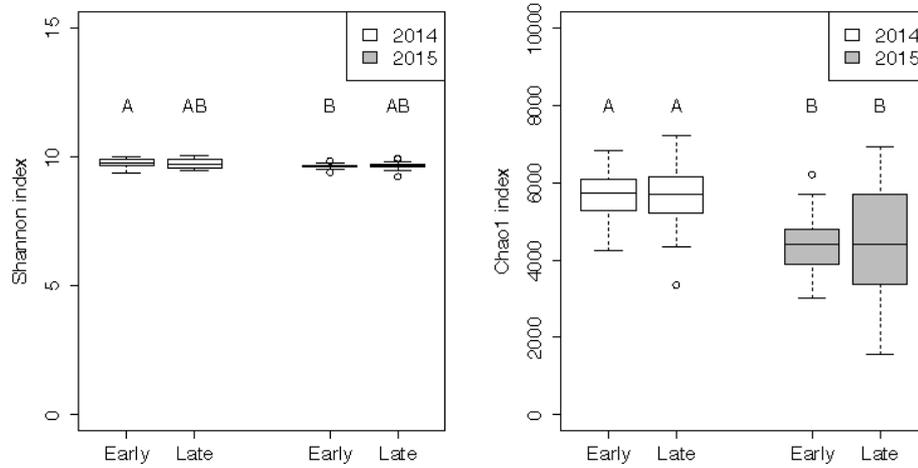
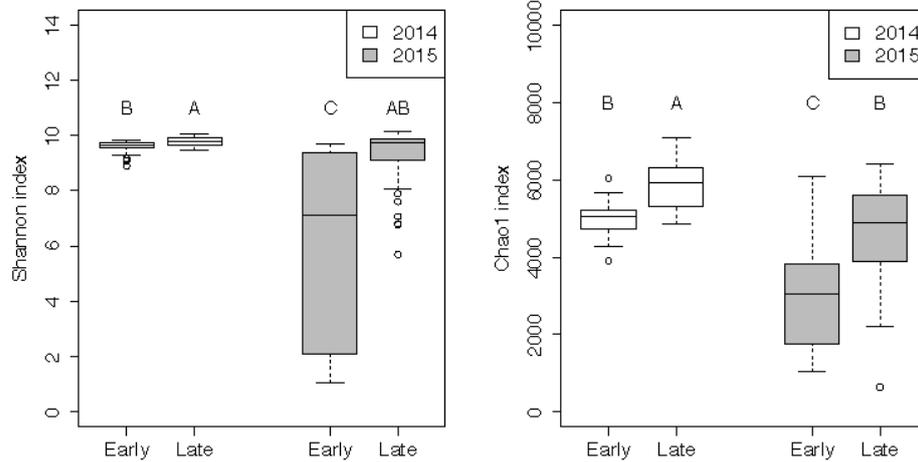


