

Molecular phylogeny of Septoria isolates associated with Septoria leaf spot on tomato in Brazil

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The Septoria leaf spot is one of the most important plant diseases on tomato in Brazil. According to the specialized literature Septoria lycopersici is the unique species associated with the disease epidemics in Brazil, however, phylogenetic studies should be done to elucidate the identity of this plant pathogen. Therefore, the main objective in this study was to carry out the phylogenetic analysis of the translation elongation factor-1 α (TEF1- α) and β -tubulin (β t) genes of 52 and 69 Septoria isolates, respectively. The isolates were obtained from tomato plants in Rio Grande do Sul, Santa Catarina, Goiás, Minas Gerais, Espírito Santo, São Paulo, Paraná, and Distrito Federal. For the phylogenetic analysis, TEF1-α and βt, sequences from Septoria species were obtained from the GenBank. The phylogenetic analysis of TEF1-α, βt, and concatenated data set were conducted using the maximum likelihood method (RAxML-HPC2) implemented in the CIPRES Science Gateway. The GTRGAMMA model was used for the search tree with 1000 replications . All isolates were clustered in the S. lycopersici clade. In addition, it was detected genetic variability among the isolates for both genes. Five haplotypes were generated for βt and TEF1-α genes with haplotype diversity of 0.140 and 0.152, respectively. The mutation rates ew (per site/per sequence) from βt and TEF1-α genes were 0.03568/8.74261 and 0.03016/4.22297, respectively. Differences of total number of mutations were detected between βt (42) and TEF1-α (19) genes. The highest nucleotide diversity (0.00875) and nucleotide diferences (2.145) were estimated for βt gene. Thus, there are evidences that S. lycopersici is the unique species associated with Septoria leaf spot on tomato with genetic variation among the isolates. Additional studies of morphological, pathogenicity and molecular characterization with calmodulin gene from these and other Septoria isolates are being conducted to confirm the results.

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