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Understanding the Begomovirus-Bemisia tabaci-Solanaceous crops pathosystem in Northwestern Argentina

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Abstract

Begomoviruses are transmitted in a persistent, circulative manner by the whitefly *Bemisia tabaci*, a complex of cryptic species. The introduction and spread of invasive *B. tabaci* in South America have intensified begomovirus outbreaks, causing severe yield losses in major vegetable crops. This study, conducted in Northwestern Argentina (NOA), a key horticultural region where tomato, pepper, and eggplant are frequently co-cultivated, aimed to genetically characterize the *Begomovirus-B. tabaci-Solanaceae* complex. Plant and whitefly samples were collected from co-cultivated crops within a representative field. Four begomovirus species were identified through metagenomic analysis and molecular characterization: soybean blistering mosaic virus (SbBMV), infecting all hosts; solanum mosaic Bolivia virus (SoMBoV), detected only in tomato; and two putative novel species, tomato common mottle virus (ToCmMoV) and pepper vein clearing virus (PepVCV), proposed here. Phylogenetic analysis grouped each virus into a distinct clade. Whitefly species were identified through PCR-RFLP analysis of the mitochondrial cytochrome c oxidase subunit I (mtCOI) gene. The invasive Mediterranean (MED) species predominated across all crops, while new world 2 (NW2) was detected only in tomato at lower abundance. Eggplant supported the highest *B. tabaci* abundance, whereas tomato harbored the greatest viral diversity, highlighting their complementary roles in vector maintenance and virus diversification. Continuous and overlapping cultivation of *Solanaceae* crops in the NOA region may promote begomovirus persistence and diversification, with crop interfaces facilitating virus exchange among host species. In addition, the dominance of the MED cryptic species highlights the need for integrated management strategies.

Introduction

Northwestern Argentina (NOA) is a key agroecological region for horticultural production, characterized by strong gradients in altitude, climate, and ecosystems. Its landscape spans the eastern Chaqueña lowlands and humid Yunga foothills, intermontane valleys, semi-arid plains, and the high-altitude Puna, giving rise to diverse agricultural systems within short distances.

Extensive crops are concentrated in the eastern lowlands and Chaqueña plains (eastern Santiago del Estero, eastern Salta, and parts of Tucumán), where flat terrain and rainfed conditions favor large-scale cultivation of common bean, soybean, maize, wheat, and sorghum. In contrast, intensive systems occur in intermontane valleys, piedmont areas, Yunga's foothills, and irrigated sections of the eastern lowlands, supporting horticulture, including tomato, pepper, eggplant, cucurbit species, sweet corn, and green beans, as well as citrus and tobacco.

Tomato (*Solanum lycopersicum*) production in the NOA relies on irrigated systems, where favorable temperatures, high solar radiation, and reliable water availability support fresh-market cultivation across approximately 3,500 hectares (Secretaría de Agricultura Ganadería y Pesca 2023). Pepper (*Capsicum annuum*) occupies around 1,200 hectares, while eggplant (*Solanum melongena*) is also cultivated, although detailed area data are less consistently reported (Food and Agriculture Organization of the United Nations 2023). These landscapes reflect a combination of intensive horticulture, family farming, and regional agribusiness shaped by the NOA's pronounced environmental gradients.

There are no quantitative estimates of yield losses caused by begomoviruses in tomato, pepper, and eggplant crops in the NOA region. Nevertheless, during years with high whitefly pressure, total losses in greenhouse tomato production and yield reductions of up to 40% in open-field tomatoes have been reported, in agreement with findings from Brazil (Inoue-Nagata et al. 2016).

Currently, the genus *Begomovirus* compromises 457 recognized species (International Committee on Taxonomy of Viruses, 2025). Begomoviruses possess either monopartite or bipartite genomes. Monopartite begomoviruses contain a single genomic component ranging from approximately 2.7 to 2.8 kilobases (kb) in length. In contrast, bipartite begomoviruses comprise two distinct genomic components, denominated DNA-A and DNA-B ranging from 2.4 to 2.7 kb

(Fiallo-Olivé et al. 2021). In Argentina, only bipartite begomoviruses have been reported. The DNA-A component encodes several proteins, including the coat protein, replication-associated proteins, transcriptional regulators, and suppressors of host defense mechanisms. DNA-B encodes proteins involved in the intracellular transport of viral DNA (from the cytoplasm to the nucleus) as well as the systemic movement of the virus throughout the plant. Notably, DNA-A and DNA-B are encapsidated separately, each within its own geminate icosahedral particle (Hesketh et al. 2018). Both components share a common region (CR) containing a hairpin structure (TAATATT/AC) and iterons, to which the Rep protein binds to introduce a nick and initiate replication (Argüello-Astorga et al. 1994; Argüello-Astorga and Ruiz-Medrano 2001). For *Begomovirus* species demarcation, a threshold of 91% genome-wide nucleotide identity for the complete genome (or DNA-A component in bipartite begomoviruses) is applied (Brown et al. 2015).

