Arbuscular mycorrhizal fungal community abundance, functions, and symbiotic interactions revealed by root metatranscriptomes.

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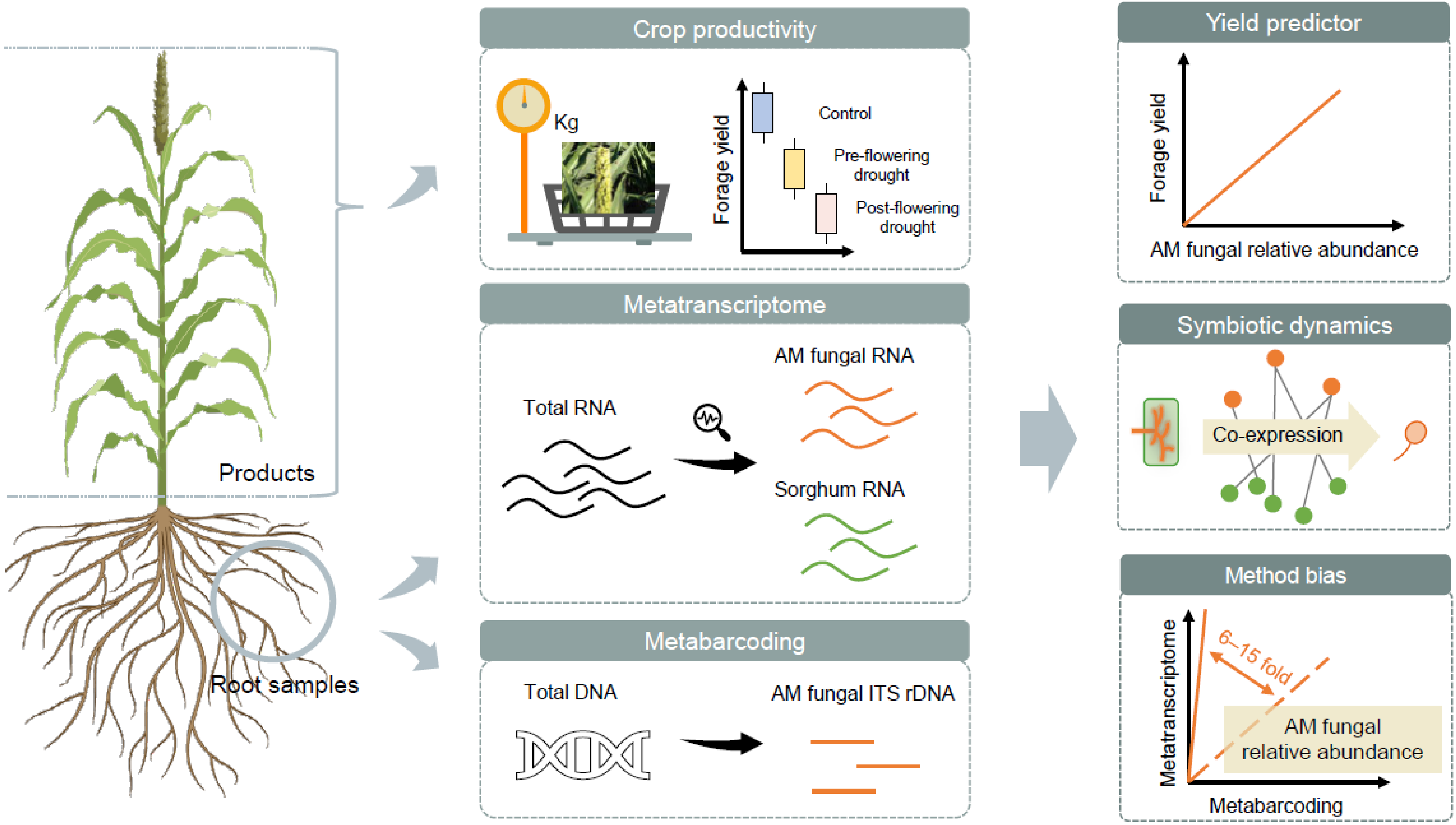
Introduction



Highlights

☐ Paradigm shift: PCR-free methods reveal 6–15-fold higher AM fungal abundance than metabarcoding, exposing systematic underestimation across decades of research.

☐ Predictive power: AM fungal abundance serves as a community-level trait that predicts crop yield under drought conditions.

☐ Symbiotic dynamics: Symbiotic life history from arbuscule formation to sporulation is governed by coupled and decoupled co-expression of plant and AM fungal genes.

