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Pest categorisation of High Plains wheat mosaic virus

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Abstract

The EFSA Panel on Plant Health conducted a pest categorisation of High Plains wheat mosaic virus (HPWMOV) for the EU territory. The identity of HPWMOV, a member of the genus *Emaravirus* (family *Fimoviridae*), is well established and reliable identification methods are available. The pathogen is not included in the EU Commission Implementing Regulation 2019/2072. HPWMOV has been reported from Argentina, Australia, Canada, Ukraine and USA, and it is not known to be present in the EU. HPWMOV infects plant species of the family Poaceae (i.e. wheat, maize and several other cultivated or wild Poaceae species). It is the causal agent of High Plains disease of wheat and maize, inducing symptoms ranging from mild to severe mosaic, chlorosis and necrosis in wheat, and chlorotic streaks in maize plants. The virus is transmitted by the wheat curl mite *Aceria tosichella*, which is present in the EU. HPWMOV transmission via seeds was reported to occur in sweet corn. Sweet corn seeds for sowing were identified as the most relevant pathway for entry of HPWMOV into the EU. Seeds from other hosts and viruliferous wheat curl mites were identified as entry pathways associated with uncertainties. Machinery not appropriately cleaned may move infected seeds and/or parts of cereals infested by viruliferous mites. Cultivated and wild hosts of HPWMOV are distributed across the EU. Would the pest enter and establish in the EU territory, economic impact on the production of cultivated hosts is expected. Phytosanitary measures are available to prevent entry and spread of the virus in the EU. HPWMOV fulfils the criteria that are within the remit of EFSA to assess for it to be regarded as a potential Union quarantine pest.

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1. Introduction

1.1. Background and Terms of Reference as provided by the requestor

1.1.1. Background

The new Plant Health Regulation (EU) 2016/2031, on the protective measures against pests of plants, is applying from 14 December 2019. Conditions are laid down in this legislation in order for pests to qualify for listing as Union quarantine pests, protected zone quarantine pests or Union regulated non-quarantine pests. The lists of the EU regulated pests together with the associated import or internal movement requirements of commodities are included in Commission Implementing Regulation (EU) 2019/2072. Additionally, as stipulated in the Commission Implementing Regulation 2018/2019, certain commodities are provisionally prohibited to enter in the EU (high risk plants, HRP). EFSA is performing the risk assessment of the dossiers submitted by exporting to the EU countries of the HRP commodities, as stipulated in Commission Implementing Regulation 2018/2018. Furthermore, EFSA has evaluated a number of requests from exporting to the EU countries for derogations from specific EU import requirements.

In line with the principles of the new plant health law, the European Commission with the Member States are discussing monthly the reports of the interceptions and the outbreaks of pests notified by the Member States. Notifications of an imminent danger from pests that may fulfil the conditions for inclusion in the list of the Union quarantine pest are included. Furthermore, EFSA has been performing horizon scanning of media and literature.

As a follow-up of the above-mentioned activities (reporting of interceptions and outbreaks, HRP, derogation requests and horizon scanning), a number of pests of concern have been identified. EFSA is requested to provide scientific opinions for these pests, in view of their potential inclusion by the risk manager in the lists of Commission Implementing Regulation (EU) 2019/2072 and the inclusion of specific import requirements for relevant host commodities, when deemed necessary by the risk manager.

1.1.2. Terms of Reference

EFSA is requested, pursuant to Article 29(1) of Regulation (EC) No 178/2002, to provide scientific opinions in the field of plant health.

EFSA is requested to deliver 53 pest categorisations for the pests listed in Annex 1A, 1B, 1D and 1E (for more details see mandate M-2021-00027 on the [Open.EFSA portal](#)). Additionally, EFSA is requested to perform pest categorisations for the pests so far not regulated in the EU, identified as pests potentially associated with a commodity in the commodity risk assessments of the HRP dossiers (Annex 1C; for more details see mandate M-2021-00027 on the [Open.EFSA portal](#)). Such pest categorisations are needed in the case where there are not available risk assessments for the EU.

When the pests of Annex 1A are qualifying as potential Union quarantine pests, EFSA should proceed to phase 2 risk assessment. The opinions should address entry pathways, spread, establishment, impact and include a risk reduction options analysis.

Additionally, EFSA is requested to develop further the quantitative methodology currently followed for risk assessment, in order to have the possibility to deliver an express risk assessment methodology. Such methodological development should take into account the EFSA Plant Health Panel Guidance on quantitative pest risk assessment and the experience obtained during its implementation for the Union candidate priority pests and for the likelihood of pest freedom at entry for the commodity risk assessment of High Risk Plants.

1.2. Interpretation of the Terms of Reference

High Plains wheat mosaic virus is one of a number of pests identified from horizon scanning and listed in Annex 1 to the Terms of Reference (ToR) to be subject to pest categorisation to determine whether it fulfils the criteria of a potential Union quarantine pest (QP) for the area of the EU excluding Ceuta, Melilla and the outermost regions of Member States (MSs) referred to in Article 355(1) of the Treaty on the Functioning of the European Union (TFEU), other than Madeira and the Azores, and so inform European Commission decision making as to its appropriateness for potential inclusion in the lists of pests of Commission Implementing Regulation (EU) 2019/2072. If a pest fulfils the criteria to be potentially listed as a Union QP, risk reduction options will be identified.

2. Data and methodologies

2.1. Data

2.1.1. Literature search

A literature search on High Plains wheat mosaic virus was conducted at the beginning of the categorisation in the ISI Web of Science bibliographic database, using the scientific name of the pest as search term. Papers relevant for the pest categorisation were reviewed, and further references and information were obtained from experts, as well as from citations within the references and grey literature.

2.1.2. Database search

Pest information, on host(s) and distribution, was retrieved from the EPPO Global Database, the CABI databases and scientific literature databases as referred above in Section 2.1.1.

Data about the import of commodity types that could potentially provide a pathway for the pest to enter the EU and about the area of hosts grown in the EU were obtained from EUROSTAT (Statistical Office of the European Communities).

The Europhyt and TRACES databases were consulted for pest-specific notifications on interceptions and outbreaks. Europhyt is a web-based network run by the Directorate General for Health and Food Safety (DG SANTÉ) of the European Commission as a subproject of PHYSAN (Phyto-Sanitary Controls) specifically concerned with plant health information. TRACES is the European Commission's multilingual online platform for sanitary and phytosanitary certification required for the importation of animals, animal products, food and feed of non-animal origin and plants into the European Union, and the intra-EU trade and EU exports of animals and certain animal products. Up until May 2020, the Europhyt database managed notifications of interceptions of plants or plant products that do not comply with EU legislation, as well as notifications of plant pests detected in the territory of the MSs and the phytosanitary measures taken to eradicate or avoid their spread. The recording of interceptions switched from Europhyt to TRACES in May 2020.

