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Rhizosphere microbiome of field-grown maize as influenced by root cortical aerenchyma

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Root cortical aerenchyma (RCA) is a selection target for maize breeding programs because it decreases the cost of soil exploration of roots and improves plant growth under drought and low-nutrient stress. RCA may modify the microenvironment of rhizosphere microorganisms by transporting oxygen to the soil or changing carbon rhizodeposition around the root. We tested the hypothesis that plants with contrasting levels of RCA will have different rhizosphere bacterial communities. The rhizospheres of maize inbreds with contrasting RCA levels and growing under low and high nitrogen conditions in Limpopo Province, South Africa and Pennsylvania, USA were studied for bacterial composition using metabarcoding of the 16s rRNA genes. Other anatomical and architectural root traits were studied as covariables in addition to RCA. The most important factor driving the rhizosphere bacterial composition was geographic location. In both sites, root phenotype, RCA included, grouped the diversity of bacterial communities better than genotype. RCA was among the significantly explanatory variables for the composition of the bacterial communities at the South African site and was neutral at the site in Pennsylvania. High-RCA rhizospheres harboured significantly enriched and depleted bacterial species compared to low-RCA plants at the two sites. Potential metabolisms related to N-cycling in soils were related to a positive effect of RCA on oxygen and a negative effect of RCA on carbon rhizodeposition in the rhizosphere. These results pave the way to further study the root phenotypes as drivers of rhizosphere microbial communities.