

141-1 **Phylotypes and sequevars of *Ralstonia solanacearum* infecting *Eucalyptus* spp. in Brazil**
(Filotipos e sequevars de *Ralstonia solanacearum* infectando *Eucalyptus* spp. no Brasil)

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Resumo

Among the bacterial pathogens of *Eucalyptus* in Brazil, *Ralstonia solanacearum* is considered one of the most important because of the characteristics of the pathogen and its damage to the crop in recent years. Given its importance and the lack of research on this pathosystem, the present study aimed to perform a molecular characterisation of different isolates of infected *Eucalyptus* plants in Brazil. A total of 19 bacterial cultures isolated from *Eucalyptus* in different regions of Brazil were analysed. A 372-bp product generated by multiplex-PCR amplification using Nmult primers identified all the isolates analysed as belonging to phylotype II. Eighteen isolates were grouped into subclade IIA and one into subclade IIB. The phylogenetic tree generated from the gene sequences of endoglucanase (*egl*) confirmed the classification of the isolates into phylotype II and separated the isolates into sequevars. Isolates AMC22, IBSBF2568 and IBSBF2576 were grouped into a single clade, as were isolates UFV18 and UFV20, with 89% and 78% *a posteriori* probability, respectively, forming two new potential sequevars not yet defined. We also identified isolates belonging to sequevars 41 (100% probability) and 37 (88% probability). However, most of the isolates did not fit into any previously described sequevar and did not form distinct clades.

Apoio: CNPq, Fapemig, CMPC