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Supplementary material

Comparison of plant growth-promoting rhizobacteria in a pine forest soil and an agricultural soil

Víctor M. Flores-Núñez[A], *Enriqueta Amora-Lazcano*[A], *Angélica Rodríguez-Dorantes*[B], *Juan A. Cruz-Maya*[C], *and Janet Jan-Roblero*[A,D]

[A]Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Prolongación de Carpio y Plan de Ayala s/n. Col. Sto. Tomás, Ciudad de México, 11340, México.

[B]Departamento de Botánica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Prolongación de Carpio y Plan de Ayala s/n. Col. Sto. Tomás, Ciudad de México, 11340, México.

[C]Unidad Profesional Interdisciplinaria en Ingeniería y Tecnologías Avanzadas, Instituto Politécnico Nacional, Av. IPN 2580, Col. La Laguna Ticoman, Ciudad de México, 07340, México.

[D]Corresponding author. Email: jjan_r@yahoo.com.mx

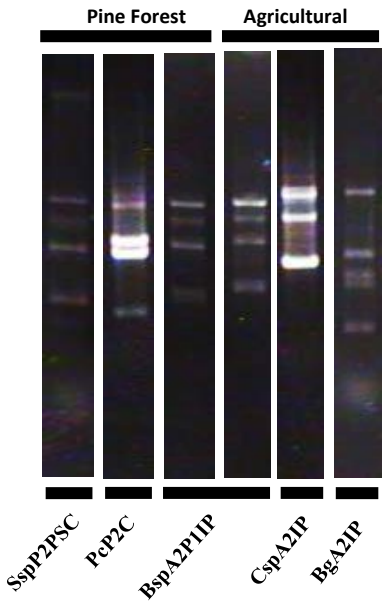

Fig. S1. Representative RAPD profiles of isolated PGPR. Each RAPD fingerprint corresponds to unique strains from pine forest soil (SspP2PSC and PcP2C), agricultural soil (CspA2IP and BgA2IP) or shared between both soils (BspA2P1IP).

