Emerald ash borer induced ash decline and its effects on belowground nutrient and microbial community dynamics

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Considerable efforts have focused on the aboveground implications of ash mortality, yet the implications for belowground microbial associations are understudied, despite the importance of soil microbial communities to soil ecological function and integrity. To characterize associations between ash trees and soil bacterial communities, we sampled soils from ash (n=23) and non-ash (n=9) plots across 7 forests in central Ohio. Concurrently, we censused the tree community and ash tree health. Soil nutrients were analyzed, DNA was extracted from soils, and paired-end sequencing of 16S rRNA amplicons was conducted. Results suggest that ash trees associate with a unique belowground community. Ash and non-ash plots differed in overall bacterial community structure (PERMANOVA; p=0.002). The most abundant bacterial phylum, Acidobacteria, had higher relative abundance in non-ash plots (Welch’s T-test; p<0.001), and of the remaining 6 most abundant phyla, all had lower abundances in non-ash plots (p<0.05). Soil pH, a major driver of bacterial abundance, was lower in non-ash plots (p<0.001), explaining the greater abundance of the acidophilic Acidobacteria. The presence of ash may mediate soil pH through cation accumulation, indirectly influencing bacterial community structure. Functionally, community differences in non-ash plots significantly increased the genetic potential for carbohydrate and nitrogen metabolic pathways. Increases in the relative abundance of these genes could indicate higher rates of decomposition and nitrogen transformations in future non-ash forests. Untangling ash tree associations with soil bacterial communities may help anticipate changes in ecosystem dynamics following the loss of ash.

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