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Shamonda virus infection in sheep and goat: First evidence from Europe

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Short Report

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Abstract

Shamonda virus (SHAV), an orthobunyavirus of the Simbu serogroup (species *Orthobunyavirus schmallenbergense*), was detected in European cattle for the first time in summer 2026, raising concerns regarding its host range and pathogenic potential. To investigate infection in small ruminants, 509 sheep and 86 goat sera collected in Baden-Württemberg, Germany, during the period of SHAV emergence were tested by real-time RT-PCR for the presence of viral genome. For comparison, 517 cattle sera were included. Viral RNA was detected in seven sheep (1.38%), three goats (3.49%) and 11 cattle (2.13%). These findings demonstrate SHAV infection in sheep and goats in Europe and suggest a broader host range than cattle only. Although clinical effects could not be assessed, the detection in small ruminants highlights the need for enhanced surveillance, particularly of reproductive disorders, given the strong abortifacient potential of related Simbu serogroup viruses.

Main text

The emergence of Shamonda virus clade Europe 1 (SHAV-EU1) in cattle in Switzerland, Germany and France in summer 2026 represents the first confirmed detection of this virus in Europe [1, 2]. That same year, a second SHAV clade (SHAV-EU2) appeared in cattle in northwestern Germany [3]. Both SHAV incursions raise important questions regarding its host range and potential impact on European livestock. SHAV belongs to the species *Orthobunyavirus schmallenbergense* within the Simbu serogroup of the genus *Orthobunyavirus*, a group of arthropod-borne viruses primarily transmitted by *Culicoides* biting midges and known to infect a range of mainly ruminant species [4]. Historically, SHAV has been detected predominantly in cattle and *Culicoides* spp. in Africa, with subsequent detections reported in Australia and Japan [5–7]. Although information on SHAV infection in small ruminants remains scarce, there is evidence suggesting that sheep and goats may be susceptible. In a molecular surveillance study in South Africa, SHAV was detected and genetically characterized in an aborted goat foetus, providing direct evidence of SHAV infection in a small ruminant and raising the possibility of an association with reproductive disease [8]. Furthermore, serological investigations in Nigeria detected antibodies against SHAV among sheep, although these findings cannot distinguish SHAV infection from exposure to antigenically related Simbu serogroup viruses and respective cross-reactions [9].

In addition to Schmallenberg virus (SBV), the first European Simbu serogroup virus, which is well established as a causative agent of abortion, stillbirth and congenital malformations in sheep and goats, several other simbuviruses, including Shuni virus (SHUV) and Akabane virus (AKAV) among others, have been associated with infections in small ruminants [10–13]. The current detection of two clades of SHAV in Europe [1–3] in cattle therefore warrants investigation of the occurrence of the first European clade (SHAV-EU1) also in local sheep and goats, in order to assesses its pathogenic potential and epidemiological significance in European livestock.

Here, we tested 509 sheep and 86 goat sera collected in the German federal state of Baden-Württemberg in summer 2026, i.e. during the period when the first indications by reported clinical diseases and

confirmation of the virus by RT-qPCR and sequence analyses in cattle emerged in this region [2]. For comparison, 517 cattle sera were included. The samples were taken by the responsible veterinarians in the context of health monitoring of the respected farms or represented routine diagnostic submissions following the rules of German mandatory surveillance programs for other diseases. Therefore, it was a random selection; the sampling did not specifically target animals with clinical signs. Nucleic acid was extracted from all samples using the King Fisher 96 Flex purification system and the NucleoMag Vet Kit (Machery Nagel, Düren, Germany) according to the manufacturer's instructions and subsequently tested by a generic RT-qPCR for viruses of the Simbu serogroup (Pan-Simbuvirus RT-qPCR) [14]. In addition, the samples were tested by an S-segment-based SBV RT-qPCR [15] to exclude the second simbuvirus present in Central Europe. Samples that gave positive results in the Pan-Simbuvirus RT-qPCR were analysed by a commercial RT-qPCR kit offered for the detection of the SHAV clade circulating in Southern Germany, Switzerland and France (ID Gene™ SHLV Duplex, Innovative Diagnostics, Grabels, France).

