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Grapevine viruses in Mexico: studies and reports

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ABSTRACT

Objective: To contribute to the knowledge of the diversity of viruses and the viral diseases reported in grapevines in Mexico, in order to benefit producers and develop comprehensive viral disease control strategies.

Design/methodology/approach: The literature search was conducted in databases such as Scopus, Google Scholar, and EBSCO host, using the following keywords alone or in combination: "virus", "plant", "grapevine", and "Mexico". In addition, the INIFAP database was consulted, alongside undergraduate and postgraduate dissertation theses.

Results: Only one academic file was found published in an indexed international journal, using the publication finder software; the report corresponds to a grapevine virus present in Mexico. However, based on all the consulted sources, several viral diseases associated with nine grapevine viruses have been reported in Mexico. These species have been grouped into seven genera and six families. The reports come from Aguascalientes (56%) and Baja California (44%). Three registered viral species are associated with the leafroll complex, three with rugose wood, one with fleck, one with infectious degeneration, and one with red blotch disease.

Findings/conclusions: Several grapevine viruses associated with major diseases have been reported in Mexico. Unfortunately, most of the reports lack detail and follow-up, and they are not readily available for international researchers; therefore, the lack of knowledge about this subject in Mexico is significant. Monitoring the epidemiology of viral diseases in the grapevine —a national and international relevant crop— is necessary.

Keywords: grapevine, viral diseases knowledge, agriculture.

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INTRODUCTION

The grapevine is a plant that belongs to the *Vitis* genera (Family: Vitaceae), which includes sixty native species from temperate regions in the northern hemisphere and some tropical regions. Twenty-five species can be found in North America alone. The most economically important species is *V. vinifera*, because its fruits are used to produce wine (about 68% of the production) and juices, as well as table grapes and raisins (Vaughan *et al.*, 2009). Grapevines are grown on more than 7,450,000 hectares around the world, which makes them the most economically important fruit-crop

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worldwide (OIV, 2016). There are about 10,000 cultivars of *V. vinifera*, and they can be classified according to color (red and white) or final use (table, wine, or raisins) (Vaughan *et al.*, 2009). In Mexico, in the 2018 agricultural cycle, 36,654.76 ha were sown with grapevines, obtaining a production of 444,446.87 tons, which amounts to over 9 million Mexican pesos (SIAP, 2020). The states with higher grape production percentages in Mexico are: Sonora (80.38%), Zacatecas (7.98%), Baja California (5.81%), Aguascalientes (3.48%), and Coahuila (1.09%). From the national production, 11% is used for raisins, 23% is used for industrial production, and 66% is used as table grapes (SAGARPA, 2018). Mexico produces 404,000 wine hectoliters, 12,000 of which are exported (OIV, 2016). Unfortunately, grapevine —just as other crops— can be impacted by different pests and pathogens. The problems that can have a high economic impact include viruses, some of which are highly pathogenic.

Nearly 80 virus species that can infect the *Vitis* genera have been identified, and around 25 grapevine viral diseases (Armijo *et al.*, 2016; Yepes *et al.*, 2018). About half of these viruses are associated with the four main complexes of the known grapevine diseases: infectious degeneration and decline, grapevine leafroll disease (GLD), rugose wood, and fleck disease. Additionally, there are recently discovered high-impact diseases such as the red blotch disease (Al Rwahnih *et al.*, 2013; Martelli, 2017). From the economic point of view, the most important grapevine viruses belong to the GLRaV complex (GLD-associated viruses), which are named in series (GLRaV-1 to -13) and can produce GLD in individual or mixed infections (Martelli *et al.*, 2012; Ito and Nakaune, 2016). Other important grapevine viruses are the grapevine virus A (GVA) and grapevine virus B (GVB), which belong to the *Vitivirus* genera. GVA causes Kober stem grooving, while GVB is associated with the corky bark symptom (Armijo *et al.*, 2016). Given that viruses cause significant economic diseases and that grapevine production is an important activity in Mexico, increasing the knowledge about grapevine virosis is necessary. Therefore, the objective of this study was to understand the situation of the grapevine viruses reported in Mexico. A literature review was carried out to expand the understanding about these viruses and the main impacted regions, as well as to share this information with the producers, in order to develop comprehensive control strategies.

