Exploring Microbial Interaction for Plant Drought Resilience in Phaseolus vulgaris L.

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Increasing global temperatures and diminishing water resources pose significant threats to food security. Exploring the role of the rhizosphere microbiome in improving plant drought tolerance presents a viable strategy to reduce crop losses and enhance stress resilience. The response of two cultivars of Phaseolus vulgaris L. to drought exposure was investigated, specifically exploring their distinct tolerance to drought. We hypothesize that the drought-tolerant (TL) genotype partially depends on the rhizosphere microbiome to manifest this trait, in contrast to the susceptible (SC) genotype. In a controlled drought stress experiment over 96 h (40% water field capacity), we observed that TL plants decreased their root mass while maintaining shoot mass stability, suggesting strategic resource allocation for drought tolerance. Additionally, prokaryotic community composition differed between TL and SC plants, with higher diversity observed in TL plants. Through network analysis and metabolic modeling, it was found that the TL genotype simplified its microbial networks under drought conditions, contrary to the SC genotype, which became more complex. This adaptation suggests a strategic shift in TL plants to modulate rhizosphere interactions, possibly reducing reliance on microbial cooperation by ensuring a steady supply of carbon through plant exudation. We mapped 17 metagenome-assembled genomes (MAGs) that exhibited differential abundance between TL (6) and SC (11), belonging to Acidimicrobia, Actinomycetia, Alphaproteobacteria, Bacteroidia, and Thermoleophilia classes. MAGs specifically associated with the TL genotype were enriched in genes linked to glycine-betaine production, halotolerance enzymes, sodium transport, and trehalose metabolism, suggesting a potential role in osmoprotection and desiccation relief. This implies that certain plant genotypes might recruit microbial taxa capable of enhancing drought tolerance through specific metabolic pathways. The findings illuminate the intricate rhizosphere microbiome dynamics in fostering plant drought resilience, offering a strategic approach to mitigate the effects of drought stress episodes and strengthen food production under climate change scenarios.

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