



Article

Enhancing Teak (*Tectona grandis*) Seedling Growth by Rhizosphere Microbes: A Sustainable Way to Optimize Agroforestry

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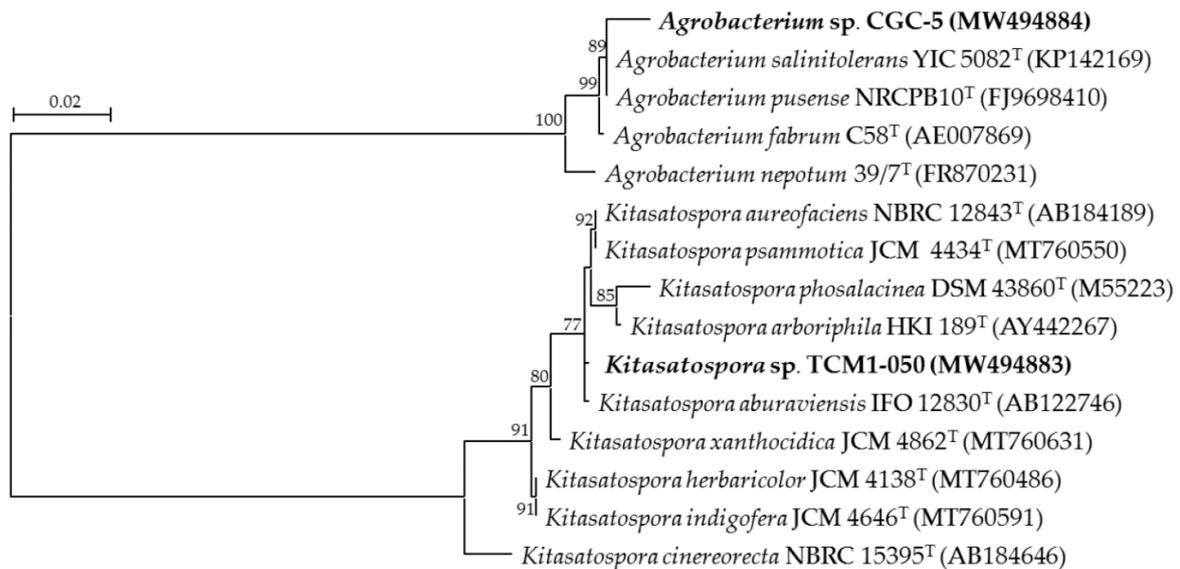


Figure S1. Unrooted maximum-likelihood phylogenetic tree of teak rhizobacteria used in this study. The tree was constructed using 16S rRNA gene sequence data derived from isolates CGC-5 and TCM1-050 (in bold) and their closely related phylogenetic species. The GenBank accession number of the gene sequence is presented in the parenthesis. Bootstrap values (based on 1,000 replications) of >60% are at the tree's nodes, and scale bar represents 2% dissimilarity.

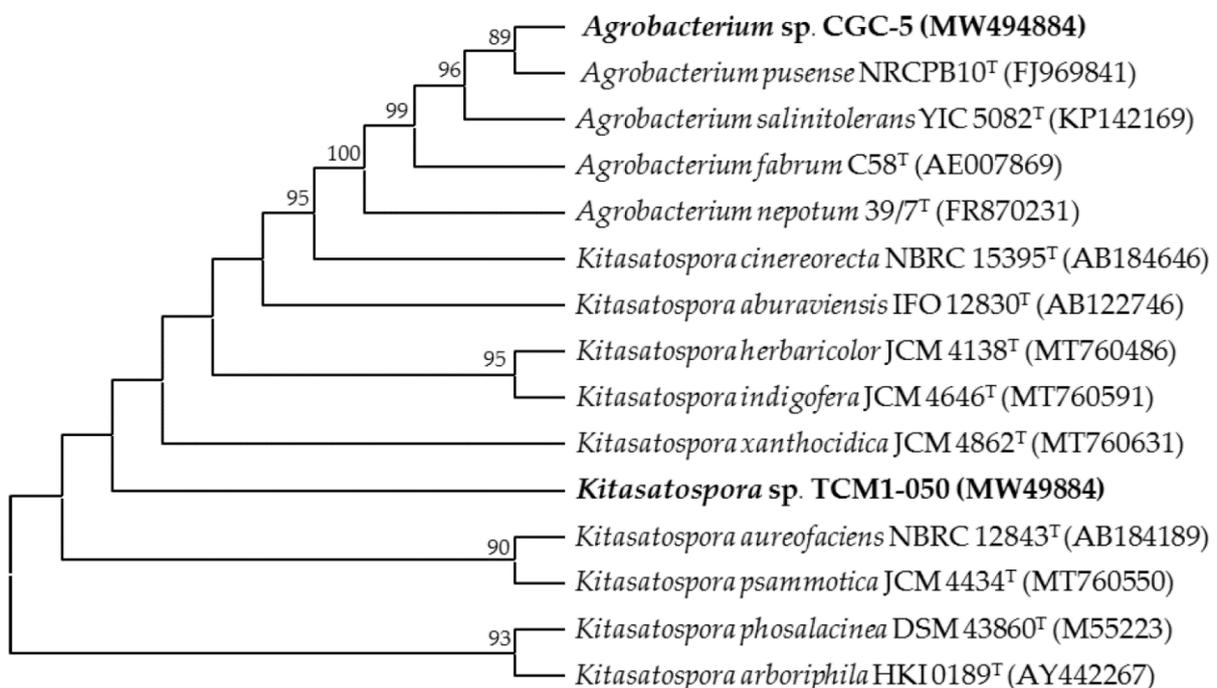


Figure S2. Unrooted maximum-parsimony phylogenetic tree of teak rhizobacteria used in this study. The tree was constructed using 16S rRNA gene sequence data derived from isolates CGC-5 and TCM1-050 (in bold) and their closely related phylogenetic species. The GenBank accession number of the gene sequence is presented in the parenthesis. Bootstrap values (based on 1,000 replications) of >60% are at the tree's nodes.