

Epidemiological Patterns of Some Plant Viruses in Brazil

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Summary

Virus epidemiology combines the virus introduction and the presence of susceptible hosts and virus vectors. The citrus tristeza virus (CTV) was introduced in Brazil from Argentina and because the presence of the aphid *Toxoptera citricidus* and susceptible combination of scion/rootstock it spread throughout the country. Bean gold mosaic virus (BGMV) has been present in Brazil in dry beans crops but at very low incidence. After the expansion of soybean culture, an excellent host for *Bemisia tabaci*, the virus was quickly spread at high incidence in nearby bean fields causing severe losses. Tospoviruses are the most important viruses in horticultural crops in Brazil. A survey in Brazil demonstrated that there is a virus species distribution in the country, that may indicate specific interactions among tospovirus species and the prevalent thrips vector species or races in different regions of Brazil.

1. Introduction

Virus transmission and spread are the requirements for a successful virus infection. There are some interesting patterns of virus distribution in Brazil considering the presence of the virus, the presence of vectors and susceptible crops. Combination of favorable conditions are necessary for virus spread. The epidemiological patterns of three important viruses in Brazil, citrus tristeza virus (CTV), bean gold mosaic virus (BGMV) and tospoviruses are shown in Table 1, and the parameters involved in the spread of these viruses are discussed in the text.

Table 1 - Epidemiological patterns in Brazil.

Virus	Favorable combinations for virus spread
TCV	Virus introduction / Presence of vector / Susceptible crop
BGMV	Presence virus / Vector + Breeding Crop / Susceptible crop
TOSPOVIRUS	Virus species / Vector species / Susceptible crops

2. Citrus Tristeza Virus (CTV)

The Citrus cultivation and processing is an important economic activity in Brazil. São Paulo State represents 85% of the total production with 200 millions trees in 900,000 hectares.

The citrus tristeza virus is a very important disease of citrus in Brazil. The virus is a member of the closterovirus group. It is a filamentous, non enveloped and usually flexous particles with 2000 nm long and 12 nm wide. It is formed by a single stranded RNA of about 20 kilobases long (1).

The virus probably has one of the most diverse ranges of strains with a wide range of biological activities. There are four major groups of strains. Mild strains also exists which are almost symptomless in sensitive indicators plants.

The long period for symptoms expression on host plants has hampered research development in CTV studies. With the introduction of the *C. aurantifolia* Swingle as a indicator host, the indexing tests became much faster and new combinations of rootstocks and scions were developed. The symptoms expression of the CTV is associated to the susceptibility level of the rootstock and the scions. When the rootstock is sour orange it causes stem-pitting and death of the infected plant. No evident symptoms does not mean absence of the virus, since tolerant varieties can grow with the virus.

The virus is commonly transmitted by the aphid *Toxoptera citricidus* in a non-persistent manner (12). Due to the high efficiency of the aphid that transmit the CTV it is almost impossible to control the virus spread. The virus can be acquired and transmit by aphids, usually after acquisition and inoculation feeding periods of at least 30 min; frequencies of transmission are positively correlated with the length of the acquisition period up to 24 h and the length of the inoculation period up to 6 h (17). There is no latent period and infectivity is lost within 48 h of acquisition (2).

2.1. Spread in Brazil

The virus was first detected in South Africa and was introduced probably through infected buds into Argentina. Because the *Toxoptera citricidus* commonly infesting citrus grooves in South America acted as a very efficient vector for CTV, it quickly spread from Argentina to Brazil, where in the forties destroyed nearly 12 millions orange tress grafted on top of sour orange rootstocks and became an endemic disease. The vector is very common in the Brazilian conditions that makes control very difficult. Fortunately use of sweet orange and mandarins as rootstocks controlled the problem, which was complemented starting in the 70's with the successful cross protection with mild strains of CTV (5).

3. Bean Gold Mosaic Virus.

Bean gold mosaic disease of common beans (*Phaseolus vulgaris*) and several other vegetables is characterized by a brilliant gold mosaic pattern on infected leaves and by stunted plants growth. The disease is a major constrain on dry beans production in North, Central and South America and in the Caribbean Basin (9).

