"Development of a Bioinformatics Pipeline Utilizing the MEMPIS Tool for Metagenomic Analysis of Soil Microbiomes to Enhance Drought Resilience in Tall Wheat Grass"

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This project focuses on the comparative analysis and modeling of metagenomes and meta transcriptomes from microbiomes associated with tall wheat grass (TWG) to explore the potential for enhancing drought resilience and contributing to sustainable agriculture. TWG, a perennial deep-rooted plant, interacts with soil microbiomes through root exudates, which influence the microbial community and its functions, including carbon cycling. The study aims to investigate how these plant-microbe interactions help TWG respond to environmental changes, such as drought, and how the soil microbiome can impact soil health and plant resilience.

The research utilizes MASH for metagenome comparison and MEMPIS for metabolic modeling, revealing distinct microbial communities between rhizosphere and bare soil samples. MASH analysis showed significant microbial diversity differences, such as between monster soil regions (p=2.27e-06). MEMPIS predicts activation of metabolic pathways by analyzing metagenomic and meta transcriptomic data, allowing mapping of microbial interactions and identifying active biochemical processes across differing environmental conditions. Heatmaps also revealed metabolic shifts in response to plant root exudates. These findings lay the groundwork for microbiome-based strategies to enhance plant growth, drought tolerance, and sustainable agricultural practices.