

Figure

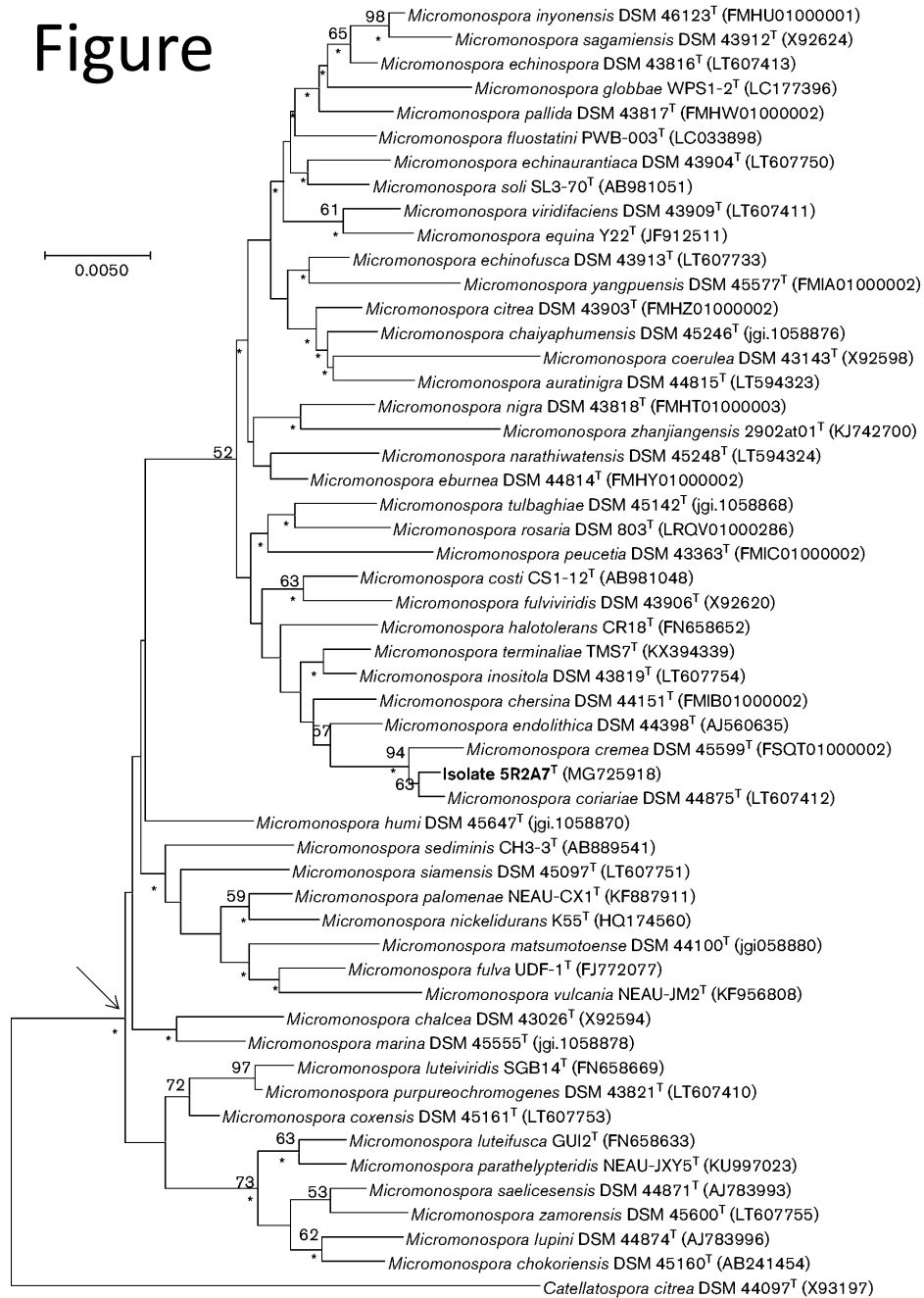


Fig. 1. Neighbour-joining phylogenetic tree based on almost-complete 16S rRNA gene sequences showing relationships between strain 5R2A7T and closely related *Micromonospora* type strains. The numbers at the nodes are bootstrap support values when >50%. Asterisks indicate branches of the tree that were recovered in the maximum-likelihood tree. *Catellatospora citrea* DSM 44097T was used as the outgroup. Bar, 0.005 substitutions per nucleotide position.