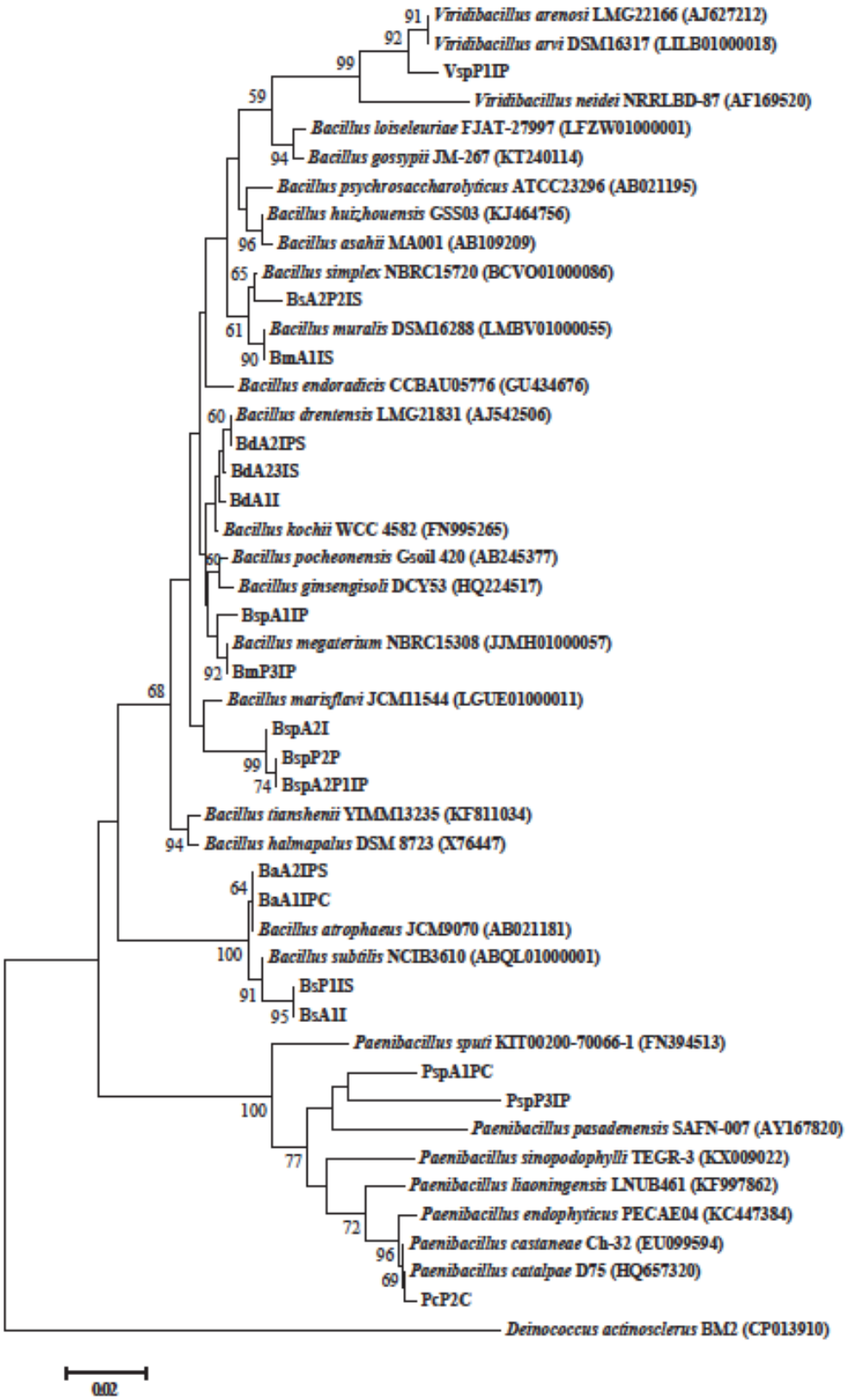

Fig. S2. Phylogenetic tree of sequences of the 16S rRNA gene of the isolates from pine forest soil and agricultural soil. Phylogenetic tree of the Firmicutes-related isolates. The tree was constructed using the neighbor-joining method; where *Deinococcus actinosclerus* BM2 (CP013910) served as an outgroup. The numbers at the branches indicate the bootstrap values of 1000 resamplings. The bar at the bottom indicates the number of substitutions per site.

