Assessing the relationship between biological nitrification inhibition of field-grown sorghum and rhizosphere microbial communities Sandra J. Simon¹, Rachel Waltermire¹, Mark B. Burnham¹, DK Lee^{1,2}, Evan H. DeLucia^{1,4}, Wendy H. Yang^{1,4,5}, Angela D. Kent^{1,3}

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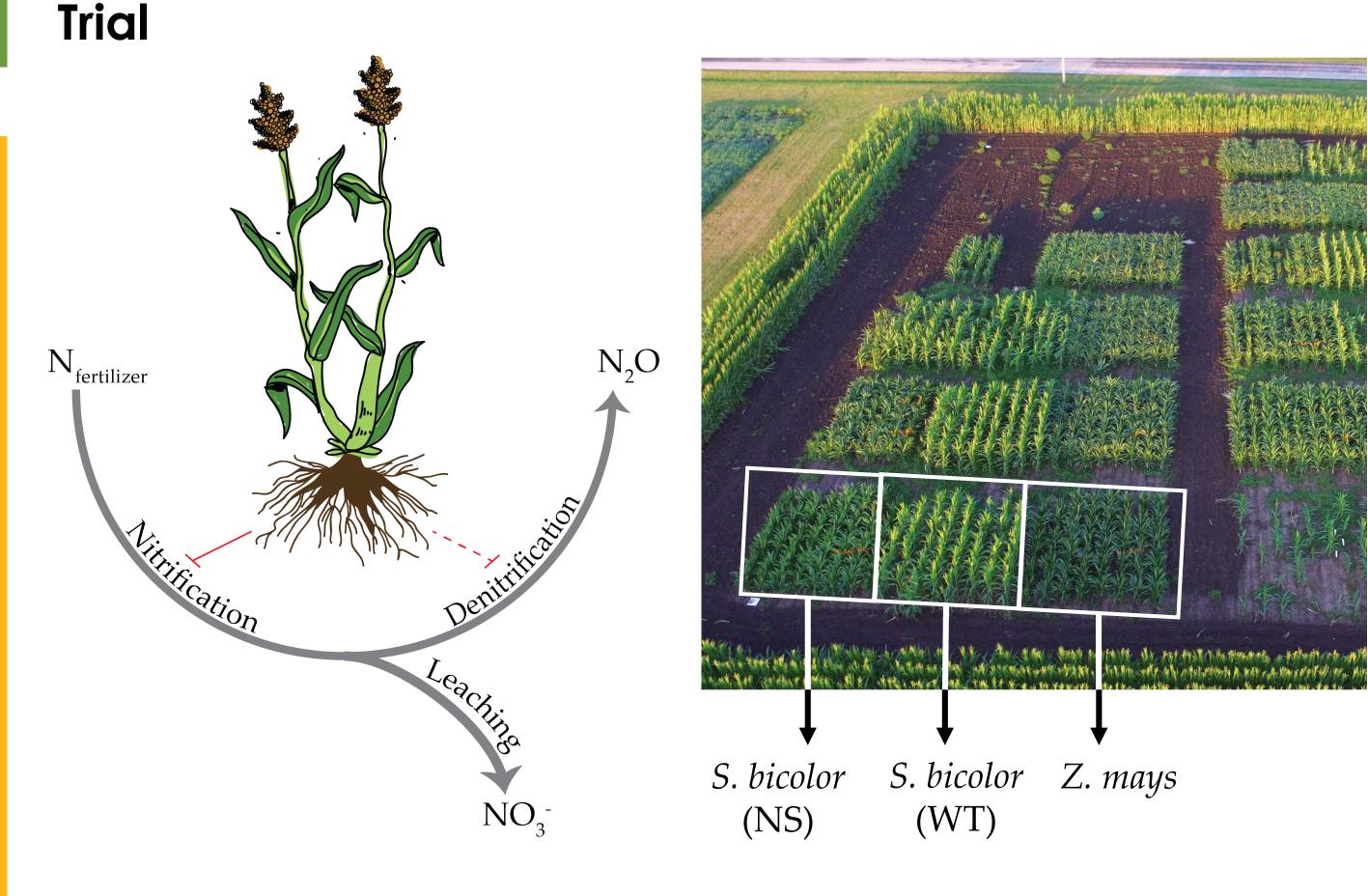
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Background

