WIDESPREAD OCCURRENCE OF TOMATO GEMINIVIRUSES IN BRAZIL, ASSOCIATED WITH THE NEW BIOTYPE OF THE WHITEFLY VECTOR.

R. Krause¹, J.J. Fernandes¹, A.C. de Avila², I.C. Bezerra², S.G. Ribeiro³, R.O. Resende⁴, M. Freites Lima⁵, E.P.B. Fontes¹ and F.M. Zerbini¹. ¹Dep. de Fitopatologia, Univ. Fed. de Viçosa, Viçosa, MG, 36571-000, Brazil, ²Embrapa-Hortaliças, Cx. Postal 218, Brasília, DF, 70359-970, Brazil, ³Embrapa-Biotecnologia, Cx. Postal 2372, Brasília, DF, 70770-900, Brazil, ⁴Dep. de Biologia Celular, Univ. de Brasília, Brasília, DF, 70910-970, Brazil, ⁵Embrapa-Semi Arido, Cx. Postal 23, Petrolia, PE, 56300-000, Brazil.

Although tomato golden mosaic virus (TGMV) was reported in Brazil more than 20 years ago (1), tomato-infecting geminiviruses have not been of economic significance in the country until recently. However, a sharp increase in the incidence of geminivirus-like symptoms in tomatoes has been reported in several areas of Brazil since 1994. This has coincided with the appearance of the B biotype of Bemisia tabaci, which, as opposed to the A biotype, readily colonizes solanaceous plants (2). We have isolated geminiviruses from symptomatic tomato plants in the Federal District, in two different areas of the state of Minas Gerais and in the state of Pernambuco. These viruses were provisionally named TGV-DF. TGV-Ig. TGV-Ub and TGV-Pel, Pe2 and Pe3. Using the primer pairs PAL1v1978/PAR1c496 and PCRc1/PBL1v2040 (3), DNA-A and -B fragments were PCRamplified, cloned and sequenced. Sequence comparisons indicated that these viruses were different from each other, and also from previously reported tomato-and bean-infecting geminiviruses, including tomato yellow vein streak virus (ToYVSV), recently described in Brazil (4). Nucleotide sequence homologies for DNA-A fragments ranged from 80% (Ub vs. Ig) to 67% (Ig vs. DF) for the 5'-end of the cp gene, and from 80% (Ub vs. DF) to 44% (Ub vs. Ig), for the 5'-end of the rep gene. Database searches indicated that the viruses are mostly related to TGMV, BGMV-Br and ToYVSV, although homologies were never greater than 80% for the fragments compared. Similar results were obtained with TGV-Ub and TGV-Ig for the DNA-B fragment (5'-end of the BC1 ORF). We are now cloning full-length genomes of these viruses to proceed with their molecular characterization. These results demonstrate that tomato-infecting geminiviruses are emerging in Brazil, posing as a major threat to the tomato industry in the country. The fact that distinct viruses are appearing in different regions of the country suggests that indigenous geminiviruses, infecting weeds and/or wild solanaceous plants, are being transferred into tomato plants by the whitefly vector. The relatively low degree of nucleotide sequence homology among these viruses might pose as a problem if host resistance is to be used as a method of control, making it necessary to search for sources of resistance that are effective against each individual virus.

References: (1) J.C. Matyis et al., Summa Phytopathologica 1:267-275, 1975. (2) F.H. França et al., An. Soc. Entomol. Bras. 25:369-372, 1996. (3) M.R. Rojas et al., Plant Disease 77:340-347, 1993. (4) J.C. Faria et al., Plant Disease 81:423, 1997.