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Assessment of the potential impact of *Scirtothrips dorsalis* through the transmission of viruses for the European Union

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1 Introduction

Scirtothrips dorsalis is a Union quarantine pest that causes direct feeding damage to crops but can also have an impact by vectoring plant pathogenic viruses (EFSA Panel on Plant Health, 2014). In the past, several outbreaks of *S. dorsalis* have been reported in the European Union (EU) that were subsequently eradicated. However, *S. dorsalis* now appears to be established in the EU (EPPO, 2026a). So far, no major damage has been reported in the EU, but the impact of *S. dorsalis* may increase due to the introduction of viruses that this species can transmit. Therefore, this study assesses the potential impact of *S. dorsalis* through the transmission of viruses. However, *Scirtothrips dorsalis* is a cryptic species complex and the species within this complex may differ in feeding damage but also in vector competence (Toda et al., 2014; Dickey et al., 2015). Therefore, this assessment begins with a brief description of the *S. dorsalis* species complex.

2 The *Scirtothrips dorsalis* species complex

Scirtothrips dorsalis is currently listed as a single species in Annex II of Commission Implementing Regulation (EU) 2019/2072[1]. However, *S. dorsalis* has been shown to be a species complex of at least nine different species with different ecological properties and host ranges (Toda et al., 2014; Dickey et al., 2015; Kumar et al., 2023). In the Netherlands, two species within this complex, East Asia 1 (EA1) and South Asia 1 (SA1), have been found in commodities during import inspections and on plants in nurseries during surveys and export inspections. SA1 has been eradicated from a single nursery but several outbreaks of EA1 are still under eradication. Both species were most likely introduced through import (including trade from other EU member states) of plants for planting of ornamentals. EA1 is probably established in the European Union (EU) because this species has been found repeatedly on plants imported from other member states (in total from three different member states). SA1 has been introduced on the Canary islands (Mouratidis et al., 2024), but it is uncertain whether it is present on Mainland Europe.

Within the *S. dorsalis* species complex, SA1 and EA1 are the species that have been reported from multiple continents but have different origins (Dickey et al. (2015); this assessment). SA1 is native to tropical regions in South Asia and appears to be less tolerant to low temperatures than EA1 that probably originates from parts of Japan and South Korea (Dickey et al., 2015). EA1 is for example present in the Kochi prefecture in Japan that has a humid subtropical climate. However, SA1 can probably not establish in that region based on observations by Tokaji & Nakao (2020) on a population of *S. dorsalis* designated as strain C that included SA1[2]. They report that "*both adults and larvae* [of strain C] *disappeared from the strawberry plants by the end of February 2014 and 2015, with no individuals being found from March onward in either year*". Thus, the potential area

[1] Commission Implementing Regulation (EU) 2019/2072 of 28 November 2019 establishing uniform conditions for the implementation of Regulation (EU) 2016/2031 of the European Parliament and the Council, as regards protective measures against pests of plants. OJ L 319, 10.12.2019, p. 1-258

[2] Dickey et al. (2015): "*The majority of their Strain C [referring to Toda et al., 2014] corresponds to South Asia 1 while the haplotype designated SdC06 (GenBank accession AB818023) belongs to South Asia 2*"

of distribution of SA1 in the EU, that is predominantly characterized by temperate and continental/cold climates (Beck et al., 2023), is likely smaller than that of EA1.

Both SA1 and EA1 are polyphagous and have different but overlapping host ranges. In Japan, where EA1 is native, *S. dorsalis* mainly affected woody plants before the introduction of 'strain C' which include haplotypes of SA1 and SA2 (South Asia 2) (Umeya et al., 1988; Toda et al., 2014; Dickey et al., 2015). However, in countries and regions where SA1 is known to be present (e.g. India, Canary Islands and the southeastern United States of America), *S. dorsalis* is known as a pest of both woody (e.g. blueberry, mango and *Rosa*) and herbaceous plants (e.g. celery, pepper and strawberry) (Dickey et al., 2015; Sridhar & Naik, 2015; Sreerama Kumar & Remani Rachana, 2021; Kumar et al., 2023; Mouratidis et al., 2024; Adhikari et al., 2025). In the Netherlands, adults and immature stages of EA1 have been found on plants of *Podocarpus macrophyllus*, while Kumar et al. (2023) did not find *P. macrophyllus* to be a host of SA1 in an experimental study in Florida. The difference in host plants (or host plant preference) is also illustrated by the fact that Japanese native populations do not prefer or do not infest *Capsicum* and other Solanaceae while *S. dorsalis* is known as a common pest of *Capsicum* in India where SA1 is present (Toda et al., 2014; Praveenkumar et al., 2025).