MATERIALS AND METHODS

The information about the viruses reported in Mexico was obtained through a literature review, based on the data gathered from Scopus, Google Scholar, and EBSCO host, using the following words or keyword combinations: “virus”, “plant”, “grapevine”, and “Mexico”. Based on the lack of academic data resulting from the search using the abovementioned keywords, the databases of the Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP) were also used, along with data gathered from undergraduate and postgraduate theses (Repositorio Institucional de CONACYT) and quotes from the consulted publications. The data was systematized by the taxonomy of the virus, the region where the virus was reported, and the disease complex to which the virus belongs.

RESULTS AND DISCUSSION

Information about grapevine viruses in Mexico

The results obtained from the search engines are reduced to just one file about a virus report in Mexico and a review. The first item is the initial report of the red blotch disease in Mexico; this disease is caused by the grapevine red blotch virus (GRBV) (Gasperin-Bulbarela *et al.*, 2019). The second item is a review of the said virus and its potential to spread the grapevine red blotch disease in Mexican vineyards (Beltrán-Beache *et al.*, 2021). The literature reviews also included international publications of interest about the subject that the search engines do not cover. These articles tackle the detection of corky bark and stem pitting symptoms, from which the term "madera rugosa" (the Spanish term for "rugose wood") was coined to describe plants that show these symptoms (Téliz *et al.*, 1980a; Téliz *et al.*, 1980b). The rest of the data obtained from the databases shows the recording of grapevine viral diseases associated with nine viral species in Mexico (Table 1).

Based on the limited data accessibility, five reports (56%) from Aguascalientes and four (44%) from Baja California were found; 50% of the viral species were reported in Aguascalientes, and 50% in Baja California (Figure 1A). These viruses are associated with different pathologies (Figure 1B). Additionally, in 2009 a technical brochure was published,

Table 1. Species of grapevine viruses documented in Mexico*.

Species	Family	Genus	Genome	Disease	Transmission
Grapevine fanleaf virus (GFLV)	*Secoviridae*	*Nepovirus*	ssRNA(+)	Fanleaf degeneration of grape	Nematode *Xiphinema index*, vegetative propagation, and grafting (Krebelj *et al.*, 2015).
Grapevine leafroll-associated virus 1 (GLRaV-1)	*Closterioviridae*	*Ampelovirus*	ssRNA(+)	Grapevine leafroll disease, (GLD)	Vegetative propagation (Rayapati *et al.*, 2014), mealybugs (Hemiptera: Pseudococcidae) and scale insects (Hemiptera: Coccidae) (Le Maguet *et al.*, 2012; Tsai *et al.*, 2010).
Grapevine leafroll-associated virus 3 (GLRaV-3)	*Closteroviridae*	*Ampelovirus*	ssRNA(+)		
Grapevine leafroll-associated virus 2 (GLRaV-2)	*Closteroviridae*	*Closterovirus*	ssRNA(+)		
Grapevine virus A (GVA)	*Betaflexiviridae*	*Vitivirus*	ssRNA(+)	Kober stem grooving	Grafting and by infected material (Yoshikawa, 2008), mealybugs and scale insects (Martelli, 2017).
Grapevine virus B (GVB)	*Betaflexiviridae*	*Vitivirus*	ssRNA(+)	Corky bark	Vegetative propagation and grafting (Maliogka *et al.*, 2015), mealybugs and scale insects (Golino *et al.*, 2002; Le Maguet *et al.*, 2012; Nakaune *et al.*, 2008).
Grapevine rupestris stem pitting-associated virus (GRSPaV)	*Betaflexiviridae*	*Foveavirus*	ssRNA(+)	Rupestris stem pitting	Vegetative propagation, grafting, and possibly via seeds (Gambino *et al.*, 2012).
Grapevine fleck virus (GFkV)	*Tymoviridae*	*Maculavirus*	ssRNA(+)	Fleck of grapevine	Infected propagative material (Martelli & Boudon-Padieu, 2006), no known vectors (Martelli, 2018).
Grapevine red blotch virus (GRBV)	*Geminiviridae*	*Grablovirus*	ssDNA	Grapevine red blotch disease	Grafting and propagative material (Cieniewicz *et al.*, 2018), *Erythroneura ziczac* Walsh y *Spisistilus festinus* (under experimental conditions) (Cieniewicz *et al.*, 2018; Poojari *et al.*, 2013).

