

The genome of the obligate endobacterium of an AM fungus reveals an interphylum network of nutritional interactions.

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Many AMF host endobacteria in their cytoplasm. To elucidate the role of the Gram negative endobacterium *Candidatus Glomeribacter gigasporarum* (CaGg), we sequenced its genome using a metagenomic approach which combined Sanger sequencing of fosmid clones from a *Gigaspora margarita* (the host) library with a 454 pyrosequencing of an enriched- endobacterial fraction. The final assembly led to 35 contigs, totalling 1.72 Mb, consisting of a chromosome and three plasmids. The genome features of CaCg place it in the Burkolderiaceae group, while metabolic networks analysis clustered CaCg with insect endobacteria, mirroring its obligate intracellular life-style. CaCg resembles an aerobic microbe, with no fermentative and limited energy-production capabilities via glycolysis and phosphate-pentose pathways. It depends upon its fungal host for C, P and N supply; its ability to synthesize amino acids is limited suggesting that most amino acids are imported from its host. In summary, the bacterial genome data of the first endosymbiont's endosymbiont revealed a novel context of intimate symbiosis between bacteria and fungi. Since the CaGg fungal host is itself an obligate biotroph dependent on its photosynthetic host, our work uncovers a network of nutritional/evolutionary interactions between plants, AM fungi and endobacteria.