

EPPO Datasheet: *Begomovirus solanumdelhiense*

Last updated: 2020-10-06

IDENTITY

Preferred name: *Begomovirus solanumdelhiense*

Taxonomic position: Viruses and viroids: Monodnaviria:
Shotokuvirae: Cressdnaviricota: Repensiviricetes: Geplafuvirales:
Geminiviridae

Other scientific names: *BGYVV*, Bitter gourd yellow vein virus,
ToLCNDV, Tomato leaf curl New Delhi begomovirus, Tomato leaf
curl New Delhi virus

[view more common names online...](#)

EPPO Categorization: A2 list, Alert list (formerly)

[view more categorizations online...](#)

EU Categorization: A2 Quarantine pest (Annex II B)

EPPO Code: TOLCND



[more photos...](#)

Notes on taxonomy and nomenclature

Tomato leaf curl New Delhi virus, ToLCNDV, is a virus species with a single-stranded DNA genome, in the genus *Begomovirus*, family *Geminiviridae*. Isolates of this virus can be grouped into several strains based on the molecular diversity of their DNA-A genome components (Moriones *et al.*, 2017). The virus isolates reported from Europe comprise the strain ToLCNDV-ES (Fortes *et al.*, 2016; Juarez *et al.*, 2019; Panno *et al.*, 2019; Ruiz *et al.*, 2017) which is genetically stable and distinct from other ToLCNDV isolates.

HOSTS

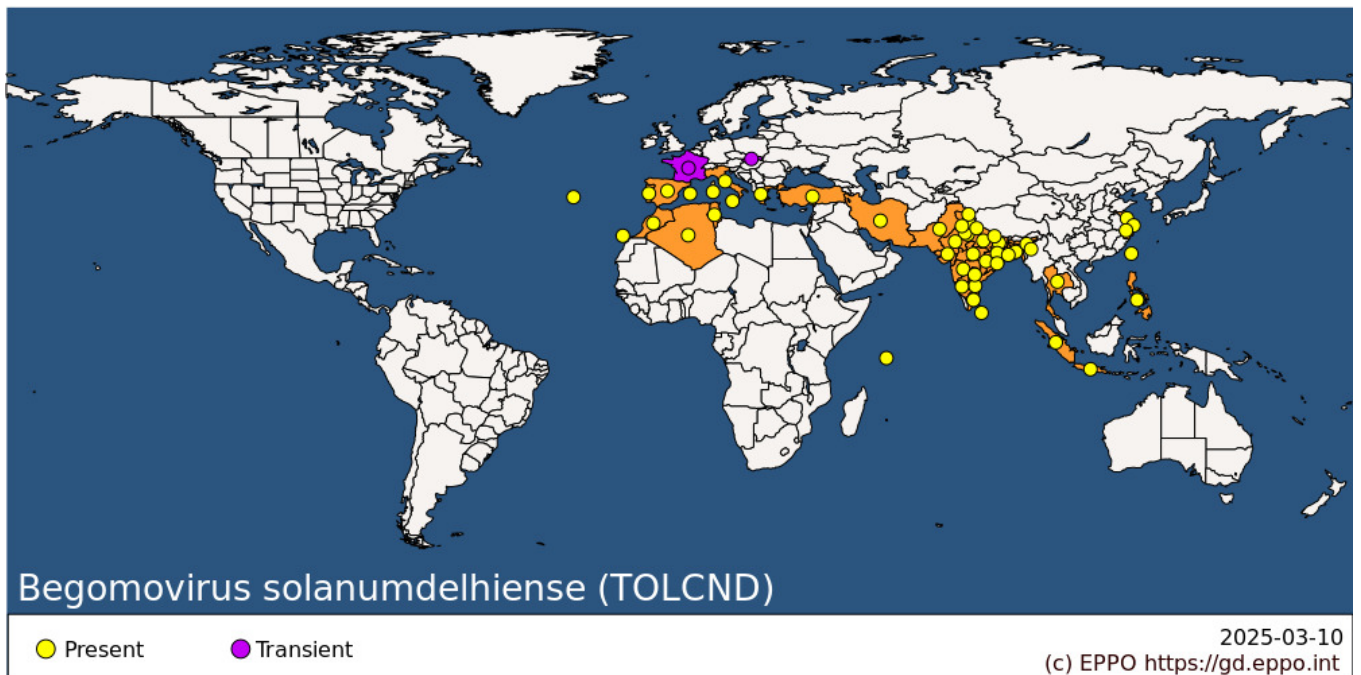
ToLCNDV has a broad host range encompassing Solanaceae, Cucurbitaceae, Fabaceae and Malvaceae species many of which are important crops and ornamental plants as well as wild species (weeds). The main crop hosts of ToLCNDV are tomato and cucurbits in particular zucchini, cucumber and melon. Wild plant hosts may not show conspicuous symptoms but can serve as virus reservoirs. Because of the broad host range and the polyphagous nature of its vector *Bemisia tabaci*, the range of susceptible plant species may be larger than reported.