Supplementary Materials

A



B



C

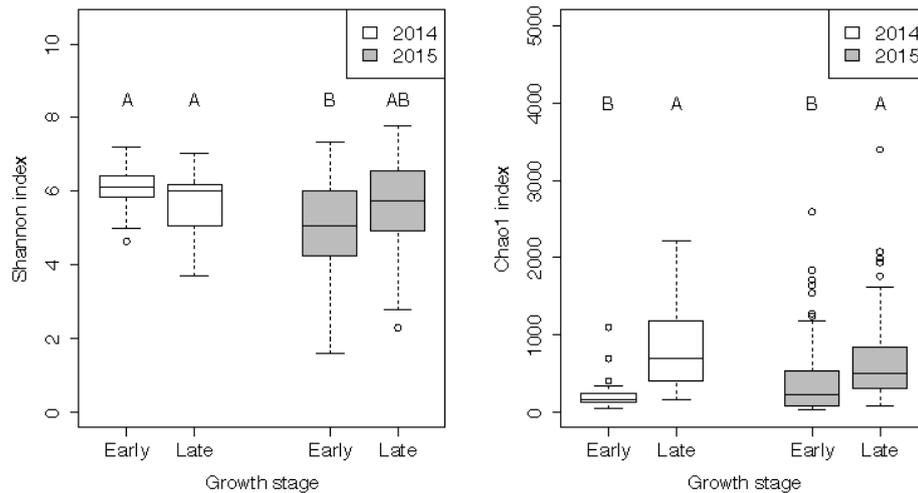


Figure S1. α -diversity differences between years and plant growth stages. Box plots of the species diversity calculated with Shannon index on left and species richness calculated by Chao 1 index on right between the two growth stages and years for the (A) soil, (B) rhizosphere and (C) root endosphere compartments. Distinct letters indicate significant differences according to Wilcoxon's pairwise test.