Figure

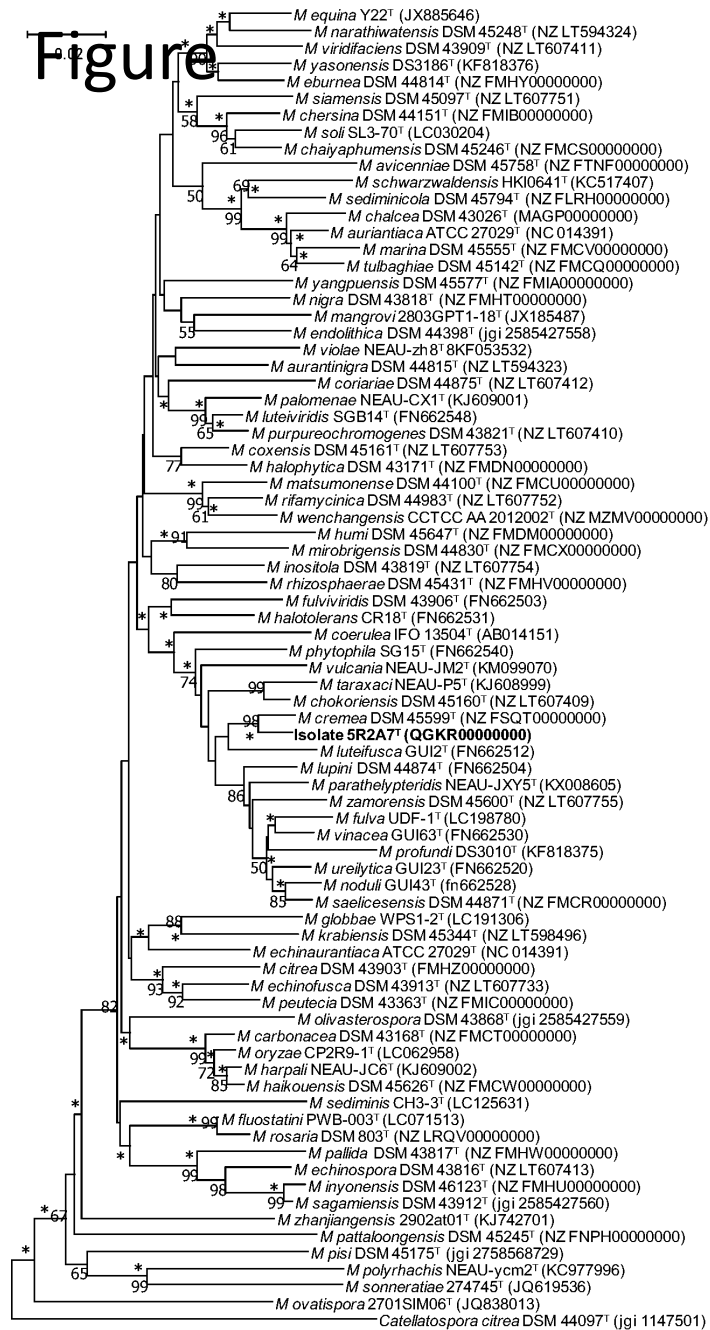


Fig. 2. Neighbour-joining phylogenetic tree based on almost-complete *gyrB* gene sequences showing relationships between strain 5R2A7T and *Micromonospora* type strains. The numbers at the nodes are bootstrap support values when >50%. Asterisks indicate branches of the tree that were recovered in the maximum-likelihood tree. *Catellatospora citrea* DSM 44097T was used as the outgroup. Bar, 0.02 substitutions per nucleotide position.

