Phenotypic Characterization of Sorghum Nitrogen Responsive Gene Edits

Hongyu Jin^{1,2}, Yufeng Ge^{1,3}, James C. Schnable^{1,2}, Thomas Clemente^{1,2}, and Jinliang Yang^{1,2}

¹Center for Plant Science Innovation, University of Nebraska-Lincoln ²Department of Agronomy and Horticulture, University of Nebraska-Lincoln ³Department of Biological Engineering, University of Nebraska-Lincoln

November 1, 2022



Phenotypic Characterization of Sorghum Nitrogen Responsive Gene Edits

Hongyu Jin^{1,2}, Yufeng Ge^{1,3}, James C. Schnable^{1,2}, Thomas Clemente^{1,2}, Jinliang Yang^{1,2} ¹Center for Plant Science Innovation, University of Nebraska-Lincoln, Lincoln, NE 68588,

USA

²Department of Agronomy and Horticulture, University of Nebraska-Lincoln, Lincoln, NE 68583, USA

³Department of Biological Engineering, University of Nebraska-Lincoln, Lincoln, NE 68583,

USA

ORCiD: [0000-0002-4562-0639]

Keywords: Sorghum, gene editing, nitrogen use efficiency, image, high throughput phenotyping, time series traits.

Crop improvement over the last few decades, especially after the Green Revolution, is partially driven by the intensive application of less expensive inorganic nitrogen (N) fertilizer. However, the unsustainable use of inorganic N fertilizer in crop production decreases farming profitability and creates a series of ecological burdens. One of the long-standing goals of crop breeding is to increase crops' nitrogen use efficiency (NUE). Studies have shown a number of phenotypic variations of sorghums grown in different N conditions, including root architecture, leaf parameters, growth parameters, yield, and biochemistry traits. Additionally, previous studies showed that the demand for N varies during the sorghum developmental stages, indicating a dynamic genetic control. In our study, taking advantage of the CRISPR-based gene editing and UNL's automatic high throughput phenotyping platform, we generated five edited sorghum lines under TX430 background and phenotyped them in two N conditions from 30 days after planting to full maturity. We extracted time-series plant growth traits from these edited lines as well as the wild type (i.e., TX430), such as plant height, plant width, and pixel counts, along with vegetation indices. Statistical analyses suggested the distinct N responses between some of the edited lines and the wild type. These N-responsive edited lines will be tested in replicated field trials and potentially be incorporated into the breeding protocol for N-resilient sorghum development.