

# European Mountain Ash ringspot associated virus – a rapid review of the wider threat to Scotland

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## Rapid Review



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Royal  
Botanic Garden  
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Forest Research

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## 1 Executive Summary

European mountain ash ringspot-associated virus (EMARaV) is an emaravirus infecting rosaceous hosts that is established and likely widespread in Scotland and elsewhere in Great Britain. Evidence suggests it has been present in the UK for several decades. The virus primarily affects species within the *Sorbus* complex and related genera (e.g. *Amelanchier*, *Aronia*). EMARaV is putatively vectored by the eriophyid mite *Phytoptus pyri* (pear leaf blister mite), enabling local spread and potential longer-distance dispersal through wind-borne movement of the vector.

EMARaV was detected in an *Aronia* tree in the wider environment in Scotland; however, there are no reports of the virus spreading to other commercially important rosaceous genera, such as *Rubus*, or to smaller-scale commercial plantings of *Aronia melanocarpa* (chokeberry) in Scotland, England or Wales. Furthermore, evidence from large-scale chokeberry orchards elsewhere in Europe indicates that EMARaV is, at most, a minor pathogen of this crop.

Based on current evidence, EMARaV does not represent a significant emerging, or escalating threat to Scotland's forestry, woodland biodiversity, or horticultural sectors. Observed impacts are largely limited to foliar symptoms in susceptible hosts. Continued surveillance, reporting of suspect cases, and laboratory confirmation will support ongoing risk monitoring.

## 2 Purpose of review

This rapid review has been commissioned to summarise the current scientific evidence on *European mountain ash ringspot-associated virus* (EMARaV), with a particular focus on its host range, distribution, transmission pathways and potential risks to Scotland's trees, woodlands and horticultural systems. The review brings together published literature, surveillance records and recent UK observations to assess whether EMARaV represents an emerging or changing threat. The aim is to support evidence-based risk assessment, surveillance prioritisation and plant health decision-making in Scotland.

### 2.1 Virus details

The taxonomic hierarchy of EMARaV can be seen in Table 1.

*Table 1. Taxonomic hierarchy of EMARaV*

Order	Elliovirales
Family	Fimoviridae
Genus	<i>Emaravirus</i>
New species name (from 2021)	<i>Emaravirus sorbi</i>
Previous Species name and common name	<i>European mountain ash ringspot-associated virus</i>

EMARaV is a multipartite (6 RNA segments), negative-strand RNA plant virus with a genome size of ~ 12.3 to 15.3 Kilobases.

There are currently 33 recognised virus species within the genus *Emaravirus*, for which EMARaV is the type-member. The 33 species split into 4 clades based on genome amino acid sequences of the RNA-dependent RNA polymerase (RdRP), Glycoprotein precursor (GPP), Nucleocapsid protein (NP) and Movement protein (MP). In emaraviruses, such as EMARaV, these proteins are typically encoded on separate genome segments with RdRP on RNA1, the glycoprotein precursor on RNA2, the nucleocapsid protein on RNA3, and the movement protein on RNA4.

EMARaV falls into Clade B for all regions except for the MP sequence which falls into Clade A. The closest species to EMARaV in clade B are shown below. Other viruses that may be of relevance to Scotland in other clades are also shown in Table 2.

*Table 2. Emaravirus species of relevance to Scotland and their respective clades*

<b>New species name</b>	<b>Old species and common name</b>	<b>Clade</b>
<i>Emaravirus lilae</i>	<i>Lilac chlorotic ringspot associated virus</i>	B
<i>Emaravirus actinidiae</i>	<i>Actinidia chlorotic ringspot associated virus</i>	B
<i>Emaravirus cercidis</i>	<i>Redbud yellow ringspot associated virus</i>	B
<i>Emaravirus rubi</i>	<i>Blackberry leaf mottle associated virus</i>	A
<i>Emaravirus fici</i>	<i>Fig mosaic virus</i>	A
<i>Emaravirus rosae</i>	<i>Rose rosette mosaic virus</i>	A
<i>Emaravirus idaei</i>	<i>Raspberry leaf blotch virus</i>	C
<i>Emaravirus quercus</i>	<i>Common oak ringspot associated virus</i>	C
<i>Emaravirus tritici</i>	<i>High plain wheat mosaic virus</i>	C
<i>Emaravirus camelliae</i>	<i>Camellia japonica associated virus</i>	D

