Title: Dataset associated with the manuscript: "Long-term compost amendment modulates wheat genotype differences in belowground carbon allocation, rhizosphere recruitment and N acquisition"

Abstract: The implementation of soil health-promoting practices, such as cover crops and compost additions, has important implications for nutrient cycling regimes in agroecosystems. At the same time, plant belowground carbon (C) allocation patterns can influence nutrient cycling and availability in soil, but the effects may depend on the crop genotype and management practices in place. The relationship between root exudation, rhizosphere communities and the processes they regulate is likely influenced by a range of soil conditions, including soil organic matter (SOM) content, nutrient status, and overall soil biological activity, but such interactions remain poorly understood. To better understand the potential role of long-term soil management (that alters of SOM) and crop genotype in regulating rhizosphere microbial communities and associated nitrogen (N) cycling processes, we collected soils from two treatments in a 10-year field trial, one with high compost inputs (108.7 Mg ha-1 every 2 years) and a control (no nutrient inputs). We then used stable isotopes to measure belowground C allocation patterns in two genotypes of winter wheat (Triticum aestivum) with distinct rooting and exudation strategies. We also measured microbial community structure and function in the rhizosphere and quantified uptake of residue-derived N from 15N-labeled residues. We found an interactive effect between soil management and genotype, where the high-exudation genotype modified its exudation more in response to soil management and was relatively better at accessing residue N in the compost-amended soils than the low-exudation genotype. The high-exudation genotype also demonstrated selection of specific rhizosphere microbial taxa, with several taxa conserved across soil treatments. Our results suggest that the high-exudation strategy influences the microbial community, and this strategy is more successful in soils with higher SOM. Understanding the relationship between crop genotype, soil management, and microbial function can help inform crop production and breeding strategies in systems seeking to leverage improved soil health and biological nutrient cycling.

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Format of data files – .csv

Location where data were collected – Fort Collins, CO

Time period during which data were collected - 2021

File Information –

Total number of files: 3

Kelly_2021_Wheat_Genotype_Wheat.Genotype.Soil.Treatment _Datafile.csv – processed primary biogeochemical and plant data used for data analysis of referenced manuscript.

README_Kelly_2021_Wheat.Genotype.Soil.Treatment.pdf – Description of data and associated publication

Codebook.csv – description of variable names in Datafile

Variable information – See Codebook

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

Software – Root data was generated using WinRhizo version 2009.

Quality assurance and quality control that have been applied

Data has been cleaned and used for analyses

Limitations to reuse – Some missing values