The risk of '*S. dorsalis*' for the EU differs per species within the complex. The probability of introduction of EA1 and SA1 is assessed to be highest among all members of the complex for reasons mentioned above: they are polyphagous, they originate from Asia but have been introduced into other continents and findings of both members have been confirmed in the EU. Dickey et al. (2015) considered the invasion potential of SA1 to be 'high', those of SA2 and EA1 'moderate' and those of the other species 'low' based on history of invasion. SA2 is like SA1 also of tropical origin but has thus far only been reported from Asia and like SA1 can likely establish in a smaller part of the EU than EA1. EA1 is probably established in the EU where it can easily spread over long distances by movement of infested plants. Most species within the complex are considered pests (Dickey et al., 2015). However, SA1 is probably the species in most studies that report impact by *S. dorsalis*, e.g. in Florida (United States of America) and India where only SA1 is known to be present (Kumar et al., 2013; Dickey et al., 2015; Kumar et al., 2023). For these reasons, the present assessment primarily focuses on EA1 and SA1.

In most papers on '*S. dorsalis',* the species within the complex is not indicated and in the present assessment the same name is used as in the reference. Where possible, it is indicated which species it probably concerns based on the location of the study and the known distribution of the species from Dickey et al. (2015).

3 Transmission of viruses and their impact

3.1 Identification of viruses

Thrips species are especially known as vectors of orthotospoviruses (previously and here referred to as tospoviruses). Therefore, the pest categorisation of tospoviruses from EFSA Panel on Plant Health (2012) and the EPPO Global Database (EPPO, 2026c) were used to identify viruses that are transmitted by *S. dorsalis*. In addition, a literature search was conducted. Biological Abstracts 1969 to February 2026 and CAB Abstracts 1973 to 2026 Week 12 were searched through Ovid® using the search string '(scirtothrips AND dorsalis) AND virus AND (transmission OR transmitted'.

EFSA Panel on Plant Health (2012) lists three tospoviruses reported as being transmitted by *S. dorsalis*:

- Groundnut bud necrosis virus (GBNV, *Orthotospovirus arachinecrosis*)
- Groundnut chlorotic fan-spot virus (GCFSV, *Orthotospovirus arachiflavi*)
- Groundnut yellow spot virus (GYSV, *Orthotospovirus arachiflavamaculae*)

EPPO (2026c) also lists these three tospoviruses and tobacco streak virus (TSV, *Ilarvirus TSV*). *Scirtothrips dorsalis* transmits TSV mechanically by carrying infected pollen and creating feeding wounds, enabling the virus to infect the plant (Rao et al., 2003; Jyothirmai Madhavi et al., 2024; ICTV, 2026). This transmission mechanism for TSV is not specific for *S. dorsalis.* Other thrips species - including species that are present in the EU - can transmit TSV in a similar way

(Tzanetakis, 2012). TSV is already present in the EU and introduction of *S. dorsalis* is not expected to increase the impact of TSV. Hence, TSV is not considered relevant in the present assessment.

In addition, EPPO (2026c) considers *S. dorsalis* a 'potential vector' of four other tospoviruses:

- Capsicum chlorosis vector (CaCV, *Orthotospovirus citrullomaculosi*)
- Water melon silver mottle virus (WSMoV, *Orthotospovirus citrullomaculosi*)
- Melon yellow spot virus (MYSV, *Orthotospovirus meloflavi*)
- Tomato spotted wilt virus (TSWV, *Orthotospovirus tomatomaculae*)

The listing of CaCV, WSMoV and MYSV is based on a study by Chiemsombat et al. (2008) who detected these viruses in *S. dorsalis* individuals but did not conduct transmission studies (i.e. did not provide evidence that these viruses are actually transmitted by *S. dorsalis*). Because of this lack of evidence for transmission by *S. dorsalis*, CaCV, WSMoV and MYSV are not considered further in the present assessment.

TSWV has been listed based on a study by Amin et al. (1981). However, EPPO (2026c) indicates that the virus in that study was actually GBNV while referring to German (1992). Therefore, TSWV is not considered further in the present assessment.

The literature search in Biological Abstracts and CAB Abstracts did not yield any viruses other than those listed above.