BGMV belongs two geminivirus group. Geminivirus is a unique group of plant virus characterized by two geminate isometric virion and a single stranded circular DNA genome (21). Geminiviruses are currently subdivided into three major groups (10): a) those that have a bipartite genome, that are transmitted by whiteflies (*Bemisia tabaci* Gennadius) and that

infect dicotyledonous plants; b) those that have a monopartite genome, that are transmitted by leafhoppers and that infect monocotyledonous plants; and c) those that have a monopartite genome, that are transmitted by leafhoppers and infect monocotyledonous. The genome of the whitefly-transmitted geminiviruses usually is divided between two DNA components, DNA-A and -B, both of which are required for infectivity (20).

The BGMV is transmitted by the whitefly *Bemisia tabaci* in a persistent-circulative manner. The *Bemisia tabaci* is a phloem feeding vector requiring a acquisition feeding period of 2-24 h, a inoculation access period of 2-3 h and has a latent period of 4-10 h. Transmission capability persists for approximately 5-20 days. The vector comprises several biotypes/races that may interact differently with the virus. The soybean plants are the main virus breeding source for the BGMV vector (9).

3.1 Spread in Brazil

Brazil is the first world producer of dry bean crop with approximately 5 million hectares cultivated each year. Around 1 million hectares were put out production due to BGMV infection in bean crops.

The BGMV has been for a long time present in Brazil in dry bean crops but of very low incidence. Around 70's soybean culture had a quick expansion from the Southern states and now is cultivated in most regions of Brazil. Soybean is an excellent host for *Bemisia tabaci*, the vector of BGMV which multiplied in huge numbers and quickly spread the virus in exceedingly high incidence in nearly all bean fields causing severe losses. Fortunately, soybean has not been affected seriously by BGMV, though being susceptible. So far, no varietal resistance of beans against BGMV was found, and the only tenable strategy has been to avoid proximity of soybean and bean crops. Attempts to produce virus resistance by transgenic bean plants expressing viral genes are under way.

4. Tospoviruses

Tomato spotted wilt virus (TSWV), a cosmopolitan plant virus which is spread in nature by some thrips species. The virus causes disease in economically important agricultural vegetable and ornamental crops predominantly in tropical regions (16). It has one of the broadest host range among plant viruses, infecting plant species out of 70 botanical families (19) causing a variable range of symptoms. Recently, TSWV also became prominent in temperate climate zones, a process which was preceded by the spread of *Frankliniella occidentalis* Perg. over the Northern hemisphere.

TSWV consists of roughly spherical, enveloped particles, ranging in diameter from 70-110 nm, which are covered with surface projections. Among plant virus TSWV appears to have a unique genome organization (11). The genome of TSWV consists of three single stranded RNA segments, denoted large (L), medium (M) and small (S). These RNA segments are complexed with nucleocapsid (N) proteins to form pseudo-circular nucleocapsid structures.

Though TSWV initially was considered as a member of a monotypic plant virus group, molecular and genomic organization data revealed that TSWV is a very similar to some arthropod transmitted animal viruses in Bunyaviridae (7, 8). To include TSWV in this family a new genus tospovirus, was created. Recent studies showed that TSWV is not the sole member of this genus, since three additional species were recognized as new members on the bases of their divergence of the nucleocapsid protein (N) encoded by the S RNA. These

new species were tomato chlorotic spot virus (TCSV), groundnut ring spot virus (GRSV) and Impatiens necrotic spot virus (INSV) (6). Other isolates found in groundnut and watermelon, although not fully characterized, have recently been proposed as a new tospovirus species named groundnut bud necrosis virus (GBNV).

In nature, tospoviruses are exclusively transmitted by several thrips species in a circulative-propagative manner (21). The vector seems to acquire the virus only during its larval stage and becomes infective afterwards for its whole lifespan.

Eight thrips species have been described in the literature as vector of tospoviruses (14, 15, 18). *Frankliniella occidentalis* is considered to be an important vector of TSWV and INSV in the Northern Hemisphere (21), whereas *Thrips palmi* is the most important vector for GRSV in India (Palmer).

4.1. Spread in Brazil

The losses caused by tospoviruses are serious in Brazil. This is due to the presence of a year round high thrips population in the field, and consequently potential virus sources. The



Figure 1 - Location of six states of Brazil where tospovirus isolates were collected. PE= Pernambuco, DF= Federal District, MG= Minas Gerais, SP= São Paulo, PR= Parana and RS= Rio Grande do Sul. Shaded areas indicate the areas where the samples were collected during 1992-1993.

total production of fresh market tomatoes is calculated to be 1.5 million tons in 25,000 ha. A rough calculation indicates that the tospoviruses cause losses of US\$ 25 million in the tomato crop yearly (de Ávila, personal communication).

