

Figure S1. Phylogenetic relationships among 63 *Pseudomonas* reference strains (in black) and the 10 strains used in this study (in green) and isolated from Andean soils. The Maximum Likelihood tree was inferred from concatenated sequences of two housekeeping genes *rpoD* and *gyrB* (1,285 bp). Only bootstrap values greater than 50 are shown. Scale bar 0.02 substitutions per site.

