in Jersey and neighbouring European countries would help to clarify the geographical distribution and movement of related viruses.

SHAV has historically been detected only sporadically in Africa [8] and Asia [9], but has recently been recognised as an emerging pathogen in Europe [10]. The detection of a virus almost identical to contemporary German clade II strains suggests that SHAV may be more widely distributed across western Europe than current surveillance data indicate. Furthermore, the identification of genetically related viruses in multiple European countries over a relatively short period supports the possibility of recent regional spread, although direct evidence for the routes and mechanisms of transmission remains lacking.

Although SHAV was detected in samples from only two holdings, the similarity of the clinical presentation observed across all four farms and the recognised limitations of testing animals outside the viraemia period mean that wider involvement cannot be excluded. Further serological investigations would be required to assess the extent of virus circulation during the outbreak. To our knowledge, this represents the first detection of SHAV in the British Isles and extends the known geographic range of European clade II SHAV into the north-west European Atlantic region.

The outbreak affected pedigree Jersey dairy herds, a breed that represents the foundation of the dairy industry in Jersey. Consequently, even limited circulation of SHAV could have disproportionate economic significance for the island's livestock sector.

Taken together, the identification of SHAV clade II in Jersey, Channel Islands, extends the known geographic distribution of this clade and demonstrates close genetic relationship to contemporary strains detected in Germany. These findings suggest wider circulation of SHAV in western Europe and highlight the importance of continued surveillance and genomic sequencing of emerging Simbu serogroup viruses.

Abbreviations

SHAV, Shamonda virus; SBV, Schmallenberg virus; S, M and L, small, medium and large genome segments

Declarations

Authors, contributions

Conceptualization: AD, VS, and NE; Methodology: AD and HD; Resources: AD, CL, RM, VS and NE; Writing—Original Draft: AD, VS and NE; Writing—Review and Editing: AD, HD, CL, RM, VS, and NE; Supervision: AD, VS and NE; Funding Acquisition: VS, and ND.

Conflict of interest

None declared

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Ethical statement

Animal samples were collected for diagnostic and clinical purposes as part of routine veterinary investigations conducted by recognised veterinary surgeons in Jersey under the Veterinary Surgeons (Jersey) Law 1999. No procedures were undertaken solely for research purposes and, therefore, ethical approval was not required.

Use of artificial intelligence

We acknowledge the use of AI to improve readability of the text.

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References

1. CHeCS (Cattle Health Certification Standards) Jersey Island Genetics Ltd. Available at: https://checs.co.uk/about-us/scheme-providers/jersey_island_genetics/ (accessed 14 September 2026)
2. Tauscher K, Wernike K, Fischer M, Wegelt A, Hoffmann B, Teifke JP et al (2017) Characterization of Simbu serogroup virus infections in type I interferon receptor knock-out mice. *Arch Virol* 162:3119–3129. <https://doi.org/10.1007/s00705-017-3475-1>
3. Golender N, Bumbarov VY, Erster O, Beer M, Khinich Y, Wernike K (2018) Development and validation of a universal S-segment-based real-time RT-PCR assay for the detection of Simbu serogroup viruses. *J Virol Methods* 261:80–85. <https://doi.org/10.1016/j.jviromet.2018.08.008>
4. Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Mol Biol Evol* 35:1547–1549. <https://doi.org/10.1093/molbev/msy096>
5. Wernike K, Pfaff F, Zeiske S, Höper D, Beer M (2026a) Two incursions, two viruses: emergence of a second novel Shamonda virus clade in Central Europe, [preprint]. *bioRxiv*. 2026 Sep 7. <https://doi.org/10.64898/2026.09.05.749452>

6. Kelleci M, Fusade-Boyer M, Chrétien D, Durand E, Mircovich M, Sécula A et al (2026) Detection of a novel Shamonda orthobunyavirus in dairy cattle, France, June 2026. Euro Surveill 31:2600689. <https://doi.org/10.2807/1560-7917.ES.2026.31.33.2600689>
7. Chiwome B, Kandiwa E, Mushonga B, Sajeni S, Habarugira G (2017) A study of the incidence of milk fever in Jersey and Holstein cows at a dairy farm in Beatrice, Zimbabwe. J S Afr Vet Assoc 88:a1457. <https://doi.org/10.4102/jsava.v88i0.1457>
8. Causey OR, Kemp GE, Causey CE, Lee VH (1972) Isolations of Simbu-group viruses in Ibadan, Nigeria 1964-69, including the new types Sango, Shamonda, Sabo and Shuni. Ann Trop Med Parasitol 66:357–362. <https://doi.org/10.1080/00034983.1972.11686835>
9. Hirashima Y, Kitahara S, Kato T, Shirafuji H, Tanaka S, Yanase T (2017) Congenital malformations of calves infected with Shamonda virus, Southern Japan. Emerg Infect Dis 23:993–996. <https://doi.org/10.3201/eid2306.161946>
10. Wernike K, Hoffmann B, Link EK, Rotheneder S, Eshak M, Pfaff F et al (2026b) It happened again: emergence of a Shamonda-like orthobunyavirus in Central Europe, [preprint]. bioRxiv. 2026 Aug 6. 10.64898/2026.08.06.743243

Tables

Table 1: Sequence identity (%) of Jersey Island SHAV 0209/2026 and representative of orthobunyaviruses across L, M and S gene segments.

Jersey SHAV 0209/2026			
L segment	M segment	S segment	
87.8 - 88.0	86.7	96.1 - 96.4	European Clade I
99.7	99.8 - 99.9	99.8 - 99.9	European Clade II
96.7	95.5 - 97.1	98.5 - 99.2	Asia (Japan)
-	-	98.1	Africa (S. Africa)
90.0	89.0	97.4	Africa (Nigeria)
88.8	52.4	96.4	SBV
84.1 - 84.3	53.3	92.0 - 93.3	Sathuperi

Figures



Figure 1

Maximum-likelihood phylogenetic trees of the L, M and S genome segments of the SHAV 0209/2026, detected in sera of affected cattle in dairy farms on Jersey Island, and representative of closely related orthobunyaviruses from 1965–2026 including the SHAV strains recently detected in Germany, France and Switzerland.