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Comparative genomics of two betaproteobacterial endohyphal symbionts: *Mycoavidus cysteinexigens* and *Burkholderia rhizoxinica*.

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Several members of the bacterial family, *Burkholderiaceae*, live as an endosymbiont associated with fungi. So far, two endohyphal bacteria belonging to this family had been isolated and characterized as new taxa, *Mycoavidus cysteinexigens*, and *Burkholderia rhizoxinica*. *M. cysteinexigens* B1-EBT is known to harbor a non-pathogenic fungus *Mortierella elongata*, whereas *B. rhizoxinica* HKI 454T is an endosymbiont of a phytopathogenic fungus *Rhizopus microspores*. In this study, we compared the genomes of these two endosymbionts to analyze the potential host-symbiont interactions, host adaptations and diverse host species distributions. The genome of strains B1-EBT and HKI 454T consisted of 2.79-Mbp and 3.75-Mbp nucleotide sequences with 48.9% and 60.7% G+C content and containing 2,317 and 3,870 coding sequences (CDSs), respectively. Despite these two bacteria have different host fungi, the whole alignment of amino acid sequences deduced from the B1-EBT and HKI 454T genome sequences using BLASTP identified 239 CDSs in chromosomal genome and 15 in two plasmids of HKI 454T with over 60% identity and 286 CDSs in chromosome with over 60% similarity. The amino acid sequence assessment analysis revealed that B1-EBT has 13 similar proteins related to DNA replication and repair, 29 ribosomal proteins, 26 proteins related to ATP synthesis, 24 membrane transport proteins and transposase and inactivated derivatives with HKI 454T. However, no common functional gene cluster involved in host-symbiont interactions was found. Our results indicated that the symbiosis between the fungus *M. elongata* and the endohyphal bacterium *M. cysteinexigens* B1-EBT was considerably different from the fungal symbiosis mechanism of *B. rhizoxinica* HKI 454T with the phytopathogenic *R. microspores*.
