**Short Note [Nota Corta]**

# REPORTE DEL VIRUS DEL MOSAICO DORADO EN CHILE APAXTLECO NATIVO EN GUERRERO, MÉXICO †

# [REPORT OF PEPPER GOLDEN MOSAIC VIRUS IN NATIVE APAXTLECO CHILI PEPPER IN GUERRERO, MEXICO]

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## SUMMARY

**Background.** The chili is a cornerstone of Mexican culture and cuisine, deeply embedded in the country's history and identity. **Objective.** To identify genetically and phylogenetically the virus that affects the native Apaxtleco chili pepper in Guerrero, Mexico, and to recognize symptoms of virosis in plants. **Methodology.** Young leaves of native Apaxtleco chili pepper plants with typical virosis symptoms were collected. The alignment of 13 sequences of DNA nucleotides was carried out, 11 of which belong to the fragment of region that codifies for the gene of "capsid protein / nuclear exportation factor BR1" of PepGMV two of these were obtained in this study, Aymedi-02 (KX641201.1) and Aymedi-01 (KX641200.1), and the nine remaining sequences were obtained from the GenBank database. Two more sequences were included for the purpose of tree rooting; one corresponds to the chlorotic leaf curl virus (AF325497.1) and another to the mosaic virus of African cassava (J02057.1), obtained from GenBank. The alignment of 13 sequences consisted of a total extension of 541 bases. To obtain descriptive information about the PepGMV sequences, only the sequences corresponding to it (11 sequences) were used, with a total of 326 conserved sites and 211 variable sites; of these, 89 are parsimony informative sites and 120 Singleton. **Results.** The sequence analysis showed 99% of identity with sequences of the PepGMV and the phylogenetic analysis confirmed the identification. **Implications.** Our results highlight a significant opportunity to enhance the control of this pathogen in this crop. **Conclusion.** Pepper Golden

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Mosaic Virus (PepGMV) was identified in Guerrero, Mexico, the symptoms presented in plants infected by this pathogen were: chlorosis, deformation, and mosaics.
**Key words:** Begomovirus; chili pepper leaf; diagnosis; nucleotide sequence.

**RESUMEN**

**Antecedente.** El chile es un pilar de la cultura y gastronomía mexicana, profundamente arraigado en la historia e identidad del país. **Objetivo.** Identificar genética y filogenéticamente el virus que afecta al chile Apaxtleco nativo de Guerrero, México y reconocer síntomas de virosis en las plantas. **Metodología.** Se colectaron hojas jóvenes de plantas de chile Apaxtleco nativo con síntomas típicos de virosis. Se realizó el alineamiento de 13 secuencias de nucleótidos de ADN, 11 de las cuales pertenecen al fragmento de la región que codifica para el gen de la "capsid protein/nuclear exportation factor BR1" de PepGMV dos de estas se obtuvieron en este estudio, Aymedi-02 (KX641201.1) y Aymedi-01 (KX641200.1), y las nueve secuencias restantes se obtuvieron de la base de datos GenBank. Se incluyeron dos secuencias más con fines de enraizamiento de árboles; una corresponde al virus del enrollamiento clorótico de la hoja (AF325497.1) y otra al virus del mosaico de la yuca africana (J02057.1), obtenidas del GenBank. El alineamiento de 13 secuencias consistió en una extensión total de 541 bases. Para obtener información descriptiva sobre las secuencias de PepGMV, se utilizaron únicamente las secuencias correspondientes a éste (11 secuencias), con un total de 326 sitios conservados y 211 sitios variables; de estos, 89 son sitios informativos de parsimonia y 120 Singleton. **Resultados.** El análisis de secuencias mostró 99% de identidad con secuencias del PepGMV y el análisis filogenético confirmó la identificación. **Implicaciones:** Nuestros resultados resaltan una oportunidad significativa para mejorar el control de este patógeno en este cultivo. **Conclusión.** El virus del mosaico dorado del chile (PepGMV) fue identificado en Guerrero, Mexico, los síntomas que presentaron las plantas infectadas por este patógeno fueron: clorosis, deformación y mosaicos.
**Palabras clave:** Begomovirus; hoja de chile; diagnóstico; secuencia de nucleótidos.

