Discussion from the GxE meeting preceding the 2017 CBR and MGC meetings – 3/8/17

A. Possible weather implementations
    a. Nick Lauter found using a T-post instead of the tripod to be more stable
    b. Mini weather stations will be tested in the canopy at a limited number of locations this season to compare to placement outside the field
B. Plans for 2018/19
    a. Natalia de Leon's proposal
        i. Use the same genetics across all locations as the division of 2016-17 experiments within G X E is not fully leveraging the breadth of environments
        ii. Consider available germplasm in addition to future experimental designs
        iii. To allow GxY estimates, could plant hybrids included in 2014/15 experiments
    b. Cinta Romay (NY): Cornell could grow 1000 plots using the same tester (potentially LH195) as the rest of GxE for 500 plots and a known working tester for the remaining 500 plots
    c. Liz Lee (ONH1) is interested in growing the yellow stripe hybrids and early design II experiment, but would prefer not to grow the mini-NAMs
    d. Other possibilities discussed
        i. Use alternative testers—different flowering times but similar genomes
            1. Use marker selection for flowering to look at testers
        ii. NIL series—672 introgression lines
            1. The temperate adapted parents' photoperiod haplotypes were replaced with tropical haplotypes
        iii. Seth Murray is interested in using material from unadapted landraces such as the GEM materials
            1. He wants to look at novel diversity not the ex-PVPs that have been extensively studied by industry
            2. Natalia's response—it has not been measured how elite the GEM germplasm is
                a. GEM germplasm has a very small amount of exotic materials
C. 2020/2021 ideas
    a. Liz Lee has developed a long ear population that accumulates biomass prior to silking and enhances sink potential
        i. Could be a platform to look at how extreme selection on a population changes the architecture of a plant
        ii. This population is exotic because of how extremely it's been selected
        iii. It doesn't shoe inbreeding depression
        iv. We could develop double haploids, cross to the stiff stalks, and test on iodents
        v. We could use 12 base lines to include all allelic combinations
        vi. Would tie in with G2F because the population could really benefit with phenotyping
    b. Another idea Liz Lee proposed was to look at early populations that when crossed lead to genome incompatibly

    c. Martin Bohn suggested we could use the data from the Design II experiments in 2014 and 2015 to design models, then generate hybrids and test these models

D. Phenotypic tools to consider
    a. Nitrate sensors, cameras in the fields, UAV
    b. Martin Bohn suggested using genotypic specific traits, such as total leaf number and area of the largest leaf, plant population, and solar radiation as variables to measure for crop models
    c. We could also contact Purdue to find out more about their hi-throughput methods for measuring leaf area