

Title: Dataset associated with the manuscript: “Divergent belowground allocation patterns of winter wheat shape rhizosphere microbial communities and nitrogen cycling activities”

Abstract: Plant roots add carbon (C) -rich rhizodeposits to the soil, which can alter microbial activity and nitrogen (N) cycling with implications for N availability and uptake by plants. We evaluated root architecture, rhizodeposit C, and microbial community structure and function across a breeding gradient of twelve winter wheat genotypes and examined how these rhizosphere traits were related to the availability and uptake of N from fresh cover crop residues in the soil. We traced wheat-derived C into soil and microbial pools using continuous isotopic labelling (^{13}C -CO $_2$) and applied ^{15}N labelled plant residues to quantify plant and microbial uptake of residue-derived N. Wheat genotypes differed in root C allocation patterns, influencing N cycling. Thicker roots released more C into soil, which enhanced N mineralization through stimulation of the microbial biomass. Microbial biomass increased N-cycling enzyme activity and residue N-uptake by wheat. Microbial communities did not differ between wheat genotypes but were strongly related to patterns in root C allocation, and several genera showed strong relationships with root C deposition and N uptake. The microbial community associated with extractable root-derived C was structurally different from the community associated with residue N uptake, indicating the N-cycling response to exudation was not necessarily carried out by the same microbial community members as those stimulated by rhizosphere C inputs. Our results indicate that differential patterns of rhizodeposition and associated belowground C allocation strategies in winter wheat can alter microbial communities and influence cycling and plant availability of residue N. Ecologically-based nutrient management in agricultural systems should consider the role of crop root traits and associated microbiomes to optimize soil nutrient dynamics.

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Format of data files – .csv

Location where data were collected – Fort Collins, CO

Time period during which data were collected - 2018

File Information –

Total number of files: 3

Kelly_Wheat_Genotype_Datafile.csv – processed primary data numbers used for data analysis in publication

README_Kelly_Wheat_Genotype.pdf – Description of data

Codebook_Kelly_Wheat_Genotype.csv – description of variable names in Datafile

Variable information – See Codebook

Method(s) – Data was collected using various biogeochemical methods, including isotope ratio mass spectrometer, amplicon sequencing, and quantitative PCR. Please see associated publication for a full description of the collection methods.

Quality assurance and quality control that have been applied – Data has been thoroughly looked-through and analyzed separately.

Limitations to reuse – Some missing values

Date dataset was last modified: October 29, 2021