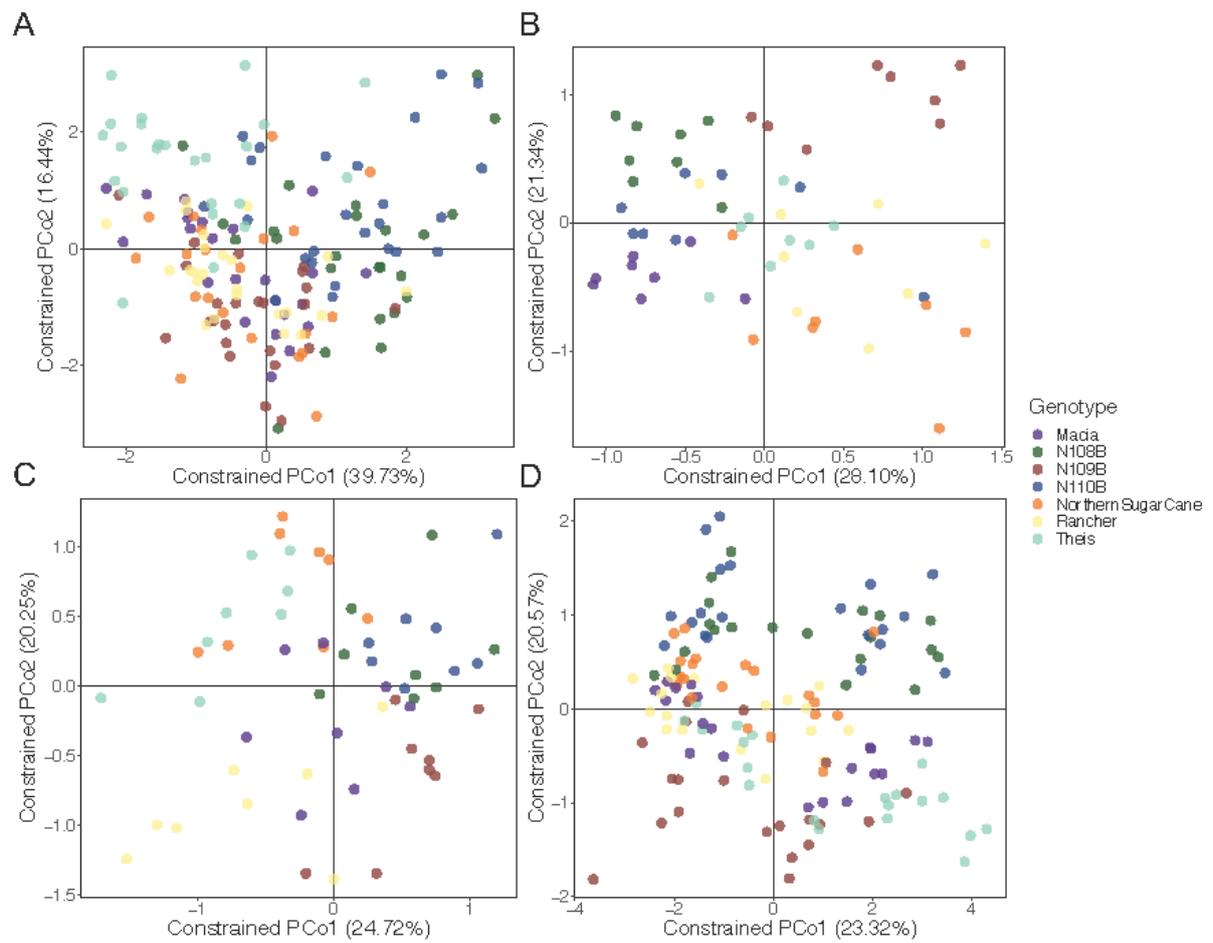


Figure S2. β -diversity differences between sweet sorghum genotypes. Canonical analysis of principal coordinates (CAP) based on the Bray-Curtis distance matrices showing samples of the different sorghum genotypes from (A) root endosphere 2014 and 2015, (B) soil 2014, (C) rhizosphere 2014, and D) rhizosphere 2015. All other factors except genotypes were conditioned in the model.

