EGU25-3250, updated on 07 May 2025
https://doi.org/10.5194/egusphere-egu25-3250
EGU General Assembly 2025

Soil microbial community response to glacial rock flour amendment: insights from a microcosm experiment

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The use of glacial rock flour as an agricultural soil amendment gained increasing interest due to its fine particle size, potential to deliver crop-essential nutrients, and capacity for Mg or Ca-rich silicates to enhance rock weathering to capture atmospheric CO_2 in carbonate form. Additionally, some studies have observed that rock flour amendments can reduce N_2O flux. Plant growth, carbon storage, and soil emissions are all influenced by microorganisms in soil, which actively participate in biotic weathering processes that release plant-essential nutrients like phosphate, potassium, and sulfur from minerals. Furthermore, microorganisms drive nitrogen and carbon cycling, which influences soil fertility and greenhouse gas emissions. Thus, the unknown impact of glacial flour application to soil microbial communities must be investigated. Our study aimed to assess a French agricultural soil microbial community responds to varying glacial rock flour application rates during a 12-week microcosm experiment. The granitic glacial flour selected for study originated from Mer de Glace (French Alps). To understand the microbial community's response, we focused on taxonomic shifts, relative abundance of genes related to nitrogen cycling and nutrient access, and geochemical shifts between baseline and 12-week samples. We hypothesized that glacial flour amendment would select for a community that would reduce nitrogen losses through N_2O and demonstrate improved ability to access flour-bound nutrients particularly at higher application rates compared to the control soil. To test this hypothesis, we conducted a 12-week microcosm study where glacial rock flour was added to 50 g of agricultural soil at rates of 0, 0.5, 2, 5, 10, 20, 30, 50, 80, 115, and 157 t ha^{-1}. Each treatment had 12 replicates and one replicate per treatment was destructively sampled each week for analysis. For the higher application rates (30-157 t ha^{-1}), a quartz powder control was included to account for potential changes in soil structure. Replicates remaining in the experiment were watered once per week up to 80% of water holding capacity to simulate agricultural irrigation or rainfall events. DNA was extracted from all samples for downstream analyses and subsamples from baseline and endpoint were retained for geochemical analyses. Quantitative polymerase chain reaction (qPCR) was performed on the 16S and 18S genes to quantify bacterial and fungal abundance, respectively. Metabarcoding of the v3-v4 region of the 16S rRNA gene (*rrs*) was done to track taxonomic changes in the bacterial population over the course of the experiment. Inorganic nitrogen species were quantified in the baseline and 12-week samples. Preliminary results showed that bacterial communities exhibited differential growth in response to amendments above 5-10 t ha^{-1} compared to those below, with shifts occurring at week 4 and week 10 of the experiment. Glacial flour application of 30 and 50 t ha^{-1} resulted in the lowest percent loss of inorganic nitrogen from baseline to week 12 compared to other application rates. These initial findings indicate that glacial rock flour application rates may significantly influence the soil microbial community, with important implications for nitrogen cycling and nutrient accessibility.