- OTU definition: 97%
- Co-occurrence corrected p-value cut-off (FDR): 0.001

Note: here, nodes represent 'sampling sites', not OTUs.

- Mendes, R., Pozzani-Kleiner, A.A., Raaijmakers, J.M.: Bacterial community associated with sugarcane in Brazil (sugarcane root)
- Han, J.G., Li, B., Liu, M., Peng, Z.H., Yang, K., Zhu, B.C.: Population diversity of rhizosphere bacteria from Bashania fangiana (rhizosphere soil of Bashania fangiana)
- Chen, Q., Zhang, K.: Phylogenetic study of the bacteria isolated from swamp and sandy soil in Ruoergai (China: Ruoergai)
- Chee-Sanford, J.C., Maxwell, S., Sim, G.K.: Distribution of tetracycline and tylosin resistance genes in bacteria isolated from swine effluent impacted environments (soil)

A

Proteobacteria: 80.3%
Actinobacteria: 8.37%
Firmicutes: 6.61%
Bacteroidetes: 3.91%
Verrucomicrobia: 0.270%
Acidobacteria: 0.270%
Planctomycetes: 0.135%
Demococcus-Thermus: 0.135%

B

Acidobacteria: 35.2%
Proteobacteria: 32.9%
Verrucomicrobia: 15.0%
Actinobacteria: 7.98%
Unclassified: 3.76%
Firmicutes: 2.35%
Gemmatimonadetes: 1.41%
Nitrospira: 0.939%
Planctomycetes: 0.469%

- Fendorf, S., Francis, C.A., Hanse, C.M., Jardine, P.M.: Changes in microbial and metabolic diversity and composition along a hydrogeochemically variable soil profile (unsaturated B horizon soil aggregate)
- Li, D., Yang, T., Zhou, H.: Phylogenetic diversity of unculturable bacteria in forest soil of Gaoligong Mountains, Yunnan (soil)
- Hugenholtz, P., Janssen, P.H., Sait, M., Schoenborn, L.: Major groups of bacteria in a pasture soil (pasture soil)
- Fendorf, S., Francis, C.A., Hanse, C.M., Jardine, P.M.: Changes in microbial and metabolic diversity and composition along a hydrogeochemically variable soil profile (unsaturated B horizon soil aggregate)
- Sacanska, G., Selenska-Pobell, S., Selenska-Pobell, S.L.: Comparative analysis of bacterial diversity in uranium mining wastes and in other heavy metal contaminated environments (soil sample from a uranium mining waste pile near the town of Johanngeorgenstadt)