Of the 509 sheep sera, seven tested positive by the Pan-Simbuvirus RT-qPCR (1.38%), with quantification cycle (Cq) values ranging from 28.7 to 38.1. Of the 86 goat sera, three gave positive results (3.49%) with Cq values of 33.3, 37.1 and 39.0. In addition, 11 of the 517 cattle sera tested positive (2.13%; Cq values 21.4 to 38.6) (Table 1). All samples gave consistently negative results in the SBV RT-qPCR, thereby excluding an SBV infection. Of the 21 Pan-Simbuvirus RT-qPCR positive samples, 13 likewise tested positive by the commercial SHAV RT-qPCR (Table 1). In particular, the samples with lower Cq values were confirmed by the SHAV follow-up PCR (Table 1), which could indicate differences in sensitivity or specificity for weakly reacting samples.

Table 1
Animal species and quantification cycle values of the samples that gave positive results in the Pan-Simbuvirus RT-qPCR.

Sample number	Animal species	Pan-Simbuvirus RT-qPCR	SBV RT-qPCR	ID Gene™ SHLV Duplex
2026BVD08794	sheep	36.6/positive	negative	negative
2026BVD08855	sheep	38.1/positive	negative	negative
2026BVD09608	sheep	35.3/positive	negative	35.5/positive
2026BVD09641	sheep	36.8/positive	negative	37.5/positive
2026BVD09658	sheep	36.3/positive	negative	35.4/positive
2026BVD09686	sheep	28.7/positive	negative	28.9/positive
2026BVD09698	sheep	28.8/positive	negative	29.5/positive
2026BVD09358	goat	39.0/positive	negative	negative
2026BVD10050	goat	37.1/positive	negative	negative
2026BVD10076	goat	33.3/positive	negative	33.4/positive
2026BVD08263	cattle	36.3/positive	negative	negative
2026BVD08282	cattle	37.2/positive	negative	negative
2026BVD08470	cattle	38.1/positive	negative	39.5/positive
2026BVD08484	cattle	23.5/positive	negative	24.4/positive
2026BVD08490	cattle	38.6/positive	negative	negative
2026BVD08492	cattle	27.2/positive	negative	26.3/positive
2026BVD08502	cattle	28.4/positive	negative	27.7/positive
2026BVD08504	cattle	35.5/positive	negative	34.9/positive
2026BVD08512	cattle	25.7/positive	negative	24.8/positive
2026BVD08541	cattle	38.1/positive	negative	negative
2026BVD09430	cattle	21.4/positive	negative	28.6/positive

Discussion

The detection of SHAV-RNA in 7/509 (1.38%) sheep and 3/86 (3.49%) goats in Baden-Württemberg during summer 2026 indicates that infection occurred in all three investigated ruminant species during the period of virus emergence. Hence, the first European SHAV clade EU1 infects a broader range than cattle alone. This finding is particularly relevant because SHAV has only recently emerged in Europe, and

little is currently known about its clinical relevance in European livestock. The observation of infected small ruminants is consistent with the broader host range known for Simbu serogroup viruses, which includes a number of ruminant species among others, although individual viruses differ considerably in their ability to infect different host species and to cause clinical disease [7]. The present study cannot establish a causal relationship between SHAV infection and clinical disease, as the animals were not specifically selected because of clinical signs. Nevertheless, the detection of viral RNA in routine surveillance samples suggests that infections may occur without obvious clinical disease in adult animals. Notwithstanding, the potential consequences of SHAV infections for animal health are of particular concern because several closely related Simbu serogroup viruses are important abortifacients of ruminants. SBV, the first Simbu serogroup virus to become established in Europe, causes relatively mild or subclinical infection in adult animals but can result in severe reproductive disease following infection during pregnancy. In sheep and goats, foetal infection may lead to abortion, stillbirth and characteristic congenital malformations [12]. Similarly, AKAV and SHUV have been associated with reproductive disorders and congenital abnormalities in ruminants [10, 11] and, most importantly, SHAV was detected and genetically characterized in an aborted goat foetus in South Africa [8]. These examples demonstrate that apparently inconspicuous infection in adult animals can have substantial consequences for herd productivity when infection occurs during susceptible stages of gestation. The emergence of SHAV in Europe therefore represents a potential new animal-health threat. Hence, surveillance of small ruminants, combined with systematic investigation of reproductive disorders, will be essential to determine whether pregnant animals are at particular risk.

Declarations

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Declaration of interest statement

The authors report there are no competing interests to declare.

Ethical statement

The samples were taken by the responsible veterinarians in the context of health monitoring of the respected farms and as part of their clinical practice, or represented routine diagnostic submissions following the rules of German mandatory surveillance programs for other diseases. No permissions were needed to collect these specimens.

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