

Evaluating Genotype-Dependent Variation in Yield & Soil Microbial Dynamics Under Continuous Alfalfa Cultivation

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Alfalfa (*Medicago sativa* L.) is a widely cultivated perennial forage crop; however, long-term monoculture has been shown to reduce productivity. The causes of this decline are multifactorial, with a recent study suggesting that shifts in soil microbial communities—particularly decreased microbial diversity and increased pathogenic populations—may play a key role. However, the investigation has focused on a single genotype, limiting our understanding of how genetic variation of alfalfa may influence these processes. We hypothesize that different alfalfa genotypes, through variation in root traits and exudates, can differentially shape soil microbial communities and thereby influence long-term plant health and productivity. To test this hypothesis, we leveraged a multi-state alfalfa variety trial established in spring 2022 at South Dakota State University. From a total of 28 genotypes representing seven U.S. states, four genotypes from Wisconsin were selected to evaluate genotype-dependent effects on biomass production and soil microbial dynamics. Plants were initially established through greenhouse propagation and transplanted to the field in a randomized design with three biological replicates. Results from 2023 to 2025 showed a steady increase in yield, reflecting the transition from establishment to peak production. Among the genotypes, Euro WI consistently exhibited the highest yield, followed by Sibir WI, while Casia WI showed comparatively lower productivity, indicating significant genotype-dependent variation. Soil samples were collected annually, and microbial DNA extraction and full-length 16S rRNA and ITS sequencing have been completed. Data are currently under analysis and will be presented at the upcoming conference.

Keywords: Alfalfa; genotype variation; soil microbial communities; continuous cultivation; biomass yield; plant–microbe interactions