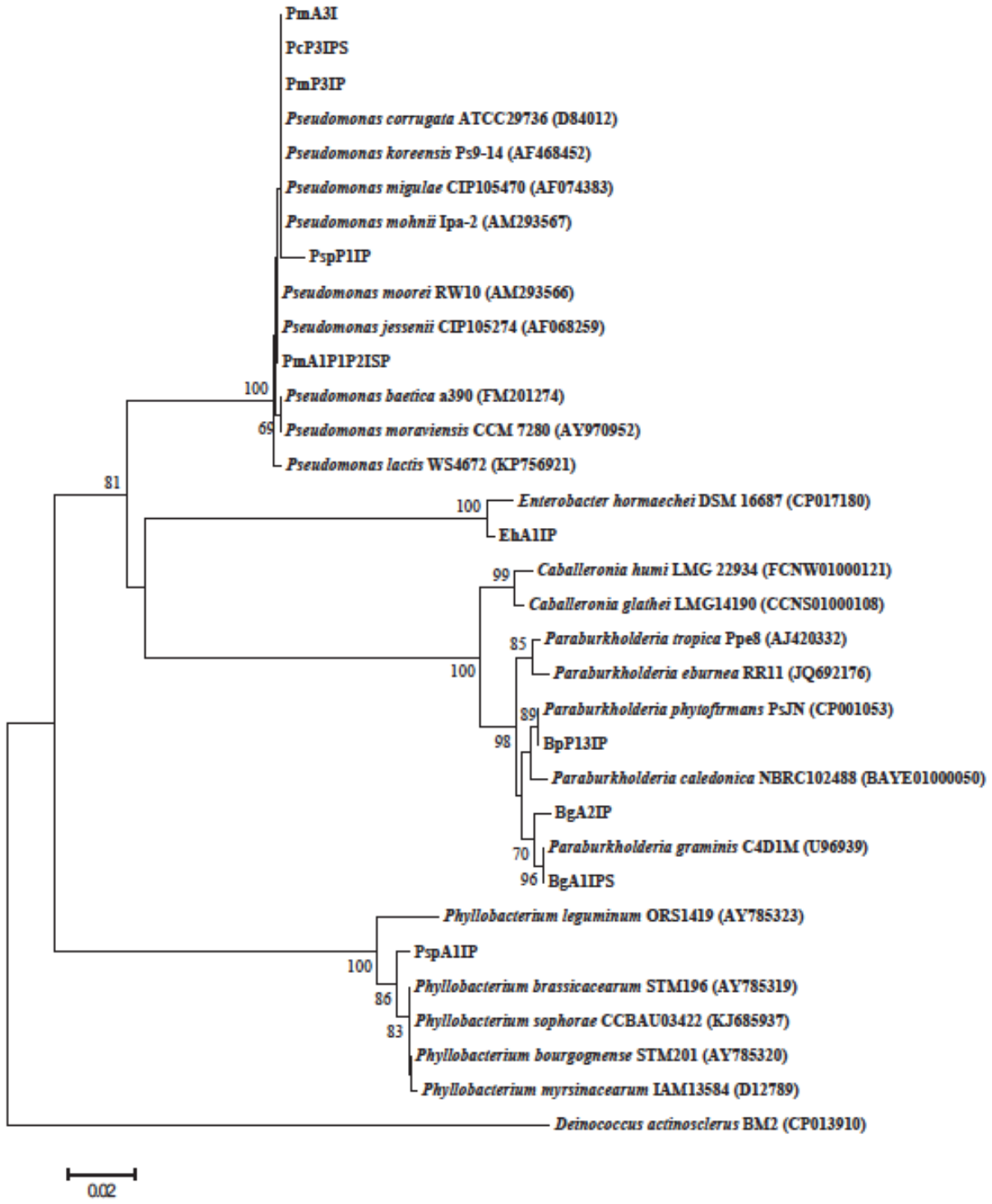

Fig. S3. Phylogenetic tree of sequences of the 16S rRNA gene of the isolates from pine forest soil and agricultural soil. Phylogenetic tree of the Proteobacteria-related isolates. The tree was constructed using the neighbor-joining method; where *Deinococcus actinosclerus* BM2 (CP013910) served as an outgroup. The numbers at the branches indicate the bootstrap values of 1000 resamplings. The bar at the bottom indicates the number of substitutions per site.