GenBank was searched to determine whether it contained any nucleotide sequences of High Plains wheat mosaic virus and the associated information. GenBank® (www.ncbi.nlm.nih.gov/genbank/) is a comprehensive publicly available database that as of August 2019 (release version 227) contained over 6.25 trillion base pairs from over 1.6 billion nucleotide sequences for 450,000 formally described species (Sayers et al., 2020).

2.2. Methodologies

The Panel performed the pest categorisation for High Plains wheat mosaic virus, following guiding principles and steps presented in the EFSA guidance on quantitative pest risk assessment (EFSA PLH Panel et al., 2018), the EFSA guidance on the use of the weight of evidence approach in scientific assessments (EFSA Scientific Committee, 2017) and the International Standards for Phytosanitary Measures No. 11 (FAO, 2013).

The criteria to be considered when categorising a pest as a potential Union QP is given in Regulation (EU) 2016/2031 Article 3 and Annex I, Section 1 of the Regulation. Table 1 presents the Regulation (EU) 2016/2031 pest categorisation criteria on which the Panel bases its conclusions. In judging whether a criterion is met, the Panel uses its best professional judgement (EFSA Scientific Committee, 2017) by integrating a range of evidence from a variety of sources (as presented above in Section 2.1) to reach an informed conclusion as to whether or not a criterion is satisfied.

The Panel's conclusions are formulated respecting its remit and particularly with regard to the principle of separation between risk assessment and risk management (EFSA founding regulation (EU) No 178/2002); therefore, instead of determining whether the pest is likely to have an unacceptable impact, deemed to be a risk management decision, the Panel will present a summary of the observed impacts in the areas where the pest occurs, and make a judgement about potential likely impacts in the EU. While the Panel may quote impacts reported from areas where the pest occurs in monetary terms, the Panel will seek to express potential EU impacts in terms of yield and quality losses and not in monetary terms, in agreement with the EFSA guidance on quantitative pest risk assessment (EFSA PLH Panel, 2018). Article 3 (d) of Regulation (EU) 2016/2031 refers to unacceptable social impact as a criterion for QP status. Assessing social impact is outside the remit of the Panel.

Table 1: Pest categorisation criteria under evaluation, as derived from Regulation (EU) 2016/2031 on protective measures against pests of plants (the number of the relevant sections of the pest categorisation is shown in brackets in the first column)

Criterion of pest categorisation	Criterion in Regulation (EU) 2016/2031 regarding Union quarantine pest (article 3)
Identity of the pest (Section 3.1)	Is the identity of the pest clearly defined, or has it been shown to produce consistent symptoms and to be transmissible?
Absence/presence of the pest in the EU territory (Section 3.2)	Is the pest present in the EU territory? If present, is the pest in a limited part of the EU or is it scarce, irregular, isolated or present infrequently? If so, the pest is considered to be not widely distributed.
Pest potential for entry, establishment and spread in the EU territory (Section 3.4)	Is the pest able to enter into, become established in, and spread within, the EU territory? If yes, briefly list the pathways for entry and spread.
Potential for consequences in the EU territory (Section 3.5)	Would the pests' introduction have an economic or environmental impact on the EU territory?
Available measures (Section 3.6)	Are there measures available to prevent pest entry, establishment, spread or impacts?
Conclusion of pest categorisation (Section 4)	A statement as to whether (1) all criteria assessed by EFSA above for consideration as a potential quarantine pest were met and (2) if not, which one (s) were not met.

3. Pest categorisation

3.1. Identity and biology of the pest

3.1.1. Identity and taxonomy

Is the identity of the pest clearly defined, or has it been shown to produce consistent symptoms and/or to be transmissible? (Yes or No)

Yes, the identity of High Plains wheat mosaic virus is established and the pest has been shown to produce consistent symptoms on its hosts and to be transmissible.

High Plains wheat mosaic virus (HPWMOV) is classified in a species (*Emaravirus tritici*) belonging to the genus *Emaravirus*, the only genus in the family *Fimoviridae*, order *Bunyavirales* (<https://talk.ictvonline.org/taxonomy/>). Over time, the virus has been named differently, that is High Plains virus, maize red stripe virus, wheat mosaic virus, which are now considered as synonyms of High Plains wheat mosaic virus. Enveloped virus particles are quasi-spherical to ovoid, 80–200 nm in diameter, containing a segmented genome consisting of eight single-stranded negative-sense RNA molecules, ca. 18.5 kb in total, which are not capped at the 5' end and not polyadenylated at the 3' end. Each genomic RNA segment (RNA 1–8) contains one open reading frame (ORF) encoding one protein, denoted P1–P8. RNA 1, 6,981 nucleotides (nt) in size, codes for P1, the 266 kDa RNA-dependent RNA polymerase (RdRp) of 2,272 amino acids (aa), containing the conserved motifs of *Bunyaviridae* RdRp (Tatineni et al., 2014). RNA 2 (2,211 nt) encodes P2 (667 aa), a glycoprotein (GP) that can undergo post-transcriptional cleavage to give proteins GP1 and GP2, 25.7 and 50.9 kDa in size, respectively. RNA 3 codes for the P3 nucleocapsid structural protein of which two variants of a 286- or 289-aa are known. RNA 4, consisting of 1,682 nt, codes for the 42 kDa P4 (364 aa), which was suggested to be the movement protein. RNA 5 and RNA 6, of 1,715 and 1,752 nt, encode for P5 (478 aa, 56 kDa) and P6 (492 aa, 58 kDa), respectively, with unknown functions, which are slightly conserved among emaraviruses. RNA 7 (1,434 nt) and RNA 8 (1,339 nt) code for P7 (305 aa, 36 kDa) and P8 (176 aa, 21 kDa), respectively (Tatineni and Hein, 2021). P7 and P8 may function as silencing suppressors (Gupta et al., 2018). The genomic RNAs of HPWMOV were completely sequenced and the sequences are publicly available in the GenBank database (Tatineni et al., 2014). RNAs 6–8 are typical of HPWMOV and do not show any sequence homology with other viruses in the GenBank (Tatineni and Hein, 2021). The first and last 14 nt at the 5' and 3' ends are conserved among all the eight HPWMOV RNA segments and are reverse complementary to each other, thus contributing to the formation of

panhandle-like structures, which are often found among negative-stranded RNA virus (Tatineni and Hein, 2021).

The EPPO code¹ (Griessinger and Roy, 2015; EPPO, 2019) for this species is: WHPV00 (EPPO, online).

