

Distribution and genetic diversity of tomato-infecting geminiviruses in

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Tomato-infecting geminiviruses have been reported throughout Brazil since the introduction of a new species of insect vector, the whitefly *Bemisia argentifolii*, in 1992. However, a detailed analysis of the biological and molecular properties of these viruses has not yet been carried out. As a first step towards the characterization of these viruses and the development of management strategies based on host resistance, we carried out a country-wide survey on the distribution and genetic diversity of tomato-infecting geminiviruses. Tomato samples with typical geminivirus symptoms were collected in seven different states, comprising the major tomato growing areas of the country, from 1994 to 1999. Geminiviruses were detected by PCR using universal primers for the genus Begomovirus. PCR-amplified fragments were cloned and sequenced. Based on sequence comparisons and phylogenetic analyses, at least five previously undescribed species of begomoviruses, plus two tentative new species, were found. Two of the new viruses were found exclusively in the Northeastern states, two exclusively in the Southeastern states, and one was found in both regions. Three of the new species were found in Minas Gerais, and two in Pernambuco. Sequence comparisons reveal strong evidence of recombination among the Brazilian geminiviruses. Together, the results indicate the existence of a high degree of pre-existing genetic diversity among tomato-infecting geminiviruses in Brazil and suggest that these viruses have emerged after being transferred from natural hosts to tomatoes, due to the introduction into Brazil of a novel polyfagous vector species.