* Not all reports specify the species; viruses associated with reported diseases are listed where appropriate. Taxonomy according to ICTV (2020).

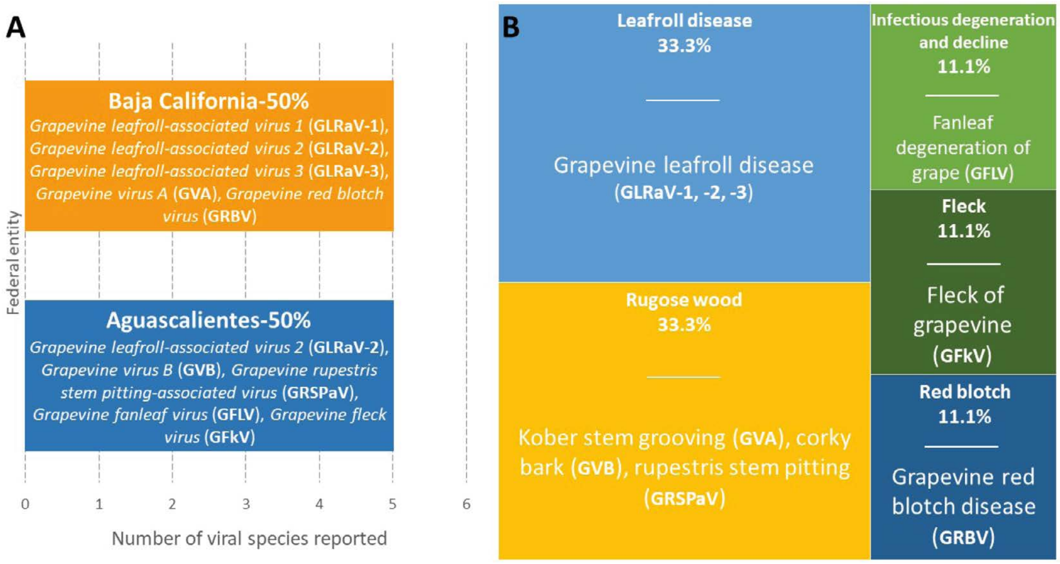

Figure 1. Reports of grapevine viruses in Mexico: A) Viral species by state (not all reports specify the species; viruses associated with reported diseases are listed where appropriate), B) Diseases and viral complexes.

including recommendations about the handling of crown gall and viral grapevine diseases in Zacatecas. Emphasis is placed on the viruses of the grapevine leafroll virus complex (GLRaV) and the grapevine fanleaf viruses (GFLV) (Velásquez-Valle *et al.*, 2009), probably because those viruses were already present in that region. There were also undergraduate virosis theses (Monroy-Corral, 2019; Palacios-Gutiérrez, 2019). However, none of the search engines used for the research included them among the results. Therefore, other similar works might not have been included in the search results, because they are not readily available.

Chronology of grapevine viruses reports in Mexico

Téliz *et al.* (1980b) reported that, in 1968, grapevines with disease-free stocks were sown in the Estación Experimental Agrícola CIANOC-Pabellón of Aguascalientes. In 1970, some of these plants started to show a curly and reddish or yellowish foliage. The disease continued to spread until 1978, and almost all the plants had stem pitting symptoms. Therefore, the authors sought to determine the relationship between the symptoms of the already known grapevine diseases, their distribution, their effects on commercial vineyards, and the development of those symptoms during the establishment of the vineyard. Corky bark and stem pitting symptoms were detected in 103 out of the 311 vineyards inspected —in 75% of the said vineyards, 4,593 plants showed stem pitting symptoms, and 3,728 showed corky bark symptoms— and in 21 out of 32 grapevine cultivars. Cardinal, Malaga Champagne, Exotic, Tokay, San Emilion, Chardonnay, and LN-33 indicator plants were the most impacted cultivars. Corky bark and stem pitting symptoms were detected in five cultivars, fluctuating from 53 to 64% and 68 to 84%, respectively. However, they were not associated with any specific virus. Additionally, the term "madera rugosa" was proposed for a set of symptoms, which included pitting and longitudinal grooves in the stem and the basal internodes of the sprouts (Téliz *et al.*, 1980a). The data was not conclusive regarding the disease found: the plants showed both corky bark and stem pitting symptoms, which led the researchers to conclude that both symptoms were related to the same disease. In the 1970s, corky bark and rugose wood symptoms were detected in Salvador, Carignan, Superior, and Red Glove cultivars in two vineyards of Aguascalientes (Téliz *et al.*, 1980b). Valle and Téliz (1983) reported that the incidence of the corky bark varied from 64 to 84% in cultivars such as Exotic, Tokay, and Red Malaga.

