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RNA-Seq: A tool for investigating the influence of biological seed treatment on crop performance during periods of osmotic stress

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While global usage of BCAs and biostimulants in maize continues to rise, the implications of these varied crop inputs are underappreciated. Among them is the potential for alteration of the maize phytobiome and how significantly that may influence crop performance. We have reported that application of a microbial or metabolite seed treatment correlates with differences in alpha diversity (16S, ITS) in the rhizosphere of *Zea mays*. Here we report on a parallel study from the same replicated trial, where gene expression in leaf tissue was analyzed by RNA-Seq. Following Illumina NGS, AgriGO's SEA tool was used to identify enriched GO terms. Later, we repeated the maize transcriptome study using similar treatments in a setting lacking the native soil microbiome. Instead, seedlings grown in sterile media were harvested within a week, with half exposed to pre-harvest osmotic stress. Analyses from the field trial revealed that genes involved in mitigating abiotic stress are upregulated in plants inoculated with the target biological seed treatments compared to controls. These findings, combined with phenotypic data and rhizosphere metagenomic analyses from the field, point to possible mechanisms for the resulting improved plant performance. The input could (1) directly influence the host transcriptome, or (2) act indirectly by recruiting and/or competing with native inhabitants to alter the phytobiome which subsequently triggers changes in host gene expression. Results highlight a need for further study of the consequences of an altered phytobiome on the maize transcriptome.