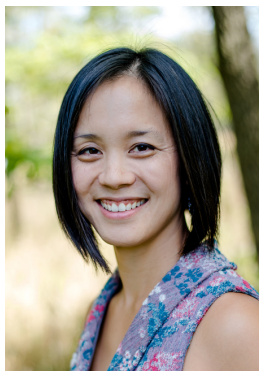


OPENING THE MICROBIAL BLACK BOX TO UNDERSTAND CONTROLS ON SOIL BIOGEOCHEMICAL PROCESSES

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103 Materials Science & Engineering Building



Join us at MSE 103

Microbes mediate biogeochemical cycling of carbon and nutrients that underlie ecosystem function, yet the explicit role of microbes is often not considered in biogeochemical studies. I will present four vignettes that demonstrate how characterizing soil microbial community composition and function can allow us to gain a better understanding of controls on soil biogeochemical processes. First, I will show how microtopographic variation in soil microbial community composition could explain spatial heterogeneity in soil greenhouse gas emissions across seemingly homogenous agricultural fields. Second, I will present how the activity of different microorganisms harboring the *nrfA* functional gene for dissimilatory nitrate reduction to ammonium, an important ecosystem nitrogen retention process traditionally thought to be restricted to anoxic conditions, could contribute to the occurrence of DNRA under oxic conditions. Third, I will explore the ecological implications of hypothesized non-respiratory functions of the nitrous oxide reductase enzyme, which has historically been associated with the anaerobic respiratory process of denitrification. Fourth, I will share evidence of how the mutualistic relationship between ectomycorrhizal fungi and their host trees can vary depending on environmental context, resulting in different drivers of ectomycorrhizal biogeochemical syndromes. Together, these studies make a strong case for opening the microbial black box to elucidate mechanisms leading to variation in soil biogeochemical processes within and across ecosystems.