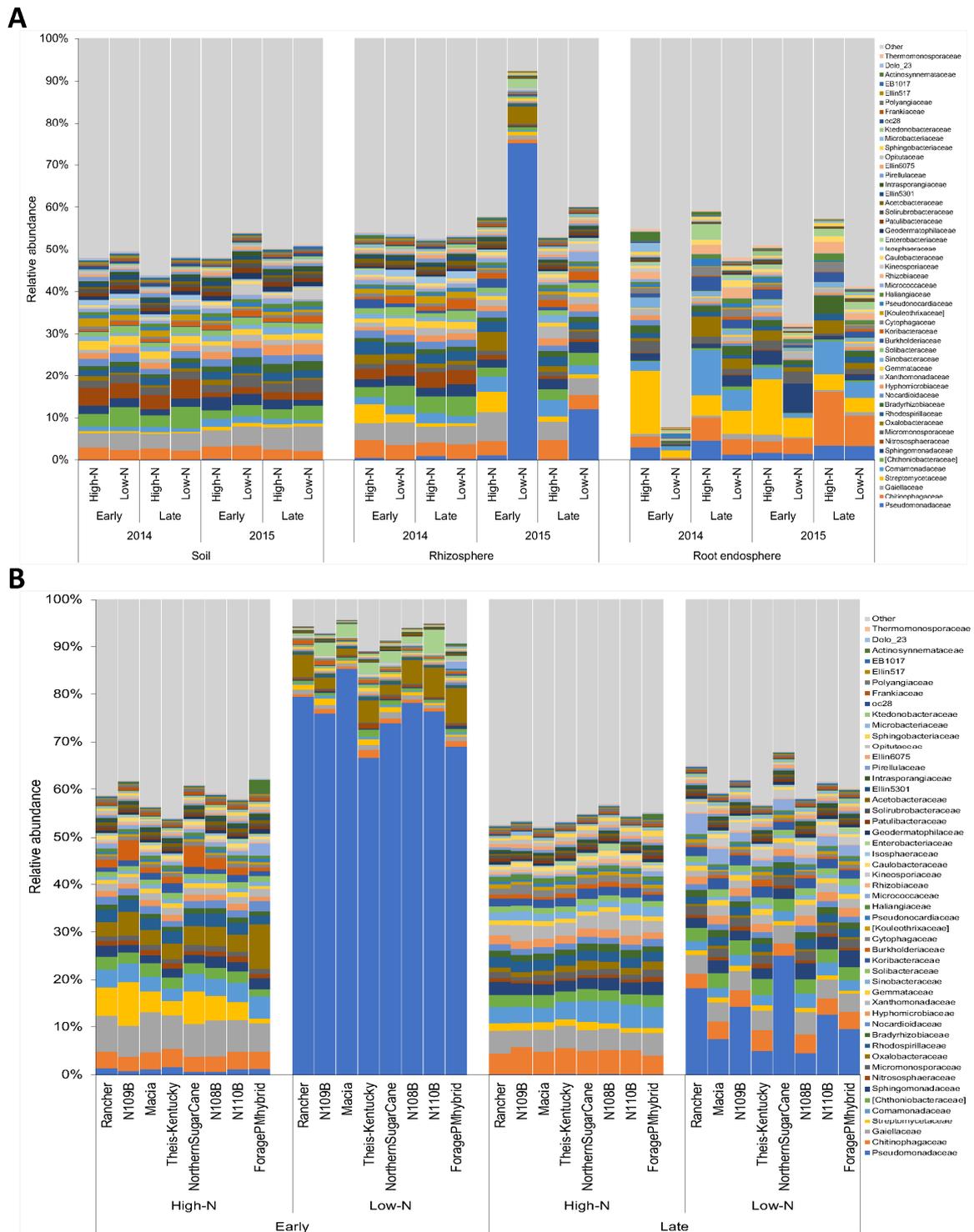


Figure S3. Bar chart showing the relative abundance of bacterial families. (A) Relative abundance of the top 50 most abundant bacterial families in the root endosphere, rhizosphere and soil compartments in 2014 and 2015 separated by growth stage and N-level. (B) Rhizosphere samples from 2015 highlighting the very high abundance of *Pseudomonas* spp. in all genotypes at the early plant growth stage under low-N. Pseudomonadaceae family is shown in blue bar. The families found in the lowest abundance were combined into “other”.

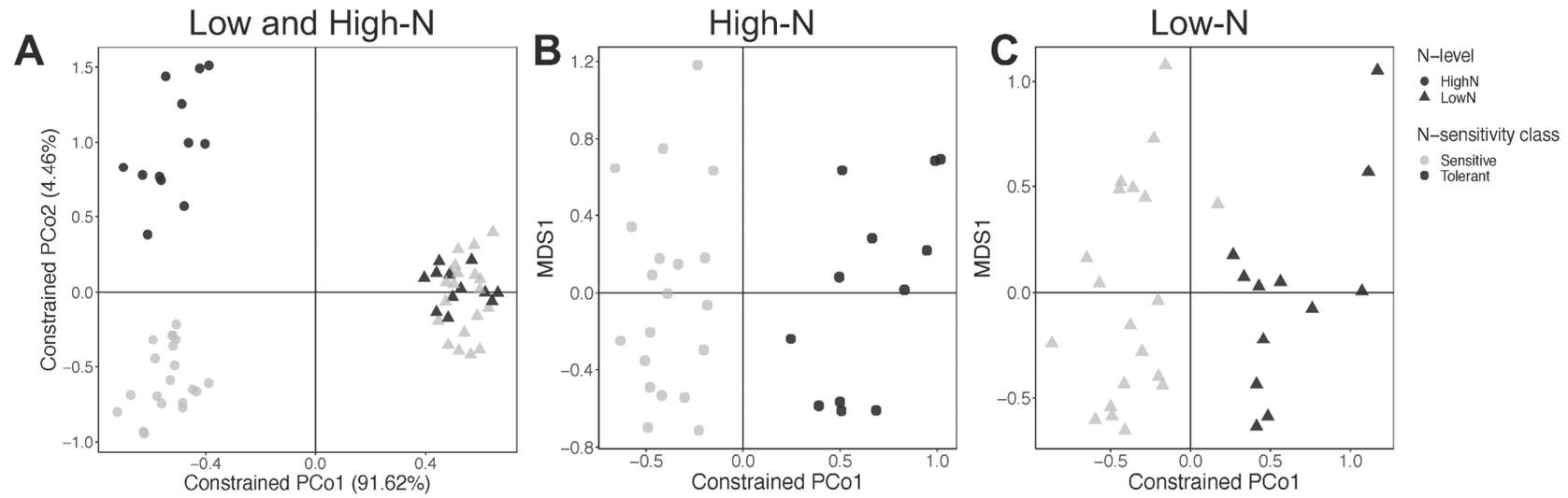


Figure S4. Bacterial community structure of soil samples from N-stress tolerant and sensitive genotypes. Canonical analysis of principal coordinates (CAP) based on the Bray-Curtis distance matrices considering soil samples from (A) both N-levels, (B) only the high-N field, and (C) only the low-N field. Soil N-levels are represented with different symbols, while sorghum genotype N-stress sensitivity classes are represented with different colors. Only samples from 2014 were used in the analysis, since samples from different genotypes were bulked in 2015.