3.2 Distribution, host range and impact of the relevant viruses

Three viruses (GBNV, GCFSV and GYSV) are reported to be transmitted by *S. dorsalis* in a specific manner (see section 3.1). Information was retrieved from literature to determine whether these viruses are a potential threat to plant health in the EU.

Information regarding the distribution, host plants and impact of GBNV, GCFSV and GYSV was initially obtained from datasheets in the CABI Compendium (CABI, 2026), the pest categorisation of the tospoviruses by the EFSA Panel on Plant Health (2012) and from a review paper on tospoviruses on the Indian subcontinent (Mandal et al., 2012). In India, GBNV is considered a major pathogen of many crops including crops that are of great economic importance to the EU (see also section 3.3). Therefore, it was not considered necessary to conduct a specific literature search to get a full list of host plants or detailed information on the distribution and impact of GBNV. For GCFSV and GYSV further information on distribution, host plants and impact was obtained by literature search (no CABI-datasheet was available for GCFSV, information in the CABI-datasheet of GYSV was very brief and Mandal et al. (2012) state that the effect of GYSV on groundnut yields is unknown). Biological Abstracts 1969 to February 2026 and CAB Abstracts 1973 to 2026 Week 12 were searched through Ovid® using the search strings '(orthotospovirus ADJ arachiflavi) OR (GCFSV OR PCFSV) OR ((groundnut OR peanut) ADJ chlorotic ADJ fan-spot ADJ (virus OR orthotospovirus))' and '(orthotospovirus ADJ arachiflavamaculae) OR (GYSV OR PYSV) OR ((groundnut OR peanut) ADJ yellow ADJ spot ADJ (virus OR orthotospovirus))'. Information from the datasources mentioned above and the literature search is briefly discussed below.

GBNV is present in many Asian countries and has a wide host range (Table 1). According to Mandal et al. (2012), GBNV is "*the most economically important tospovirus*" in India that affects important crops like cowpea, mung bean, pea, potato, soybean and tomato. Many studies are available on GBNV (see also section 3.3).

GCFSV (synonym: peanut chlorotic fan-spot virus, PCFSV) has only been reported from Taiwan (Table 1) where it was sporadically found in groundnut during a survey made in central Taiwan in 1992 – 1993 (Chen & Chiu, 1996; Chu et al., 2001). GCFSV has also been detected in symptomatic cowpea plants in Taiwan (Huang et al., 2018) but no records of economic damage were found for cowpea.

GYSV (synonym: peanut yellow spot virus, PYSV) has been reported from three Asian countries from a few plant species (Table 1). Information on impact is scarce. Thakur & Agarawal (1996) reported groundnut plants with severe leaf spotting caused by GYSV in Raipur in India in 1993 but did not mention yield losses. Mandal et al. (2012) state the following about impact of GYSV in

groundnut in India: "*Incidence of PYSV up to 90% has been observed in southern India, but impact on yield loss is not known*". Groundnut is the only known host plant in India according to Pradeep et al. (2024). In a study in Thailand, Sirisingh & Pitak (1987) reported that repeated applications of an insecticide in groundnut reduced thrips populations and the "*incidence of PYSV*" and increased the yield by 20%. No details are, however, presented (abstract in conference proceedings) and it is uncertain to which extent the increase in yield was due to a decrease in GYSV-infections. In addition, groundnut is not grown commercially in the EU or at least not on a large scale due to unfavourable climatic conditions (CBI, 2023; Research and Markets, 2025). Ding et al. (2007) detected GYSV in fruit of sweet pepper (*Capsicum annuum*) with "*severe necrotic ringspot symptoms*" in Yunnan (China). Symptoms on fruit will generally lead to yield or quality losses, but no information was found regarding GYSV incidence in pepper crops or whether GYSV actually causes significant yield or quality losses. Therefore, the impact of GYSV remains highly uncertain.

Because of uncertainties about the impact of GCFSV and GYSV in their current area of distribution, the potential impact of *S. dorsalis* as a vector of viruses was only assessed in relation to GBNV (section 3.3). However, studies on thrips-mediated transmission of these viruses were used to assess which of the species in the *S. dorsalis* complex can actually transmit tospoviruses (see section 3.3.2).

