Characterization of an endophytic bacterial community associated with *Eucalyptus* spp

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ABSTRACT. Endophytic bacteria were isolated from stems of *Eucalyptus* spp (*Eucalyptus citriodora, E. grandis, E. urophylla, E. camaldulensis, E. torelliana, E. pellita*, and a hybrid of *E. grandis* and *E. urophylla*) cultivated at two sites; they were characterized by RAPD and amplified rDNA restriction analysis (ARDRA). Endophytic bacteria were more frequently isolated from *E. grandis* and *E. pellita*. The 76 isolates were identified by 16S rDNA sequencing as *Erwinia/Pantoea* (45%), *Agrobacterium* sp (21%), *Curtobacterium* sp (9%), *Brevibacillus* sp (8%), *Pseudomonas* sp (8%), *Actinobacter* sp (4%), *Burkholderia cepacia* (2.6%), and *Lactococcus lactis* (2.6%). Genetic characterization of these endophytic bacteria isolates showed at least eight ARDRA haplotypes. The genetic diversity of 32 *Erwinia/Pantoea* and 16 *Agrobacterium* sp isolates was assessed with the RAPD technique. There was a high level of genetic polymorphism among all the isolates and there was positive correla-
tion between the clusters and the geographic origin of the strains. These endophytic bacteria were further analyzed for in vitro interaction with endophytic fungi from Eucalyptus spp. We found that metabolites secreted by Erwinia/Pantoea and B. cepacia isolates had an inhibitory growth effect on some endophytic fungi, suggesting that these metabolites play a role in bacterial-fungal interactions inside the host plant. Apparently, these bacteria could have an important role in plant development; in the future they may be useful for biological control of diseases and plant growth promotion, as well as for the production of new metabolites and enzymes.

**Key words:** Endophytic bacteria; Plant-bacteria interaction; Erwinia; Pantoea