In NOA, several distinct begomovirus have been identified infecting tomato crops, including tomato dwarf leaf virus (ToDfLV, *Begomovirus solanumparvi*), tomato mottle wrinkle virus (ToMoWV, *Begomovirus solanumargentinaense*), soybean blistering mosaic virus (SbBMV, *Begomovirus glycinis*), tomato yellow spot virus, (ToYSV, *Begomovirus solanumflavusmaculae*), tomato yellow vein streak virus (ToYVSV, *Begomovirus solanumflavusvenae*), and sida golden mosaic Brazil virus (SiGMBRV, *Begomovirus sidagolbrazilense*) (Vaghi Medina and López Lambertini 2012; Vaghi Medina 2015; Vaghi Medina et al. 2015). In pepper, reported begomoviruses include SbBMV, ToYSV, ToYVSV, ToDfLV, SiGMBRV, and pepper blistering leaf virus (PepBLV, *Begomovirus capsicumannui*) (Bornancini et al. 2020). To date, there are no published reports of begomoviruses infecting eggplant in Argentina.

Begomoviruses are transmitted in a persistent, circulative manner by the whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), which is considered one of the most important agricultural pests worldwide (Rosen et al. 2015). *B. tabaci* is a polyphagous insect that causes direct damage to host plants through phloem feeding and the deposition of honeydew, which facilitates the proliferation of saprophytic sooty molds, ultimately diminishing the plant's photosynthetic efficiency (Perring et al. 2018). Additionally, *B. tabaci* inflicts indirect damage by serving as a vector for the transmission of various plant viruses (Choudhary et al. 2025).

B. tabaci is recognized as a species complex comprising more than 44 distinct cryptic species described to date (Wang et al. 2025). The delineation of these cryptic species is primarily based on genetic variability within the mitochondrial cytochrome c oxidase subunit I (mtCOI) gene, using a 4% sequence divergence threshold for species delimitation (Lee et al. 2013). Although morphologically indistinguishable, these cryptic species exhibit considerable genetic and biological diversity, including variation in host-plant range, induction of physiological disorders in plants, and differing levels of insecticide resistance during both nymphal and adult stages (Horowitz et al. 2005; Wang et al. 2010; Sun et al. 2013). They also differ in invasiveness and various ecological and behavioural traits (Zang and Liu 2007; Crowder et al. 2010). Moreover, each cryptic species varies in its efficiency to acquire and transmit specific plant viruses (Polston et al. 2014; Wei et al. 2014). The Middle East-Asia Minor 1 (MEAM1) and Mediterranean (MED) genotypes, recognized as the most invasive cryptic species within the *B. tabaci* complex, have been reported in Argentina alongside the native New World lineages, New World 1 (NW1) and New World 2 (NW2) (Viscarret et al. 2003; Grille et al. 2011; Alemandri et al. 2012).

Species-rich ecological compartments within agrosystems may facilitate the evolution of diverse viral strategies for survival and transmission, by facilitating complex interactions among multiple host plants, vector species, and environmental factors. These interactions drive viral adaptation, host range expansion, and increased transmission efficiency (Nigam 2021). Cultivated plants are typically grown within complex agroecosystems, where interactions between crops and surrounding wild vegetation play a critical role in shaping plant health and pathogen dynamics. Most previous studies examining the agroecological interface have focused on identifying viruses shared between cultivated and wild plant communities (Barreto SS, Hallwass M, Aquino OM 2013; Alexander et al. 2014; Hančinský et al. 2020; Maliano et al. 2021). This study focuses on the agroecological interactions among tomato, pepper, and eggplant crops

cultivated in proximity in NOA, with particular emphasis on their relationships in the begomovirus pathosystem context. Consequently, the objective was to perform a genetic characterization of the begomovirus-*B. tabaci*-tomato-pepper-eggplant complex in this region.

Materials and Methods

Sample collection

Plants and whiteflies were collected from tomato, pepper and eggplant crops cultivated alongside one another on a farm located in Embarcación, Salta Province, in NOA (coordinates: 23º 13’ 52” S; 64º 6’ 54” O) during the 2022. Planting took place in late February and harvesting lasted until September for tomato and pepper and November for eggplant. The study was conducted in a commercial production farm where insecticide applications for whitefly control were performed.

Three distinct sampling zones were established at the beginning, middle, and end of each selected plot of tomato, pepper, and eggplant to ensure spatially representative sampling across the cultivation area. Each sampling zone comprised two crop rows, which were thoroughly surveyed by walking the full length of each row. Plants exhibiting characteristic symptoms of viral infection were identified and sampled for further analysis. Whiteflies were collected randomly within each plot using an entomological aspirator. Samples were collected at two time points (late March and early June, corresponding to the flowering and fruiting stages of the crops, respectively.

