



Brussels, 10th September 2026

UECBV Ref: MV - 33740

UECBV Situation Note: 2026 Shamonda-like Virus Outbreak in Europe

Introduction

More than a decade after the emergence of Schmallerberg virus in 2011, a new *Orthobunyavirus* of the Simbu serogroup emerged in Central Europe in the summer of 2026 and is currently affecting seven countries: **France, Germany, Switzerland, the Netherlands, Belgium, Liechtenstein and Austria.**

Whole-genome sequencing revealed that the detected virus has the highest sequence similarity to Shamonda virus, hence its designation as “**Shamonda-like virus**”.

The latest test results point to a **second incident** of introduction and spread in Germany. Sequence analyses of PCR-positive samples from north-western and eastern Germany reveal the presence of a further variant related to the Shamonda virus, which differs significantly from the Shamonda virus/DE/2026 variant initially detected. To facilitate distinction, the two variants are now designated **Shamonda virus Europe 1** (SHAV-EU1) and **Shamonda virus Europe 2** (SHAV-EU2) respectively.

The current outbreak therefore comprises **two independent events** which are already overlapping in some federal German states.

At the EPIZONE Conference in Bern in early September, it was reported that this second type of Shamonda virus had been detected in Belgium, the Netherlands, northern Germany and north-western France, while the first type continues to circulate in France, southern Germany, Austria and Switzerland.

Background on Shamonda virus (SHAV)

Shamonda virus (SHAV) is transmitted by blood-sucking midges of the genus *Culicoides* and is closely related to other viruses of the Simbu serogroup, such as Schmallerberg virus (SBV) and Akabane virus (AKAV).

Shamonda virus was first detected in Nigeria in the mid-1960s and, up until 2026, had been reported sporadically in western, eastern and southern Africa, as well as in Japan. In the summer of 2026, it appeared in Central Europe for the first time, with farmers and veterinarians in Germany, France and Switzerland reporting clinical signs since mid-June.

Susceptible species and clinical signs

Infections with Shamonda virus Europe 1 have so far been detected in cattle, horses, alpacas, sheep, and goats. As of 1 September, all positive samples for SHAV-EU2 in Germany have come from cattle.



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Cattle with acute infections show mild clinical signs such as fever, reduced milk yield and diarrhoea. Neurological disorders are also possible, as has been observed in relation to SHAV-EU1 in horses.

Vertical transmission and foetal effects

The virus has been identified in aborted bovine foetuses, providing strong evidence of transplacental infection and suggesting a possible role in abortion, although a causal relationship has not yet been conclusively established.

Similarly, while the virus has recently been detected in a congenitally abnormal newborn calf in the Netherlands, its role in causing foetal malformations remains unproven.

Legislation

SHAV infection is not currently categorised under the European Union's animal health legislation and is therefore not subject to any official surveillance or control measures. The infection is also not regulated at international level by the World Organisation for Animal Health (WOAH).

No official communication has been issued at EU level so far.

Situation by affected country

Germany

The first detection of Shamonda virus in Germany was confirmed by the Friedrich-Loeffler-Institut (FLI) on 3 August 2026. The virus was identified on a cattle farm in southern Germany, in the state of Baden-Württemberg.

On 1 September 2026, the FLI reported the introduction and spread of a second genotype (SHAV-EU2) among cattle herds in north-western and eastern Germany, particularly in the states of North Rhine-Westphalia, Lower Saxony, Hesse and Thuringia.

France

In June 2026, veterinarians reported acute diarrhoea, fever, lethargy and reduced milk yield in dairy cattle in Doubs and Ain, followed by similar cases in Savoie and Haute-Savoie in July.

The virus was identified on 31 July by the FLI and ENVT through genomic analysis of cattle samples. By 6 September, it had been detected by RT-PCR in 37 departments.

Switzerland

The virus was first identified in Switzerland by the Institute of Virology and Immunology (IVI) on 31 July 2026. By 24 August, 22 cantons had been affected.



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On the same date, the virus was detected for the first time in horses showing neurological signs. It was identified only in brain tissue, while blood and cerebrospinal fluid samples tested negative, possibly reflecting a shorter viraemic period in horses than in cattle.

The Netherlands

In early September, Royal GD detected Shamonda-like virus for the first time in a **newborn calf** showing underdevelopment, abnormal limbs and neurological signs. A causal link between the infection and these abnormalities has not yet been established.

Genetic analysis confirmed two variants circulating in the Netherlands. The predominant variant, also detected in the affected calf, corresponds to that circulating in northern Germany. The second variant, previously identified in southern Germany, France and Switzerland, has so far been detected in one cattle in the Netherlands.

Belgium

Cases have been confirmed in both Wallonia and Flanders in both sheep and cattle.

Austria

The first case of Shamonda-like virus was detected in Austria in mid-August 2026. The disease is currently spreading rapidly across the country. Infections have been detected in Vorarlberg, Upper Austria, Tyrol, Salzburg, Styria, Carinthia and Lower Austria. Further spread is expected. To date, cases in Austria have been limited exclusively to cattle.

Concerns

Given the demonstrated capacity for genome reassortment among viruses of the Simbu serogroup, the co-circulation of the newly identified SHAV and Schmallenberg virus (SBV) in Europe could lead to increased genetic diversity and the emergence of novel reassortant viruses. Although reassortment between SHAV and SBV has not yet been demonstrated, their close evolutionary relationship highlights the need for continued genomic surveillance.

In Germany, for example, SBV and the two SHAV variants are currently co-circulating. It is therefore likely that these viruses will exchange genome segments and mutate.

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