3.1.2. Biology of the pest

HPWMOV infects plant species of the family Poaceae and is the causal agent of High Plains disease of wheat and maize. Infected wheat plants show symptoms ranging from mild to severe mosaic, chlorosis and necrosis, whereas red striping and chlorotic streaks are typically displayed by infected maize plants (Jensen et al., 1996). In the USA, HPWMOV is frequently found in fields also infected by the potyvirids wheat streak mosaic virus (WSMV) and/or Triticum mosaic virus (TriMV) (Mahmood et al., 1998; Seifers et al., 2002, 2008; Hein et al., 2012; Redila et al., 2021). Typical symptoms caused by single infections of these viruses are difficult to distinguish from each other and co-infected plants may show exacerbated symptoms (Burrows et al., 2009). HPWMOV, TriMV and WSMV form a complex of viruses transmitted by the same mite vector (*Aceria tosichella*) and cause one of the most important diseases of wheat in the USA (Tatineni and Hein, 2021).

Transmission of HPWMOV to several hosts in the family Poaceae by the wheat curl mite *Aceria tosichella* Keifer has been documented (Seifers et al., 1997). As for other mite-transmitted viruses, the transmission mode of HPWMOV by *A. tosichella* is not known (Tatineni and Hein, 2021). A high level of genetic diversity in wheat curl mite has been reported, with at least 29 different lineages identified (Seifers et al., 2002; Carew et al., 2009; Skoracka et al., 2012; Skoracka et al., 2013; Szydlo et al., 2015; Skoracka et al., 2018, Khalaf et al., 2020). The efficiency of virus transmission is determined by the mite lineage as documented by Seifers et al. (2002), who showed that three out of five wheat curl mite lineages of different geographic origin in the USA were unable to transmit, or able to transmit at very low rate, the five tested HPWMOV isolates. The other two lineages differed in the efficiency of HPWMOV transmission: one population ('Nebraska', type 2) transmitted HPWMOV efficiently, the other one ('Montana', type 1) efficiently transmitted HPWMOV only if the plants were coinfecting by WSMV (Seifers et al., 2002; Hein et al., 2012). Therefore, uncertainty exists on the transmission efficiency of the virus by some mite biotypes. Type 1 and type 2 lineages occur in Australia, Europe, South America and the Middle East, and are known as MT-8 and MT-1 in Europe and South America, respectively (Skoracka et al., 2017, 2018; Khalaf et al., 2020). Wind contributes to passive spatial dispersal of the wheat curl mite *A. tosichella* up to several kilometres (Stilwell et al., 2019). Whether other eriophyid mite species are involved in the virus spread is unknown, but this possibility is considered unlikely due to the specificity of virus-mite interactions generally involved in this kind of vector-mediated transmission (de Lillo et al., 2021).

Seed transmission was initially reported to occur in sweet corn (*Zea mays* subsp. *saccharata*), at a very low frequency (Foster et al., 2001). However, recent studies clarified that HPWMOV transmission through sweet corn seed may occur at higher rates (2–4%) (Blunt and Hill 2004; Nischwitz, 2020). In a greenhouse experiment, among 179 seedlings emerging from sweet corn seeds originated from infected plants, only 6 were tested positive for HPWMOV and showed the typical symptoms described above on maize (Nischwitz, 2020). In Brazil, HPWMOV has been detected by phytosanitary inspections using serological and molecular tests, in seedlings of maize emerged from seeds of two accessions imported from USA, although no information on the tested maize subspecies was provided (Alves Botelho et al., 2016). No experimental data are available on seed transmission for other hosts of HPWMOV.

HPWMOV is not mechanically transmissible by inoculation of sap from infected tissues, however the virus was successfully inoculated by vascular puncture of maize embryos (Seifers et al., 2004; Louie et al., 2006). Transmission by pollen is not reported for HPWMOV and members of the genus *Emaravirus* are not known to be pollen transmitted (Mielke-Ehret and Mühlbach, 2012).

The viral disease epidemiology and disease cycle largely depend on the wheat curl mite behaviour, and on the presence of 'green bridge' host plants that allow the viruliferous mites to survive in the absence of host crops. Volunteer wheat plants, infested by virulent mites migrating from HPWMOV-infected maturing wheat, is the most efficient green bridge in the central Great Plains of North America

¹ An EPPO code, formerly known as a Bayer code, is a unique identifier linked to the name of a plant or plant pest important in agriculture and plant protection. Codes are based on genus and species names. However, if a scientific name is changed the EPPO code remains the same. This provides a harmonized system to facilitate the management of plant and pest names in computerized databases, as well as data exchange between IT systems (Griessinger and Roy, 2015; EPPO, 2019).

(Tatineni and Hein, 2021). At the emergence of winter wheat, these viruliferous mites moving to newly emerged seedlings may introduce the virus to these crops (Tatineni and Hein, 2021). In addition, maize and grass hosts also can act as green bridges. Although most commercial maize hybrids cannot be systemically infected by HPWMoV (Marçon et al., 1997a,b) they can still serve as green bridges and support viruliferous mites (Knoell, 2018; Tatineni and Hein, 2021).

3.1.3. Host range/Species affected

Natural HPWMoV infections have been originally reported in cultivated species of the family Poaceae, such as wheat (*Triticum aestivum* L.) and maize (*Zea mays* L.) (Jensen et al., 1996). In 1994 and 1995, yellow foxtail (*Setaria glauca* L.) and green foxtail (*Setaria viridis* L.) plants were found to be infected by HPWMoV (Seifers et al., 1998). More recently, one infected foxtail barley (*Hordeum jubatum* L.) plant was reported to be infected by HPWMoV in Canada (Abdullahi et al., 2020). Other natural hosts may also exist. Due to the lack of mechanical transmission, the HPWMoV host range is difficult to study in laboratory conditions, however several additional species of the family Poaceae, such as oat (*Avena sativa* L.), barley (*Hordeum vulgare* L.), rye (*Secale cereale* L.), rye brome (*Bromus secalinus* L.), yellow foxtail, have been successfully infected by using the wheat curl mite as a vector. In contrast, green foxtail infection in greenhouse experiments failed (Seifers et al., 1998). A detailed list of natural and experimental hosts of HPWMoV is reported in Appendix A.

3.1.4. Intraspecific diversity

Due to the error-prone viral replication system and the subsequent selection of the fittest variants in a certain environment, viruses have the typical features of quasi-species (Andino and Domingo, 2015). This means that, even in a single host, they accumulate as a cluster of closely related sequence variants slightly differing from each other. Therefore, a certain level of intraspecific diversity is expected for all viruses. This genetic variability may interfere with the efficiency of detection methods.