## 2.2 Host range

The reported hosts of EMARaV are members of the Rosaceae, a large family comprising approximately 4,828 species across 91 genera. Within this family, EMARaV infections are predominantly recorded in the genus *Sorbus*. However, recent taxonomic revisions of the *Sorbus* complex have resulted in several former *Sorbus* species being reassigned to other genera, including *Aria*, *Cormus* and *Karpatiosorbus*.

*S. aucuparia* subsp. *moravica*, *S. aucuparia* × *Crataegus sanguinea* cv. *Granatnaja*, and (*Sorbus aria* × *Aronia arbutifolia*) × *S. aucuparia* cv. *Burka*, cv. *Finskaja* (a *Sorbus* hybrid of unknown origin) were reported as new hosts in production orchards in the Czech Republic in 2015 (1). EMARaV was first reported in serviceberry (*Amelanchier* sp.) in Germany in 2018 (2) and *Karpatiosorbus x hybrida* in Finland in 2020 (3). EMARaV has more recently been reported in Scotland in *Amelanchier* and *Aronia* (A. Inman Personal communication, 2025); these two genera along with *Sorbus*, *Aria*, *Cormus* and *Karpatiosorbus* all belong within the subfamily Amygdaloideae, Tribe, Maleae and subtribe Malinae. A complete list of known hosts is provided below.

- *Sorbus aucuparia* (Rowan)
- *Aria edulis* (previously *Sorbus aria*) (Whitebeam)
- *Karpatiosorbus x hybrida* (previously *Sorbus hybrida*) (Finnish Whitebeam)
- *Cormus domestica* (previously *Sorbus domestica*) (Service tree)
- *Sorbus torminalis* (Wild service tree)
- *Sorbus Intemedia* (Swedish Whitebeam)
- *Sorbus rehderiana*
- *Amelanchier* spp. (Serviceberry)
- *Aronia melanocarpa* (Black chokeberry)
- *S. aucuparia* subsp. *moravica*,
- *S. aucuparia* × *Crataegus sanguinea* cv. *Granatnaja*,
- (*Sorbus aria* × *Aronia arbutifolia*) × *S. aucuparia* cv. *Burka*, cv. *Finskaja*

The above species vary significantly in range in Scotland. *S. aucuparia* and *A. edulis* are very widespread in both planted and natural landscapes (4). The other species mentioned above are much less frequently found according to the Plant Atlas (2020) (5).

It is worth noting that EMARaV **has not** been reported on any of the rarer Scottish whitebeam species such as *Hedlundia arranensis* (previously *Sorbus arranensis*), which is an endemic species to the island of Arran. However, no full-scale targeted surveys for EMARaV have been conducted in Scotland.

Given the information above, the impact of EMARaV to the natural environment and production horticulture in Scotland is therefore thought to be low. A targeted survey could be initiated to confirm this.

## 2.3 Distribution

EMARaV appears to be widespread in Northern Europe with reports from Norway, Sweden (6), Finland (7,8), Poland (9), Germany (6,10), the Czech Republic (9), Russia and the United Kingdom (6,7). European iNaturalist records include reports from Sweden, Finland, Lithuania, Russia, Austria, Germany, Poland and Northern Italy, N. Ireland, Scotland and Northern England (A. Inman, Personal communication 6 February 2026).

It is likely that the virus has been present (and established) in GB for more than 30 years based on symptoms reported by Cooper in 1979 (7). Reports from GB suggest the virus is widespread in Scotland based on samples taken from symptomatic trees found in diverse locations in the Central and West Highlands of Scotland (regions include Stirlingshire, Perth, Kinross and Highlands, Killin, Eilean Donan Castle, West Highlands and Ullapool).