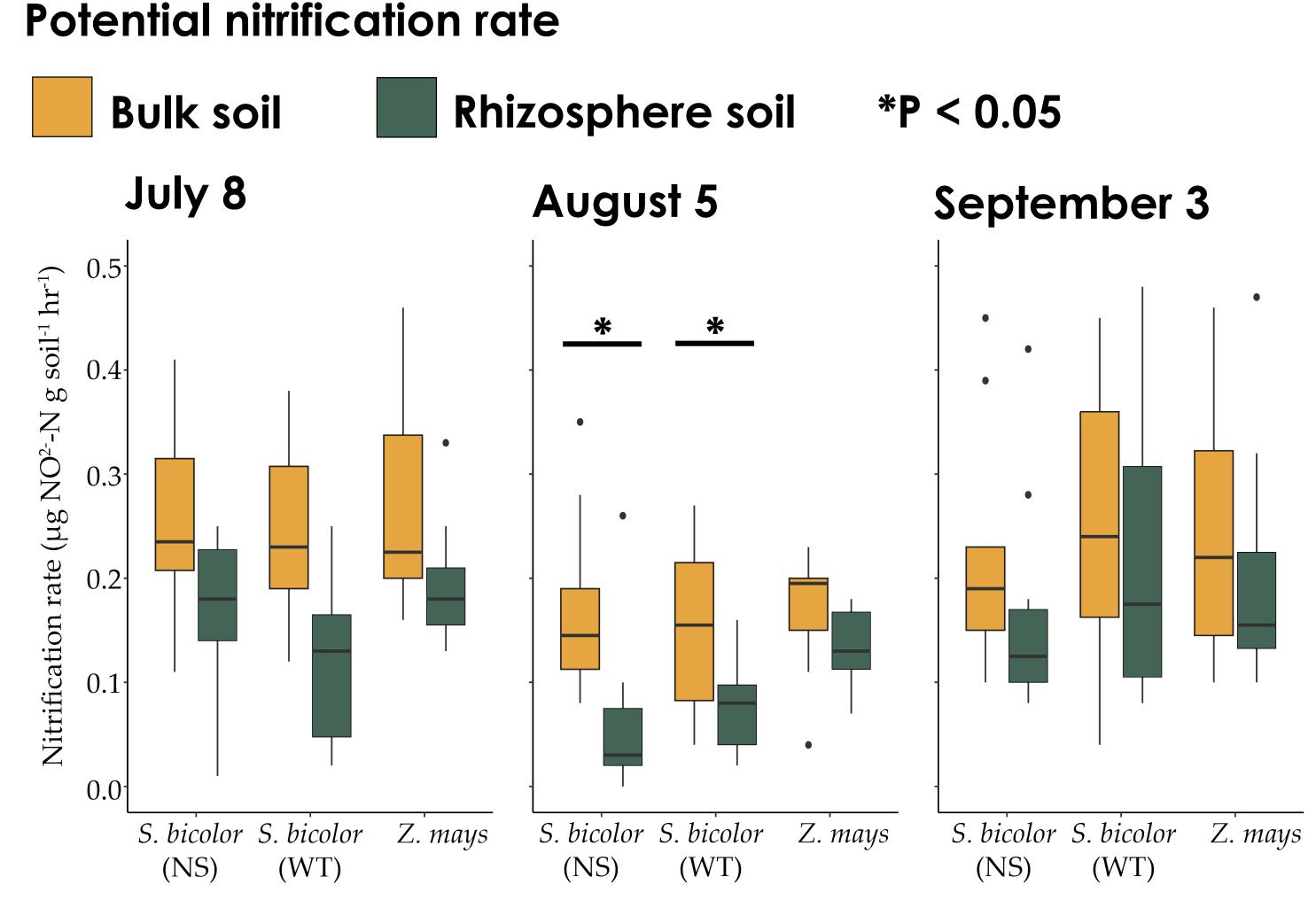
Given the large contribution of fossil fuel burning to greenhouse gas emission, there is high demand to implement renewable cropping systems for biofuel production. However, the heavy use of nitrogen (N) fertilizers to maximize crop yield leads to additional forms of pollution, such as high levels of nitrate (NO_3^-) leaching into groundwater. Determining ways to reduce NO_3^- production and leaching will thus increase the environmental benefit of bioenergy cropping systems. The nitrification of ammonium (NH_4^+) by bacteria and archaea in the soil is a key step leading to NO_3^- production. Studies have shown that the candidate bioenergy crop sorghum is capable of exuding secondary metabolites in its rhizosphere that inhibit nitrification. Nevertheless, the relationship between sorghum's biological nitrification inhibition (BNI) ability and its rhizosphere microbial community has yet to be explored in field conditions.