Detection of begomovirus infection in plants

A total of 75 plants exhibiting virus-like symptoms, including 40 tomato plants, 29 pepper plants, and 6 eggplant plants, were analysed by multiplex PCR to determine begomovirus infection. Total DNA was extracted from plant samples using the Dot-Blot method described by (Mason et al. 2008). The amplification was performed using the degenerate primer pair PAL1v1978 and PAR1c496 (Rojas 1993). As an internal control, the primer pair RBCL-H535 and RBCL-C705 was included in the reaction (Nassuth et al. 2000). PCR-positive samples were subjected to rolling circle amplification (RCA) using the TempliPhi kit (Cytiva, Marlborough, United States) to amplify circular DNA molecules. Restriction fragment length polymorphism (RFLP) analysis was then performed using the restriction enzyme *Hpa*II, and the resulting fragments were resolved by electrophoresis. Due to the low number of begomovirus positive plants observed per cultivar in each sampling event, samples collected in both surveys were combined and analysed together.

Next generation sequencing (NGS) and data analysis

RCA products (3 from tomato, 2 from pepper, and 1 from eggplant) were subjected to NGS. Libraries were prepared using the Nextera XT DNA kit and sequenced with paired-end reads (2 × 150 bp). One sample was sequenced on the Illumina NovaSeq 6000 platform at the Genomics and Bioinformatics Unit of ANLIS (Buenos Aires, Argentina), three samples were sequenced at Macrogen Inc. (Seoul, South Korea), and two samples were sequenced on the Illumina NextSeq 2000 platform at CEPROCOR (Centro de Excelencia en Productos y Procesos de Córdoba, Unidad de Biología Molecular, Santa María de Punilla, Córdoba, Argentina).

Pre-processing of RCA-NGS reads involved quality filtering using Trim Galore v0.6.10 (Krueger 2021). To reconstruct complete begomovirus genomes, the following assembly strategy was employed:

1. **Primary Assembly**: Reads were first assembled using metaviralSPAdes v4.0 (Antipov et al. 2020).
2. **Secondary Assembly**: If either the DNA-A or DNA-B component was not fully assembled, reads were reassembled using metaSPAdes v4.0 (Nurk et al. 2017).

3. **Host Read Removal**: If either component remained incomplete, reads were mapped to the host genome using Bowtie2 v2.4.4 (Langmead and Salzberg 2012), and host-derived reads were removed using Samtools v1.21 (Danecek et al. 2021). Steps 1 and 2 were then repeated with the filtered dataset.
4. **Reference-Guided Assembly**: If genome components were still incomplete, contigs were compared to the NCBI non-redundant (nr) database (Sayers et al. 2025) using the BLAST online server. The best-matching viral reference genome was used for reading mapping with Bowtie2, followed by extraction of mapped reads using Samtools and reassembly according to steps 1 and 2.

To evaluate the integrity of the coding sequences, open reading frames (ORFs) were identified and analysed using Geneious v9.0.5 (Kearse et al. 2012). In addition, the common region between DNA-A and DNA-B components of each isolate was compared to verify the presence and similarity of iteron sequences. To validate the assembly pipeline, *in silico* restriction digestion was performed using *HpaII*, and the resulting profiles were compared with those obtained through RCA-RFLP analysis.

Begomovirus species identification and phylogenetic analysis

A dataset comprising 97 DNA-A and 65 DNA-B begomovirus sequences from the countries of the Southern Cone of South American including Ecuador, Brazil, Uruguay, Bolivia, Peru, and Argentina was retrieved from the (NCBI Virus Database). To date, no complete begomovirus genome sequences have been reported from Chile or Paraguay. Multiple sequence alignments were performed using the MUSCLE algorithm (Edgar 2004). For species-level identification of begomoviruses recovered from metagenomic data, pairwise nucleotide identity analyses were performed using the Sequence Demarcation Tool (SDT) v1.3 (Muhire et al. 2014). Sequences U15015 (DNA-A) and U15017 (DNA-B), corresponding to tomato leaf curl New Delhi virus (ToLCNDV, *Begomovirus solanumdelhiense*)and AF141922 (DNA-A) and AF141897 (DNA-B) corresponding to tomato yellow leaf curl Thailand virus (ToYLCTHV, *Begomovirus solanumflavusthailandense*)were used as outgroups references.

Phylogenetic inference was performed using the maximum likelihood method available in the web-based version of IQ-TREE (Trifinopoulos et al. 2016). The best-fitting nucleotide substitution model was selected using ModelFinder in the IQTREE software (Kalyaanamoorthy et al. 2017). Tree confidence was assessed using Ultrafast Bootstrap approximation (UFBoot) and the Shimodaira–Hasegawa approximate likelihood ratio test (SH-aLRT) with 1000 replicates (Guindon et al. 2010; Hoang et al. 2018). The perturbation strength was seated in 0.9 points and the IQ-TREE stopping rule in 300. The resulting phylogenetic treefiles were visualized and annotated using FigTree (Rambaut A. 2010).