EMARaV is currently a priority pest for Observatree. There are around 50 reports of EMARaV recorded across GB from 2016 to 2025 indicating the widespread nature of the virus. Reports are based on visual images of symptoms only; these have not been confirmed by sequencing or other lab tests (Figure 1).

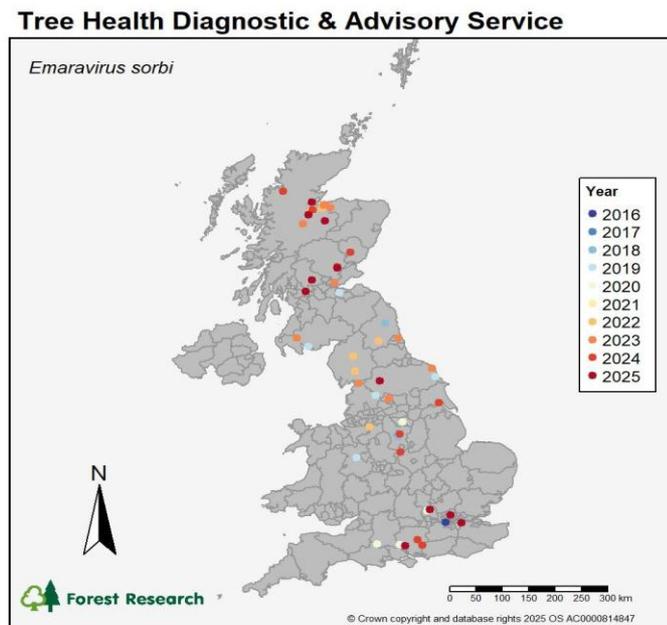


Figure 1: TreeAlert reports of suspected EMARaV across GB. Reports are based on visual images only and not by confirmation by sequencing or other lab tests (Credit Tree Health Advisory Service and TreeAlert, Forest Research).

## 2.4 Symptoms

Symptoms are usually observed as ringspots, line patterns and oak leaf patterns on foliage of affected trees (Figure 2).

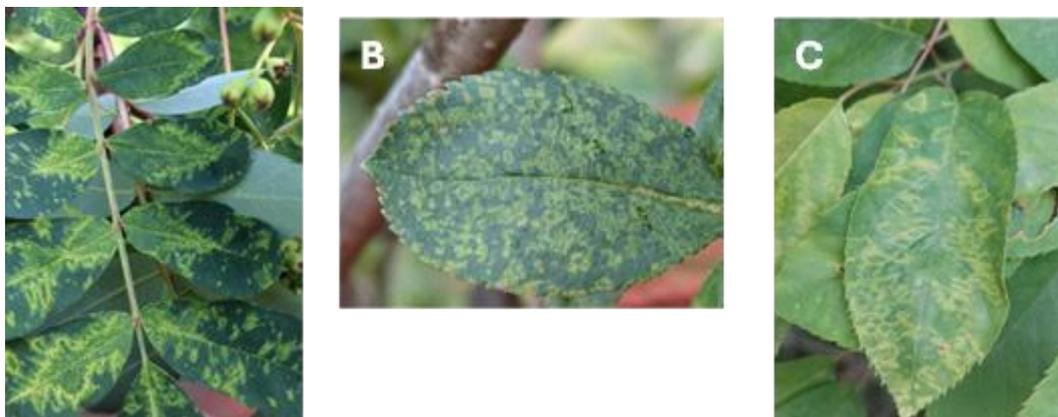


Figure 2: Symptoms of EMARaV on (A) *Sorbus aucuparia* (Credit FERA), (B) *Aronia* sp. (Credit A. Inman), (C), *Amelanchier* sp. (possibly *A. lamarckii*), (Credit A. Inman)

## 2.5 Transmission

EMARaV is putatively reported to be naturally transmitted in *Sorbus aucuparia* (European mountain ash) by the eriophyid mite *Phytoptus pyri* (pear leaf blister mite) (Figure 3) (11). This mite occurs on multiple rosaceous hosts, including economically important genera such as *Pyrus* (pear) and *Malus* (apple), which also belong to the subtribe Malinae. There is, however, no evidence to date that suggests EMARaV infects pear or apple. Confirmed hosts of EMARaV are provided in Section 2.2.

