

Title: Comparative Genomics of Intracellular Mollicutes-related Bacterial Endosymbionts of Fungi

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Project Goals: The goal of this SFA is to obtain mechanistic insights into Bacterial-Fungal Interactions to inform predictive models of their function in soil and their responses to environmental perturbations, such as changing climate and agricultural practices.

Abstract Text: Diverse members of the early-diverging Mucoromycota including arbuscular mycorrhizal fungi and soil fungi in the Mortierellaceae are capable of harboring both Gram-positive Mollicutes-related endobacteria (MRE) and Gram-negative Burkholderia related endobacteria (BRE). Previous work has shown that MRE are dependent on their fungal host and their genomes are thought to be severely reduced in size. Given this, it has been hypothesized that MRE bacterial endosymbionts were acquired early, prior to the diversification of Mucoromycota. Alternatively, these myco-symbionts could have been acquired after the divergence of these lineages and spread horizontally between lineages. To address these hypotheses, we obtained four complete MRE genomes from two genera in the Mortierellaceae: *Linnemannia* (LMRE) and *Benniella* (BMRE). The size of these genomes ranged from 326 to 615 Kbp and includes the smallest known complete bacterial genomes of myco-symbionts. Comparative analyses of these genomes revealed unique content and organization with respect to each MRE lineage and provides insight as to how bacterial genomes may adapt to a particular fungal host. Homology based comparisons of predicted proteins revealed differences in genome reduction as a result of the endosymbiosis. Additionally, MRE protein lengths were significantly shorter on average compared to closely related *Mycoplasma* and *Spirioplasm* relatives. Multigene phylogenetic analysis also indicated that the MRE genomes within *Benniella* were more closely related to MRE from Glomeromycotina compared to MRE in more closely related *Linnemannia*. These results indicate that *Linnemannia* and *Benniella* isolates may have acquired their MRE after divergence from a common ancestor. The outcomes of this work expand upon foundational knowledge of the evolutionary impacts of bacterial-fungal interactions, towards the goal of continued investigations of evolution and impacts of these interactions on host and endosymbiont.

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