

Domestication-driven Metaorganism Evolution of Wheat

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There is evidence that the composition of microbial communities of the plant phyllosphere is maintained over different host generations. This observation suggests a conserved mechanism to assemble and maintain microbial communities in spite of changing environments. Furthermore, it points to the presence of an internal reservoir of microbes transmitted vertically from generation to generation. Here, we examine the microbial community composition of seeds of different wheat species as a source for early microbial colonization of plant seedlings. We hypothesize that vertically transmitted microbes represent tightly co-evolving endophytes possibly with beneficial effects. Furthermore, we hypothesize that domestication of wheat has impacted the ability to assemble and maintain microbial communities. To address this, we have collected seeds from *Triticum dicoccoides*, *T. boeoticum* and *T. urartu* wild wheat species and from domesticated *T. aestivum* in a region of South Turkey located in the Fertile Crescent. We characterize the microbial species by amplification and sequencing of the bacterial 16S locus and the fungal inter transcribed sequence locus (ITS) from seed derived DNA. Our preliminary data has revealed the occurrence of fungal species including species of the genera *Alternaria* and *Antridium* genus, and bacterial species from the genera *Pseudomonas*, *Luteibacter* and *Halomonas*. Some of these microbes are associated with plant growth promotion in previous studies. To examine the in-planta occurrence and abundance of the seed-borne endophytes, we moreover germinate the wheat seeds under sterile conditions to characterize the microbial species migrating from seeds to leaves and roots. Ultimately, this will allow us to characterize the core endophytic communities of wild and cultivated wheat species from the Fertile Crescent.