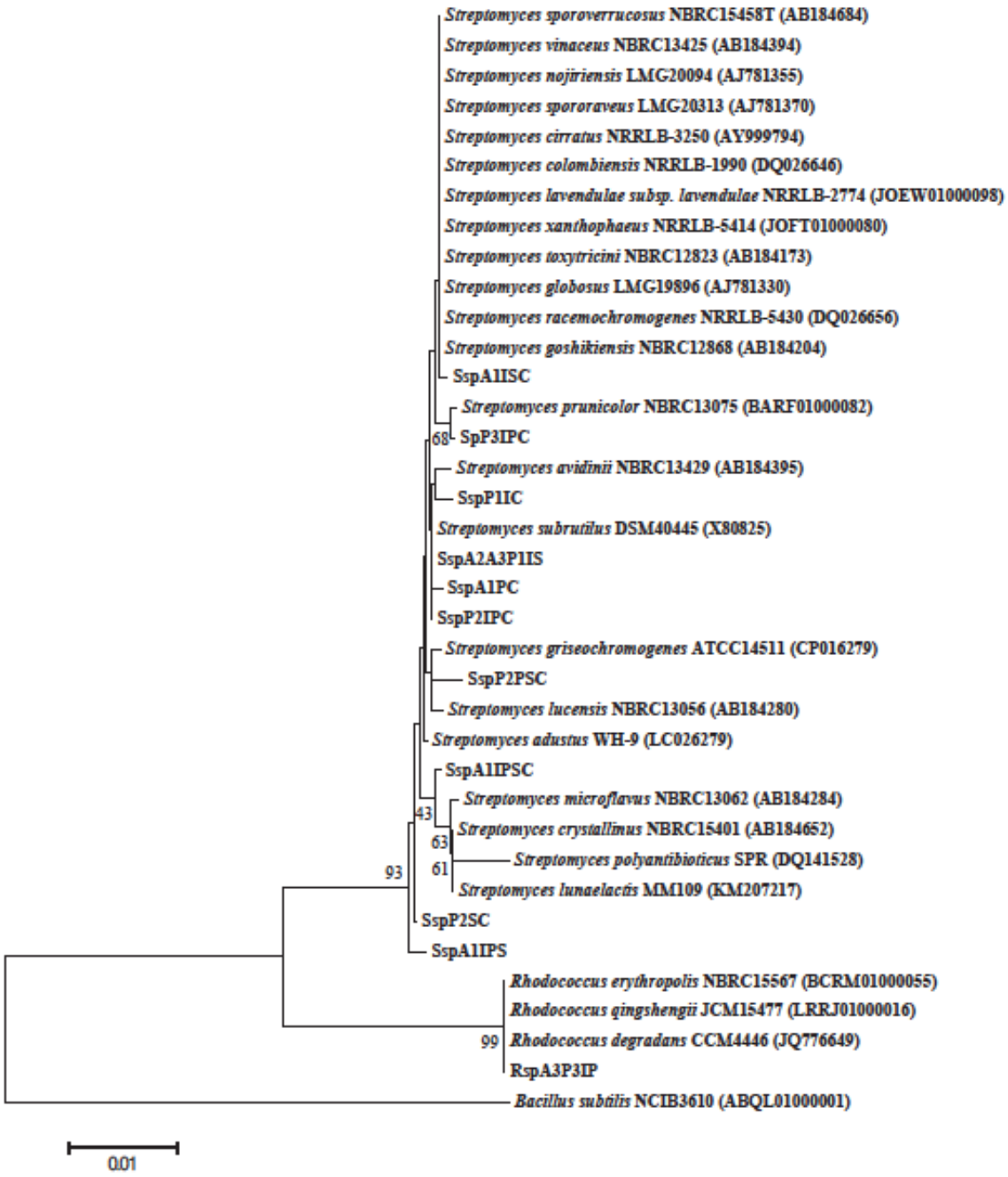

Fig. S4. Phylogenetic tree of sequences of the 16S rRNA gene of the isolates from pine forest soil and agricultural soil. Phylogenetic tree of the Actinobacteria-related isolates. The tree was constructed using the neighbor-joining method; where *Bacillus subtilis* NCIB3610 (ABQL01000001) served as an outgroup. The numbers at the branches indicate the bootstrap values of 1000 resamplings. The bar at the bottom indicates the number of substitutions per site.