Two full genome sequences, including all the eight RNA components, and two complete coding sequences of HPWMoV, as well as partial genomic sequences from several HPWMoV isolates are currently available in the NCBI GenBank database (<https://www.ncbi.nlm.nih.gov/nucleotide/>). An overall sequence variability at the nucleotide level allowed to identify two distinct isolates (Stewart, 2016). The nucleocapsid protein shows the highest sequence variability among HPWMoV isolates, often associated with differences in symptomatology and infection ability (Seifers et al., 2004). Two serologically distinct virus isolates U04-82 and U04-83, have been described, slightly differing in the nucleocapsid protein (Seifers et al., 2009).

3.1.5. Detection and identification of the pest

Are detection and identification methods available for the pest?

Yes, detection and identification methods are available for High Plain wheat mosaic virus.

Serological and molecular tests have been developed for the detection and identification of HPWMoV, including DAS-ELISA (Seifers et al., 1997) and several RT-PCR amplification-based assays. The existence of at least two different HPWMoV serotypes may hamper detection of some isolates by ELISA assay (Seifers et al., 2009). An early molecular detection protocol was based on RT-PCR (Lebas et al., 2005). The identification methods have been improved by the use of SYBR green RT-qPCR, TaqMan RT-qPCR, endpoint RT-PCR, RT-helicase dependent amplification (RT-HDA) and a field deployable system (Razor-Ex) using a single primer set containing 5' modifications to detect a 96 nt fragment from different HPWMoV variants (Arif et al., 2014). In a comparative study, all these detection methods were considered rapid, reliable, sensitive and efficient (Arif et al., 2014). Loop-mediated isothermal amplification (LAMP) was also successfully employed for HPWMoV detection (Arif et al., 2012). The higher sensitivity of RT-qPCR versus ELISA test was shown by Bryan et al. (2019).

3.2. Pest distribution

3.2.1. Pest distribution outside the EU

To date, HPWMoV has been reported in Argentina, Australia, Canada, Ukraine and the USA (Snihur et al., 2020; CABI, 2022). Details on HPWMoV worldwide distribution are summarised in the

Appendix B. The presence of HPWMOV in the USA is known since the early identification of the virus as the causal agent of High Plains disease in 1993 (Jensen et al., 1996), although the presence of the virus in the USA has been dated back possibly to early 1950s (Tatineni and Hein, 2021). HPWMOV was then reported in Australia (Skare et al., 2006; Coutts et al., 2014) and, in 2017, in Argentina and Canada (Alemandri et al., 2017; Abdullahi et al., 2020). The recent report of HPWMOV in Ukraine, on wheat from four regions (Dnipropetrovsk, Donetsk, Zaporizhia and Kharkiv) and on maize from another region (Vinnytsia) (Snihur et al., 2020), shows that the virus is now present and established also in one European country (Figure 1).

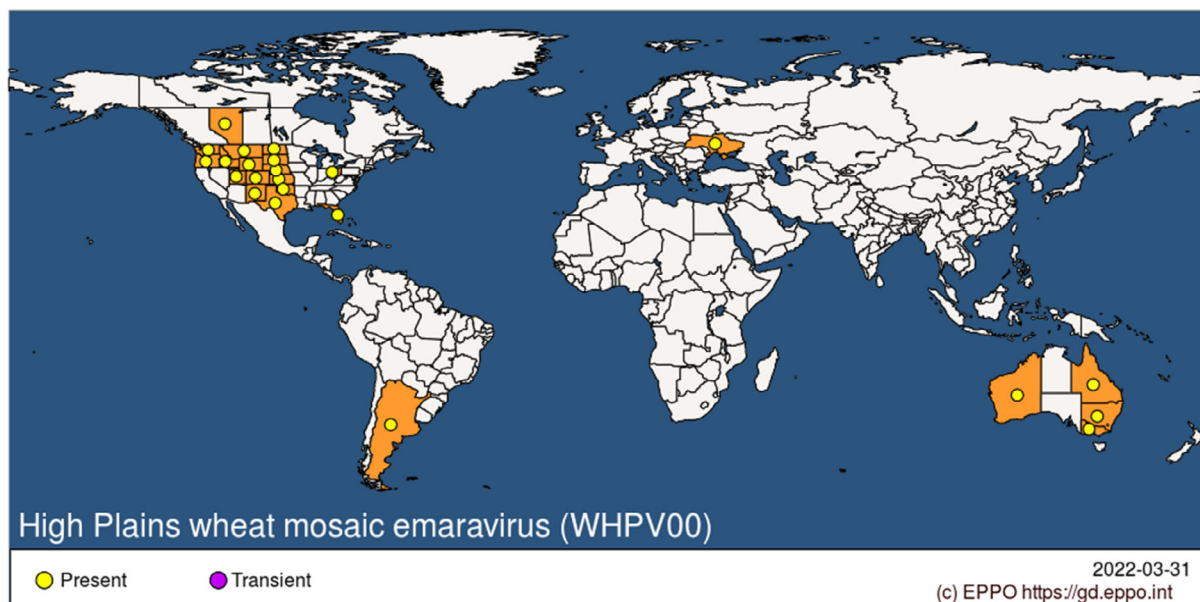


Figure 1: Global distribution of High Plains wheat mosaic virus (Source: Eppo Global database accessed on 31 March 2022)

3.2.2. Pest distribution in the EU

Is the pest present in the EU territory? If present, is the pest in a limited part of the EU or is it scarce, irregular, isolated or present infrequently? If so, the pest is considered to be not widely distributed.

No, High Plains wheat mosaic virus has not been reported in the EU.

To date, HPWMOV has not been reported in the EU.

3.3. Regulatory status

3.3.1. Commission Implementing Regulation 2019/2072

High Plains wheat mosaic virus is not listed in Annex II of Commission Implementing Regulation (EU) 2019/2072, an implementing act of Regulation (EU) 2016/2031.

3.3.2. Hosts or species affected that are prohibited from entering the Union from third countries

None of the host plants of High Plains wheat mosaic virus are prohibited from entering the Union from third countries under Commission Implementing Regulation (EU) 2019/2072.

3.3.3. Legislation addressing the organisms that vector High Plains wheat mosaic virus (Commission Implementing Regulation 2019/2072)

The known vector of HPWMOV, the wheat curl mite *Aceria tosichella*, is not regulated under Commission Implementing Regulation 2019/2072.

3.4. Entry, establishment and spread in the EU

3.4.1. Entry

Is the pest able to enter into the EU territory? If yes, identify and list the pathways

Yes, High Plains wheat mosaic virus may enter into the EU with seeds for sowing of sweet corn. Seeds of other cereal hosts, viruliferous wheat curl mite *Aceria tosichella* and machinery not appropriately cleaned may also represent entry pathways, with uncertainties.

Comment on plants for planting as a pathway

Host plants for planting is not a pathway of entry as cereals are not traded as plants.

