

Sequence Diversity among Avocado Sunblotch Viroids Isolated from Single Avocado Trees

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In previous studies we developed an avocado sunblotch viroid (ASBVd) specific reverse transcription-polymerase chain reaction (RT-PCR) protocol and tested all avocado germplasm accessions in the U.S. National Germplasm Repository (NGR) for ASBVd. It was found that 19% of the accessions were infected with the viroid. To characterize the population of sequence variants, single trees of seven accessions with a history of infection were selected. RT-PCR products were cloned and sequenced from these trees and a total of 60 sequence variants were identified from 122 clones. Most of the variants were found to be unique to the individual tree from which they were isolated. The fraction of unique variants was 81% in 'Lima Late', 81% in 'Aycock Red', 67% in 'Hawaii', and 60% in 'Young Special'. Analysis of the sequence data suggests that variants evolved within a tree rather than arising from multiple infection events, supporting the quasispecies concept for ASBVd. Changes in the right terminal loop (R_{TL}), previously associated with leaf variegation and bleaching, were found in all variants isolated from bleached tissue; however, 16 clones isolated in non-symptomatic tissue also had changes in the R_{TL} . The addition of a U between bases 115 and 118 was found in 21 of the 23 clones isolated from the bleached tissue but not found in the 99 clones isolated from green tissue. These data suggest that the insertion of a U between bases 115 and 118 is responsible for the bleaching condition.

KEY WORDS: Viroids; capillary electrophoresis; sequence variants; quasispecies.

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