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## Review

# Emergence and epidemiology of *Cucurbit yellow stunting disorder virus* in the American Desert Southwest, and development of host plant resistance in melon

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## ABSTRACT

*Cucurbit yellow stunting disorder virus* (CYSDV), emerged in the Sonoran Desert region of the southwestern USA in 2006 and has become well established. Symptoms induced by CYSDV infection include a striking interveinal chlorosis or yellowing and reduced yield and quality. The virus is transmitted by *Bemisia tabaci*, and the cryptic species MEAM1 has been present in the region since the early 1990s. CYSDV has now become the most economically important of the viruses affecting cucurbit production in the southwestern US. Here, we present a review of recent studies on CYSDV in the southwestern US, with implications for management of this virus throughout the world. Field surveys have established that CYSDV results in late-season infection of spring melon crops with limited economic impact; however, all summer and fall cucurbits become infected shortly after emergence due to high *B. tabaci* populations and abundant sources of inoculum. Studies have also demonstrated that CYSDV has an extensive host range among crops and weeds prevalent in the region. Recent studies demonstrated considerable variation in virus accumulation and transmission rates among the host plants evaluated as potential reservoirs. Cucurbit hosts had the highest CYSDV titers, were efficient sources for virus acquisition, and showed a positive correlation between titer in source plants and transmission to cucurbit plants. Non-cucurbit hosts had significantly lower CYSDV titers and varied in their capacity to serve as sources for transmission. Experiments demonstrated that multiple factors influence the efficiency with which a host plant species will be a reservoir for vector transmission of CYSDV to crops. Melon PI 313970 was identified as a new source of host plant resistance to CYSDV, in addition to the previously identified TGR 1551 (=PI 482420) and TGR 1937 (=PI 482431). Potential new sources of CYSDV resistance were identified by field screening of ca. 500 melon accessions with naturally occurring inoculum from 2007 through 2012. Host plant resistance to *B. tabaci* has also been identified in melon germplasm resistant to CYSDV and could be an important factor in reducing losses to CYSDV. Resistance to CYSDV is being transferred to US western shipping type cantaloupe and honeydew.

## 1. Introduction and history of CYSDV

Numerous plant viruses cause yellowing symptoms in cucurbit crops. Most are caused by viruses in the genus *Crinivirus*, although such symptoms can also be caused by viruses that are members of other genera or by nutrient deficiencies. Symptoms of yellowing viruses are difficult if not impossible to distinguish from one another visually, and differentiation requires tests such as ELISA, RT-PCR, and sequencing. *Cucurbit yellow stunting disorder virus* (CYSDV; genus *Crinivirus*, family *Closteroviridae*), is one of the most widely distributed viruses among cucurbit production regions. The virus was initially discovered in the United Arab Emirates (Hassan and Duffus, 1991), but is now common

throughout many tropical and subtropical production areas, including the Middle East and Mediterranean basin, as well as North and Central America (Abou-Jawdah et al., 2000; Brown et al., 2007; Celix et al., 1996; Desbiez et al., 2000; Kao et al., 2000; Kuo et al., 2007; Louro et al., 2000; Polston et al., 2008; Tzanetakis et al., 2013; Wisler et al., 1998; Yakoubi et al., 2007).

Most CYSDV isolates from throughout the world are closely related genetically based on comparisons of the capsid protein (CP) sequences; however, sequence comparisons did reveal two groups of isolates. One group contained the majority of isolates (e.g., from Europe; North and Central America; Africa and some from the Middle East), and these are referred to as Western isolates (Rubio et al., 2001). A second distinct

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Fig. 1. Interveinal yellowing symptoms on melon typical of *Cucurbit yellow stunting disorder virus* infection.

group of isolates from Iran, Saudi Arabia, and Sudan share a higher degree of identity with one another, and are referred to as Eastern isolates (Rubio et al., 2001; Yakoubi et al., 2007; Mohammed et al., 2014). An analysis of the genetic variation within a localized CYSDV population from southern Spain was conducted over an eight-year period beginning two years after the virus was first identified in the region. Five different regions of the CYSDV genome were sequenced for each isolate to provide a more complete evaluation of genetic variation than could be achieved with a single gene. This study revealed an exceptionally high level of genetic conservation among the isolates examined (Marco and Aranda, 2005). Results suggested that, at least under the production conditions in southern Spain, there appears to have been insufficient selection pressure placed on the virus to cause genetic divergence of isolates within the population. It remains to be determined how factors may influence divergence of other regional CYSDV populations or what factors led to the divergence of the Western and Eastern CYSDV isolates.