The panel identified sweet corn seeds for sowing as the main entry pathway of HPWMOV in the EU. Seeds for sowing of other cereal hosts have been identified as potential entry pathways, with uncertainties due to the lack of experimental evidence on seed transmission in these hosts. The viruliferous wheat curl mite *Aceria tosichella* provides an additional entry pathway associated with uncertainty due to lack of information on the persistence of its transmission ability. Viruliferous mites may enter by natural means (i.e. wind) and/or by import of infested fresh corn cobs and sprouts. However, phytosanitary certificate is required to import such fresh corn cobs and sprouts or other vegetable products of maize from third countries other than Switzerland (Annex XI, A, 3). Machinery not appropriately cleaned may move infected seeds and/or part of cereals infested by viruliferous mites, thus contributing to the spread of the virus. Grain of cereal hosts for feed and food are identified as a minor entry pathway of HPWMOV: although it is unlikely that grain for feed and food will be sown, grain spillage may occur during unloading operation and transport (EFSA PLH Panel, 2010). Phytosanitary certificate is required to import grains of genera *Triticum* L., *Secale* L. and *xTriticale* Wittm. ex A. Camus from several countries, including the USA in which HPWMOV has been reported to be present (2019/2072, Annex XI, A, 1). Interestingly, the Ukrainian wheat and maize isolates of HPWMOV, recently reported for the first time in Europe, were found in distant geographic regions and showed significant sequence diversity from each other, suggesting possible multiple introductions in this country (Snihur et al., 2020), either through seeds for sowing or through viruliferous mites. Possible entry by natural means (i.e. by wind) of viruliferous mites into EU MSs neighbouring Ukraine cannot be excluded.

There are no prohibitions (Annex VI) or specific requirements (Annex VII) in place regulating HPWMOV hosts in the EU. Phytosanitary certificate is required for some commodities as indicated in Table 2 where main pathways are listed.

Table 2: Potential pathways for High Plains wheat mosaic virus into the EU 27

Pathways	Life stage	Relevant mitigations [e.g. prohibitions (Annex VI), special requirements (Annex VII) or phytosanitary certificates (Annex XI) within Implementing Regulation 2019/2072]
Seeds for sowing of <i>Zea mays</i> subsp. <i>saccharata</i> (sweet corn)	N/A	Phytosanitary certificate required to import sweet corn and corn from third countries other than Switzerland (Annex XI, A, 8)
Seeds for sowing of other HPWMOV hosts	N/A	Phytosanitary certificate is required to import seeds of Poaceae from some country in which HPWMOV has been reported to be present (Argentina and Australia) and seeds of genera <i>Triticum</i> L., <i>Secale</i> L. and <i>xTriticale</i> Wittm. ex A. Camus from several countries, including USA, where the virus has been reported (Annex XI, A, 8)
Viruliferous wheat curl mite <i>Aceria tosichella</i>	Adult and possibly young mite stages	
Machinery and vehicles	N/A	Official statement that the machinery or vehicles are cleaned and free from soil and plant debris is required (Annex VII, 2) Phytosanitary certificate for the introduction into the Union territory of machinery and vehicles from third countries other than Switzerland is required (Annex XI, A, 1)

EU 27 annual imports of cereals (CN 10) and maize seed for sowing (CN100510) from countries where HPWMoV is present are provided in Appendix C and D, respectively.

Notifications of interceptions of harmful organisms began to be compiled in Europhyt in May 1994 and in TRACES in May 2020. As at 26 January 2022 there were no records of interception of HPWMoV in the Europhyt and TRACES databases. However, HPWMoV has been intercepted in Brazil in seedlings of maize emerged from seeds of two accessions imported from USA (Alves Botelho et al., 2016). There were no records of interception of the mite vector *A. tosicHELLa* in the Europhyt and TRACES databases.

3.4.2. Establishment

Is the pest able to become established in the EU territory?

Yes, the virus can potentially establish wherever the hosts and the vector are available in the EU.

HPWMoV could potentially establish in the EU in areas where its hosts and vector, *A. tosicHELLa*, are present (see Section 3.4.3 for the distribution of *A. tosicHELLa* in the EU). *A. tosicHELLa* is the only known vector of the virus and is necessary for the virus establishment, including its transfer to suitable hosts after entry. Whether other vectors may also contribute to the establishment of HPWMoV in the EU is not known. Moreover, the wheat curl mite plays a major role in the virus epidemiology due to its ability to preserve the virus on the green bridges when the crops are not in the field (see Section 3.1.2). *A. tosicHELLa* has been reported in several EU MSs (see Section 3.4.3).

3.4.2.1. EU distribution of main host plants

Natural hosts of HPWMoV are widespread in the EU. Cereal crops widely occur in the EU. Details on cereal crops production areas in individual EU MSs are provided in Table 3.

Table 3: Cereals (excluding rice) for the production of grain (including seed) [C1000] area (cultivation/harvested/production) (1,000 ha). Eurostat database, date of extraction 10 December 2021.

MS/Time	2016	2017	2018	2019	2020
Belgium	337,02	305,43	304,52	313,11	304,34
Bulgaria	1.804,65	1.718,83	1.806,78	1.915,74	1.953,69
Czechia	1.359,01	1.354,68	1.338,78	1.352,53	1.344,88
Denmark	1.464,80	1.442,80	1.416,29	1.373,66	1.366,92
Germany	6.325,00	6.276,20	6.148,90	6.380,00	6.074,90
Estonia	351,40	330,68	350,43	364,36	370,12
Ireland	280,34	271,68	260,97	266,66	265,63
Greece	952,81	808,22	757,63	698,29	703,79
Spain	6.130,53	5.907,63	5.922,60	5.872,34	5.967,17
France	9.513,27	9.323,15	9.042,03	9.378,93	8.889,92
Croatia	508,66	461,48	459,70	490,88	535,76
Italy	3.022,86	2.906,45	2.875,50	2.846,49	2.784,41
Cyprus	23,80	20,22	24,01	23,07	31,97
Latvia	706,10	633,40	679,80	733,90	750,00
Lithuania	1.326,70	1.199,51	1.257,23	1.349,57	1.382,43
Luxembourg	27,86	27,96	26,31	27,39	25,48
Hungary	2.563,85	2.400,41	2.365,03	2.455,80	2.334,66
Malta	0,00	0,00	0,00	0,00	0,00
Netherlands	179,16	161,93	166,38	178,16	172,27
Austria	784,31	776,18	778,94	776,40	764,87
Poland	7.400,26	7.602,00	7.806,31	7.891,43	7.410,54
Portugal	230,20	209,61	202,38	197,43	189,89
Romania	5.480,77	5.186,37	5.253,03	5.565,08	5.605,25

MS/Time	2016	2017	2018	2019	2020
Slovenia	98,36	98,46	98,25	98,62	101,28
Slovakia	752,32	717,47	743,15	769,12	747,32
Finland	998,10	864,56	906,80	946,50	951,60
Sweden	1.004,68	993,10	922,11	977,05	993,34

3.4.2.2. Climatic conditions affecting establishment

Except for those affecting the hosts and the vector, no eco-climatic constraints exist for HPWMoV.