Table 1: Distribution and host plants of tospoviruses reported to be transmitted by *Scirtothrips dorsalis*

Groundnut bud necrosis virus (GBNV)	
Distribution	Bangladesh, China (Yunnan), India, Indonesia, Iran, Nepal, Pakistan (CABI, 2021a)[1].
Host plants	wide host range including common bean (*Phaseolus vulgaris*), groundnut (*Arachis hypogeae*), onion (*Allium cepa*), pea (*Pisum sativum*), pepper (*Capsicum annuum* and *C. frutescens*), potato (*Solanum tuberosum*), soybean (*Glycine max*) and tomato (*S. lycopersicum*) (CABI, 2021a).
Groundnut chlorotic fan-spot virus (GCFSV)	
Distribution	Taiwan (Chu et al., 2001)
Host plants	cowpea (Huang et al., 2018), groundnut (Chu et al., 2001; EFSA Panel on Plant Health, 2012),
Groundnut yellow spot virus (GYSV)	
Distribution	India and Thailand (Sirisingh & Pitak, 1987; Thakur & Agarawal, 1996; CABI, 2019), China (Ding et al., 2007)
Host plants	groundnut (Gopal et al., 2010; EFSA Panel on Plant Health, 2012; CABI, 2019), pepper (Ding et al., 2007)

[1]CABI (2021a) also lists Turkey referring to Uzunogullari & Gumus (2020) but this reference only includes findings of tomato spotted wilt virus in Turkey

3.3 Groundnut bud necrosis virus

3.3.1 Vector species

EFSA Panel on Plant Health (2012) list three thrips species that transmit GBNV: *Frankliniella schultzei*, *S. dorsalis* and *Thrips palmi*. More recently, *T. parvispinus* has also been reported to transmit GBNV (Sharanya et al., 2025). A literature search was conducted to assess the relevance of *S. dorsalis* as a vector of GBNV (synonym: peanut bud necrosis virus, PBNV). Biological Abstracts 1969 to February 2026 and CAB Abstracts 1973 to 2026 Week 12 were searched through Ovid® using the search string '((GBNV OR PBNV OR TSWV) OR (tomato ADJ spotted ADJ wilt ADJ virus) OR (orthotospovirus ADJ arachinecrosis) OR ((groundnut OR peanut) ADJ bud ADJ necrosis ADJ (virus OR orthotospovirus)) AND (scirtothrips AND dorsalis))'. References were selected that include experimental studies on transmission of GBNV by *S. dorsalis*. The same databases were also searched for original research papers on the ability of *F. schultzei* and *T. parvispinus* — thrips species that are present in the EU — to transmit GBNV. *Thrips parvispinus* is native to Asia and was recorded for the first time in the EU (in Greece) in 2000 (Collins & Mound, 2000). Since then, but especially since 2017 the number of records of *T. parvispinus* has increased in the EU (Pijnakker, 2023; Cantó et al., 2024; EPPO, 2026d). *Frankliniella schultzei* was already recorded in the EU (the

Netherlands) in 1965 but its distribution seems still limited (Vierbergen, 1995; CABI, 2021b). In addition to the databases mentioned above, the pest categorisation of the tospoviruses from EFSA Panel on Plant Health (2012) was screened for relevant references. The results of the literature search are discussed in section 3.3.3.

3.3.2 Vector species within the *Scirtothrips dorsalis* complex

In general, relatively few thrips species are known as vector of tospoviruses (EFSA Panel on Plant Health, 2012). Rotenberg et al. (2015) list 15 thrips species that have been reported as a vector of tospoviruses while more than 6.500 thrips species are known today (ThripsWiki, 2026). EFSA Panel on Plant Health (2012) also state: "*There is ample evidence that the virus–vector relationships linking tospoviruses to their thrips vectors demonstrate a high level of specificity, which also determines vector competence".* Therefore, it is likely that the different species within the *S. dorsalis* species complex differ in vector competence and SA1 is probably the species reported to be associated with GBNV and other tospoviruses (GCFSV and GYSV). All *S. dorsalis* - GBNV - transmission studies found in the present assessment (see section 3.3.3) were conducted in India where SA1 is the only member of the *S. dorsalis* species complex known to be present (Dickey et al., 2015). Therefore, these studies probably concerned SA1. In one transmission study (Bhat et al., 2021), sequences of the mitochondrial cytochrome c oxidase subunit I (COXI) gene of thrips individuals had been deposited in NCBI GenBank and these sequences had the highest similarity with those of SA1 isolates deposited by Dickey et al. (2015) (see section 3.3.3). Transmission studies with GCFSV and GYSV found in the literature search (see section 3.2) were carried out in Taiwan and India, respectively (Chen & Chiu, 1996; Chu et al., 2001; Gopal et al., 2010). In these countries only SA1 (India) or SA1 and SA2 (South Asia 2, Taiwan) are known to be present (Dickey et al., 2015). No evidence was found that EA1 transmit any virus. Dickey et al. (2015) also state: "*South Asia 1 is likely the species implicated in tospovirus transmission as it is present in India, Taiwan, and Thailand where vectoring has been documented*".