Tospoviruses as TSWV has been described in Brazil since 1938 (3, 4). Since the last decade TSWV became the most threatening virus disease on vegetable crops in Brazil.

A recently survey was conducted in several regions of Brazil (15) to investigate the epidemiological status of tospovirus spread in the country (Fig. 1). Out of 150 tospovirus isolates, the existence of at least three tospovirus species was demonstrated to occur in Brazil using the classification based on the divergence of the N gene (4). Isolates, identical to TSWV, TCSV and GRSV, were detected, while no isolates identical to INSV were detected in our survey. Sixty nine isolates (46.0%) were identified as TSWV, 54 (36.0%) as TCSV and 12 as GRSV (8.0%). Fifteen isolates (10.0%) did not show any positive reaction with antibodies against the four tospovirus species TSWV, TCSV, GRSV and INSV. Despite the limited number of samples randomly collected in each state, the isolated tospovirus species displayed a peculiar geographical distribution (Fig. 2).

Our study demonstrated a great variability and a wide distribution of tospoviruses in Brazil as it has recently been reported. The results confirmed the occurrence of at least three tospovirus species in Brazil: TSWV, TCSV and GRSV.

The natural occurrence of the virus species TSWV, TCSV and GRSV in different states suggests that the tospovirus situation is more complex in Brazil than in other parts of the world. While in most parts of the world one tospovirus species seems to infect a certain crop, at least three different tospovirus seems to infect the tomato crop in Brazil. The fact that INSV was not detected in this survey was not surprising since the occurrence of this virus is mainly restricted to ornamentals and not to vegetables (22). Only one chrysanthemum plant was examined in this survey.

Although a limited number of samples and crops were analyzed, the prevalence of a tospovirus species in a certain geographical region, e.g. the occurrence of TSWV in the

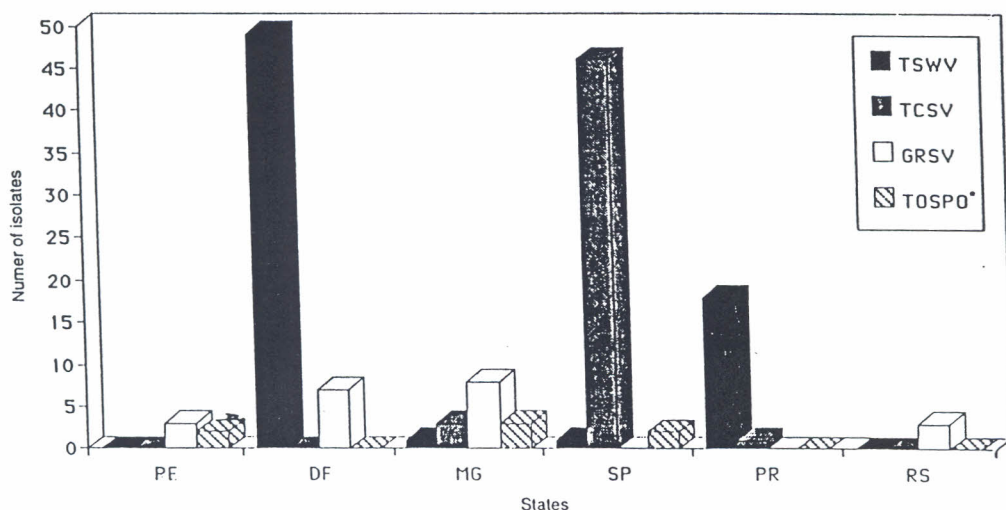


Figure 2 - Occurrence of tospovirus species in six states of Brazil. The virus species were identified by DAS-ELISA using polyclonal antisera specific to the TSWV, TCSV, GRSV and INSV N protein. (*) Tospo = unknown tospovirus isolates.

Federal District and in Paraná, TCSV in São Paulo and Rio Grande do Sul, and GRSV in Pernambuco, suggests that these different species may not spread at the same rate in all states. This spread is ecologically and epidemiologically difficult to explain at this moment. This different spread may partly be explained by the presence of different weeds and crops functioning as virus sources in different states. In addition, the thrips population may differ in race and species in the different states. Differences in the thrips population may result in a preferential and differential transmission.

The present survey showed a characteristic regional distribution of the tospoviruses. Either TSWV or TCSV and GRSV predominantly occurred in the states. The 15 isolates (10.0%) which did not show any reaction in ELISA with the antisera to TSWV, TCSV, GRSV and INSV are possibly members of one or more new serogroups and eventually new tospovirus species.

5. References

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