

Utilizing new *Citrullus colocynthis* sources to enhance resistance to papaya ringspot virus type W (PRSV-W) in watermelon cultivars

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Background

Potviruses, including papaya ringspot virus (PRSV) and zucchini yellow mosaic virus (ZYMV) are the most common aphid-transmitted viruses and considered among the most serious impediments for the watermelon crop in the southeast of the United States in the last 40 years. Watermelon plants infected with squash vein yellowing virus (SqVYV) that cause sudden vine decline and significant losses to the watermelon crop in Florida are also frequently infected with PRSV-W. Development of PRSV-resistant cultivars is essential to ensure and maintain successful watermelon production in the U.S.

There is a great interest by the watermelon community in developing PRSV-resistant cultivars. In order to expedite this process there is a need to identify new genetic sources and utilize them to enhance watermelon cultivars with resistance to potviruses.

Objectives of this study

1) Develop germplasm lines and genetic populations derived from the PRSV-W resistant versus susceptible, homozygote lines and study the genetic inheritance of PRSV-W in the desert watermelon *C. colocynthis*, and 2) incorporate PRSV-resistance from these wild type-desert watermelons into watermelon cultivars.

Accomplishments

Objective 1

We have screened the United States Plant Introduction (PI) accessions representing the desert watermelon *Citrullus colocynthis* collected in Asia, the Middle East and North Africa, and identified several sources that show high resistance to papaya ringspot virus of watermelon (PRSV-W) (Figure 1). We have selected and self-pollinated plants that showed high resistance and confirmed that the resistance to PRSV-W still exists in the subsequent generation's homozygous S_3 lines. At the same time, we self-pollinated *C. colocynthis* PI accessions that showed high susceptibility to PRSV-W and have been using them in constructing genetic populations (F1, F2 and BC1) derived from crossing the PRSV-resistant versus susceptible lines. The genetic populations are being used in inheritance studies aimed to determine the mode of PRSV-resistance inheritance and the gene loci conferring the resistance.

Objective 2

We have made crosses of the most resistant *C. colocynthis* accessions (collected in Asia and north-western Africa) with watermelon cultivars (Charleston Gray and Sugar Baby) and have been developing genetic populations (BC1F2) that will be screened for PRSV-resistance. The BC1F2 plants that are most resistant to PRSV will be further backcrossed to watermelon cultivars to develop advanced watermelon breeding lines with PRSV-resistance and desirable fruit quality. The advanced lines could be further used by public researchers and seed companies in breeding programs aimed to incorporate the resistance into elite watermelon cultivars.



Figure 1. Leaves of a wild type watermelon (*Citrullus colocynthis*) accession showing high resistance to papaya ringspot virus (PRSV) (upper row) versus leaves of a watermelon accession highly susceptible to PRSV, showing extensive deformation and mosaic patterns (lower row).



Figure 2. Watermelon fruits of a plant derived from a cross between a *Citrullus colocynthis* plant resistant to papaya ringspot virus and the heirloom cultivar Charleston Gray.

Scientific Publications resulting from this project:

Levi, A., J. Coffey, N. Guner, K. Tadmor and K. Ling. Resistance to papaya ringspot virus-watermelon strain (PRSV-W) in the desert watermelon *Citrullus colocynthis*. HortScience (manuscript in preparation).

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