We implemented a field experiment and sampled bulk and rhizosphere soils from *Zea mays*, wild type *Sorghum bicolor* (WT), and a *Sorghum bicolor* (NS) transgenic line, developed to reduce production of rhizosphere nitrification-inhibiting sorgoleone, to better understand the mechanisms of BNI in sorghum through plant development to answer the following questions:

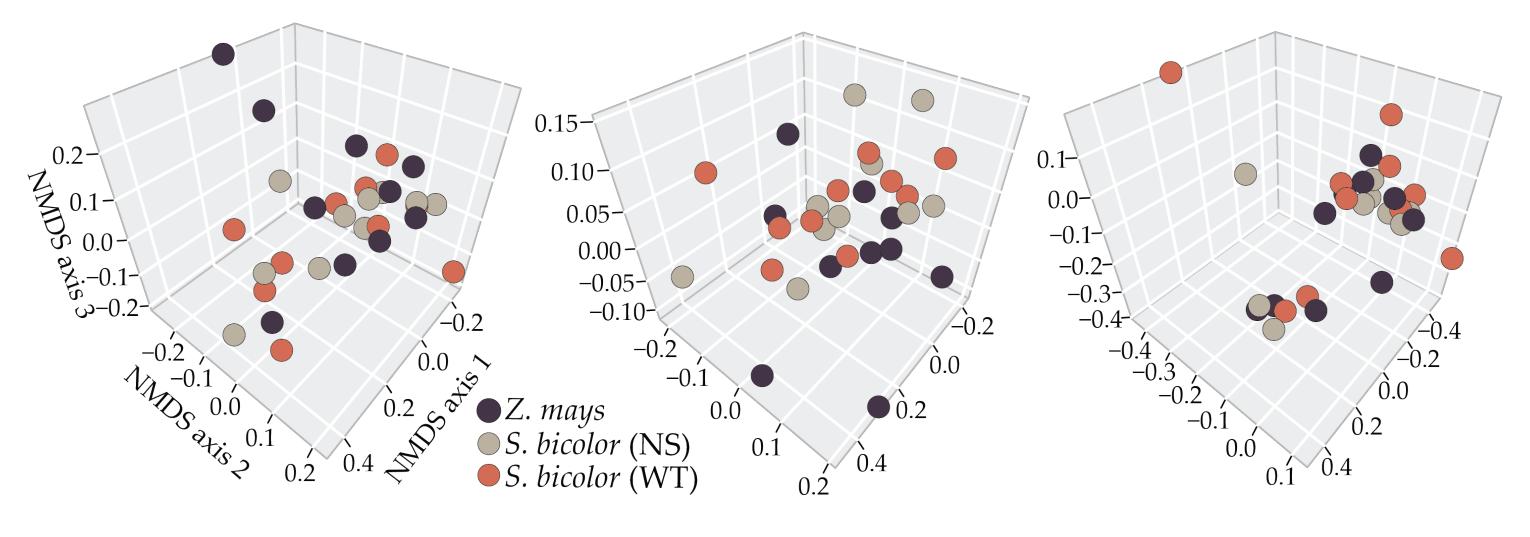
- 1. How does the BNI effect that field-grown *S. bicolor* exerts on the soil compare to Z. mays?
- 2. How does microbial community composition and recruitment of nitrifiers change in relation to BNI compounds?
- 3. Does sorgoleone production contribute to BNI under field conditions?