***Bemisia tabaci* cryptic species identification**

Out of a total of 377 whiteflies collected, 51 were obtained from tomato, 23 from pepper and 303 from eggplant. The collected specimens were initially differentiated as either *Bemisia tabaci* or *Trialeurodes vaporariorum* based on the structure of their compound eyes. *B. tabaci* is characterized by two eye facets connected by a bridge of simple ocelli, whereas *T. vaporariorum* displays distinctly separated eye facets (Carapia Ruiz and Castillo-Gutiérrez 2013; Patel et al. 2022). Following identification, each specimen was sexed and subsequently preserved in 90% ethanol at refrigerated temperatures. A total of 118 females (40 from tomato, 22 from pepper, 56 from eggplant) were selected for cryptic species identification. DNA purification was performed following the Chelex protocol described by (Xavier et al. 2021). Due to the low number of begomovirus positive plants observed per cultivar in each sampling event, samples collected in both surveys were combined and analysed together for virus and whitefly characterization. The mtCOI fragment was amplified by PCR using the degenerate primer 2195Bt and the primer CO12/Bt-sh2 (Mugerwa et al. 2018). For the discrimination among *B. tabaci* cryptic species, 12µl of each PCR product was digested with the restriction enzyme *Taq*I in a final volume of 20µl. Reactions were performed at 65 °C, and the resulting fragments were visualized as distinct

patterns on 1.2% agarose gels stained with GelRed (Biotium, Fremont, CA, USA). To validate the PCR-RFLP patterns used for species identification, representative PCR amplicons corresponding to the different RFLP profiles detected among host plants were sequenced: three from *B. tabaci* MED samples collected from tomato, pepper, and eggplant, and one from an NW2 sample collected from tomato. The amplicons were gel-purified and sequenced bidirectionally using primers 2195Bt and CO12/Bt-sh2 at Macrogen (Seoul, South Korea). The mtCOI sequences obtained from each representative sample were compared against the GenBank database to determine the percentage of nucleotide identity.

Results

Begomovirus species identification by metagenomic analysis

75 symptomatic plants were analysed, of which 14 tested positive for begomoviruses (9/40 from tomato, 4/29 from pepper, and 1/6 from eggplant). Due to the low number of positive samples, results from both sampling events were pooled. The remaining symptomatic plants were not analysed further in this study and may be infected with other viruses. High-throughput sequencing analysis of RCA products (3 from tomato, 2 from pepper, and 1 from eggplant) enabled the reconstruction of seven complete DNA-A and six DNA-B genomic components of begomoviruses (Table S1). The comparison of the in silico RFLP patterns generated using *Hpa*II from the assembled sequences with those obtained experimentally through RCA-RFLP for each sample showed consistent results, confirming the accuracy of the assembled genomes. Solanum mosaic Bolivia virus (SoMBoV, Begomovirus solanumboliviense) was identified in one sample collected in tomato (Table 1). On the other hand, SbBMV (*Begomovirus glycinis*) was identified from tomato, pepper, and eggplant plants (Table 1).

One putative novel begomovirus species was identified in tomato and one in pepper crops. Tomato sample 823 exhibited symptoms characterized by mottle, upward leaf curling predominantly affecting the apical regions of the plant (Figure 1a). DNA-A reconstructed from this tomato sample shared 89.29% sequence identity with tomato vein clearing leaf deformation virus (ToVCLDeV, *Begomovirus solanumvenadepravationis*) (Table 1). The assembled DNA-B component also showed a maximum identity of 89.64% with ToVCLDeV (Table 1). We propose this as a new begomovirus species, with the name tomato common mottle virus (ToCmMoV), according to symptoms observed in tomato field plant (Figure 1a). The DNA-A component of ToCmMoV is 2711 bp in length and contained six open reading frames (ORFs): AV1, AC1, AC2, AC3, AC4, and AC5. DNA-B is 2655 bp and encoded two ORFs: BV1 and BC1, consistent with the bipartite genome organization characteristic of new world begomoviruses (Figure 1a). The common region (CR) shared between DNA-A and DNA-B exhibited 98.7 % nucleotide identity and the same iterons sequences (TCTCCA and TGGAGT) identified (Figure S1).

Pepper plant corresponding to sample 828 showed symptoms of vein clearing, leaf curling, distortion, and reduction in the size of apical leaves (Figure 1b). DNA-A (2661 bp) assembled exhibited a maximum nucleotide identity of 86.68% with sida mosaic Bolivia virus 1 (SiMBoV1, *Begomovirus sidaboliviaenseprimi*, whereas the DNA-B (2653 bp) showed a maximum identity of 83.26% with tomato interveinal chlorosis virus 2 (ToICV2) (Table 1). Consequently, we proposed this as a new begomovirus species, with the name pepper vein clearing virus (PepVCV) according to symptoms observed in pepper field plant (Figure 1b). Both components exhibit the typical genome organization of bipartite new world begomoviruses (Figure 1b). The CR of DNA-A and DNA-B from this sample shared 95.4 % nucleotide identity, and the presence of the iteron motifs TCACCA and TGGTGA in both genomic components further support the accuracy of the assembly strategy (Figure S1).

