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Genetic characterization of *Ralstonia solanacearum* causing bacterial wilt in Brazil.

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[1]PhD student, [2]Researcher Embrapa Hortaliças, [3]Professor Universidade Federal de Viçosa. Email: thais.santiago@ufv.br. Caracterização genética de *Ralstonia solanacearum* causando a murcha bacteriana no Brasil.

Ralstonia solanacearum (RS) causes bacterial wilt, a highly destructive disease, in more than 200 plant species. Despite the widespread occurrence of the disease in Brazil, no thorough pathogen population genetics studies were conducted yet. A total of 120 isolates of RS from 19 states and 12 host species were characterized for biovar, phylotype, and sequevar. Additionally, the genetic diversity was estimated using BOXAIR. Biovar was determined using physiological tests. Phylotype was determined by multiplex PCR using a set of phylotype-specific primers (Nmult:21:1F, Nmult:21:2F, Nmult:22:InF, Nmult23:AF and Nmult21:RR) and the 759/760 primers. PCR amplification of a 750 bp fragment of the endoglucanase gene (egl) was performed using the primer pair Endo-F and Endo-R and the genetic diversity of RS isolates was determined by repetitive PCR assay using the BOXAIR primer. Brazilian isolates were classified as biovar 1 (N=51), 2 (N=54) and 3 (N=15). Phylotypes II (115 isolates; 372 bp fragment) and I (5 isolates; 155 bp) were detected among the isolates. All phylotype I isolates were from the Northern region. Based on the *egl* sequences isolates could be grouped in phylotype I and phylotype II subclusters IIA and IIB and sequevars 1, 4A, 5, 6, 18 and 36 could be identified. A heterogeneous group of isolates was formed with the banding pattern generated by BOX-PCR assay. There is high genetic variability in the Brazilian population of RS and this makes bacterial wilt control using host resistance a challenging task. Financial support: FAPEMIG and CNPq.

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