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Alice MacQueen
University of Texas at Austin, alice.macqueen@utmail.utexas.edu

Jeffrey W. White
USDA-ARS, jeffrey.white@ars.usda.gov

Phillip E. McClean
North Dakota State University, phillip.mcclean@ndsu.edu

Tom Juenger
University of Texas at Austin

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GENETICS OF YIELD VARIATION AND GENOTYPE BY ENVIRONMENT INTERACTIONS IN THE COOPERATIVE DRY BEAN NURSERIES

Alice MacQueen[1], Jeffrey W. White[2], Phil McClean[3], Tom Juenger[1]

[1]The University of Texas at Austin; [2]USDA ARS; [3]North Dakota State University

Common bean (*Phaseolus vulgaris*) yields have improved in multiple long-term breeding efforts across the world. An important long-term trial that supports these breeding efforts is the Cooperative Dry Bean Nursery (CDBN), an ongoing 60+ year collaboration across the United States and Canada. However, large genotype-by-environment interactions (GxE) persist in common bean (Figure 1). Though genomics assisted breeding tools and analyses to study GxE are rapidly improving (Heffner *et al.,* 2009; Perez & de los Campos 2014), accurate phenotyping in relevant field conditions remains a major limitation of these analyses. Major phenotyping efforts such as the CDBN, when combined with genomic data, offer unparalleled opportunities to determine how major genetic factors affect genotype by environment interactions.

Figure 1. Examples of genotype by environment interactions for yield of four CDBN varieties in response to a precipitation related principal component.

To characterize the genetics of phenotypic variation in common bean, phenotypes and fitness in a wide range of environments must be connected to the alleles that influence them. In collaboration with current common bean sequencing efforts, we are sequencing 320 varieties and breeding lines from the CDBN to establish a genome-wide association (GWA) mapping population. We will use this panel to determine the genomic regions associated with phenology, yield, and other traits phenotyped by the CDBN. We will also use weather data associated with each location and year to determine the genetics of, and the abiotic factors leading to, GxE interactions between these phenotypes and climate.

Variety, phenotype and weather collection

117 varieties in the CDBN have single nucleotide polymorphism (SNP) data through genotyping by sequencing (GBS), as part of the Mesoamerican Diversity Panel (Moghaddam *et al.*, 2016). Breeders with ties to the CDBN generously provided seed that allowed GBS sequencing of an additional 203 varieties from the CDBN, currently underway.

Collaborators in the CDBN have collected phenotypic data for a suite of agronomic traits for over 500 common bean varieties grown at various subsets of 84 locations. There are between
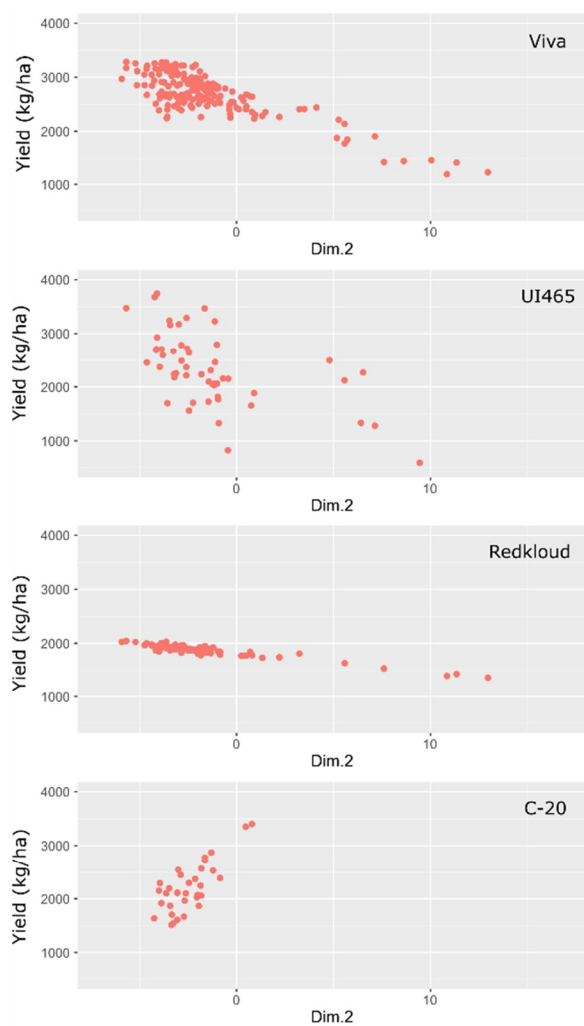
nine and twelve phenotypes for which we will have sufficient data for an analysis of GxE through environmental PCA (ePCA) and GWA. The dataset also includes monthly weather data associated with each trial year at each site. We are working to add and compare daily weather data from NOAA to environmental PCA derived from monthly weather data.

Planned Analyses

We will perform a PCA on all monthly and daily weather variables. In a preliminary analysis with monthly weather variables, the first two PCs explained 39.1% and 22.6% of the variance, and loaded strongly with temperature and precipitation variables, respectively. We will determine the slopes and variance for variety yields in response to these environmental PCs. This will allow us to identify varieties in two categories: "yield stable", with small slopes and low variance, and "yield labile" varieties, with significant positive or negative slopes (reaction norms) and low variance. Preliminary results indicate that reaction norms and environmental sensitivity differ by race: we observe more stable varieties than expected for PC2 in Andean lines, and more negative reaction norms than expected for PC2 in Durango lines.

Work is currently in progress to link datasets containing phenotypic, weather, pedigree, and genetic variables. When the genotype data is complete, we will screen for genomic regions associated with yield variation by using the GEMMA software to conduct genome-wide association (GWA) for yield and other phenotypes in multiple environments simultaneously while controlling for population structure (Zhou and Stephens 2014). Multivariate analyses substantially increase power to detect pleiotropic variants and variants that affect only one of multiple correlated phenotypes (Stephens 2013). The kinship matrix correction applied by GEMMA will be essential to account for breeding relationships among lines and past introgression events between varieties. Factors such as domestication clade, market class, ePCAs, and pedigree information will be included as additional cofactors in the models.

ACKNOWLEDGEMENTS

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