Phylogenetic analysis

Phylogenetic analysis of DNA-A sequences revealed that each of the four identified begomovirus species belongs to a separate clade. SbBMV shared a common ancestor with ToDfLV and ToMoWV, both of which have previously been reported in Argentina (Figure 2). In a different clade, SoMBoV evolved from a shared ancestral lineage with bean bushy stunt virus (BBSV, *Begomovirus phaseoliretorridi*), pepper leafroll virus (PepLRV, *Begomovirus capsicumcontorsioris*), muntingia yellow spot virus (MuYSV, *Begomovirus muntiflavi*), ToYVSV and tomato golden vein virus (TGVV, *Begomovirus solanumaureivenae*) (Figure 2). This clade comprises begomovirus species from different countries, including Argentina, Brazil, Peru, and Ecuador. The novel proposed species ToCmMoV shared a common ancestor with ToVCLDeV, also reported in Argentina. Both begomoviruses share a common evolutionary origin with hyptis golden mosaic virus (HyGMV, *Begomovirus hyptidis*), described in Ecuador (Figure 2). Phylogenetic analysis indicated that the newly proposed species PepVCV shares a common evolutionary origin with SiMBoV1 and sida yellow mosaic Alagoas virus (SiYMAV, *Begomovirus sidaflavalagoense*), which have been reported in Bolivia and Brazil, respectively. The begomovirus species identified in this study exhibited similar clustering patterns in the phylogenetic analysis of the DNA-B component (Figure S2).

B. tabaci species identification using PCR-RFLP of the mtCOI fragment

Eggplant exhibited the highest abundance of *B. tabaci* individuals collected (303/377), compared to tomato (51/377) and pepper (23/377). PCR-RFLP analysis of 118 female whiteflies collected from the three crops revealed two distinct *Taq*I RFLP patterns: one consisting of fragments of approximately 700 and 200 bp, corresponding to the MED cryptic species, and another showing a single strong band above 400 bp, corresponding to NW2. Identification of MED and NW2 by PCR-RFLP was validated by sequencing representative amplicons from each RFLP pattern obtained from tomato, pepper, and eggplant samples. MED-associated mtCOI sequences from tomato (745 bp, PZ387685), pepper (756 bp, PZ387684), and eggplant (758 bp, PZ387686) showed 100%, 99.87%, and 100% nucleotide identity with *B. tabaci* MED cryptic species sequences KC661292.1, EU192071.1, and KUG82840.1, respectively. The mtCOI sequence (734 bp, PZ387687) from the single NW2 individual identified in tomato by PCR-RFLP showed 99.05% nucleotide identity with the NW2 cryptic species sequence LR535718.1. The proportion of *B. tabaci* cryptic species identified by PCR-RFLP in tomato crops was 97.5% (39/40) MED and 2.5% (1/40) NW2. All individuals analysed from pepper (22/22) and eggplant (56/56) were identified as MED. Overall, MED was the predominant species in tomato, pepper, and eggplant, whereas MEAM1 was not detected in any of these hosts. Results are presented based on the combined analysis of samples collected in both sampling events.

Discussion

This research provides the first report of SbBMV infecting eggplant, thereby expanding its known host range. Previously reported hosts in Argentina include soybean (*Glycine max*), chia (*Salvia hispanica*), common bean (*Phaseolus vulgaris*), pepper and tomato (Rodríguez-Pardina et al. 2011; Vaghi Medina 2015; Bornancini et al. 2020; Luciani et al. 2024). Furthermore, this represents the first detection of a begomovirus infecting eggplant in Argentina. Another begomovirus species identified in tomato was SoMBoV, which has been detected exclusively in tomato crops. Notably, the virus was originally reported in Bolivia, where it was first identified in a *Solanum* sp. weed host (Wyant et al. 2011). The identification of two novel begomoviruses, ToCmMoV and PepVCV, contributes to the expanding diversity of begomovirus species identified in NOA. Notably ToCmMoV and PepVCV does not cluster within the same clade in the phylogenetic tree, indicating distinct evolutionary origins. Despite their distinct phylogenetic positions, both viruses cluster with begomoviruses that infect alternative host species beyond tomato and pepper, and which have also been reported in other South American countries. ToCmMoV share a common evolutionary origin with ToVCLDeV and HyGMV, the latter of which has been reported infecting *Hytis pectinate* in Ecuador (Reyes-Proaño et al. 2022). In contrast, PepVCV clusters with SiMBoV1 reported infecting *Sida micrantha* in Bolivia and SiYMAV identified infecting *Sida urens* and *Passiflora edulis* in Brazil (Wyant et al. 2011; Tavares et al. 2012; Mituti et al. 2019).

B. tabaci exhibited differential population abundance across tomato, pepper, and eggplant in the current research. Notably, 80.4% of the individuals were collected from eggplant, indicating a clear preference for this host over tomato and pepper. The abundance of whitefly on eggplant can be influenced by multiple factors. Shah and Liu (2013) reported that immature stages of *B. tabaci* exhibited high survival rates ranging from 80 % to 98 % and the shortest developmental duration on eggplant, compared to tomato, cucumber, and pepper, indicating superior host suitability. Furthermore, adult *B. tabaci* demonstrated distinct host related behavioural patterns influenced by their natal plant. Eggplant was not only preferred as an oviposition site but also effectively retained adults that had developed and fed on it during earlier life stages (Shah and Liu 2013). Additionally, eggplant attracted adults originating from other hosts, such as tomato and pepper, suggesting a strong inter-host preference. However, this attraction was superseded in the presence of cucumber, which emerged as the most attractive host overall. Notably, eggplant also supported the highest egg-to-adult survivorship among the tested host plants (Shah and Liu 2013). Previous studies investigating the host selection behaviour of *B. tabaci* have demonstrated that morphological leaf traits such as trichome density, trichome length, leaf lamina thickness, and leaf coloration significantly influence both host attractiveness and oviposition preferences (Hasanuzzaman et al. 2016). It has been proposed that the propensity of adult *B. tabaci* to oviposit near trichomes may be driven by selective pressures from natural enemies or by the favourable microhabitat conditions that trichomes provide on the leaf surface (Chu Chang-Chi et al. 1995; Heinz and Zalom 1995). The above may explain the higher abundance of whiteflies observed on eggplant compared to tomato and pepper.