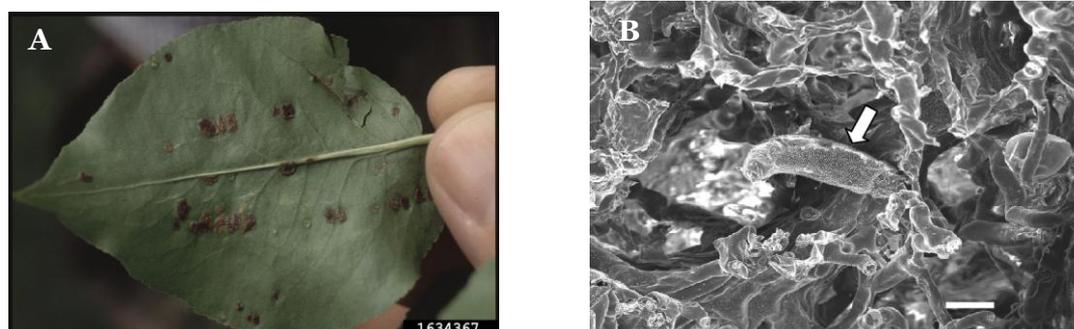


Figure 3: (A) Typical blister damage caused by the Pearleaf blister mite on pear (Credit Penn State Department of Plant Pathology & Environmental Microbiology Archives, Penn State University, Bugwood.org). (B) *Phytoptus pyri* (white arrow) within gall tissue from the undersurface of a leaf of an EMARaV infected mountain ash tree. Scanning electron microscopy. Bar represents 50  $\mu\text{m}$  (replicated from Mielke-Ehret & Muehlbach, 2012 DOI:10.3390/v4091515 (12))

The mite lives in galls on the lower surface of *S. aucuparia* leaves. In their study, Mielke-Ehret et al. 2010 (11) investigated mites from galls in both EMARaV infected and uninfected *S. aucuparia* leaves. Immunofluorescence microscopy showed that the EMARaV N protein P3 was present in entire mites prepared from galls on infected *S. aucuparia*. In *P. pyri* collected from non-infected plants, no or only very weak fluorescence signals were detected. RT-PCR analysis of *P. pyri* individuals from EMARaV infected leaves also revealed the presence of both virus genomic RNAs and antigenomic RNAs (signifying the active replication of a negative-sense RNA virus), suggesting that *P. pyri* can acquire the virus and is a candidate vector of EMARaV. No virus was detected by RT-PCR in mites from uninfected leaves. This notion is supported by the fact that eriophyid mites are well known vectors of other *Emaraviruses*. Other examples of eriophyid mites transmitting viruses include *Phyllocoptes fructiphilus* (Rose bud mite) which transmits *Rose rosette virus*, *Aceria tosichellai* (Wheat curl mite) which transmits *High Plains wheat mosaic virus*, *Phyllocoptes parvoflori* which transmits *Blackberry leaf mottle-associated virus* and *Phyllocoptes gracilis* (Raspberry leaf and bud mite), putatively reported to transmit *Raspberry leaf blotch virus*.

Spread of EMARaV in Scotland is likely to dependent on vector presence and EMARaV host distribution. *P. pyri* is likely to facilitate transmission of EMARaV to hosts locally and at a potentially longer-distance spread, given the wind-dispersed nature of these mites. However, there is currently no evidence of other mechanisms of spread such as seed or pollen or mechanical transmission (11).

## 2.6 Risk to other hosts

The Rosaceae family includes many plants that are native to Scotland (e.g., lady's mantle (*Alchemilla vulgaris*), hawthorn (*Crataegus monogyna*), and apple (*Malus domestica*), and several species which are important crops (e.g., *Rubus* species such as raspberries and blackberries).