The range of susceptible host plants and those found to be infected in nature may not correspond. Thus, the virus strain ToLCNDV-ES present in Europe is predominantly found on Cucurbitaceae plants and while the virus strain infects tomato (Janssen *et al.*, 2017; Ruiz *et al.*, 2017) it appears to be poorly adapted to this host and is better adapted to cucurbits which are efficiently infected by ToLCNDV-ES (Juarez *et al.*, 2019; Panno *et al.*, 2019).

Host list: *Abelmoschus esculentus*, *Acalypha indica*, *Benincasa fistulosa*, *Benincasa hispida*, *Calotropis procera*, *Capsicum annuum*, *Capsicum chinense*, *Capsicum frutescens*, *Carica papaya*, *Catharanthus roseus*, *Cestrum nocturnum*, *Chenopodium album*, *Chenopodium giganteum*, *Chrysanthemum indicum*, *Citrullus lanatus*, *Coccinia grandis*, *Commelina benghalensis*, *Convolvulus arvensis*, *Crossandra infundibuliformis*, *Cucumis melo* subsp. *agrestis*, *Cucumis melo* subsp. *melo* var. *cantaloupensis*, *Cucumis melo* var. *flexuosus*, *Cucumis melo*, *Cucumis sativus*, *Cucurbita maxima*, *Cucurbita moschata*, *Cucurbita pepo* var. *giromontiina*, *Cucurbita pepo*, *Cyamopsis tetragonoloba*, *Dahlia pinnata*, *Datura stramonium*, *Daucus carota*, *Ecballium elaterium*, *Eclipta prostrata*, *Euphorbia hirta*, *Glycine max*, *Gossypium hirsutum*, *Hibiscus cannabinus*, *Ipomoea cairica*, *Jasminum multiflorum*, *Jatropha*, *Lagenaria siceraria*, *Luffa acutangula*, *Luffa aegyptiaca*, *Momordica charantia*, *Momordica dioica*, *Papaver somniferum*, *Parthenium hysterophorus*, *Phyllanthus niruri*, *Physalis minima*, *Ricinus communis*, *Rumex dentatus*, *Sauropus androgynus*, *Sechium edule*, *Solanum lycopersicum*, *Solanum melongena*, *Solanum nigrum*, *Solanum tuberosum*, *Sonchus oleraceus*, *Tagetes erecta*, *Trichosanthes cucumerina*, *Trifolium repens*, *Vicia lens*, *Vigna radiata*

GEOGRAPHICAL DISTRIBUTION

ToLCNDV was first described from India (Padidam *et al.*, 1995) and it is mainly present in Asia where many host plants and various virus isolates (strains) are described. The occurrence of the virus coincides with the presence of the *Bemisia tabaci* whitefly vector and the availability of suitable host plants. ToLCNDV occurs in the Mediterranean regions, in areas where *B. tabaci* is endemic. ToLCNDV findings outside the climate suitable for the insect vector are linked with the horticulture pathway and plants produced under protected cultivation (glasshouses).



EPPO Region: Algeria, France (mainland), Greece (mainland), Italy (mainland, Sardegna, Sicilia), Morocco, Portugal (mainland, Azores), Slovakia, Spain (mainland, Islas Baleares, Islas Canárias), Tunisia, Türkiye

Africa: Algeria, Morocco, Seychelles, Tunisia

Asia: Bangladesh, China (Jiangsu, Shanghai, Zhejiang), India (Andhra Pradesh, Assam, Bihar, Chhattisgarh, Delhi, Gujarat, Haryana, Himachal Pradesh, Jammu & Kashmir, Jharkand, Karnataka, Madhya Pradesh, Maharashtra, Manipur, Odisha, Punjab, Rajasthan, Tamil Nadu, Telangana, Uttarakhand, Uttar Pradesh, West Bengal), Indonesia (Java, Sumatra), Iran, Nepal, Pakistan, Philippines, Sri Lanka, Taiwan, Thailand