In the present study, the introduced MED specie was found to be predominant whitefly species in tomato, pepper, and eggplant crops in NOA. Notably, MEAM1 specie was not detected in this analysis in contrast to previous reports (Viscarret et al. 2003; Alemandri et al. 2015). A single specimen of the native species NW2 was detected, associated with tomato crops. These results indicate that NW2 was present at a significantly lower abundance compared to the invasive MED specie. This emergence highlights the phytosanitary implications of their efficiency as vectors of plant viruses, particularly species within the genera *Begomovirus* and *Crinivirus* (Ning et al. 2015; Shi et al. 2018; Fiallo-Olivé et al. 2020). To our knowledge, the transmission efficiency of the MED cryptic species has not yet been evaluated for the begomovirus species present in Argentina, representing an important area for future research. The MED species have emerged as significant agricultural pests in Argentina and across South America, following their initial detection on red pepper and cucurbit crops in Argentina (Grille et al. 2011; Krause-Sakate et al. 2020). In Brazil, MED has exhibited a progressive expansion in its geographical distribution across multiple regions of the country, demonstrating a pronounced affinity for both ornamental plant species and a range of vegetable cropping systems (de Moraes et al. 2017; Bello et al. 2020). The displacement of one *B. tabaci* cryptic species by another has been previously documented (Watanabe et al. 2019; Tang et al. 2020). Furthermore, studies have shown that MED exhibits a more complex and diverse population structure than MEAM1, which is considered the second most invasive *B. tabaci* species globally (Gautam et al. 2020). This high level of intraspecific genetic variability is frequently attributed to repeated biological re-invasions by new MED populations into areas already occupied by earlier ones. Such re-invasions introduce novel haplotypes into established populations, thereby increasing local genetic diversity and promoting the emergence of new variants (de Barro and Ahmed 2011; de Moraes et al. 2018; Tang et al. 2020; Paredes-Montero et al. 2021). The greater genetic variability observed in MED may enhance its phenotypic plasticity, facilitating adaptation to new environments and host plants. This adaptability, in combination with its pesticide resistance, may explain the ability of MED to establish and dominate in new areas, ultimately displacing other cryptic species previously present in the same productive regions. In addition, the prevalence of the MED species in NOA may be explained by its greater tolerance to high temperatures, as supported by studies indicating that MEAM1 exhibits higher mortality rates than MED at 37 °C and 40 °C (Mahadav et al. 2009). Although the average maximum temperature in Orán in 2022 was 29.2 °C, days with maximum temperatures above 36°C were recorded, potentially favoring MED (https://www.smn.gob.ar/estadisticas).

This study identified four begomovirus species co-occurring within a single agricultural field where tomato, pepper, and eggplant were cultivated side by side, highlighting the complex interactions among host plants, viruses, and their vector, with a particular focus on the crop interface and its role in shaping these interactions. Notably, eggplant harbored the highest abundance of *Bemisia tabaci*, yet only six plants showed virus-like symptoms and a single begomovirus-positive sample was detected, suggesting the possible presence of additional asymptomatic infections that remain undetected. Few studies have reported begomovirus infections in eggplant in the Americas (Moura et al. 2018). In contrast, tomato exhibited a markedly higher frequency of symptomatic plants and the greatest diversity of begomovirus infections among the surveyed crops, indicating a strong host-virus association and a high degree of viral adaptation.

The agroecological context of the NOA is characterized by the continuous and overlapping cultivation of Solanaceae species under both open-field and greenhouse systems, resulting in year-round host availability. This production structure may facilitate the persistence of begomoviruses in the region. The results also highlight the ecological role of eggplant in sustaining whitefly populations and the importance of tomato in promoting begomovirus diversity. At the same time, the predominance of the MED cryptic species in vegetable production systems represents a significant challenge for vector management. Overall, these findings support the development of farming systems that reduce the spread and impact of begomoviruses and their insect vectors, contributing to more stable and sustainable production systems.

Declarations

Compliance with Ethical Standards

The authors declare that there are no conflicts of interest.

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Tables

Table 1. Details of begomoviruses identified per sample from rolling circle amplification and next generation sequencing (RCA-NGS) data.