3.4.3. Spread

Describe how the pest would be able to spread within the EU territory following establishment?

Trade of HPWMoV-infected seeds may spread the virus at long distances. Natural spread in the field is mediated by wheat curl mite (*A. tosichella*), which is known to be present in the EU territory and can be dispersed by wind and human activities.

Comment on plants for planting as a mechanism of spread

Generally, there is no trade of plants for planting (excluding seeds) of HPWMoV hosts.

HPWMoV may spread at large distances by seeds for sowing of HPWMoV-infected hosts. Natural spread in the field is mediated by wheat curl mite (*A. tosichella*), which is reported to be present in Bulgaria, France, Germany and Romania by CABI. However, its distribution in the EU is certainly wider because this mite has been reported also in Poland (Kozłowski, 2000; Skoracka et al., 2017). Moreover, the presence of WSMV, which is also transmitted by *A. tosichella*, in several EU MSs (Bulgaria, Czech Rep., Hungary, Italy, Romania, Slovakia, Spain) (Byamukama et al., 2020; CABI, 2022), suggests that this mite is widely distributed in the EU, thus making possible mite-mediated spread of HPWMoV in several MSs. Viruliferous mites could be naturally spread by wind moving the virus up to several kilometres from an infected field (Stilwell et al., 2019). Perennial or biennial wild graminaceous hosts could act as reservoir for HPWMoV.

Human-assisted HPWMoV spread may occur by trade of seeds for sowing of HPWMoV-infected hosts. Machinery not appropriately cleaned may carry seeds and cereals debris infested by viruliferous mites, thus contributing to the spread of the virus. Trade of fresh corn cobs and sprouts infested by viruliferous wheat curl mites may also contribute to further spread the virus.

Minor risk of spread was identified in traded potted plants for planting where the soil or growing medium carries Poaceae weeds infested by the viruliferous mite *A. tosichella*.

3.5. Impacts

Would the pests' introduction have an economic or environmental impact on the EU territory?

Yes, would the virus be introduced in the EU an economic impact can be expected.

It has been shown that HPWMoV may induce symptoms of mosaic and necrosis on wheat, and chlorotic streaks and red striping on corn (Tatineni and Hein, 2021), and possibly kill susceptible maize plants, especially sweet corn, infected at early stages (CABI, 2022). In 1993, about a 30–85% disease incidence was reported in 304 ha of sweet corn fields in Idaho (Foster et al., 2001). During a field survey in Alberta (Canada) in 2017, disease incidence in wheat fields reached up to 75%; however, the symptomatic plants were mostly coinfecting by WSMV and HPWMoV (Abdullahi et al., 2020). Indeed, HPWMoV has been frequently found in mixed infections with WSMV and, together with this virus and Triticum mosaic virus (TriMV), form a complex of viruses causing one of the most important diseases of wheat in the USA (Tatineni and Hein, 2021). Due to the frequent mixed infections, it is difficult to determine the yield losses caused by each virus. Moreover, mixed infection may also affect HPWMoV epidemiology (Seifers et al., 2002; Hein et al., 2012), thus making even more complex the estimation of yield losses caused by this virus alone. Anyway, it has been estimated that HPWMoV infections can cause yield losses up to 75% in dent corn (*Zea mays* var. *indentata*) and 100% in sweet corn (Jensen, 1994, quoted in CABI, 2022). Wheat yields can also be deeply affected by virus infection. In a

greenhouse experiment, wheat varieties infected by HPWMoV isolate U04-82 showed a 27–79.6% reduction in seed production (Seifers et al., 2009). Lower seed germination and a 40% yield loss for sweet corn were reported by a grower in 2016 (Nischwitz, 2020). Coinfections of WSMV and HPWMoV have been reported to correlate with increased severity of symptoms in wheat (Burrows et al., 2009). Therefore, entry of HPWMoV in areas where WSMV is already present, like in several EU MSs, could give rise to mixed infections that are expected to increase yield losses already caused by WSMV alone.

The HPWMoV impact on corn yield can be mitigated by using resistant hybrid maize lines (Marçon et al., 1997a,b, 1999). Such a resistance is not available for sweet corn and wheat. In the case of wheat, resistant cultivars against WSMV are available, but whether they are also resistant against HPWMoV and the effect of this resistance on the virus epidemiology are still unknown (Tatineni and Hein, 2021).

Besides yield reduction, HPWMoV infections may impair seed quality.

Based on the above, if the pest would become established in the EU, an economic impact can be expected. However, there is uncertainty on the magnitude of this impact.

3.6. Available measures and their limitations

Are there measures available to prevent pest entry, establishment, spread or impacts such that the risk becomes mitigated?

Besides the request of phytosanitary certificate for seeds for some hosts and for vegetable products of maize, no other measures are currently applied to HPWMoV hosts (see Section 3.3 and 3.4.1).

3.6.1. Identification of potential additional measures

Additional potential risk reduction options and supporting measures are shown in Sections 3.6.1.1 and 3.6.1.2.

3.6.1.1. Additional potential risk reduction options

Potential additional control measures are listed in Table 4

Table 4: Selected control measures (a full list is available in EFSA PLH Panel, 2018) for pest entry/establishment/spread/impact in relation to currently unregulated hosts and pathways

Control measure/ Risk reduction option	RRO summary	Risk element targeted (entry/establishment/ spread/impact)
Require pest freedom	Use of cereal seeds for sowing and grains from a country officially free from HPWMoV or from a pest free area or from a pest free place of production is highly effective.	Entry/Spread
Crop rotation, associations and density, weed/volunteer control	Crop rotation, associations and density, weed/volunteer control are used to prevent problems related to pests and are usually applied in various combinations to make the habitat less favourable for pests. The measures deal with (1) allocation of crops to field (over time and space) (multi-crop, diversity cropping) and (2) to control weeds and volunteers as hosts of pests/vectors. Control of volunteer plants is an effective measure to interrupt disease cycle and reduces both mite and virus spread during the next growing season (Wegulo et al., 2008). When this measure is adopted over wide wheat production areas, it is considered particularly effective (CABI, 2022). Crop rotation with non-host plants could reduce the mite population.	Entry/Establishment/Spread/ Impact
Use of resistant and tolerant plant species/varieties	Resistant plants are used to restrict the growth and development of a specified pest and/or the damage they cause when compared to susceptible plant varieties under similar environmental conditions and pest pressure.	Entry/Establishment/Spread/ Impact

