

## 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%), *Acinetobacter* 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*