Underestimated AM fungal abundance

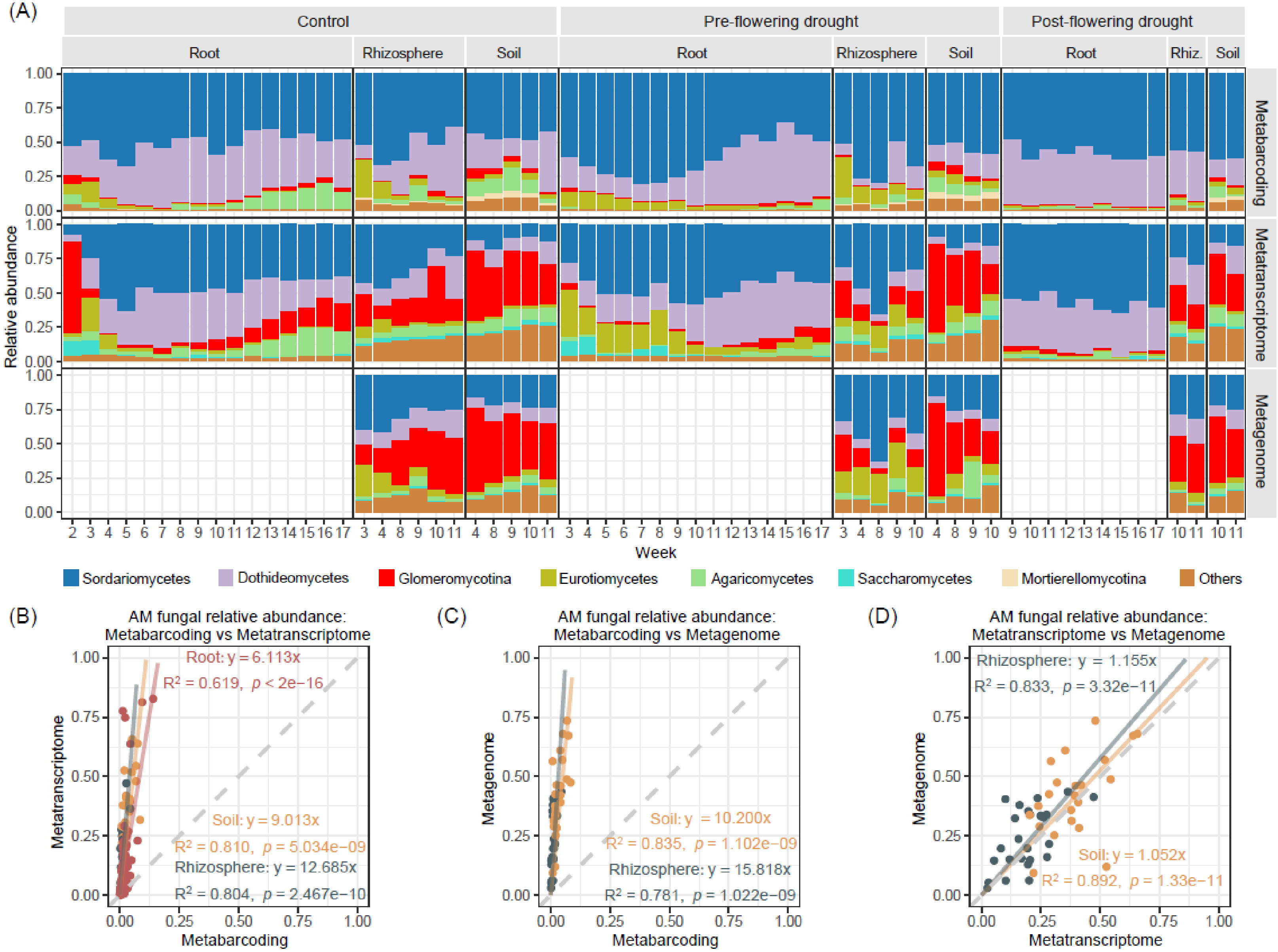