## INTRODUCTION

In Mexico, the chili crop, *Capsicum annuum* (Solanaceae), has a special place because it is a basic component in nearly all popular dishes, and contributes, proteins and minerals. Most of the national production is consumed in the domestic market, and many agronomic tasks are carried out manually during the productive process; this is reflected in a source of jobs in irrigation and rainfed farming, which constitute an alternative to increase producers' income (Ayvar *et al.,* 2007). Large economic losses have been reported in the production of this crop, caused by phytopathogenic viruses (Bhatt *et al.,* 2016; Hernández *et al.,* 2018); the virus group known as Geminivirus is located mainly in tropical and subtropical zones, and the most widely diversified and distributed group is that of Begomovirus, with 322 species reported to date which infect mostly dicotyledonous plants and are transmitted by *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae) (Fiallo-Olivé *et al.,* 2021). However, in Guerrero state (in southern of Mexico), different genotypes of native chili peppers are grown, which are adapted to different micro-regions, and there is a high incidence of virosis, of which the etiology is unknown and there are no formal reports of the viruses that cause the symptoms. Because of this, this research aimed was to identify genetically and phylogenetically the virus that affects the native Apaxtleco chili pepper in Guerrero, and to recognize symptoms of virosis in plants.

## MATERIALS AND METHODS

### Plant material collection

In July 2024 young leaves of native Apaxtleco chili pepper plants with typical symptoms of virosis were collected, such as: bright yellow mosaics, epinasty, marginal leaf chlorosis, leaf enations, leaf area reduction, dwarfism, and growth delay (Polston and Anderson, 1997). Sampling was random, 3 leaves per plant and total of 15 plants. The collection site was the experimental field of Colegio Superior Agropecuario del Estado de Guerrero (CSAEGRO), in Cocula, Guerrero, Mexico (18° 14' N, 99° 39' W and 640 m above sea level altitude).

### Sequence alignment

The alignment of 13 sequences of DNA nucleotides was carried out, 11 of which belong to the fragment of region that codifies for the gene of "capsid protein / nuclear exportation factor BR1" of PepGMV two of these were obtained in this study, Aymedi-02 (KX641201.1) and Aymedi-01 (KX641200.1), and the nine remaining sequences were obtained from the GenBank database. Two more sequences were included for the purpose of tree rooting; one corresponds to the chlorotic leaf curl virus (AF325497.1) and another to the mosaic virus of African cassava (J02057.1), obtained from GenBank. The alignment of 13 sequences consisted of a total extension of 541 bases. To obtain descriptive information about the PepGMV sequences, only the sequences corresponding to it (11 sequences) were

used, with a total of 326 conserved sites and 211 variable sites; of these, 89 are parsimony informative sites and 120 Singleton.

**Phylogenetic analysis**

An analysis was conducted using the maximum parsimony method for the phylogenetic reconstruction which would allow the identification and location of the materials under study. The analysis considered that all the traits present had the same value, and the empty spaces present between the aligned sequences (GAP) were considered as lost data ("complete deletion"). To obtain the more parsimonious trees, a heuristic search was used with 1000 random taxa addition repetitions and an exchange of bifurcations of bisection-reconnection of trees; the best 100 trees in the analysis were saved. A "bootstrap" resampling test of 1000 repetitions was applied to estimate the level of confidence of consensus tree topology. This analysis was done using MEGA 7.026 software (Kumar *et al.*, 2016).

**Sequences**

The viral syndrome detected in native Apaxtleco chili pepper plants included leaf deformation, presence of roughness, yellow mosaics, reduction in size, edema with chlorosis, and leaf chlorosis (Figure 1). The sequences obtained (540 and 537 bp) from the amplified product had 99% of similarity with the region that codifies for capsid protein, with sequences reported in GenBank for squash leaf curl virus. The sequences were deposited in the National Center for Biotechnology Information (NCBI) with accession numbers KX641201.1 Aymedi 02 and KX641200.1 Aymedi 01. The strict consensus tree showed the grouping of materials obtained in this study, Aymedi-02 (KX641201.1) and Aymedi-01 (KX641200.1), together with those that correspond to the PepGMV, that is, they were identified with the corresponding virus (bootstrap= 100). Additionally, both sequences present 100% of identity (bootstrap= 99). On the other hand, the analysis showed differences in level of divergence of two samples of this study regarding to the 11 obtained from the GenBank database; that is, there are intra-specific evolutionary differences in PepGMV (bootstrap>60).