Symptoms of CYSDV infection in cucurbit host plants are predominantly characterized by interveinal chlorosis or yellowing (Fig. 1), with major veins remaining green until late in disease development (Celix et al., 1996; Wisler et al., 1998; Tzanetakis et al., 2013). Early symptoms on some hosts include a yellow-green chlorotic mottle (Fig. 2) that eventually develops into full interveinal chlorosis. Symptoms initially appear on older leaves and progress acropetally over time. In the case of melon (*Cucumis melo*) or watermelon (*Citrullus*



Fig. 2. Chlorotic mottle symptoms characteristic of early stage symptom development on melon caused by *Cucurbit yellow stunting disorder virus*.



Fig. 3. Typical pattern of symptom development resulting from infection of melon by *Cucurbit yellow stunting disorder virus*. Yellowing symptoms begin on older leaves near the crown and progress over time toward younger parts of the plant.

*lanatus*) plants, this involves a progression of symptom development beginning with leaves near the crown and gradual development of symptoms extending along the vines (Fig. 3); in extreme cases entire branches are yellowed. Yellowed leaves often become thickened and brittle. Fruit do not show obvious symptoms, but studies have shown that sugar levels ( $^{\circ}$ Brix) are reduced in CYSDV-infected plants (Abou-Jawdah et al., 2000; López-Sesé and Gómez-Guillamón, 2000). These symptoms are similar to those caused by other yellowing viruses, including other members of the genus *Crinivirus*, such as *Beet pseudoyellows virus* (BPYV) (Duffus, 1965), *Cucurbit chlorotic yellows virus* (CCYV) (Gyoutoku et al., 2009; Okuda et al., 2010), and *Lettuce infectious yellows virus* (LIYV) (Duffus et al., 1986) (reviewed by Tzanetakis et al., 2013; Wisler et al., 1998). Other viruses genetically and structurally distinct from criniviruses can cause virtually identical symptoms on cucurbit hosts. These include *Cucurbit aphid-borne yellows virus* (CABYV), a member of the genus *Polerovirus*, family *Luteoviridae* (Lecoq et al., 1992; Lecoq and Desbiez, 2012), and *Melon yellowing associated virus* (MYaV), a member of the genus *Carlavirus*, family *Betaflexiviridae* (Nagata et al., 2003, 2005).

CYSDV is transmitted exclusively by the sweet potato whitefly, *Bemisia tabaci*, in a semipersistent manner (Celix et al., 1996). It is efficiently transmitted by both of the widely prevalent cryptic species, MEAM1 and MED (formerly known as Biotypes B and Q, respectively). Although studies have not thoroughly examined transmission by other cryptic species of *B. tabaci* (Dinsdale et al., 2010; De Barro et al., 2011), it is likely that other *B. tabaci* cryptic species may be vectors of this virus. Seminal work by Celix et al. (1996) thoroughly documented the transmission parameters of CYSDV by *B. tabaci* to and from melon. Transmission is enhanced with longer feeding periods on both acquisition and transmission hosts. The virus can be acquired by whiteflies from infected melon plants with feeding periods as short as two hours, but acquisition periods of at least 18 h resulted in transmission to greater than 80% of test plants (Celix et al., 1996). CYSDV transmission efficiency by viruliferous whiteflies also increased with longer feeding periods up to 48 h. Although the virus can be transmitted by individual whiteflies, feeding by large numbers of viruliferous insects improves transmission rates (Celix et al., 1996). In other words, it is possible to obtain transmission in the field with low whitefly populations, but as populations increase, transmission rates to cucurbit crops usually increase as well. Recent studies have demonstrated that infected reservoir host plants vary in their capacity to serve as acquisition hosts for the whitefly vector, with some far more efficient than others as sources for whitefly acquisition and transmission of CYSDV into cucurbit crops (Wintermantel et al., 2016). It is also important to note the long latent period of CYSDV in melon and other cucurbit host plants, during which plants can remain asymptomatic for three to four weeks after infection

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