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Soil legacy is associated with microbiome assembly and smut disease outcome in sugarcane

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Smut disease, caused by *Sporisorium scitamineum* infection, remains a major constraint to sugarcane production. Although host–pathogen interactions are central to disease development, soil legacy effects and associated microbiomes may also influence disease outcome and host resistance. Here, we investigated whether contrasting soils are associated with differences in microbiome assembly, host transcriptional state, and smut outcome in two sugarcane genotypes. Plants were cultivated for 10 months in sandy loam and clayey soils. Buds were then subjected to controlled inoculation with *Sporisorium scitamineum*, followed by transcriptome analysis at 48 h post-inoculation and disease evaluation under greenhouse conditions. Bacterial communities were characterized by amplicon sequencing. The microbiome structure was strongly shaped by plant compartment, with soil effects more pronounced in rhizosphere+root and a relatively stronger host influence in internal tissues. Communities associated with clayey soil showed greater compositional consistency and were enriched in functions related to nutrient acquisition and microbial interactions, whereas sandy loam-associated communities were more variable and environmentally responsive. These patterns were accompanied by clear differences in host responses and disease outcome under greenhouse conditions. Plants derived from sandy loam soil developed smut symptoms, whereas those from clayey soil remained symptom-free under the conditions tested, regardless of genotype. After inoculation, plants from clayey soil displayed transcriptional profiles consistent with regulated defense responses, including oxidative stress modulation, hormone signaling, and cell wall-related processes. In contrast, plants from sandy loam soil exhibited transcriptional signatures dominated by stress-response pathways, including heat shock-related processes, without evidence of coordinated defense activation. These results indicate that soil of origin is associated with microbiome assembly, host physiological state, and smut disease outcome in sugarcane, and highlight the potential for soil- and microbiome-based management strategies to modulate disease expression.

KEYWORDS: soil legacy, microbiome assembly, plant defense, sugarcane smut.

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