## RESULTS AND DISCUSSION

The first report of Geminivirus in Mexico was in Huasteca zone in Tamaulipas state, which is why it was called Pepper Huasteco Virus (PHV), and later the name changed to Pepper Huasteco Yellow Vein Virus (PHYVV), because of symptoms that it causes on leaves; on the other hand, reports indicated that Pepper Golden Mosaic Virus (PepGMV) was distributed in a more restricted way (Torres *et al.*, 1993; Torres *et al.*, 1996). The PepGMV is widely distributed in Mexico, so it is not strange for it to be detected in other Solanaceae such as tobacco *Nicotiana tabacum* L. (Solanaceae) (Torres *et al.*, 1996). This virus has other variants in Sinaloa, Tamaulipas and Baja California Sur (Holguín *et al.*, 2004). The detection of phytopathogenic viruses

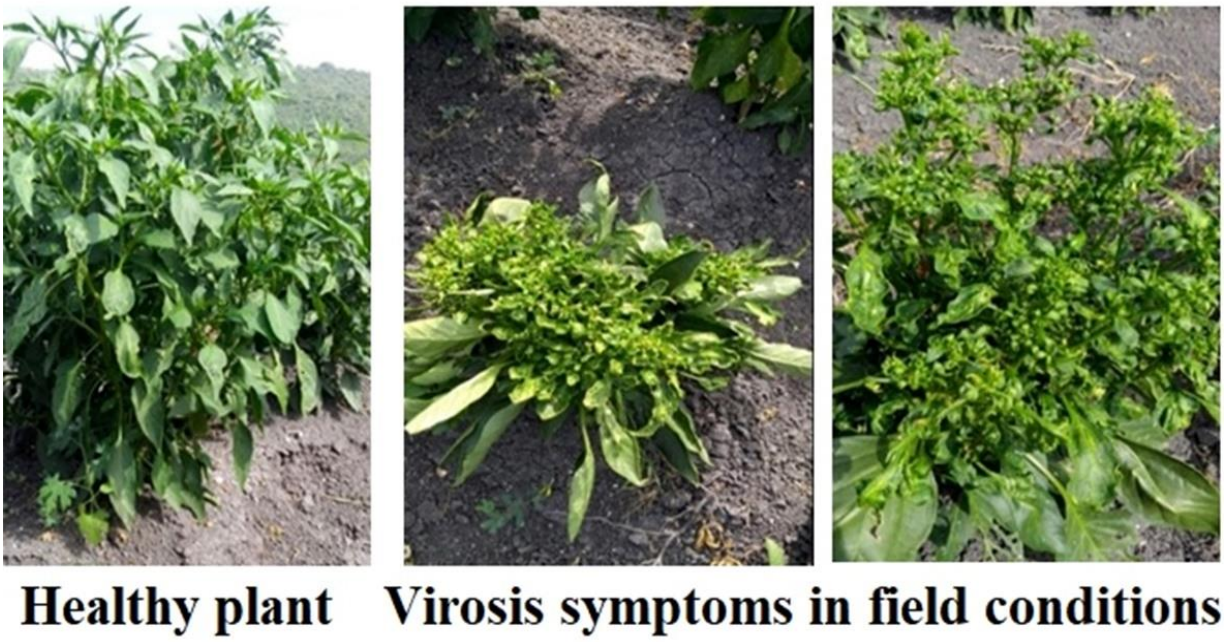


**Figure 1.** PepGMV. Symptoms of chlorosis, deformation, and mosaics associated with begomovirus infection in native Apaxtleco chili pepper.