BIOLOGY

ToLCNDV is transmitted by *Bemisia tabaci* whiteflies and persists in the vector insect. Adult insects acquire the virus by sucking on phloem sap, and once ingested the virus circulates in the insect body. The insect can further transmit the virus to another plant when feeding. The virus does not replicate in the insect and transmission efficiency decreases with age but the vector remains viruliferous throughout its life span. Even in the temporary absence of host plants suitable for ToLCNDV, the virus can persist in the vector and when hosts are again present then virus transmission by sap sucking is generally very effective and even a few insects can cause disease outbreaks. The broad host range of the virus and the polyphagous nature of the whitefly vector, in particular the invasive MEAM1 (Middle East-Asia Minor) and MED (Mediterranean) species present in Southern Europe and the Mediterranean Basin, assure virus establishment in the environment.

Seedling infection arising from germinating seeds of ToLCNDV-infected zucchini fruits was reported (Kil *et al.*, 2020). It is likely that this happened by wounding of the germinating seeds and mechanical transmission of the virus present on the seed coat. While rare cases of mechanical virus infection through wounding exist, insect transmission is the primary mode of ToLCNDV spread and virus incidence is closely linked to the geographical distribution of *B. tabaci*, which is determined by climate variables, temperature and humidity (EFSA, 2013; Gilioli *et al.*, 2014). *B. tabaci* has short acquisition and inoculation access periods (< 30 min) for efficient virus transmission and virus spread and disease incidence is linked to the density of whitefly populations.

DETECTION AND IDENTIFICATION

Symptoms

Symptoms become apparent on plants infected with ToLCNDV approximately 10 to 14 days after vector feeding. ToLCNDV causes systemic infections in its hosts and early symptoms become visible in youngest uppermost plant parts showing leaf curling, distortion, and blistering. In cucurbit hosts this is associated with discoloration, chlorotic mottling and vein banding followed by upward rolling and general chlorosis of older leaves. In tomato, leaf curling of the apical portions of the plant are the first signs of a developing begomovirus infection, somewhat similar to symptoms caused by *Tomato yellow leaf curl virus* (TYLCV) and other begomoviruses. In later infections, chlorotic spots and mottling can be observed on older leaves. Early infections with ToLCNDV interferes with flowering and fruit development resulting in reduced flower setting and low numbers of fruits. Fruits are small with unappealing discoloration, indents or blisters and lacking in taste, and may prematurely drop, which can eventually result in complete crop failure (EFSA, 2020a, b).

ToLCNDV can occur in mixed infection with other viruses, in particular other begomoviruses, and with alpha- and betasatellites. Mixed infections can result in synergism and more severe symptoms than ToLCNDV infections alone.

ToLCNDV causes pronounced symptoms in infected plants and while uncertainty exists on symptoms on wild hosts, virus-infected crops are generally recognised.

Morphology

ToLCNDV has distinctive virus particles composed of two incomplete icosahedra fused to form a paired (geminata) particle of 18x30 nm. The virus particles are unique and characteristic for geminiviruses only.

Detection and inspection methods

ToLCNDV causes obvious symptoms in most infected hosts however, these symptoms are not adequate to identify the virus because they are similar to those caused by other begomoviruses and because of other viruses present in mixed infections. Thus, for unambiguous virus detection and identification, laboratory methods are required. Inspection and tracing of symptomatic plants guide sampling with leaves of apical portions of plants being used for virus testing. Even when symptoms are mild or absent, ToLCNDV can be detected. ToLCNDV can be reliably detected using commercial ELISA tests (DAS-ELISA) which can be used for surveillance to trace infections (Juarez *et al.*, 2019). Subsequent identification of ELISA positive samples can be done using molecular tests to identify ToLCNDV (Figas *et al.*, 2017; Panno *et al.*, 2019; Parrella *et al.*, 2018; Ruiz *et al.*, 2015; Saez *et al.*, 2016). For identification of virus strains and in particular to identify the European strain ToLCNDV-ES, sequence analysis of the complete DNA-A genome component ToLCNDV is required. This is achieved by combining DNA amplification (Rolling circle amplification RCA or PCR) with sequencing (Fortes *et al.*, 2016; Moriones *et al.*, 2017).

