EPPO Datasheet: *Nepovirus solani*

Last updated: 2023-02-08

IDENTITY

Preferred name: *Nepovirus solani*
Taxonomic position: Viruses and viroids: Riboviria: Orthornavirae: Pisuviricota: Pisoniviricetes: Picornavirales: Secoviridae
Other scientific names: *PBRSV, Potato Andean calico virus, Potato black ringspot nepovirus, Potato black ringspot virus, Tobacco ringspot nepovirus Andean calico strain, Tobacco ringspot virus Andean calico strain*
Common names: Andean calico of potato
view more common names online...
EPPO Categorization: A1 list
view more categorizations online...
EU Categorization: A1 Quarantine pest (Annex II A)
EPPO Code: PBRSV0

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Notes on taxonomy and nomenclature

A previously undescribed virus was isolated from the potato cultivar Antarqui (*Solanum tuberosum* x *S. tuberosum* subsp. *andigenum*) showing necrotic spotting on the tip leaves (Salazar, 1972) and was subsequently named *Potato black ringspot virus* (PBRSV) (Salazar & Harrison, 1977). At around the same time another previously undescribed virus was isolated from the potato cultivar Ticahuasi (*Solanum tuberosum* x *S. tuberosum* subsp. *andigenum*) showing calico leaf symptoms (Fribourg & Salazar, 1972) and was named as the calico strain of *Tobacco ringspot virus* (TRSV-Ca) (Fribourg, 1977). Subsequently it was proposed that TRSV-Ca was a strain of PBRSV since they were similar, but not identical, both antigenically and in their host plant reactions (Salazar & Harrison, 1978b). Analysis of the complete genome sequences of two isolates of PBRSV from potato have confirmed that PBRSV is a distinct virus species but closely related to TRSV (Souza Richards *et al*., 2014). The genomes of PBRSV and of the TRSV-Ca strain have 90% amino acid (aa) identity in the Pro-Pol region (RNA1) (Pacheco, 2021) but it does not appear that the region encoding the coat protein (RNA2) of the TRSV-Ca strain has been sequenced. Furthermore, PBRSV isolates from *Arracacia xanthorrhiza* (arracacha) and *Solanum tuberosum* hybrids (potato) formed two distinct groups, with identities of approximately 94% for the Pro-Pol (proteinase and RNA polymerase protein domains) region of RNA1 and 81% for the CP (coat protein) gene of RNA2 (Souza Richards *et al*., 2014). This is above the sequence demarcation limit for a new species of less than 80% amino acid (aa) identity in the Pro-Pol region and 75% aa identity in the CP region of RNA2 (ICTV, 2022a). A new PBRSV variant, possibly representing a new strain, was detected in Peru using high throughput sequencing (Fuentes *et al*., 2019; Krueze *et al*., 2019).

Nepoviruses are divided into three subgroups A, B and C based on sequence and genome organisation. PBRSV is in subgroup A. This subgroup has an RNA-2 of 3700–4000 nucleotides (nts) in length, present in both B and M components, which represent the bottom (B) and middle (M) components obtained after buoyant density centrifugation, during virus purification. Subgroup B has an RNA-2 of 4400–4700 nts in length, present only in the M component. Subgroup C has an RNA-2 of 6400–7300 nts in length, present in the M component, particles that are sometimes barely separable from those of B component. The three subgroups also differ in the cleavage sites recognized by their proteinase (ICTV, 2022b).

HOSTS

The principal natural host of PBRSV is potato (*Solanum tuberosum*), although there are only reports of natural infection of *S. tuberosum* subsp. *andigenum* (Fribourg, 1977) and *S. tuberosum* x *S. tuberosum* subsp. *andigenum* (Fribourg, 1977; Salazar & Harrison, 1978a). Other natural hosts in the Andean region are *Arracacia xanthorrhiza* (family Apiaceae) (Lizarraga *et al*., 1994), and *Oxalis tuberosa* (oca, family Oxalidaceae) (Lizarraga *et al*., 1997; Jeffries, 1998; Kreuze *et al.,* 2020), which may be grown in the same field, in rotation with or intercropped with

potato (Bianco & Sachs, 1998; Lizarraga *et al*., 1997; NRC, 1989).

Experimentally, plant species of at least 9 families have been infected, including plants in the Amaranthaceae, Aizoaceae, Cucurbitaceae, Fabaceae, Oxalidaceae and Solanaceae (Fribourg, 1977; Salazar & Harrison, 1978a).

Host list: *Arracacia xanthorrhiza*, *Solanum tuberosum subsp. andigenum*, *Solanum tuberosum*

GEOGRAPHICAL DISTRIBUTION

Despite Fribourg (1983) suggesting that PBRSV (reported as TRSV-calico strain in his publication) may have a wider distribution it has currently only been reported from Peru; primarily from the Andean region but also other areas in Peru which have received seed tubers from this region. Interestingly, in Costa Rica, TRSV was found to be infecting 42% of potato leaf samples tested using ELISA (Vásquez *et al*., 2006). However, confirmation of TRSV is required, since the supplier of the TRSV polyclonal antibody used in this study has reported cross reaction with PBRSV (Agdia, 2021). TRSV antibodies from other sources have also been reported to cross react with PBRSV (EPPO, 2017a).

