

16S rRNA phylogenetic analysis of the plant growth-promoting rhizobacteria associated with pepper(Piper nigrum L.).

ABSTRACT

Fourteen indigenous rhizobacterial isolates from pepper (*Piper nigrum* L.) rhizosphere were successfully identified by 16S rRNA sequencing, namely *Acinetobacter radioresistens* (UPMLH1), *Bacillus* spp. (UPMLH8, UPMLH23, UPMLH34 and UPMLH43), *Bacillus cereus* (UPMLH1, UPMLH13, UPMLH24, UPMLH41 and UPMLH42), *Bacillus megaterium* (UPMLH3 and UPMLH22), *Bacillus subtilis* (UPMLH5) and *Leclercia* sp. (UPMLH2). All the identified strains were successfully positioned in the 16S rRNA based phylogenetic tree at the nucleotide and the amino acid sequence levels. Present study found that the relationship structure of translated amino acid phylogenetic tree was simpler than nucleotide based phylogenetic tree. Both phylogenetic trees contained two phyla, Firmicutes and Proteobacteria, with the Firmicutes were the largest proportion of the isolates recovered from this study.

Keyword: 16S rRNA; Pepper; *Piper nigrum* L.; Plant growth-promoting rhizobacteria