Figure

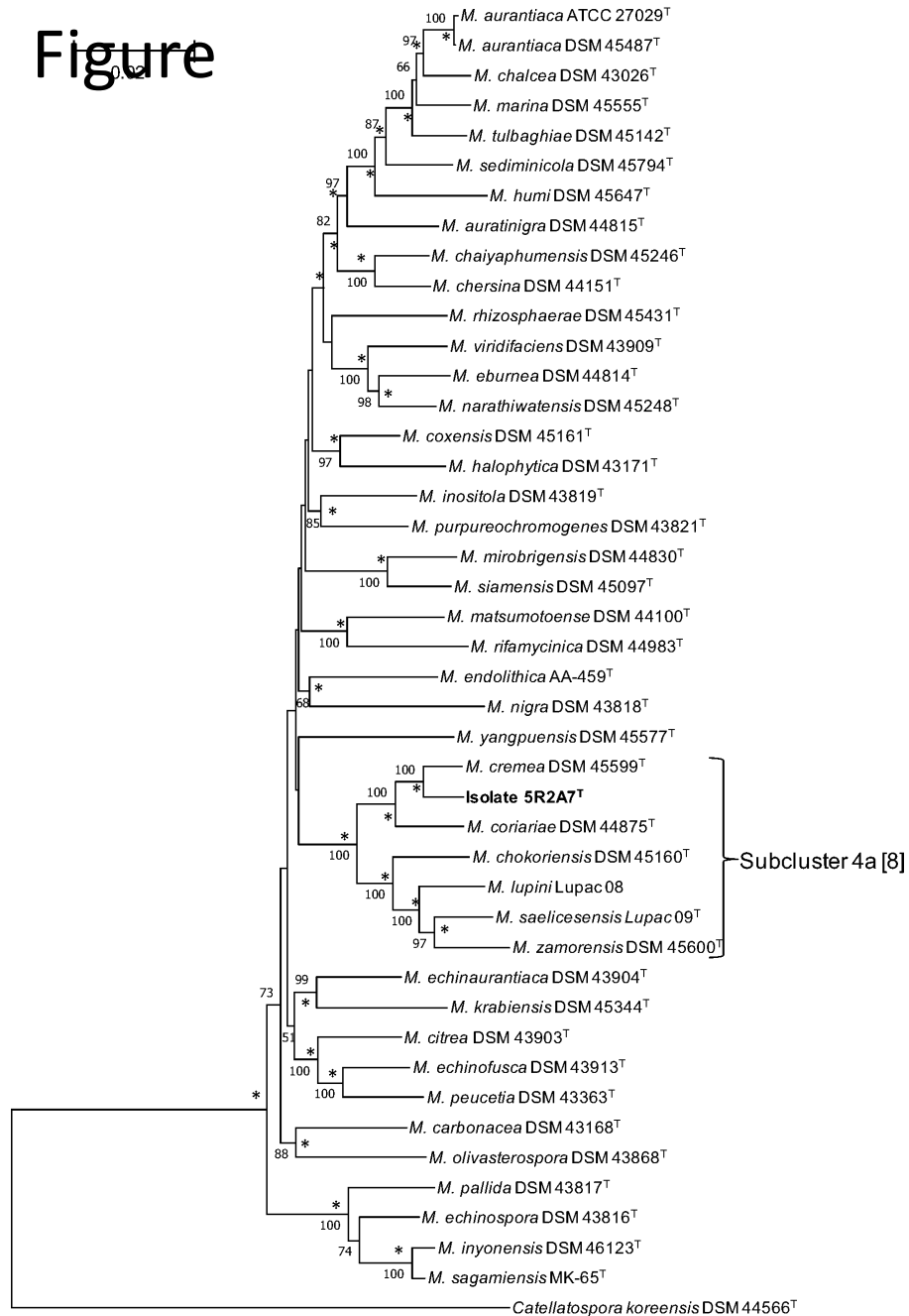


Fig. 3. Neighbour-joining phylogenetic tree based on multilocus sequence alignment of 16rRNA, gyrB, rpoB, atpD, and recA gene sequences showing relationships between strain 5R2A7T and *Micromonospora* type strains. Strain *M. lupini* Lupac 08 is not the type strain but is included in the MLSA tree as a genome sequence in place of that of the type strain (Lupac 14NT), which is not available. The numbers at the nodes are bootstrap support values when >50%. Asterisks indicate branches of the tree that were recovered in the maximum-likelihood tree. *Catellatospora citrea* DSM 44097T was used as the outgroup. Bar, 0.005 substitutions per nucleotide position.