3.3.3 Transmission studies

Six GBNV-transmission studies were found with *S. dorsalis, F. schultzei* and/or *T. parvispinus.* Three of these studies also include *T. palmi* (according to the thrips names used in the references). These studies are briefly discussed below. Details of these studies are presented in the Annex (Excel-document). In addition, a study by Meena et al. (2005) on the detection of GBNV in *S. dorsalis* is discussed. This reference was included because it has been referred to as evidence for GBNV-transmission by *S. dorsalis* (e.g. EFSA Panel on Plant Health (2012) and Bhat et al. (2021))

Amin et al. (1981) reported that *S. dorsalis* transmitted GBNV[3] from infected peanut plants (groundnut, *Arachis hypogaea*) to healthy peanut and urdbean plants (blackgram, *Vigna mungo*) with 10-15 thrips per test plant in an experimental study in Hyderabad (Andhra Presh, India). Additionally, Amin et al. (1981) reported transmission of GBNV by *Frankliniella schultzei* from peanut to urdbean (the only host plant tested with this thrips species). They found *F. schultzei* to be a more efficient vector than *S. dorsalis*. However, Palmer et al. (1990) examined the thrips collection at ICRISAT Center in Hyderabad and found that specimens labelled as *F. schultzei* were in fact *T. palmi*. They also carried out a survey in groundnut fields near Hyderabad and Raichur (Karnataka) in February 1989. They found all three species (*S. dorsalis, F. schultzei* and *T. palmi*) with *S. dorsalis* being the most abundant one and *Thrips palmi* and *F. schultzei* having an irregular distribution. They tested individual specimens for the presence of GBNV[3] by dot immunobinding assay and found a positive result for *T. palmi*; results with *S. dorsalis* and *F. schultzei* were inconclusive. Based on these results, Palmer et al. (1990) state "*that there is a need to reexamine the vector relationships of BND [bud necrosis disease] in Asia*". Later, Reddy et al. (1995) reported that *T. palmi* had transmitted GBNV (synonym: peanut bud necrosis virus, PBNV) in the study of Amin et al. (1981) and not S. *dorsalis* or *F. schultzei*: "*Amin et al. (1981) reported that the virus causing PBND in India is transmitted by Frankliniella schultzei and Scirtothrips dorsalis. Subsequent investigations, which involved accurate identification of thrips, showed that in fact Thrips palmi transmits PBNV, and not F. schultzei or S. dorsalis, which are also present on the plants*". A

[3] In the reference indicated as tomato spotted wilt virus (TSWV), but in the 90s the virus causing bud necrosis disease in groundnut (peanut) turned out to be different from TSWV and was named groundnut bud necrosis virus (Mandal et al. 2012).

possible misidentification of the thrips has also been suggested by Vijaya Lakshmi (1994) who could not reproduce the results of Amin et al. (1981) (see below).

Vijaya Lakshmi (1994) conducted transmission studies with *T. palmi, F. schultzei* and *S. dorsalis* colonies reared from thrips collected in the field at the ICRISAT Asia Center (Hyderabad) and from Raichur Karnataka in India. Transmission studies were done from infected groundnut leaves to healthy groundnut and urdbean (*V. mungo*) plants. Vijaya Lakshmi (1994) found that only *T. palmi* transmitted GBNV (37.8% transmission to groundnut and 36.8% to blackgram with one thrips per plant). No transmission was found with *F. schultzei* and *S. dorsalis*.

Meena et al. (2005) detected GBNV in a *S. dorsalis* population collected in and around Coimbatore, Tamil Nadu (India) by RT-PCR but did not conduct transmission studies (i.e. did not provide evidence that GBNV is actually transmitted by *S. dorsalis*).