Testing of *B. tabaci* for the presence of ToLCNDV and other circulative, persistent plant viruses is critical to detect and intercept viruliferous insects which may, for example, be carried along with imported plant materials. Virus detection and identification in vectors is achieved by molecular methods including real-time PCR (Bertin *et al.*, 2018; Luigi *et al.*, 2020).

An EPPO Diagnostic Protocol for Begomoviruses is under development and will cover detection and identification of ToLCNDV. As surveys should be carried out in all the EU member countries, a pest survey card was prepared by the European Food Safety Authority (EFSA, 2020b) to assist EU Member States in planning their annual survey activities for ToLCNDV.

PATHWAYS FOR MOVEMENT

ToLCNDV spread is predominantly with viruliferous whiteflies thus virus distribution coincides with the geographic distribution of its vector and is limited by the spread capacity of the insect. The insect carrying the virus can transmit

it throughout its lifetime thus passive transport of viruliferous adults through wind, or infesting host or non-host plants and other materials (cut flowers and fresh herbs) traded internationally constitute means of virus long-distance movement and virus introduction into new areas. Import of many host plants of ToLCNDV and other commodities are regulated in the EU and in many EPPO countries and the introduction of *B. tabaci* is forbidden. However, the number of whiteflies intercepted at points of entry indicate a putative pathway for ToLCNDV to enter the EPPO region.

PEST SIGNIFICANCE

Economic impact

In the regions where ToLCNDV occurs, the virus presents a threat to solanaceous and cucurbit plants including economically important crops, such as tomato, eggplant, pepper, potato, zucchini, cucumber and melon. In addition, the virus also causes serious economic losses in vegetable and fibre crops grown in Asia, potato (Jeevalatha *et al.*, 2017a,2017b; Usharani *et al.*, 2004) cotton and okra (Venkataravanappa *et al.*, 2015, 2018; Zaidi *et al.*, 2016) and many other food crops. It is assumed that ToLCNDV causes serious economic losses wherever it occurs and has severe impacts on quality and yield of the vegetable harvest. These products are important sources of healthy diets and income security. Plant protection products used for vector control may have negative impacts on the environment and biodiversity if they are not used appropriately.

Control

Effective control of ToLCNDV rely on the control of the insect vector *B. tabaci*. In regions where *B. tabaci* occurs in nature and open fields, control should both exclude the insect (physical barriers, protected cultivation) and reduce whitefly populations using IPM practices combining biological and chemical control strategies (Crespo *et al.*, 2019; Rodriguez *et al.*, 2019; Tellez *et al.*, 2017) to suppress virus spread. Eliminating virus-infected plants or groups of plants is only relevant in the absence of established *B. tabaci*, this is the case for example when outbreaks occur in protected cultivation and temporary whitefly populations can be eradicated. Managing ToLCNDV and whitefly-transmitted viruses in general is challenging in open-field crops. Thus, in open-field horticulture, the control of whitefly transmitted viruses relies on insecticides to reduce vector populations and host plant resistance to the virus combined with selected IPM strategies (Lapidot *et al.*, 2014). Crop rotation and planting outside of periods with high vector populations may contribute to reduce impact from virus diseases.

Genetic resistance is the most promising strategy for ToLCNDV control and resistance provided by Ty-2 and Ty-3 genes conferring resistance against TYLCV can provide a level of protection against ToLCNDV (Akhtar *et al.*, 2019; Lata *et al.*, 2019; Prasanna *et al.*, 2015). In cucurbits, *Cucurbita moschata* lines that had little or no symptoms of ToLCNDV infections may be potential sources of ToLCNDV resistance (Saez *et al.*, 2017,2016). Resistance has been reported in sponge gourd (Islam *et al.*, 2010) and in five accessions of melon (Romay *et al.*, 2019). Breeding ToLCNDV resistant crops may be a long-term solution but currently no ToLCNDV resistant crops are cultivated.