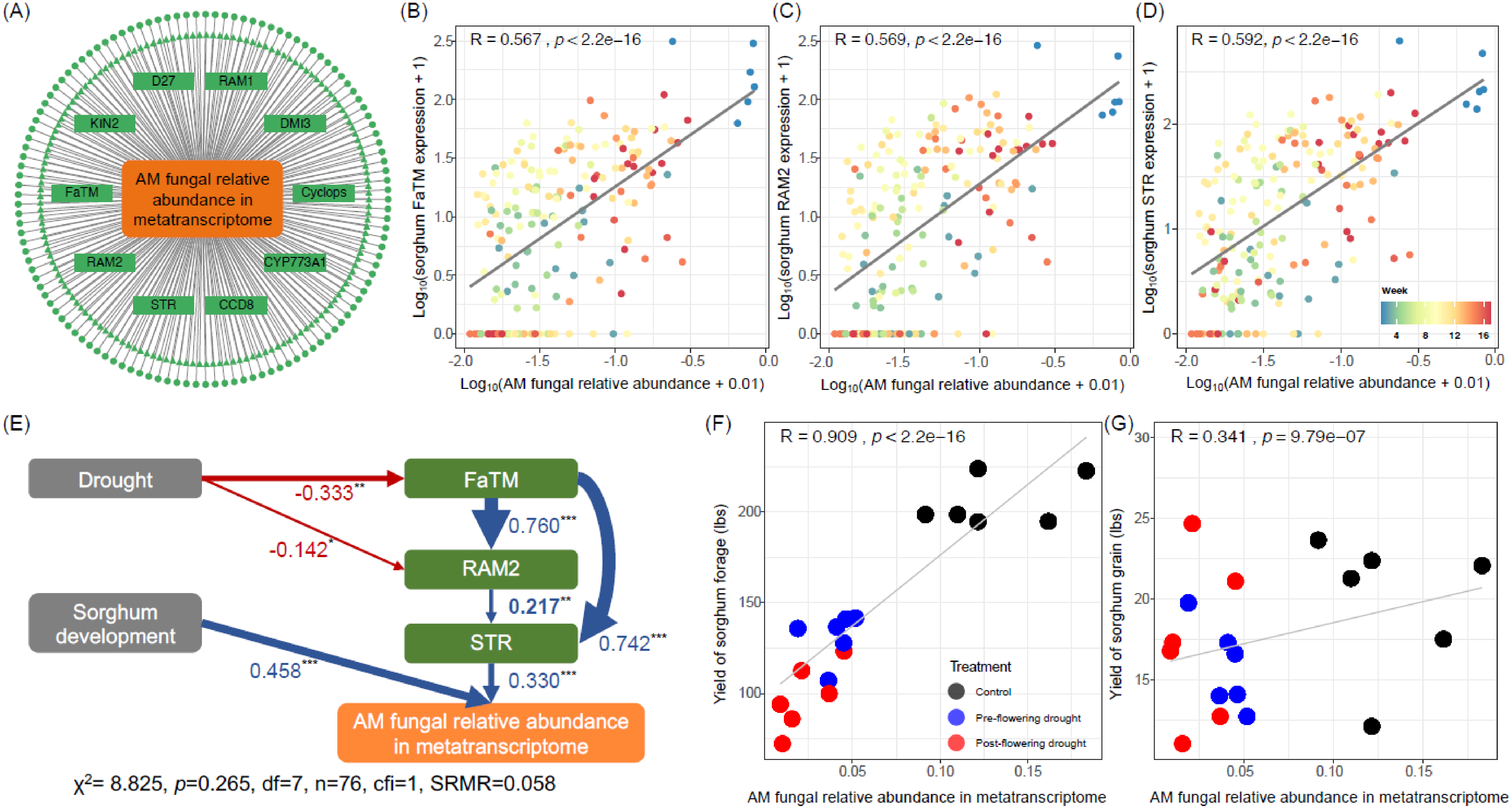


