Title: Leaf Carbon Isotope Composition in Diverse Sorghum Lines

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Project Goals:
The *overall project goal* is to establish a foundational, systems-level understanding of plant, microbial, and environmental interactions that will lead to strategies for enhancing growth and sustainability of sorghum through genetic and microbial adaptations to water and nitrogen limited environments.

The ***specific objective*** of the research presented here is to screen diverse panels of sorghum genotypes to determine the genetic factors influence leaf carbon isotope composition ($\delta^{13}C_{leaf}$). Towards achieving our project goals, we have conducted several phenotyper, greenhouse and field experiments on various populations of sorghum genotypes. Data will be presented on greenhouse experiments used to determine the relationship of whole plant water use efficiency (WUE_{plant}) with leaf intrinsic transpiration efficiency (TE_i) and $\delta^{13}C_{leaf}$ in a select number of sorghum lines. As predicted from theoretical models of C_4 photosynthesis we have demonstrated that $\delta^{13}C_{leaf}$ is related to TE_i, when efficiency of CO_2 concentrating mechanism (leakiness) remains constant. Accordingly, $\delta^{13}C_{leaf}$ has been proposed as a high-throughput phenotyping tool for TE_i in C_4 plants. We have scaled this research up to test the variation in $\delta^{13}C_{leaf}$ in 30 diverse line of sorghum grown under controlled environment growth conditions in the Bellweather Phenotyping System at the Danforth Plant Science Center and in the field near Scottsbluff, Nebraska. We have followed up on these initial experiments with screens of $\delta^{13}C_{leaf}$ across the sorghum biomass association panel (BAP) grown under both field and controlled environment growth conditions. Given the large genetic and phenotypic diversity within the BAP it is likely that variation in $\delta^{13}C$ exists in this population that can be associated with genetic loci.

Future directions
Leaf and whole plant traits will be assessed across sorghum genotypes to help identify and select for genomic traits and potentially elite lines for enhanced water use efficiency.

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