The recent report of EMARaV in *Aronia* in the wider environment in Scotland raises questions regarding the potential risk to commercially grown Rosaceae berry fruit such as *Rubus* and *Aronia melanocarpa* (Chokeberry). Within the three decades that EMARaV is known to have been present in GB, there has been no reported movement of EMARaV from *Sorbus* to commercial *Rubus* crops. This is consistent with their taxonomic separation: *Rubus* (Subfamily Rosoideae, Tribe Rubeae) is distantly related to the Malinae subtribe (i.e. *Sorbus*, *Aronia*, *Amelanchier*), a factor that typically restricts virus and vector host ranges. Even if a host jump occurred, EMARaV's impact would likely be no more damaging to the 24 *Rubus* pathogens already regulated or monitored via the UKPHRR.

Although chokeberry production in the GB is currently limited, several small-scale commercial plantations exist. These include a plantation established in 2011 in the North Downs, Kent ([Aroniaberriesuk.co.uk](http://Aroniaberriesuk.co.uk)), as well as smaller operations in North Wales ([Aerona](#)) is cultivated within some UK agroforestry systems ([The Agroforestry Research Trust](#)). *Aronia* is cultivated in parts of Europe, but Poland is the world's leading producer with about 90% of global production on more than 6,000 hectares ([Aronia, the Native American superfood that conquered Poland](#)). Cultivation is also widespread in other Eastern European countries (Germany, Austria, Slovenia, Croatia, Serbia, Ukraine) and, more recently, in Italy through pilot projects and crops mainly in Friuli.

A scan of the literature on EMARaV infection of *Aronia* doesn't yield any published reports of EMARaV affecting commercial *Aronia* in Europe except for the virus being found in production orchards in the Czech Republic (1). The lack of reports across other parts of Europe suggest EMARaV isn't a major pathogen of this crop despite likely proximity and presumably frequent exposure to EMARaV. Similarly, there don't appear to be any reports of EMARaV on the genus *Rubus* outside of the UK. Observed impacts are largely limited to foliar symptoms in susceptible hosts.

### 3 Conclusion

Current evidence indicates that EMARaV is established and likely widespread in Scotland and across GB generally, primarily affecting species within the *Sorbus* complex and closely related genera in the Rosaceae such as *Aronia* and *Amelanchier*. Symptom reports and confirmed detections suggest the virus has been present for several decades and is not a recent introduction. It is worth noting that EMARaV has not been reported on any of the rarer Scottish whitebeam species such as *Hedlundia arranensis* (previously *Sorbus arranensis*), which are an endemic species to the island of Arran. However, no full-scale targeted surveys for EMARaV have been conducted in Scotland.

There is no evidence to date that EMARaV poses a significant threat to commercially important rosaceous crops in Scotland such as *Rubus* and small-scale commercially grown *Aronia melanocarpa* (chokeberry). The taxonomic distance of *Rubus* to *Sorbus*, *Aronia* and *Amelanchier* is likely to be a factor restricting virus and vector host range. There is limited published evidence of infection in larger-scale commercial *Aronia melanocarpa* production in Europe. The absence of widespread reports from major chokeberry-producing regions in Europe suggests that EMARaV is unlikely to represent a major threat to commercial chokeberry cultivation in Scotland.

Spread of EMARaV in Scotland is likely to be dependent on vector presence and EMARaV host distribution. *P. pyri* is likely to facilitate transmission of EMARaV to hosts locally and at a potentially longer-distance spread, given the wind-dispersed nature of these mites. However, there is currently no evidence other mechanisms of spread such as seed or pollen or mechanical transmission.

Overall, based on current knowledge, EMARaV does not appear to represent an emerging or escalating threat to Scotland's forestry, woodland biodiversity, or horticultural systems. Observed impacts are largely limited to foliar symptoms in susceptible hosts. Continued passive surveillance and reporting of suspect cases, and laboratory confirmation will support ongoing risk monitoring and would improve confidence in this assessment.

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