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GENETIC STRUCTURE OF *Tomato severe rugose virus* POPULATIONS/ Estrutura genética de populações do begomovírus *Tomato severe rugose virus* (ToSRV). O.F.L. SANDE<sup>1,2</sup>; E. MIZUBUTI<sup>1</sup>; B. HORA-JUNIOR<sup>1</sup>; F.M. ZERBINI<sup>1</sup>. <sup>1</sup>Dep. de Fitopatologia/BIOAGRO, Universidade Federal de Viçosa, Viçosa, MG, Brazil; <sup>2</sup>Instituto Superior Politécnico de Manica, Mozambique. E-mail: [oslasande@hotmail.com](mailto:oslasande@hotmail.com)

The genus *Begomovirus* (family *Geminiviridae*) includes viruses with a genome composed of one or two molecules of circular, single-stranded DNA encapsidated in twinned icosahedral particles. The incidence of begomoviruses in Brazil has increased since the 1990's with the introduction of the vector *Bemisia tabaci* Middle East-Asia Minor 1 (MEAM1). The objective of this work was to evaluate the spatio-temporal dynamics of populations of *Tomato severe rugose virus*, the most common begomovirus in tomato crops in southeastern Brazil. Foliar samples with begomovirus-like symptoms including dwarfing, yellow mosaic and leaf curl were collected in tomato fields located in rural areas of the municipalities of Coimbra (MG) in 2013 and 2014 and Florestal (MG) in 2014. Total DNA was extracted and used as a template for the amplification of viral genomes using the phi29 DNA polymerase. Viral genomes were cloned in plasmid vectors and fully sequenced. A total of 75 full-length DNA-A clones were obtained. The isolates obtained from tomato samples indicate an almost absolute predominance of ToSRV in Florestal and Coimbra (replacing *Tomato common mosaic virus* as the dominant begomovirus in Coimbra). Phylogenetic analysis, including additional ToSRV sequences from a number of cultivated and non-cultivated hosts available in GenBank, divided ToSRV isolates into four major clades: Florestal/2008; São Paulo, Goiás and the Federal District; Florestal/2014 and Viçosa, Coimbra, Carandaí and Jaíba. The genetic variability of the ToSRV population is not equally distributed among subpopulations. Subpopulations from Viçosa and Florestal/2008 have a greater contribution to the variability. Coalescence analysis mapped the mutations occurring along the viral genome. All mutations observed in peppers and in non-cultivated hosts are common to tomatoes and show the same relative age, suggesting that ToSRV is well adapted to tomatoes, with occasional transfer to other hosts by the insect vector.

**Key words:** Begomovirus; Tomato; ToSRV; Variability; Mutations.