South America: Peru

BIOLOGY

Many species of nepovirus are transmitted non-persistently by nematodes (ICTV, 2022b) and *Xiphinema* spp. are assumed to transmit PBRSV (Salazar, 1996). Some *Xiphinema* ssp. are present in the EPPO region, but it is not known whether these are able to transmit PBRSV (EFSA, 2020). It is easily transmitted by contact between plants, mechanically and vegetatively through tubers. Transmission through true potato seed of 2 – 9% (for the TRSV-Ca strain) has been demonstrated, but although the virus is detected in pollen no evidence of pollen transmission has been found (Jones, 1982). As far as it is known there are no reports of seed transmission of PBRSV in arracacha and oca.

DETECTION AND IDENTIFICATION

Symptoms

Symptoms of PBRSV in potato (*Solanum tuberosum* hybrids) are cultivar and environment dependent, and may also be virus strain dependent. Under cool Andean highland conditions these range from no symptoms to systemic necrotic leaf spotting (Salazar & Harrison, 1977) and calico-like symptoms (Fribourg, 1977). These bright yellow calico-like symptoms are particularly noticeable in some cultivars notably Ticahuasi (Salazar & Harrison, 1977). Under warmer conditions the calico symptoms are less pronounced (Fribourg, 1977). Calico symptoms only appear to have been reported for the TRSV-Ca strain.

Morphology

Virus particles are isometric, non-enveloped of two types but similar in size, 25–30 nm in diameter, and exhibit icosahedral symmetry (T = 1, pseudo T = 3) (ICTV (2022a)). The genome is a bipartite, linear positive-sense, single-stranded RNA. Complete sequences are available for a number of PBRSV isolates. RNA1 ranges from 7,579-7,598 bases between the different isolates and contains one single open reading frame (ORF), which is translated into a large polyprotein with 2 325 amino acids and a molecular weight of 257 kDa. RNA2 ranges from 3857 to 3918 bases for the different isolates, and it encodes a polyprotein of 1079–1082 amino acids with a molecular weight of 120 kDa (Souza Richards *et al*., 2014). The complete coding sequence of PBRSV isolates are available at https://www.ncbi.nlm.nih.gov/nuccore/?term=potato+black+ringspot+virus.

Detection and inspection methods

Field inspection of potato plants and other host plants may enable detection of the virus (see section on Symptoms); EPPO Standard PM 3/71 General crop inspection procedure for potatoes (EPPO, 2007). PBRSV is reliably detected in *in vitro* plants (4–6 weeks old and with stems of at least 5 cm) and plants grown from infected tubers, using indicator plants and serological and molecular methods. The reliability of testing tubers has not been reported.

Indicator plants

Indicator plants for use in quarantine testing are listed in PM 3/21 *Post-entry quarantine for potato* (EPPO, 2019a) and symptoms are described by Verhoeven & Roenhorst (2000). Recommended indicator plants are: *Chenopodium giganteum* (synonym *C. amaranticolor*) and *C. quinoa* (necrotic local lesions followed by systemic apical necrosis; *Nicotiana benthamiana* (local chlorotic and necrotic lesions and rings, systemic chlorosis, chlorotic and necrotic rings); *N. occidentalis* P1 (local necrotic lesions and rings, systemic dwarfing and veinal necrosis) and *N. tabacum* (local and systemic chlorotic and necrotic ringspots and line patterns)**.**

Serological detection methods

High-titre antisera can be prepared against PBRSV. ELISA has been successfully used for virus detection (Schroeder & Weidemann, 1990) and both polyclonal and monoclonal antibodies are available commercially.

Molecular methods

Two step (Wei & Clover, 2008) or one-step RT-PCR (EPPO, 2017) using forward and reverse primers A NepoA-F and NepoA-R for detection of nepoviruses in subgroup A may be used followed by sequencing the PCR amplicon (?340 bp) for confirmation of virus identity. Validation data is available for this test (Anses, 2015). Other primers for detection of nepoviruses and PBRSV are listed by Pacheco (2021) but these do not appear to have been validated.