Figure 1. PCR-free methods reveal higher AM fungal relative abundance than metabarcoding.

Good predictor of crop productivity



$\chi^2 = 8.825$, $p=0.265$, df=7, n=76, cfi=1, SRMR=0.058

Figure 2. AM fungal relative abundance in association with sorghum genes and productivity.

AM fungi-sorghum co-expression network

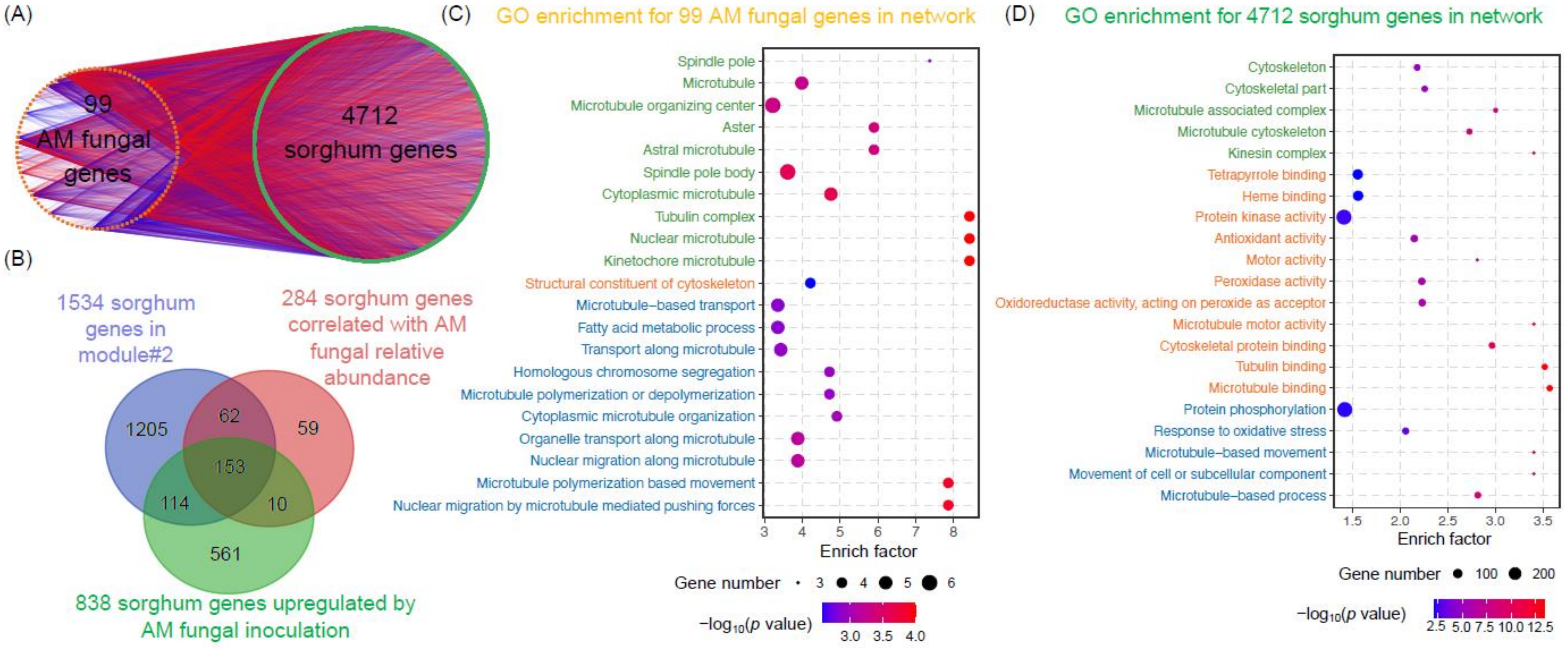


Figure 3. Plant and AM fungal genes responsible for cytoskeleton organization are enriched in the gene co-expression network.