Host	Sample ID	Genomic Components assembled	Sequence Length (bp)	High Identity Score (SDT %)	Best BLAST Hit (Virus acronym, GenBank accession number)	Species identified	Genbank Accession ID
Tomato	822	DNA-A-1	2602	93.78	SoMBoV (HM585435)	SoMBoV (*Begomovirus solanumboliviense*)	PX770009.1
		DNA-A-2	2601	93.55	SoMBoV (HM585435)	SoMBoV (*Begomovirus solanumboliviense*)	PX770015.1
		DNA-B	2581	92.00	SoMBoV (HM585436)	SoMBoV (*Begomovirus solanumboliviense*)	PX770010.1
Tomato	823	DNA-A	2711	89.29	ToVCDeV (MK423208)	ToCmMoV (tomato common mottle virus)	PX531287.1
		DNA-B	2655	89.64	ToVCDeV (MK423207)	ToCmMoV (tomato common mottle virus)	PX531288.1
Tomato	829	DNA-A	2603	98.73	SbBMV (MN486871)	SbBMV (*Begomovirus glycinis*)	PX770013.1
		DNA-B	2589	96.91	SbBMV (MN486872)	SbBMV (*Begomovirus glycinis*)	PX770014.1
Pepper	826	DNA-A	2603	98.96	SbBMV (MN486871)	SbBMV (*Begomovirus glycinis*)	PX770011.1
		DNA-B	2589	96.91	SbBMV (MN486872)	SbBMV (*Begomovirus glycinis*)	PX770012.1
Pepper	828	DNA-A	2661	86.68	SiMBoV1 (HM585441)	PepVCV (pepper vein clearing virus)	PX531289.1
		DNA-B	2653	83.26	TolCV2 (MK087039)	PepVCV (pepper vein clearing virus)	PX531290.1

Eggplant	1052	DNA-A	2603	99.00	SbBMV (MN486871)	SbBMV (*Begomovirus glycinis*)	PX703140.1
		DNA-B	2587	95.38	SbBMV (MN486872)	SbBMV (*Begomovirus glycinis*)	PX703141.1

