Improving Soil C Dynamic Models Through the Incorporation of Microbial Processes

Melanie A Mayes[1,2], Chris Schadt[1,3], Gangsheng Wang[1,3], Laurel Kluber[1,3], J Meg Steinweg[4], J Nick Hendershot[2], Sindhu Jagadamma[5], and Colin Averill[6]

[1]Climate Change Science Institute, Oak Ridge National Laboratory, [2]Environmental Sciences Division, Oak Ridge National Laboratory, [3]Biosciences Division, Oak Ridge National Laboratory [4]University of Wisconsin Baraboo/Sauk County, [5]University of Tennessee Knoxville, [6]University of Texas Austin

The focus of our research is to develop robust parameters and an improved conceptual understanding of microbial-facilitated decomposition of organic matter, and apply these to improve model representation of microbial decomposition using the Microbial ENzyme Decomposition (MEND) Model. We used incubation-derived experimental data to calibrate MEND, where calibration targets were CO_2 fluxes from native soil C, $^{14}CO_2$ fluxes from substrate additions, microbial biomass carbon (MBC), and dissolved organic carbon (DOC). We found that predicted MBC values were substantially less than measured at 150 days and longer, which we attributed to unaccounted dormancy in the microbial community. We developed a microbial physiological model to account for both dormant and active fractions, and refined the MEND decomposition model. The new model improved the simulation of MBC values, but further testing of simulated microbial growth and maintenance rates required greater temporal resolution of MBC and CO_2 fluxes. Therefore, we are performing a new set of incubations with a detailed series of short-term measurements (0, 2, 4, 8, 24, 48, 72, 96, 120, 144 h) using ^{13}C glucose addition, and long-term measurements (0, 1, 2, 4, 6, 10, 20, 38, 60, 90….730 d) using ^{13}C cellulose addition. Specifically, the maximum specific growth and maintenance rates, the Michaelis-Menten half-saturation constant, the initial active fraction in microbes, and the growth yield efficiency can be calibrated from short-term data and applied to long-term data. Furthermore, because MEND currently uses only one C pool for microbes (MBC) and does not have the capability to capture microbial community dynamics, we tested alternate measures of MBC, including quantitative PCR (QPCR), phospholipid fatty acid analysis (PLFA), and direct counts, which would facilitate modeling simple forms of community dynamics. We have identified good correlations between MBC, QPCR, and PLFA that are substantially stronger than relationships between MBC and soil physical parameters such as moisture, temperature, or texture. This suggests that QPCR or other data may be substituted for MBC in future model calibration targets, with the added advantage of providing better information on microbial community composition and greater scalability for data generators. Paired forest and grassland soils were collected from four sites including Alfisols in Missouri near MOFLUX and Athens OH, Ultisols from the Freel's Bend site in TN, and Mollisols from the Chichaqua Bottoms Greenbelt site in IA. These incubation experiments will allow us to test and calibrate the MEND model, but also explore how microbial community dynamics can be incorporated into future versions of the MEND model.