Decoupled co-expression of cytoskeleton genes

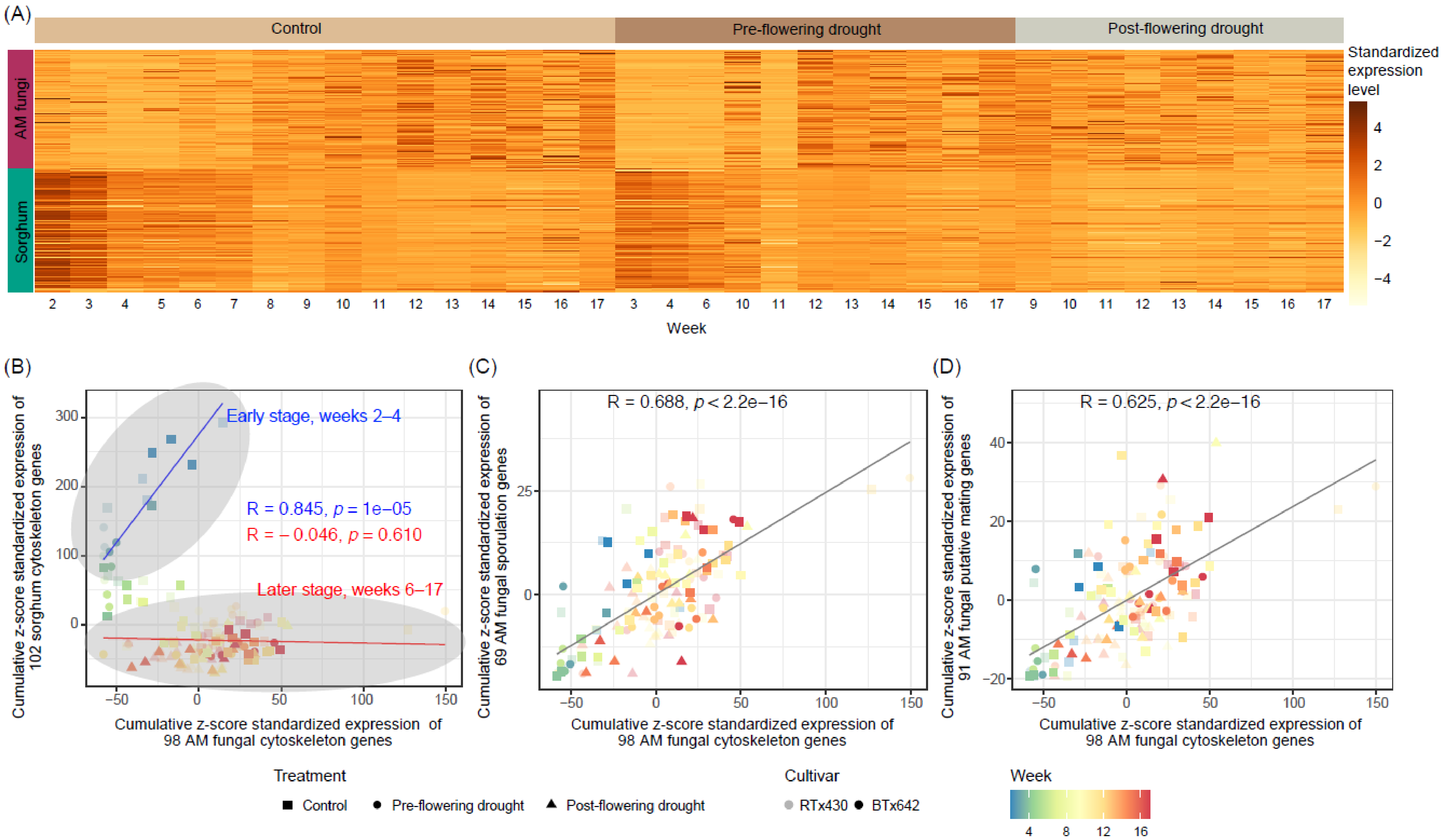


Figure 4. Cytoskeleton gene expression co-occurrence in plant and AM fungal transcriptomes from roots over time.

Summary

- PCR-free metatranscriptomes and metagenomes estimate AM fungal relative abundance 6–15-fold higher than ITS rDNA metabarcoding across compartments, indicating that decades of metabarcoding-based surveys likely undercounted AM fungi in host-associated and soil environments.
- Root AM fungal relative abundance strongly predicts sorghum forage yield and moderately predicts grain yield and quality. These results elevate AM fungal abundance from a descriptive community metric to an integrative indicator of crop productivity under water stress.
- Dual RNA-seq reveals early-season coordination between plant and AM fungal cytoskeleton gene expression consistent with arbuscule biogenesis. In late season, plant cytoskeleton expression declines while AM fungal cytoskeleton genes remain upregulated and align with transcriptional signatures of sporulation and putative sexual processes.

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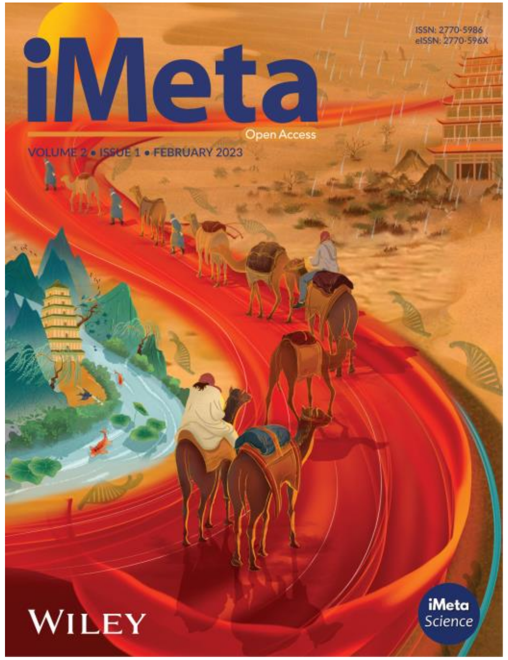

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