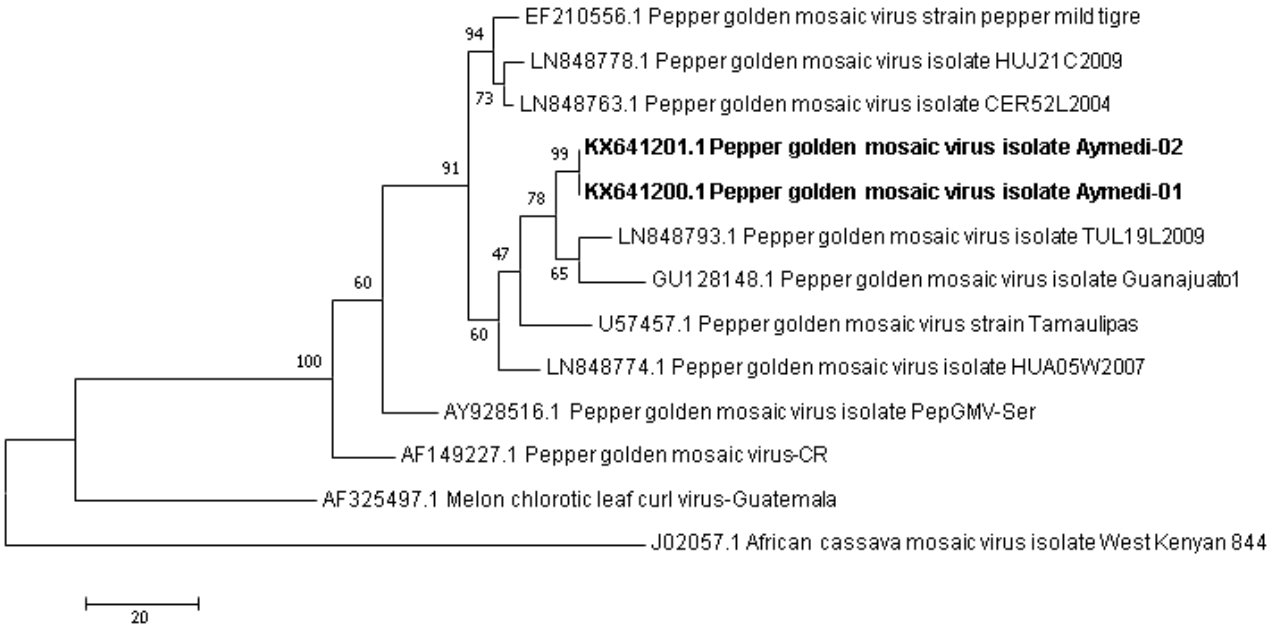


**Figure 2.** Strict consensus tree of DNA region that codifies for the gene of "coat protein" nuclear export factor BR1" with the maximum parsimony method, 1000 heuristic searches, and bootstrap test of 1000 repetitions. The tree includes 11 samples of golden mosaic virus, one sequence of chlorotic leaf curl virus (AF325497.1), and another of the African cassava mosaic virus (J02057.1). The "bootstrap" values >60 are under the branches.

through molecular methods can be used when there is knowledge of at least part of the sequence of the virus genome (Jeong *et al.*, 2014). In southern of Mexico, in Guerrero state, there have been reports about grave problems caused by phytopathogenic viruses in chili pepper crop, although no serious or formal reports have been found in the region mentioned; however, in this research study there is information about the molecular detection and identification of PepGMV based on the gene sequence analysis of complete capsid protein associated with the leaf mosaic, whose color varies from dull yellow to a bright gold in the native genotype of smooth Apaxtleco Ancho in southern of Mexico under rainfed conditions, which will allow implementing management strategies for the vector associated to PepGMV and its natural reservoirs such as weeds (Díaz *et al.*, 2018). For example, some of the management strategies would be that the producer uses certified seed, removal of infected plants, and control of natural vectors, although numerous researchers have emphasized the importance of integrated management strategies for protecting plants against viral diseases (Devi *et al.*, 2024).

## CONCLUSION

Pepper Golden Mosaic Virus (PepGMV) was identified in Guerrero state, Mexico, this pathogen's symptoms in infected plants were chlorosis, deformation, and mosaics.

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**Conflict of interest.** The authors declare non existing personal or institutional conflict of interest.

**Compliance with ethical standards.** Due to the nature of the study this does not apply.

**Data availability**. The data are available upon request from the corresponding authors.

**Author contribution statement (CRediT). J.F Díaz-Nájera** – Investigation, Methodology and Writing – original draft. **S. Ayvar- Serna** – Investigation and Writing – revision and editing. **J.L. Arispe-Vázquez** – Investigation, Methodology and Writing – revision and editing. **J. Terrones-Salgado** – Software and Writing – original draft. **A. Flores-Yáñez** – Methodology. **M. Vargas-Hernández** – Supervision and Writing – original draft. **K.V. De Lira Ramos** – Software and Writing – original draft. **L. Carnero-Avilés** – Investigation and Supervision. **M. Felipe-Victoriano** – Software. **J. Mayo-Hernández** – Visualization, Writing – review & editing. All authors

have read and agreed to the published version of the manuscript.

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