Control measure/ Risk reduction option	RRO summary	Risk element targeted (entry/establishment/ spread/impact)
	<ul style="list-style-type: none"> It is important to distinguish resistant from tolerant species/varieties. <p>Maize hybrids resistant to HPWMOV are available (Marçon et al., 1997a, b and 1999). Sweet corn and wheat varieties/cultivars resistant to HPWMOV are not available (Tatineni and Hein, 2021). Resistance against <i>A. tosichella</i> has been reported in wheat (Thomas et al., 2004) although the stability of such a resistance is considered uncertain (Tatineni and Hein, 2021).</p>	
Timing of planting and harvesting	<p>The objective is to produce phenological asynchrony in pest/crop interactions by acting on or benefiting from specific cropping factors such as: cultivars, climatic conditions, timing of the sowing or planting and level of maturity/age of the plant seasonal timing of planting and harvesting.</p> <p>Avoiding overlapping cultivation of <i>A. tosichella</i> hosts that may act as green bridges may contribute to interrupt the disease cycle (Tatineni and Hein, 2021).</p>	Entry (reduce contamination/infestation)/Spread/Impact
Chemical treatments on crops including reproductive material	Chemical treatments against the HPWMOV vector <i>A. tosichella</i> are ineffective in controlling the mite because of its hidden niches on the plants (Navia et al., 2013 and references therein). However, these treatments may only reduce the spread of the virus.	Impact/Spread
Cleaning and disinfection of facilities, tools and machinery	<p>The physical and chemical cleaning and disinfection of facilities, tools, machinery, transport means, facilities and other accessories (e.g. boxes, pots, pallets, palox, supports, hand tools). The measures addressed in this information sheet are: washing, sweeping and fumigation.</p> <p>These cleaning measures may remove the vector.</p>	Entry/Spread
Waste management	Treatment of the waste (deep burial, composting, incineration, chipping, production of bio-energy, etc.) in authorised facilities and official restriction on the movement of waste.	Establishment/Spread

3.6.1.2. Additional supporting measures

Potential additional supporting measures are listed in Table 5.

Table 5: Selected supporting measures (a full list is available in EFSA PLH Panel, 2018) in relation to currently unregulated hosts and pathways. Supporting measures are organisational measures or procedures supporting the choice of appropriate risk reduction options that do not directly affect pest abundance

Supporting measure	Summary	Risk element targeted (entry/establishment/ spread/impact)
Laboratory testing	Examination, other than visual, to determine if pests are present using official diagnostic protocols. Diagnostic protocols describe the minimum requirements for reliable diagnosis of regulated pests.	Entry
Sampling	According to ISPM 31, it is usually not feasible to inspect entire consignments, so phytosanitary inspection is performed mainly on samples obtained from a consignment. It is noted that the sampling concepts presented in this standard may also apply to other	Entry

Supporting measure	Summary	Risk element targeted (entry/establishment/spread/impact)
	<p>phytosanitary procedures, notably selection of units for testing.</p> <p>For inspection, testing and/or surveillance purposes, the sample may be taken according to a statistically based or a non-statistical sampling methodology.</p>	
Phytosanitary certificate and plant passport	<p>An official paper document or its official electronic equivalent, consistent with the model certificates of the IPPC, attesting that a consignment meets phytosanitary import requirements (ISPM 5)</p> <p>a) export certificate (import)</p> <p>b) plant passport (EU internal trade).</p> <p>A phytosanitary certification confirming that the seeds originate outside of the range of occurrence of HPWMOV is an effective measure.</p>	Entry
Certification of reproductive material (voluntary/official)	<p>Plants come from within an approved propagation scheme and are certified pest free (level of infestation) following testing; Used to mitigate against pests that are included in a certification scheme.</p> <p>The risk is reduced if seeds for sowing are produced under an approved certification scheme and tested free of the virus.</p>	Entry/spread
Delimitation of Buffer zones	<p>ISPM 5 defines a buffer zone as 'an area surrounding or adjacent to an area officially delimited for phytosanitary purposes in order to minimize the probability of spread of the target pest into or out of the delimited area, and subject to phytosanitary or other control measures, if appropriate' (ISPM 5). The objectives for delimiting a buffer zone can be to prevent spread from the outbreak area and to maintain a pest free production place (PFPP), site (PFPS) or area (PFA).</p>	Spread
Surveillance	<p>HPWMOV is not reported to be present in the EU.</p> <p>Surveillance would be an efficient supporting measure.</p>	Spread

3.6.1.3. Biological or technical factors limiting the effectiveness of measures

- Asymptomatic host plant species and similarity of symptoms caused by HPWMOV with those induced by other viruses (i.e. WSMV) may reduce the efficacy of inspections.
- Volunteers or other natural hosts providing green bridges for viruliferous mites that may favour virus establishment and spread could reduce the efficacy of measure addressing establishment and spread.
- The dispersal potential of the vector via wind could reduce the efficacy of the buffer zone.
- WSMV present in the EU may increase the transmission efficiency of HPWMOV by some *A. tosichella* lineages.
- The small size of the eriophyid mites may impair detection especially at low population size.

3.7. Uncertainty

- Natural host range of HPWMOV and the presence of asymptomatic hosts
- Seed transmission for natural hosts other than sweet corn
- Transmission mechanism of the virus by the wheat curl mite, persistence and efficiency of transmission by the mite biotypes already present in the EU
- Existence of other mite vectors of HPWMOV
- The distance over which the vector could be dispersed by the wind
- Magnitude of the impact of HPWMOV under the EU conditions

4. Conclusions

High Plains wheat mosaic virus fulfils the criteria that are within the remit of EFSA to assess for it to be regarded as a potential Union quarantine pest. Table 6 provides a summary of the PLH Panel conclusions.

Table 6: The Panel's conclusions on the pest categorisation criteria defined in Regulation (EU) 2016/2031 on protective measures against pests of plants (the number of the relevant sections of the pest categorisation is shown in brackets in the first column)

Criterion of pest categorisation	Panel's conclusions against criterion in Regulation (EU) 2016/2031 regarding Union quarantine pest	Key uncertainties
Identity of the pest (Section 3.1)	The identity of High Plains wheat mosaic virus is established	None
Absence/presence of the pest in the EU (Section 3.2)	HPWMOV has not been reported from the EU	None
Regulatory status (Section 3.3)	The pest is not regulated in the EU	None
Pest potential for entry, establishment and spread in the EU (Section 3.4)	HPWMOV could enter in the EU with seeds of sweet corn for sowing, which have been shown to be able to transmit the virus. Seeds of other hosts and viruliferous wheat curl mite <i>Aceria tosichella</i> have been identified as additional entry pathways. Would the pest enter in the EU it may establish and spread within the EU territory.	Natural host range and the presence of asymptomatic hosts. Seed transmission for natural hosts other than sweet corn. Transmission mechanism of the virus by the wheat curl mite.
Potential for consequences in the EU (Section 3.5)	Introduction and further spread of HPWMOV could have negative impact on the EU yield and quality production of the cultivated hosts.	Magnitude of the impact of HPWMOV under the EU conditions.
Available measures (Section 3.6)	No specific phytosanitary measures are currently in place, but potential control measures are available to mitigate the risk of entry, establishment, spread and impact of HPWMOV in the EU	None
Conclusion (Section 4)	High Plains wheat mosaic virus fulfils the criteria that are within the remit of EFSA to assess for it to be regarded as a potential Union quarantine pest.	
Aspects of assessment to focus on/scenarios to address in future if appropriate:	Information on potential seed transmission of HPWMOV by hosts other than sweet corn and on the transmission mechanism by <i>A. tosichella</i> .	

