Wild progenitor species of maize (teosintes) have greater seedborne microbial diversity than domesticated maize

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Maize (*Zea mays*) is a globally vital cereal crop that sustains billions of people as a food staple while supporting livestock, biofuel, and industrial applications. Maize was domesticated from teosintes, a group of *Zea mays* subspecies that originated in ancient Mesoamerica. Plant domestication and intensive agriculture may have reduced beneficial endophytic diversity in maize, underscoring the need to characterise microbial roles in plant performance. Investigating seed and seedling microbiomes is critical for unravelling how microbial communities influence plant ecology and function. The study tested the hypothesis that the seedborne microbial communities of teosintes were more diverse than those of domesticated maize. Seedborne microbial endophytic communities were surveyed from 85 geographical diverse *Zea* accessions, 65 cultivars and 20 teosintes accessions, originating from 28 countries sourced from international genebanks. The fungal ITS2 region and bacterial 16S rRNA genes were sequenced using the Illumina MiSeq platform to analyse the microbiomes associated with the shoot, root and kernel from five seedlings of each accession. The teosintes accessions, on average, had a significantly higher bacterial and fungal Shannon diversity index and observed taxon indices than the domesticated maize accessions. *Pseudomonadota* and *Actinomycetota* were the most abundant and prevalent bacterial phyla across all accessions of teosintes, comprising an average of 80% and 17% of the total reads, respectively. In contrast, *Pseudomonadota* was extremely abundant in domesticated maize, comprising an average of 98% of the bacterial reads, compared to 71% in teosintes. *Sarocladium* and *Fusarium* were the most abundant fungal genera across the accessions averaging 90% of the total reads. This study revealed significant differences in seed and seedling microbiomes between domesticated maize and teosintes, with accessions of the latter harbouring greater microbial diversity. The dominance of *Pseudomonadota* in domesticated maize and the reduced microbial richness suggest that domestication has resulted in specialised microbial associations, potentially impacting plant resilience. These findings highlight the importance of preserving and restoring microbial diversity in modern crops that have the potential to enhance stress tolerance, nutrient uptake, and disease resistance.

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