Phytosanitary risk

ToLCNDV is present in several countries of the EPPO region, in Southern European and neighbouring countries bordering the Mediterranean Sea, in areas where *B. tabaci*, its insect vector, is established. Virus dissemination and spread is bound to the geographic range distribution of the vector and this is limited by suitable eco-climatic conditions (EFSA, 2020, 2013). In open fields, adequate pest management often is not possible and adaption of whiteflies to less favourable conditions and range expansion triggered by climate change and intensified agriculture aggravates ToLCNDV damage (Bertin *et al.*, 2018). Outside the areas where *B. tabaci* is endemic, the virus may spread if the vector expands its range due to adaptation to less favourable conditions or climate change. In climates less suitable for the vector and where crop production is under protected conditions, ToLCNDV infections can occur but are transient because vector populations only occurs during part of the year and cannot establish.

In Europe, all ToLCNDV isolates described so far belong to one strain, ToLCNDV-ES, which is genetically homogenous and probably derived from a single introduction. This ToLCNDV strain comprises virus isolates that are adapted to cucurbit hosts (cucumber, melon, and zucchini), and which circulate mainly in cucurbits whereas tomato and other solanaceous crops are less important host plants. An increased risk to crop production in the EPPO

region would arise from additional virus diversity introduced from Asia where various isolates of the virus are reported and in addition the virus is associated with other viruses and satellite molecules. In this case additional host plants, such as tomato, potato could be strongly affected and current crop management strategies may be jeopardized.

PHYTOSANITARY MEASURES

The import of some host plants for planting (e.g. Solanaceae) is prohibited in many EPPO countries. Other host plants for planting should only be imported from pest-free areas for the virus. They may also come from areas where the virus occurs if they are produced in pest-free sites of production e.g. under isolation or where measures are implemented to avoid the presence of *B. tabaci* (e.g. green/ screenhouses, trapping) and no symptoms of the virus are observed during the cycle of vegetation on. Surveillance (visual inspection followed by laboratory testing) contributes to early detection of ToLCNDV infected plants and assessment of vectors for targeted insecticide application.

REFERENCES

- Akhtar KP, Akram A, Ullah N, Saleem MY, Saeed M (2019) Evaluation of Solanum species for resistance to *Tomato leaf curl New Delhi virus* using chip grafting assay. *Scientia Horticulturae* **256**.
- Bertin S, Luigi M, Parrella G, Giorgini M, Davino S, Tomassoli L (2018) Survey of the distribution of *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Lazio region (Central Italy): a threat for the northward expansion of *Tomato leaf curl New Delhi virus* (Begomovirus: Geminiviridae) infection. *Phytoparasitica* **46**, 171-182.
- CABI (2020) Datasheet on Tomato leaf curl New Delhi virus (Tomato New Delhi virus). Available online <https://www.cabi.org/isc/datasheet/118179>
- Crespo O, Robles C, Ruiz L, Janssen D (2019) Antagonism of Cucumber green mottle mosaic virus against *Tomato leaf curl New Delhi virus* in zucchini and cucumber. *Annals of Applied Biology*.
- EFSA (2013) Scientific Opinion on the risks to plant health posed by *Bemisia tabaci* species complex and viruses it transmits for the EU territory. *EFSA Journal* **11** (4), 3162. <https://doi.org/10.2903/j.efsa.2013.3162>
- EFSA (2020a), Bragard C, Dehnen-Schmutz K, Di Serio F, Gonthier P, Jacques MA, Jaques Miret JA, Justesen AF, MacLeod A, Magnusson CS, Milonas P, Navas-Cortes JA, Parnell S, Potting R, Reignault PL, Thulke HH, Van der Werf W, Vicent Civera A, Yuen J, Zappala L, Candresse T, Chatzivassiliou E, Winter S, Bottex B (2020) Pest categorisation of tomato leaf curl New Delhi virus. *EFSA Journal* **18**(7), 6179, 36 pp. <https://doi.org/10.2903/j.efsa.2020.6179>
- EFSA (2020b), van Gemert J, Schenk M, Candresse T, Bottex B, Delbianco A, Vos S. Pest survey card on tomato leaf curl New Delhi virus. EFSA supporting publication EN-1904. 26 pp. <https://doi.org/10.2903/sp.efsa.2020.EN-1904>
- Figas MR, Alfaro-Fernandez A, Font MI, Borrás D, Casanova C, Hurtado M, Plazas M, Prohens J & Soler S (2017) Inoculation of cucumber, melon and zucchini varieties with *Tomato leaf curl New Delhi virus* and evaluation of infection using different detection methods. *Annals of Applied Biology* **170**, 405-414.
- Fortes IM, Sanchez-Campos S, Fiallo-Olive E, Diaz-Pendon JA, Navas-Castillo J, Moriones E (2016) A novel strain of *Tomato leaf curl New Delhi virus* has spread to the Mediterranean Basin. *Viruses* **8**.
- Gilioli G, Pasquali S, Parisi S, Winter S (2014) Modelling the potential distribution of *Bemisia tabaci* in Europe in light of the climate change scenario. *Pest Management Science* **70**, 1611-1623.
- Islam S, Munshi AD, Mandal B, Kumar R, Behera TK (2010) Genetics of resistance in *Luffa cylindrica* Roem. against *Tomato leaf curl New Delhi virus*. *Euphytica* **174**, 83-89.
- Janssen D, Simon A, Crespo O, Ruiz L (2017) Genetic population structure of *Bemisia tabaci* in Spain associated