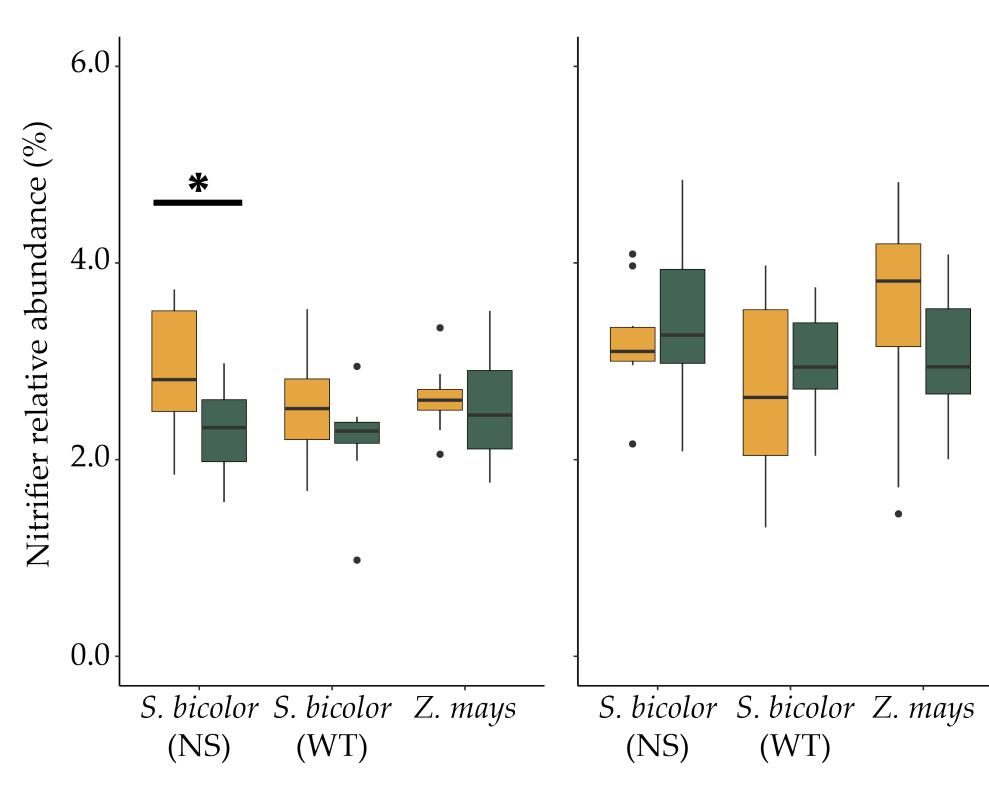


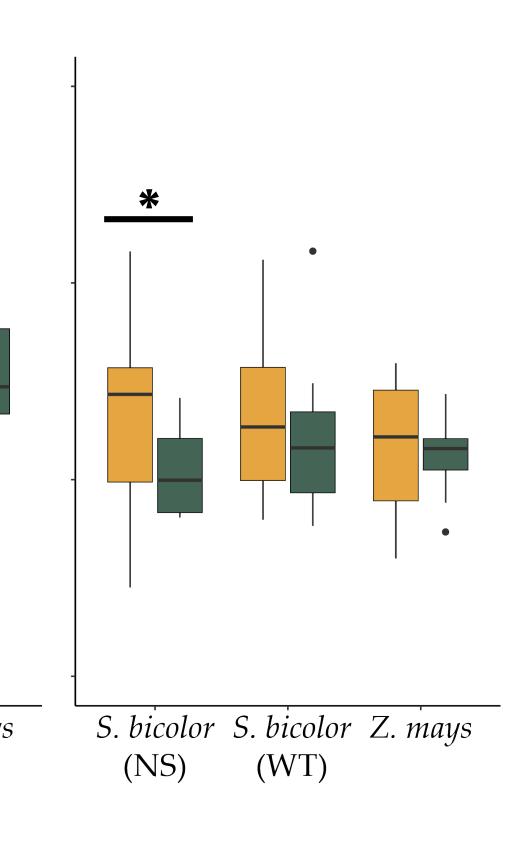


Microbial community composition in the rhizosphere



Nitrifier recruitment









Key results

Both *S. bicolor* genotypes inhibited potential nitrification during the mid-season sampling date while at peak growth (~65 days after sowing).

Microbial community composition in the rhizosphere was not different among species or transgenic type.

Nitrifier relative abundance was not lower in the rhizosphere zone mid-season when the greatest BNI effect was observed, but was reduced in the transgenic *S. bicolor* (NS) rhizosphere zone in early and late season.

Conclusions

S. bicolor exhibited greater nitrification inhibition in field conditions than Z. mays.

BNI depends on plant growth stage and growing season conditions. Since BNI was expressed despite the reduction of sorgoleone production, it appears that other BNI mechanisms were active in the rhizosphere in the 2019 growing season.



Nitrifier abundance did not appear to be directly influenced in mid-season when BNI was highest, suggesting that other factors exert influence over rhizosphere potential nitrification rates in the field, including the suppression of nitrifier activity through direct

competition for NH₄⁺ by heterotrophic microbes and plant roots in the rhizosphere ecosystem.



