Readme for Plant Exudate Data

**Basic Data Overview:** Using the protocol and a glass bead semi-hydroponic system setup outlined in (Lopez-Guerrero et al. 2022), plant exudates were collected, including amino acids, from several different maize genotypes. By using phenotypic measurements also collected from the different maize genotypes, we can see if there are correlations between amino acid exudates and phenotypic traits amongst these maize genotypes.

Genotype ID: maize genotype identity

Planting Date: day of planting

# seeds planted: number of seeds planted per that genotype

# Final Plants: number of final plants that sprouted and were used for measurement

Exudates collection date: day that the exudates were collected.

Exudates collection method: solution that the exudates were collected in.

Analysis LC-MS Amino Acids: status on if the LC-MS process is complete (just kept the ones that were complete when cleaning up the data)

Analysis GC-MS: status on if the GC-MS process is complete (just kept the ones that were complete when cleaning up the data)

Plant health notes: notes on the basic health of the plant

Final result: final view of the health of the plant

Columns M through AW: phenotypic traits taken or measured from the plants

Date AA/OA Data received: date the amino acid exudate data was collected

LCMS/GCMS ID: identification of the LCMS/GCMS sample

Columns AZ-BI: Amino acids that had good enough recovery to be analyzed further. These are the amino acids I will be analyzing for my project