with *Tomato leaf curl New Delhi virus* - Short Communication. *Plant Protection Science* **53**, 25-31.

Jeevalatha A, Chakrabarti SK, Sharma S, Sagar V, Malik K, Raigond B, Singh BP (2017) Diversity analysis of *Tomato leaf curl New Delhi virus*-[potato], causing apical leaf curl disease of potato in India. *Phytoparasitica* **45**, 33-43.

Jeevalatha A, Siddappa S, Kumar A, Kaundal P, Guleria A, Sharma S, Nagesh M, Singh BP (2017) An insight into differentially regulated genes in resistant and susceptible genotypes of potato in response to tomato leaf curl New Delhi virus-[potato] infection. *Virus Research* **232**, 22-33.

Juarez M, Legua P, Mengual CM, Kassem MA, Sempere RN, Gomez P, Truniger V, Aranda MA (2013) Relative incidence, spatial distribution and genetic diversity of cucurbit viruses in eastern Spain. *Annals of Applied Biology* **162**, 362-370.

Juarez M, Rabadan MP, Martinez LD, Tayahi M, Grande-Perez A, Gomez P (2019) Natural hosts and genetic diversity of the emerging *Tomato leaf curl New Delhi virus* in Spain. *Frontiers in Microbiology* **10**, 140.

<https://doi.org/10.3389/fmicb.2019.00140>

Kil E-J, Vo TTB, Fadhila C, Ho PT, Lal A, Troiano E, Parrella G, Lee S (2020) Seed Transmission of *Tomato Leaf Curl New Delhi Virus* from Zucchini Squash in Italy. *Plants* **9**(5), 563. <https://doi.org/10.3390/plants9050563>.

Lapidot M, Legg JP, Wintermantel WM, Polston JE (2014) Management of whitefly-transmitted viruses in open-field production systems. *Plant Virus Epidemiology* **90**, 147-206. <https://doi.org/10.1016/B978-0-12-801246-8.00003-2>

Lata S, Hussain Z, Mangal M, Yadav RK, Vinutha T, Jat GS, Gosavi G, Kumar P, Perveen S, Tomar BS (2019) qPCR analysis of Ty-2 and Ty-3 gene pyramided lines of tomato for resistance to tomato leaf curl New Delhi virus (ToLCNDV). *Indian Journal of Agricultural Sciences* **89**, 1719-1722. <https://doi.org/10.1111/ppa.12267>

Luigi M, Manglli A, Bertin S, Donati L, Tomassoli L, Ferretti L & Faggioli F (2020) Development and validation of a specific real-time PCR protocol for the detection of tomato leaf curl New Delhi virus. *European Journal of Plant Pathology* **157**, 969-974 <https://doi.org/10.1007/s10658-020-02038-1>

Moriones E, Praveen S, Chakraborty S (2017) *Tomato Leaf Curl New Delhi Virus*: an emerging virus complex threatening vegetable and fiber crops. *Viruses* **9**(10), 264. <https://doi.org/10.3390/v9100264>.

Padidam M, Beachy RN, Fauquet CM (1995) Tomato leaf curl geminivirus from India has a bipartite genome and coat protein is not essential for infectivity. *Journal of General Virology* **76**(1), 25-35. <https://doi.org/10.1099/0022-1317-76-1-25>

Panno S, Caruso AG, Troiano E, Luigi M, Manglli A, Vatrano T, Iacono G, Marchione S, Bertin S, Tomassoli L, Parrella G, Davino S (2019) Emergence of tomato leaf curl New Delhi virus in Italy: estimation of incidence and genetic diversity. *Plant Pathology* **68**, 601-608. <https://doi.org/10.1111/ppa.12978>

Parrella G, Troiano E, Formisano G, Accotto GP, Giorgini M (2018) First report of *Tomato leaf curl New Delhi virus* associated with severe mosaic of pumpkin in Italy. *Plant Disease* **102**, 459-460.