PATHWAYS FOR MOVEMENT

Local spread of PBRSV is by contact between plants and probably nematode vectors. Plants for planting (including tubers) of arracacha, oca and potato moved locally or internationally for commercial planting or as germplasm constitute major pathways for movement. Potentially other Andean root crops may present a risk since these are often grown in association with, or in the same area as potato. Additionally, for potato the virus may be spread by true potato seed (TPS) through its movement as potato germplasm, although the significance of this in practice is less clear since it has only been rarely reported infecting gene bank accessions. However, the increasing interest in use of TPS for commercial potato production means that care should be taken to ensure that parent plants used to produce

the TPS are free from PBRSV. Additionally, infected pollen moved for potato breeding may possibly present a risk, of introducing the virus into breeding programmes, although there is currently no evidence of pollen transmission. Whether PBRSV may be spread by seed and pollen of other hosts has not been reported. Infective *Xiphinema* spp. in soil and growing media attached to plants (host or non-host plants) from areas where the nematode occurs may be a major entry pathway (EFSA, 2020). Although soil and growing media attached to (agricultural) machinery, tools, and packaging materials was identified as an entry pathway, it was not considered as an important pathway (EFSA, 2020).

PEST SIGNIFICANCE

Economic impact

PBRSV causes damaging symptoms in some potato cultivars under certain conditions. Although Fribourg (1977) describes it as widespread in Peru, it has not been recorded as causing any particular losses in potato production, and it appears to be no more important than the nepoviruses *Beet ringspot virus* and *Tomato black ring virus* are on potato in Europe. Moreover, PBRSV was only recorded once in a recent survey in Peru using high throughput sequencing (Fuentes *et al*., 2019; Krueze *et al*., 2019).

Control

Control depends on the production of high-quality planting material from virus-free nuclear stock or true potato seed that is produced from PBRSV-free parents in a pest free area or facility. Planting should be in in fields free from potential vectors and volunteer plants. Measures to minimize mechanical transmission may be used.

Phytosanitary risk

Climatic conditions will not impair the ability of PBRSV to establish in the EPPO region. Potato is widely grown and is the main crop at risk. Although EFSA (2020) concluded that PBRSV met the criteria to qualify as an EU quarantine pest, the magnitude of potential impact in the EU was unclear.

PHYTOSANITARY MEASURES

EPPO recommends its member to prohibit the import of all breeding material of potato, of whatever origin, except under a special permit, subject to post?entry quarantine (EPPO, 2017b; EPPO, 2019a). Once tested and found to be free from pests it may be released from quarantine and moved within the EPPO region.

Certified seed potatoes (micropropagative material and minitubers) may be traded if they meet the requirements of EPPO Standards PM 3/62 *Production of pathogen-free microplants of potato* (EPPO, 2019c) and PM 3/63 *Production of pathogen-free minitubers of potato* (EPPO, 2019d) respectively. For import of seed potatoes and ware potatoes EPPO recommends that trade should be subject to transitional arrangements described in PM 8/1 *Co mmodity-specific phytosanitary measures for potato* (EPPO, 2017a), which requires for countries where PBRSV occurs, import from a pest-free area and from a pest-free potato production and distribution system, according to EPPO Standard PM 3/61 *Pest-free areas and pest-free production and distribution systems for quarantine pests of potato* (EPPO, 2019b). Additionally for ware potatoes, for countries in Central and South America where PBRSV does not occur, recommendations are confirmation by detection survey that PBRSV does not occur and inspection or testing of tubers on import.

Import of potato is regulated/prohibited in many EPPO countries. In the EU, the import of seed potatoes and plants (including true potato seed for planting of stolon-or tuber-forming species of *Solanum* or their hybrids is prohibited from third countries, other than Switzerland, by Annex VI of Commission Implementing Regulation (EU) 2019/2072 (EU, 2022). Furthermore, such material stored in gene banks or genetic stock collection are subject to quarantine restrictions. Entry of ware potatoes is also regulated, and import is only permitted from specified countries, which currently does not include countries in Central and South America. However, as long as ware potatoes are not planted and only used for consumption or processing, the ability of PBRSV to establish is likely very low (EFSA,

2020).

Currently, EPPO countries do not prohibit the import of the other potential hosts of PBRSV, the Andean root crops arracacha and oxalis from South America for planting although prohibitions for example in the EU, have been introduced for plants for planting (other than seeds and *in vitro* material) of another Andean root crop, *Ullucus tuberosus* by Commission Implementing Regulation (EU) 2018/2019 (EU, 2018).

The pathway of viruliferous vectors of PBRSV is possibly open, because the existence of the pathway cannot be excluded based on comparisons with the biology of closely related viruses (in the same genus or family) (EFSA, 2020).

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ACKNOWLEDGEMENTS

This datasheet was extensively revised in 2023 by C Jeffries (SASA, UK) with help from L Salazar (formerly CIP, Peru). Their valuable contribution is gratefully acknowledged.

How to cite this datasheet?

EPPO (2025) *Nepovirus solani*. EPPO datasheets on pests recommended for regulation. Available online. https://gd.eppo.int

Datasheet history

This datasheet was first published in the EPPO Bulletin in 1984 and revised in the two editions of 'Quarantine Pests for Europe' in 1992 and 1997, as well as in 2023. It is now maintained in an electronic format in the EPPO Global Database. The sections on 'Identity', 'Hosts', and 'Geographical distribution' are automatically updated from the database. For other sections, the date of last revision is indicated on the right.

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Co-funded by the European Union