The soybean rhizosphere microbiome: who is a key player and what factor drives differences in soybean productivity?

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Crop productivity largely depends on not only the structural and nutritional status of soils, but also the microbial composition and activities in soils, specifically rhizosphere soils. The objectives of this research are to correlate the soybean productivity in Nebraska (NE) and Oklahoma (OK) in the U.S. with the physicochemical properties and the distribution of microbiome in the rhizosphere. NE and OK were chosen among 9 states because of a significant difference in soybean yields: the former was the highest soybean yield state while the latter was the lowest in soybean production. Fourteen rhizosphere samples from NE and OK were measured for organic carbon, nitrogen, phosphorus, potassium, calcium, magnesium, sulfur, sodium, iron, zinc, manganese, copper, and pH along with precipitation and average temperature during soybean cultivation. Principal component analysis (PCA) based on variance-covariance matrix was conducted to examine correlations among variables in NE and OK. Two marker genes, *nifH* and 16S rDNA, were PCR amplified and sequenced in Illumina MiSeq. Taxonomic analysis showed relatively higher abundance of Firmicutes and Acidobacteria in OK where as Actinobacteria was more abundant is NE. A clear pattern of distribution and evenness of microbiota was observed based on pH range, irrespective of the state. Among predicted functions, TCA cycle and pentose phosphate pathway were more abundant in NE than OK rhizosphere. Overall, TM7 bacteria at the phylum level are closely related with NE soils, whereas they are not with OK samples. In addition, organic matter, potassium, and pH are major factors that could derive soybean yield difference. This research has given insight into the microbial community in the rhizosphere between the high-yield state (NE) vs. the low-yield state (OK) for soybean production in accordance with correlated environmental factors.