Figures

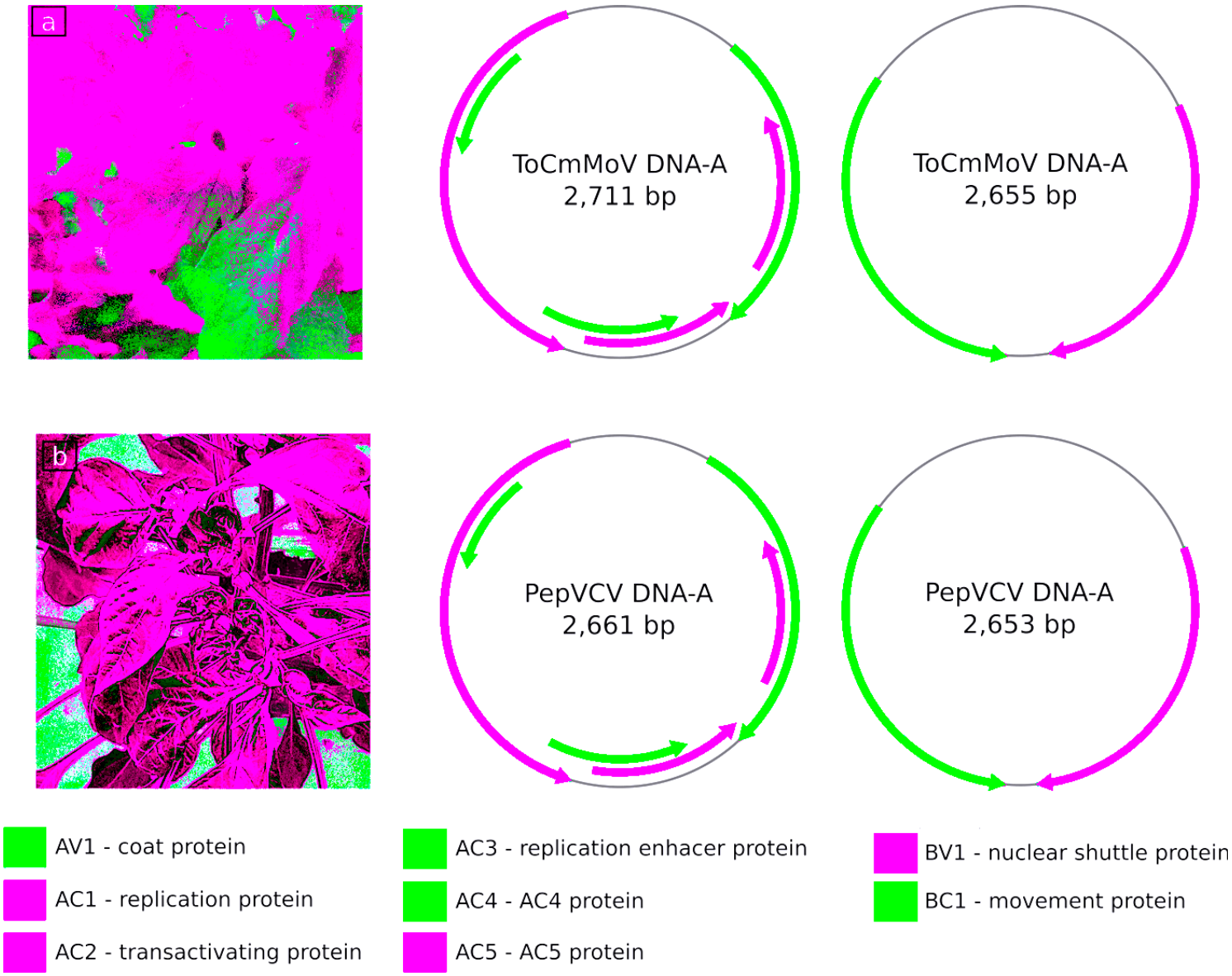


Figure 1

(a) Symptoms of mottle, upward leaf curling infected with tomato common mottle virus (ToCmMoV) and alongside the genome organization of ToCmMoV. (b) symptoms of vein clearing, leaf curling, distortion, and reduction in the size of apical leaves infected with pepper vein clearing virus (PepVCV) and alongside the genome organization of PepVCV. The genome organization of each novel virus is shown, with annotated open reading frames (ORFs) and corresponding protein references.

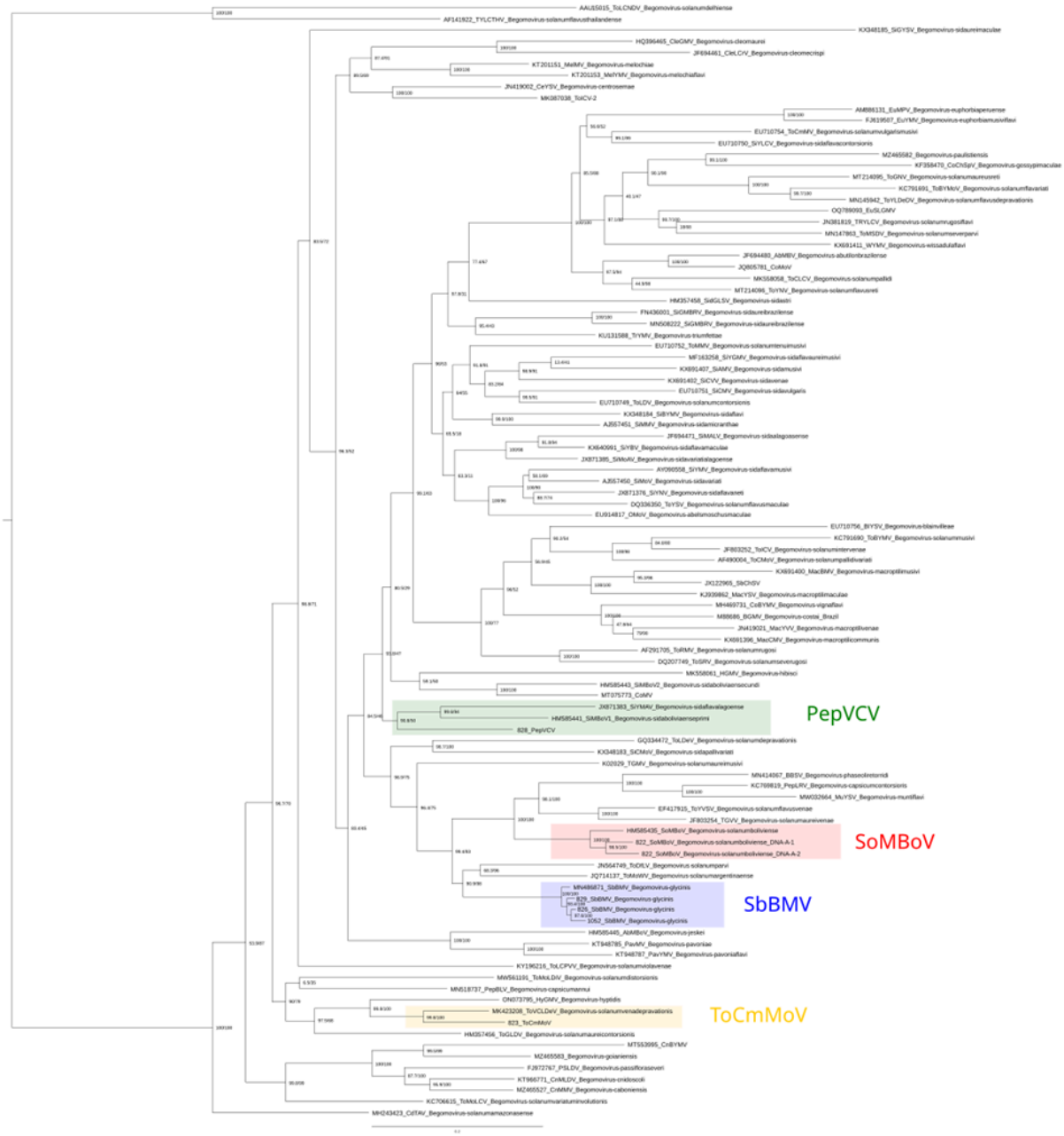


Figure 2

Phylogenetic tree of DNA-A components of begomoviruses from the Southern Cone of South America. Identified species are shown in coloured boxes.

Supplementary Files

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