Prasanna HC, Sinha DP, Rai GK, Krishna R, Kashyap SP, Singh NK, Singh M, Malathi VG (2015) Pyramiding Ty-2 and Ty-3 genes for resistance to monopartite and bipartite tomato leaf curl viruses of India. *Plant Pathology* **64**, 256-264.

Rodriguez E, Tellez MM, Janssen D (2019) Whitefly control strategies against *Tomato Leaf Curl New Delhi Virus* in greenhouse zucchini. *International Journal of Environmental Research and Public Health* **16**(15), 2673.

<https://doi.org/10.3390/ijerph16152673>

Romay G, Pitrat M, Lecoq H, Wipf-Scheibel C, Millot P, Girardot G, Desbiez C (2019) Resistance against *Melon Chlorotic Mosaic Virus* and *Tomato Leaf Curl New Delhi Virus* in melon. *Plant Disease* **103**, 2913-2919.

<https://doi.org/10.1094/PDIS-02-19-0298-RE>

Ruiz L, Simon A, Velasco L, Janssen D (2017) Biological characterization of *Tomato leaf curl New Delhi virus* from Spain. *Plant Pathology* **66**, 376-382.

Ruiz ML, Simon A, Velasco L, Garcia MC, Janssen D (2015) First report of *Tomato leaf curl New Delhi virus* infecting tomato in Spain. *Plant Disease* **99**, 894-894.

Saez C, Esteras C, Martinez C, Ferriol M, Dhillon NPS, Lopez C & Pico B (2017) Resistance to tomato leaf curl New Delhi virus in melon is controlled by a major QTL located in chromosome 11. *Plant Cell Reports* **36**, 1571-1584.

Saez C, Martinez C, Ferriol M, Manzano S, Velasco L, Jamilena M, Lopez C & Pico B (2016) Resistance to *Tomato leaf curl New Delhi virus* in Cucurbita spp. *Annals of Applied Biology* **169**, 91-105.

Tellez MD, Simon A, Rodriguez E, Janssen D (2017) Control of Tomato leaf curl New Delhi virus in zucchini using the predatory mite *Amblyseius swirskii*. *Biological Control* **114**, 106-113.

Usharani KS, Surendranath B, Paul-Khurana SM, Garg ID, Malathi VG (2004) Potato leaf curl - a new disease of potato in northern India caused by a strain of Tomato leaf curl New Delhi virus. *Plant Pathology* **53**, 235-235.

Venkataramanappa V, Reddy CNL, Jalali S & Reddy MK (2015) Association of tomato leaf curl New Delhi virus DNA-B with bhendi yellow vein mosaic virus in okra showing yellow vein mosaic disease symptoms. *Acta Virologica* **59**, 125-139.

Venkataramanappa V, Reddy CNL, Saha S & Reddy MK (2018) Recombinant *Tomato leaf curl New Delhi virus* is associated with yellow vein mosaic disease of okra in India. *Physiological and Molecular Plant Pathology* **104**, 108-118.

Zaidi SSEA, Shafiq M, Amin I, Scheffler BE, Scheffler JA, Bridson RW & Mansoor S (2016) Frequent occurrence of *Tomato Leaf Curl New Delhi Virus* in Cotton Leaf Curl Disease affected cotton in Pakistan. *Plos One* **11**(5).
<https://doi.org/10.1371/journal.pone.0155520>

ACKNOWLEDGEMENTS

This datasheet was prepared in 2020 by Stephan Winter, Plant Virus Department, Leibniz Institute- German Collection of Microorganisms and Cell Cultures, DSMZ, Germany. His valuable contribution is gratefully acknowledged.

How to cite this datasheet?

EPPO (2025) *Begomovirus solanumdelhiense*. EPPO datasheets on pests recommended for regulation. Available online. <https://gd.eppo.int>

Datasheet history

This datasheet was first published in 2020. It is 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.



Co-funded by the
European Union