Ruth (2018) conducted transmission studies with *T. palmi, F. schultzei* and *S. dorsalis* populations collected from tomato plants at the Horticultural Research Station, Mahanandi, Andhra Pradesh (India). Transmission studies were done from infected tomato leaves (*Solanum lycopersicum*) to healthy tomato and cowpea (*Vigna unguiculata*) plants (10 thrips per plant). They found that only *T. palmi* transmitted GBNV (transmission efficiencies were 33.35 and 36.73% for tomato and cowpea, respectively). The author describes how the thrips species were identified but not how the virus was identified.

Bhat et al. (2021) conducted a transmission study with *S. dorsalis* and reported transmission of GBNV from infected gerbera (*Gerbera jamesonii*) plants to cowpea and tulsi (*Ocimum sanctum*) plants by *S. dorsalis.* Thrips had been collected from infected gerbera plants in Bengaluru (Karnakata, India) and released on the cowpea and tulsi test plants (10 thrips per plant). Thrips collected from the gerbera plants were identified as *S. dorsalis* morphologically and by molecular means (for three individuals). However, the authors do no describe how it was ascertained that each specimen used in the transmission experiment was *S. dorsalis* as *T. palmi* is for example also known to infest gerbera in Bengaluru (Reddy & Aswath, 2008). The transmission efficiency was not determined (the authors do not present the number of test plants that were exposed to the thrips and how many of them got infected). In the present assessment, the sequences of the COXI gene of the three thrips individuals that had been deposited in NCBI GenBank (accession numbers KX929020-KX929022) were analysed to determine to which species within the *S. dorsalis* complex the individuals most likely belonged. Therefore, sequences were compared with those of isolates deposited by Dickey et al. (2015) using NCBI blastn (standard settings, align two or more sequences). Accession numbers KX929020 and KX929021 had the highest similarities (97.86-99.85%) with the SA1-isolates deposited by Dickey et al. (2015). Accession number KX929022 did not have a high sequence similarity with any *S. dorsalis* sequence in NCBI GenBank (NCBI blastn, standard settings, core nucleotide database, closest match with KX929020: query cover 96%, identity 78.91%). However, KX922022 still clusters with other SA1 sequences, be it with a long branch (the accessions KX929020–KX929022 and the sequences from Dickey et al. (2015) were downloaded for analysis in Geneious Prime v2025.2.2. MAFFT alignment shows 100% coverage for a DNA fragment 649 nucleotides in length that was used for FastTree cluster analysis).

Jyothirmai Madhavi et al. (2024) conducted transmission studies with *T. palmi, F. schultzei* and *S. dorsalis* colonies reared from thrips collected from apparently healthy blackgram and greengram (*V. radiata*) plants in the field at Hyderabad (India). Transmission studies were done from infected leaflets of blackgram and greengram to healthy blackgram, greengram and cowpea plants. They found that only *T. palmi* transmitted GBNV (50 – 87.5% transmission with 10 thrips per plant). The authors describe how the thrips species were identified but not how the virus was identified.

Sharanya et al. (2025) conducted a transmission study with *T. parvispinus* reared on cowpea plants in Tabil Nadu (India). They did various tests to determine the acquisition access period (AAP), inoculation access period (IAP) and number of thrips required for transmission of GBNV in cowpea. Highest transmission efficiencies were recorded at 72 h IAP and AAP: 6.66% with one thrips per plant and 86.66% with 10 thrips per plant. In tomato, three thrips per plant did not yield any symptomatic plant but the release of 10, 15, 20 or 25 thrips per plant (72 h IAP and AAP) resulted in 100% transmission (5 out of 5 plants).

3.3.4 Impact

3.3.4.1 Impact in the current area of distribution

Many references describe GBNV as a damaging pest in India, for example:

Gayathri et al. (2025) calls GBNV a 'devastating' virus in tomato: "*Early infection resulted in chlorotic and necrotic lesions on the leaves and drying of young buds followed by stem necrosis and stunting*".

Kunkalikar et al. (2011) state the following about the impact of GBNV in vegetables (synonym: PBNV): "*Until the mid-2000, the occurrence of PBNV was limited to a few regions. Beginning in 2001, epidemics of PBNV were reported in several tomato-growing regions of India, including Hoskote and Nasik regions of Karnataka and Maharashtra States, respectively, that are the major tomato-producing areas. Consequently, PBNV has become a major constraint (…), there by [sic] limiting the sustainability of tomato that contributes nearly 8% of the total production of vegetables in India".*

Mandal et al. (2012): "*GBNV is the most widespread of all the tospoviruses known in India. In addition to groundnut, important crops such as cowpea, mungbean, pea, potato, soybean, and tomato are known to be affected by GBNV*".

