

PLANT SUCCESS POSTGRADUATE PROJECT CONCEPTS: PREDICTION & ANDROPOGONEAE

Andropogoneae: Experimental and theoretical explorations of transferability of “Successful” genome-to-phenome multi-trait solutions across phylogenomic and ecophysiological context.

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BACKGROUND

The tropical grass tribe Andropogoneae has been identified as one of the CoE targets for experimental and theoretical investigations of “Plant Success”, with relevance for both natural and agricultural systems (CI-Jordan, CI-Wright, CI-Henry, CI-Holland, CI-Brodribb, CI-Hammer, CI-Beveridge). There are many possible Andropogoneae PhD projects that can be undertaken in association with the CoE CI projects. The objective of this PhD project concept document is to identify some of the possible PhD projects that CI-Cooper could undertake in partnership with other CoE-CIs and through partnerships with our CoE collaborators and Associate investigators. The focus herein is on development and application of predictive methodology focused on multi-trait “workable solutions” for “Plant Success” within drought-affected environments.

The primary interest of CI-Cooper is in studying and testing predictive transferability of genome-to-phenome knowledge of different trait combinations contributing to “Plant Success” (Tardieu et al. 2021) across different levels of divergence within the Andropogoneae and related grasses. One of the specific crop-focussed experimental-theoretical targets of interest to investigate predictive transferability of drought adaptation related “Plant Success” trait combinations is the transferability between maize and sorghum (e.g., Mace et al. 2013, Choudhary et al. 2020, Vadez et al. 2021). This maize-sorghum crop focus aligns with the ongoing Sorghum-Andropogoneae interests of CI-Jordan and AI-Mace, the crop modelling focus of CI-Hammer and PI-Messina (Corteva), and the genomics focus of PI-Morris (CSU), PI-Hearne (CIMMYT), and a range of other collaborators, including Buckler (USDA-Cornell). The maize-sorghum comparison could be extended to include comparisons with pearl millet (Choudhary et al. 2020), which would expand the diversity dimension for studying branching diversity and other drought and heat adaptation trait complexes. There is a lot of background genomics, trait physiology and modelling research to be done that provides many opportunities for predictive modelling focussed PhD projects. An example of a coordinated set of such projects is listed below.

PROJECT CONCEPTS

PhD Project Topic 1.

Informatics and Statistical Modelling: Mining the CIMMYT maize “Seeds of Discovery” data resources to test for signatures of “Plant Success” for abiotic stress adaptation that could transfer to the working hypotheses for “Plant Success” in tropical maize (Atanda et al. 2021) and temperate maize (Cooper et al. 2014).

PhD Project Topic 2.

Modelling: Explore uses of the APSIM sorghum, maize and millet crop growth models to examine the “ideotype” and “multiple workable solution” hypotheses to enable accelerated breeding for crop yield and yield stability in drought-prone environments: Integrated assessments of Canopy Systems Architecture, Root Systems architecture and biomass partitioning to determine yield potential and reproductive resiliency.

PhD Project Topic 3:

Experimental-Modelling: Predict and test the “Plant Success” hypotheses that are the expected outcomes from PhD Projects 1 and 2 above within the data resources of the sorghum “map and select” CoE sorghum project of CI-Jordan.

PhD Project Topic 4:

ARGOS gene family evolutionary history, focussed on characterising diversity and adaptation efficacy within the Andropogoneae tribe, and efficacy for crop yield potential and yield stability (maize and sorghum) under abiotic stresses associated with water availability and high temperature. The ARGOS gene family has been investigated in detail in temperate maize. Native allelic variation (Guo et al. 2014), transgenic variation (Simmons et al. 2021) and gene edit generated variation (Shi et al. 2017) have all been demonstrated to have yield efficacy in maize influencing both yield potential and yield stability. Advances in crop model architecture to enhance yield prediction for maize (Messina et al. 2019) will be used to undertake novel analyses of existing Corteva (CoE Partner) data sets. This would provide an entry point for the phylogenomic analyses of the ARGOS gene family within the Andropogoneae and the design of experiments to test predictions.

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