The GVB, grapevine rupestris stem pitting-associated virus (GRSPaV), GVA, and grapevine virus D (GVD) belong to the rugose wood diseases complex. These viruses can cause four distinct disorders: rupestris stem pitting, corky bark, Kober stem grooving, and LN33 stem grooving (Moradi *et al.*, 2018). The corky bark damage is attributed to the infection by GVB, a virus of the *Vitivirus* genera (Boscia *et al.*, 1993; ICTV, 2020). For its part, GRSPaV has been associated with rupestris stem pitting (Martelli, 1993). Therefore, the two species were likely present since the vineyards were established, because at least GVB was later identified in the region. From 2007 to 2009, research work was carried out in two commercial vineyards from Aguascalientes, in order to quantify the incidence and severity of corky bark, with various cultivar and rootstock combinations, including Red Globe/Franco, Superior/Franco, Red Globe/Salvador, and Salvador/1103-P. The researchers determined a 27.5-66.1% incidence of plants with corky bark-rugose wood symptoms in one vineyard and up to an 81.6% incidence in the other. GVB and the grapevine leafroll-associated virus 2 (GLRaV-2), one of the causative agents of GLD, were identified using an RT-PCR protocol (Velásquez-Valle *et al.*, 2010). Most of the varieties and rootstocks of the infected plants came from Ojocaliente, Zacatecas, although not necessarily from the same vineyard; they had originally been obtained from the USA, as "virus-free" material. Additionally, as a result of monitoring carried out in 2006, symptomatic plants were detected, and GVB was identified in SH-3 and Dog Ridge rootstocks, along with grapevine fleck virus (GFkV) in SH-3 rootstocks (Velásquez-Valle *et al.*, 2010).

In 2013, random samples were collected from 12 out of the 22 commercial vineyards in Aguascalientes to determine the incidence of viral diseases. The DAS-ELISA analysis of the samples from the plants collected —which included the Chenin Blanc, Chenin Blanc/Dog Ridge, Salvador Franca, Red Globe Franca, Red Globe/Rupestris, and Salvador varieties— revealed the presence of the grapevine fanleaf virus (GFLV), with a 6.7-37.5% incidence in the Chenin Blanc, Red Globe/Rupestris, and Salvador varieties. Samples from 5 out of the 12 vineyards tested positive for the virus (Velásquez-Valle *et al.*, 2013). GFLV is the causative agent of the infectious degeneration of the grapevine leaf that has spread throughout the world (Andret-Link *et al.*, 2004). The DAS-ELISA serological analysis carried out by Velásquez-Valle *et al.* (2013) in Aguascalientes also recorded the presence of a non-specified GLRaV in the Chenin Blanc, Chenin Blanc/Dog Ridge, Salvador Franca, Red Globe Franca, and Salvador varieties, with a 3.8-80% incidence. The authors suggest that the original infected plant material is the primary contamination source.

Meanwhile, evaluating the potential regional vectors of viral diseases is highly important. The main vectors for GLRaVs are mealybugs (Hemiptera: Pseudococcidae) and scales (Hemiptera: Coccidae). Vine mealybugs (*Planococcus ficus*) were first detected in

Baja California in 2014 (CESVBC, 2018); subsequently, samples from plants with GLD symptoms were collected in 2018. Following RT-PCR protocols, the GLRaV-1, GLRaV-2, and GLRaV-3 viruses were first detected in Baja California, along with GVA —another virus transmitted by vine mealybugs. GLRaV-1 was the dominant GLRaV virus (26%), followed by GLRaV-3 (24%) (Monroy-Corral, 2019). At the same time, massive sequencing techniques (RNA-seq) and bioinformatics analysis were used to identify and search for viruses with RNA or DNA genomes. The aim was to know the viruses found in *P. ficus*, in order to propose alternatives to control the insect populations. According to the results, the presence of one or more putative RNA viruses which could be specifically associated with *P. ficus* has been detected, as well as another virus potentially associated with the plant; however, their characterization is an ongoing effort (Duarte-De Jesús, 2020; Martinez-Mercado *et al*. 2022).