Rahul Dev et al. (2022) carried out a survey for GBNV-symptoms (synonym: PBNV) in tomato fields in Coimbatore district, Tamil Nadu and confirmed the presence of GBNV by mechanical inoculation, electron microscopy and RT-PCR-sequencing: "*The disease incidence ranged from 8.33 % (Narasipuram village) to a maximum of 36.67 % (Viraliyur village) (…). The disease occurred in all the stages of the crop from young stage to flowering stage. The survey implies the natural distribution and symptomatology of PBNV in tomato. PBNV initially produced chlorotic ring spots (…) which later turned to necrotic ring spots (…) on the leaves. Severe infection on young shoots lead to budblight necrosis (…). On stem and petioles, PBNV caused necrotic streaks (…). PBNV infection on early crop stage caused wilting and stunting of the whole plant (…). On the fruit, it caused chlorotic ring symptom".*

3.3.4.1 Potential impact for the EU

GBNV is a potential threat to the production of varies crops in the EU including economically important crops like common bean, potato and tomato. The impact of GBNV (and tospoviruses in general) depends, however, on the presence of a vector species. At least one vector species of GBNV, *T. parvispinus,* is present in the EU. This species that is native to tropical Asia has a wide host range including GBNV-host plants and appears to expand its range within the EU (Pijnakker, 2023; EPPO, 2026d;2026b). Whether the presence of *S. dorsalis* will further increase the potential impact of GBNV in the EU is uncertain because of (i) uncertainties about the identity of the thrips used in transmission studies (see section 3.3.3.) and (ii) possible differences in vector competence between species within the *S. dorsalis* species complex (see section 3.3.2).

4 Summary and conclusions

- *Scirtothrips dorsalis* is a cryptic species complex of at least nine different species with different distribution areas, host ranges and ecological properties:
  - within the complex, South Asia 1 (SA1) and East Asia 1 (EA1) are the species with the highest probability of introduction into the EU: SA1 and EA1 originate from Asia but have been introduced into other continents and findings of both members have been confirmed in the EU,
  - EA1 is probably native to parts of Japan and South Korea and can likely establish in a larger part of the EU than SA1 that is native to tropical regions in South Asia.
  - SA1 and EA1 are polyphagous and have different but overlapping host ranges. EA1 seems to affect mainly woody plants, while SA1 is known as a pest of both woody and herbaceous plants.
  - EA1 is probably established in the EU; the pest status of SA1 is uncertain.
- *Scirtothrips dorsalis* has been reported to transmit three tospoviruses: groundnut bud necrosis virus (GBNV, *Orthotospovirus arachinecrosis*), groundnut chlorotic fan-spot virus (GCFSV, *Orthotospovirus arachiflavi*) and groundnut yellow spot virus (GYSV, *Orthotospovirus*

arachiflavamaculae). The potential impact of *S. dorsalis* in the EU as a vector of these viruses is, however, uncertain:
  - GBNV is known as a pest of many crops including economically important crops like many legumes, potato and tomato, but there is uncertainty about the ability of *S. dorsalis* to transmit GBNV. Besides *S. dorsalis*, three other thrips species have been reported to transmit GBNV: *Thrips palmi*, *T. parvispinus* and *Frankliniella schultzei* of which the latter two are present in the EU. Experimental evidence was found for transmission of GBNV by *T. palmi* and *T. parvispinus* but the ability of *S. dorsalis* and *F. schultzei* to transmit GBNV may need confirmation because of conflicting information.
  - GCFSV and GYSV: little information is available on GCFSV and GYSV and their impact is uncertain. GCFSV has been reported from groundnut and cowpea in Taiwan but without information on economic damage. GYSV has been reported from groundnut in India and Thailand but without conclusive evidence on impact. It has also been reported from symptomatic pepper (*Capsicum*)-fruit in Yunnan (China), but no information was found on yield or quality losses in this crop caused by GYSV.
- SA1 is probably the species reported to be associated with GBNV and other tospoviruses. No evidence was found that EA1 can act as a vector of GBNV or any other tospovirus.
- *Scirtothrips dorsalis* can mechanically transmit tobacco streak virus (TSV, *Ilarvirus TSV*) but this transmission mechanism is not specific for *S. dorsalis.* Other thrips species including species that are present in the EU can transmit TSV in a similar way.

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