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Abbreviations

DG SANTÉ	Directorate General for Health and Food Safety
EPPO	European and Mediterranean Plant Protection Organization
FAO	Food and Agriculture Organization
IPPC	International Plant Protection Convention
ISPM	International Standards for Phytosanitary Measures
MS	Member State
PLH	EFSA Panel on Plant Health
PZ	Protected Zone
TFEU	Treaty on the Functioning of the European Union
ToR	Terms of Reference

Glossary

Containment (of a pest)	Application of phytosanitary measures in and around an infested area to prevent spread of a pest (FAO, 2018)
Control (of a pest)	Suppression, containment or eradication of a pest population (FAO, 2018)
Entry (of a pest)	Movement of a pest into an area where it is not yet present, or present but not widely distributed and being officially controlled (FAO, 2018)
Eradication (of a pest)	Application of phytosanitary measures to eliminate a pest from an area (FAO, 2018)
Establishment (of a pest)	Perpetuation, for the foreseeable future, of a pest within an area after entry (FAO, 2018)
Greenhouse	A walk-in, static, closed place of crop production with a usually translucent outer shell, which allows controlled exchange of material and energy with the surroundings and prevents release of plant protection products (PPPs) into the environment.
Hitchhiker	An organism sheltering or transported accidentally via inanimate pathways including with machinery, shipping containers and vehicles; such organisms are also known as contaminating pests or stowaways (Toy and Newfield, 2010).
Impact (of a pest)	The impact of the pest on the crop output and quality and on the environment in the occupied spatial units
Introduction (of a pest)	The entry of a pest resulting in its establishment (FAO, 2018)
Pathway	Any means that allows the entry or spread of a pest (FAO, 2018)
Phytosanitary measures	Any legislation, regulation or official procedure having the purpose to prevent the introduction or spread of quarantine pests, or to limit the economic impact of regulated non-quarantine pests (FAO, 2018)

Quarantine pest	A pest of potential economic importance to the area endangered thereby and not yet present there, or present but not widely distributed and being officially controlled (FAO, 2018)
Risk reduction option (RRO)	A measure acting on pest introduction and/or pest spread and/or the magnitude of the biological impact of the pest should the pest be present. A RRO may become a phytosanitary measure, action or procedure according to the decision of the risk manager
Spread (of a pest)	Expansion of the geographical distribution of a pest within an area (FAO, 2018)

Appendix A – High Plains wheat mosaic virus host plants/species

Source: EPPO Global Database (EPPO, online)

Host status	Host name	Plant family	Common name	Reference
Cultivated hosts	<i>Triticum aestivum</i>	Poaceae	Wheat	Jensen et al. (1996)
	<i>Zea mays</i>	Poaceae	Maize, corn	Jensen et al. (1996)
Cultivated/wild hosts	<i>Setaria glauca</i> (syn. <i>Pennisetum glaucum</i>)	Poaceae	Yellow foxtail	Seifers et al. (1998), EPPO (online)
	<i>Setaria viridis</i>	Poaceae	Green foxtail	Seifers et al. (1998)
	<i>Hordeum jubatum</i>	Poaceae	Foxtail barley	Abdullahi et al. (2020)
Experimental hosts	<i>Avena sativa</i>	Poaceae	Oat	Seifers et al. (1998)
	<i>Bromus secalinus</i>	Poaceae	Rye brome	Seifers et al. (1998)
	<i>Hordeum vulgare</i>	Poaceae	Barley	Seifers et al. (1998)
	<i>Secale cereale</i>	Poaceae	Rye	Seifers et al. (1998)

Appendix B – Distribution of High Plains wheat mosaic virus

Distribution records based on EPPO (EPPO, online)

Region	Country	Sub-national (e.g. State)	Status
Europe	Ukraine		Present
North America	Canada	Alberta	Present, no details
	United States	Colorado	Present, no details
		Florida	Present, no details
		Idaho	Present, no details
		Kansas	Present, no details
		Montana	Present, no details
		Nebraska	Present, no details
		New Mexico	Present, no details
		North Dakota	Present, no details
		Ohio	Present, no details
		Oklahoma	Present, no details
		Oregon	Present, no details
		South Dakota	Present, no details
		Texas	Present, no details
		Utah	Present, no details
Washington	Present, restricted distribution		
Wyoming	Present, no details		
South America	Argentina		Present, restricted distribution
Oceania	Australia	New South Wales	Present, no details
		Queensland	Present, no details
		Victoria	Present, no details
		Western Australia	Present, no details

Appendix C – Import data of cereals

EU 27 annual imports of cereals (HS 10) from countries where HPWMOV is present, 2016–2020 (Hundreds of kg) Source: Eurostat. Extraction date: 24 February 2022.

Partner/Period	2017	2018	2019	2020	2021
Argentina	2,154,677.48	2,816,072.77	1,889,615.48	2,037,412.84	2,118,019.81
Australia	2,484,138.93	1,680,467.25	7,564.72	15,652.85	4,306,217.55
Canada	17,890,571.83	21,796,462.48	19,934,220.07	26,453,348.45	26,101,151.27
Ukraine	98,925,332.89	124,259,144.21	157,635,985.38	97,165,451.20	78,867,610.73
United States	11,505,750.57	28,983,977.56	12,491,999.10	10,177,325.13	3,590,277.33

Appendix D – Import data of maize for sowing

EU 27 annual imports of maize for sowing (HS 100510) from countries where HPWMOV is present. 2016–2020 (Hundreds of kg) Source: Eurostat. Extraction date: 22 February 2022.

Partner/Period	2017	2018	2019	2020	2021
Argentina	790.35	42.23	53.45	64.57	87.41
Australia	0.90	0.38	30.26	0.47	1.32
Canada	1.87	20.32	10.55	25.54	5.88
Ukraine	2,090.61	8,872.22	2,488.57	7,572.38	20,077.58
United States	46,241.68	35,856.15	20,771.26	24,027.41	15,730.92