The grapevine plant is frequently co-infected by one or more GLRaV species, in addition to GVA and GVB (Le Maguet *et al*., 2012); therefore, when plants show inconclusive symptomatology, various viruses should be subject to a joint monitoring. A clear example of this problem was the discovery in 2008 of the red blotch disease in plants showing GLD-like symptoms, in a Cabernet Sauvignon vineyard at the Oakville Station of the University of California (Calvi, 2011). GRBV is now known to be the cause of this disease (Sudarshana *et al*., 2015; Cieniewicz *et al*., 2017). The first report about the presence of GRBV in Mexico was made in 2019 (Gasperin-Bulbarela *et al*., 2019). Throughout 2016 and 2017, samples with amplification of the expected products were found by PCR-based diagnosis of *Vitis vinifera* Pinot noir, Merlot, and Nebbiolo plants which showed red blotch symptoms at Ensenada, Baja California. A representative amplicon sequence had a high identity (98%) with Canadian GRBV isolates. Likewise, Gasperin-Bulbarela *et al*. (2019) reported the full sequence of two new Mexican GRBV isolates. In a follow-up work, in 2018 and 2019, they carried out a sample focused on plants with reddening symptoms in Baja California and found positive samples in red and white varieties, using PCR. The main symptoms in plants from positive red varieties were red blotches in the leaf blade and the secondary and tertiary red veins, while foliar chlorosis was recorded in white varieties. Additionally, an analysis of the viral DNA restriction patterns of 21 positive samples enabled the identification of isolates from Washington, New York, California, and Canada; this suggests several points of origin or entry paths for GRBV (Palacios-Gutiérrez, 2019). Beltrán-Beache *et al*. (2021) reviewed the current global situation of the red blotch virus and the risk it entails for Mexico, and they emphasized the lack of knowledge about the incidence and geographical distribution of the virus in the country. The only official report about the situation was developed by Gasperín-Bulbarela *et al*. (2019). However, those authors do not discard the presence of the virus in other areas; therefore, detecting the disease is fundamental to avoiding its transmission.

CONCLUSIONS

According to our review, the following viruses have been reported in Mexico: GFLV, GLRaVs, GVA, GVB, GRBV, GFkV, and GRSPaV. Most of those reports lack detail and follow-up. Although grapevine is a highly important crop for the country, there is scant information about viral diseases. Additionally, none of the reports we reviewed evaluated the economic impact of the diseases; such data should be transferred to the producers and technicians who manage the vineyards. In general terms, this information is not readily available, which hinders the appreciation and knowledge of the contributions made by students and others parties interested in the area. Therefore, we strongly suggest publishing information in formal media (particularly international media), in order to provide easy access for members of the academia and the industry. The management and characterization of grapevine viral diseases are a highly complex process, due to their chronic nature and their symptomatology, which may change from one grapevine variety to another. Therefore, accessible, quick, and sensitive new diagnosis techniques are required. Likewise, integrated disease management would benefit from establishing interactions between members of the academia and producers, facilitating management decision-making.

Mexico lacks significant knowledge about viral infections of grapevine; therefore, much work is to be done. Some potential initial steps could include: studying viral epidemiology in grapevines; carrying out accurate diagnoses in places where suspicious (symptomatic) plants have been detected; monitoring areas where viruses have been detected in the past; identifying and follow-up current vectors; and studying the effects of viral infection in plants and the economic impact on crops. Additionally, the potential co-infection of plants, the impact of mixed infections in crops, and the agents that take part in transmission could be addressed. Both the collection of field data and the application of molecular biology tools help to understand the etiology of viral diseases, as well as the host-pathogen-vector interaction.

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