Seedling Salinity Tolerance Assay

Joseph Barham[1], Brent Hulke[2], Qi Zhang[1], Tom DeSutter[3]
[1]Dept. of Plant Sciences, NDSU | [2]USDA-ARS | [3]Dept. Soil Sciences, NDSU

Summary

A genetically diverse panel of sunflowers from the SAM population will be grown in controlled, lethally saline conditions to evaluate variation in early vegetative growth under these conditions. These data will be used, along with existing salinity tolerance data, to further elucidate the genetic architecture of salinity tolerance in sunflower.

Motivation

Sunflower is a moderately salt-tolerant crop with significant variation in tolerance across genotypes[1]; however, relatively little is known of variation in survival when exposed to extremely high salinity. Additional insight into the genetic architecture underpinning of salt tolerance will also be generated through this project.

Previous work[2] has had success in characterizing sunflower salinity stress responses and their variation by genotype, but this work focused on a labor-intensive hydroponic setup that limited replication significantly and thus affected statistical power. While these findings have been field verified[3] and provided insight into the genetic architecture of salt tolerance, there remain questions about sunflower and salinity tolerance that may be experimentally answered.
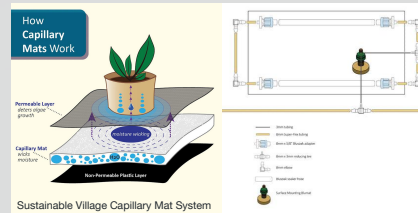

A field with a visible crust of salt or sodic compounds. Nearly all fields in ND have an EC greater than 1.[4]
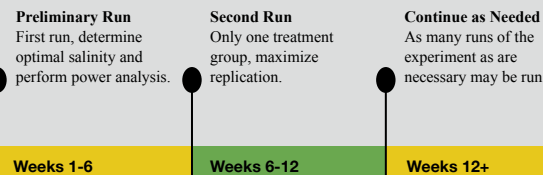
Methodology

Ray Leach "conetainer" pots with a 2.7" diameter and 10" depth will be filled with a sandy growth medium and placed on greenhouse benches in an Randomized Complete Block Design on top of the capillary watering mats. Units given the treatment will have NaCl mixed into the substrate directly, measured as a percentage of mass. A preliminary experiment will be conducted to establish an appropriate salinity level.

A single achene from each genotype from the genetically diverse SAM population (consisting of 288 genotypes) will be planted per pot, at a depth of ~1 cm. The date of emergence, date of first visible evidence of salt damage, the date of the first true leaf (defined in this case as reaching 1 cm in length), and date of death (defined as date on which the apical meristem is dead) will all be measured. After death or six weeks' survival, plants will be harvested and the greenhouse space will be prepared for the next run of the experiment. Data collected will be analyzed in R and SAS, both in survival analysis and as phenotypic data for GWAS. This experiment will be run several times to generate a high level of replication, with the exact number of runs TBD by statistical power analysis after the preliminary experiment is complete.

Sustainable Village Capillary Mat System

Timeline

Preliminary Run
First run, determine optimal salinity and perform power analysis.

Second Run
Only one treatment group, maximize replication.

Continue as Needed
As many runs of the experiment as are necessary may be run.

Weeks 1-6 | Weeks 6-12 | Weeks 12+

Relevance

This project is just one part of a widespread increased interest in sunflower salinity tolerance. This interest is driven by the increasing salinization of farmland as a consequence of climatic and cultural effects[5], and although other mitigation strategies exist and are improving year to year, breeding for salinity tolerance has not been meaningfully successful in sunflower thus far.

The data produced by this project will provide immediate value to our understanding of sunflower salt tolerance in early vegetative growth and lethally saline conditions (such as sunflower planted directly into salt-crusted soil), and will also be valuable in the future as new genetic resources are developed. In particular, additional genome assemblies of SAM population genotypes will be of great value, as traits like salt tolerance are often linked to complex genetic architecture such as transposons and structural variation, which may be difficult to detect with association mapping.

References

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