

Paenibacillus–Pseudomonas consortium improves barley performance with minimal impact on native rhizobacterial community

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>*gyrB* Z15

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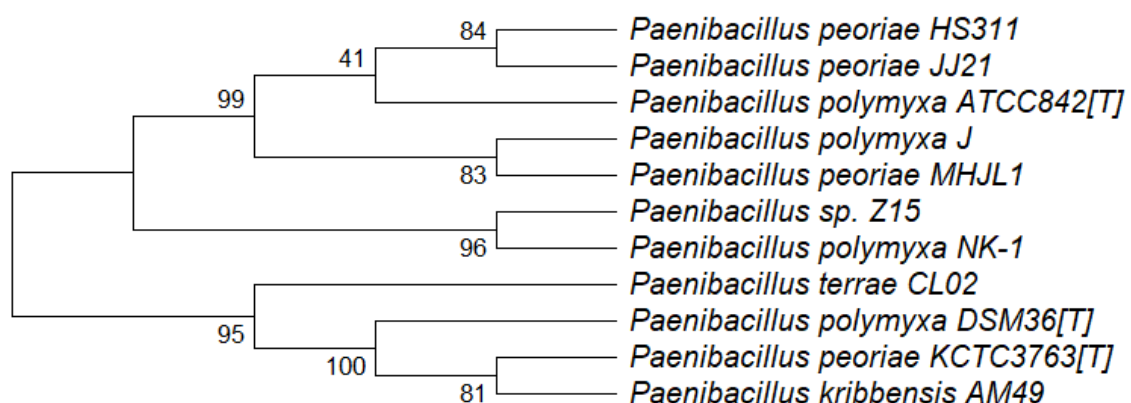
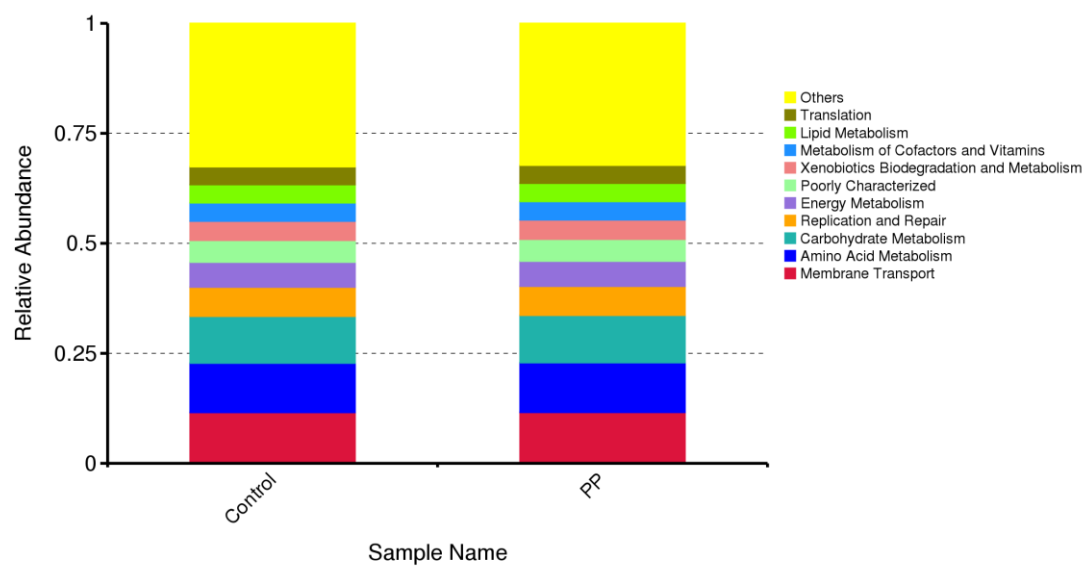


Figure S1. Sequence of *gyrB* and phylogenetic tree based on concatenated 16S rRNA and *gyrB* sequences showing the relationship of strain Z15 to selected *Paenibacillus* strains. The tree was constructed using the Maximum Likelihood method (Tamura–Nei model, 1000 bootstrap replicates) in MEGA 12.

a)



b)

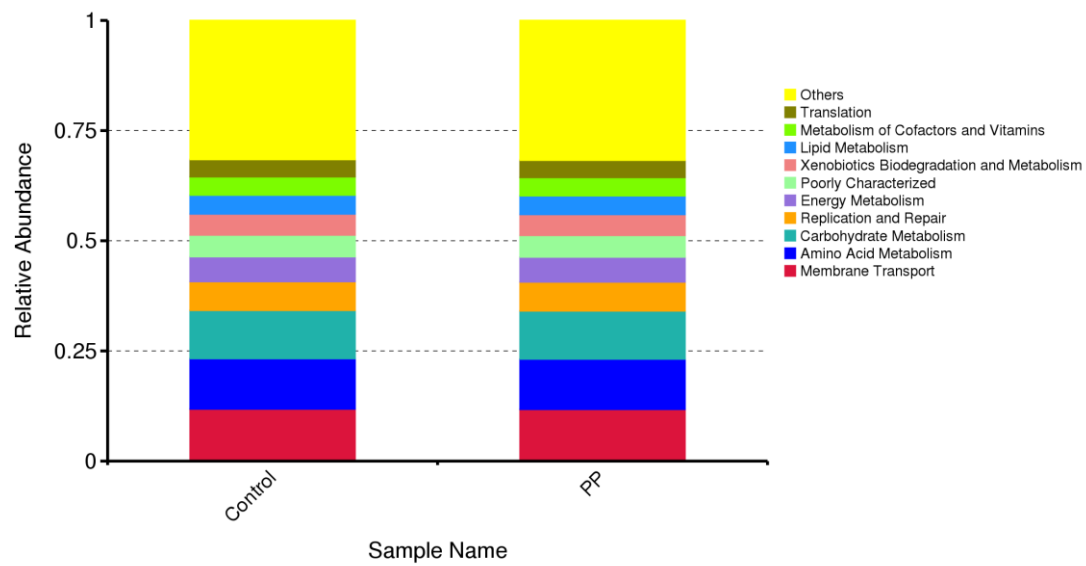


Figure S2. Barplot of PICRUSt function annotation; a – first time point, b – second time point