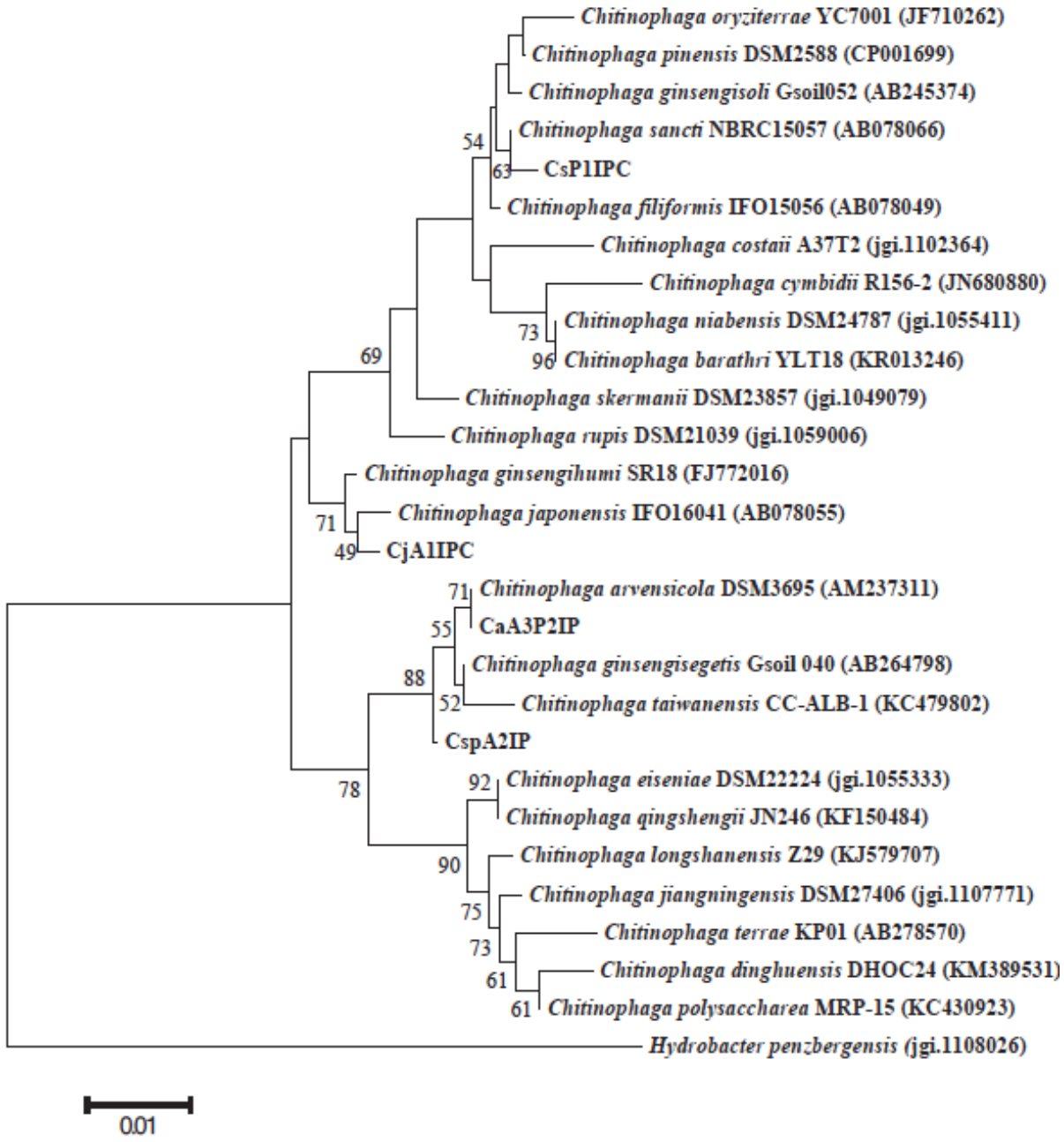

Fig. S5. Phylogenetic tree of sequences of the 16S rRNA gene of the isolates from pine forest soil and agricultural soil. Phylogenetic tree of the Bacteroidetes-related isolates. The tree was constructed using the neighbor-joining method; where *Hydrobacter penzbergensis* (jgi.1108026) served as an outgroup. The numbers at the branches indicate the bootstrap values of 1000 resamplings. The bar at the bottom indicates the number of substitutions per site.