

Increasing Genetic Gains in Wheat through Physiological Genetics and Breeding

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Introduction

In order to meet future wheat demand it is necessary to increase yield potential and develop stress adapted genotypes. To do so, research and breeding is conducted at CIMMYT through the International Wheat Yield Partnership (IWYP) platform combining physiology, genetics, and breeding. Physiological breeding focuses on understanding the physiology and genetics of key traits and conducting complementary crosses among them based on conceptual models to utilize the diversity present in the CIMMYT germplasm. Physiological breeding combined with genetic approaches (GWAS, QTLs, Genomic Selection) are used in the program to achieve genetic gains. (Reynolds and Langridge 2016 Current opinion in plant biology)

Methods and Results

Conceptual models for yield under yield potential and stress conditions

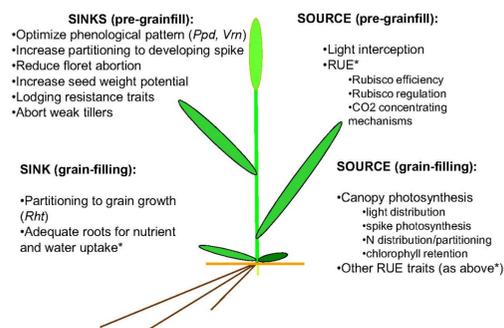


Fig. 1. An example of a conceptual platform for designing crosses that combine complementary yield potential traits in wheat.

Matthew Reynolds et al. *J. Exp. Bot.* 2011;62:439-452

RUE = Radiation use efficiency; N = nitrogen.

Development of new tools for rapid and precise phenotyping

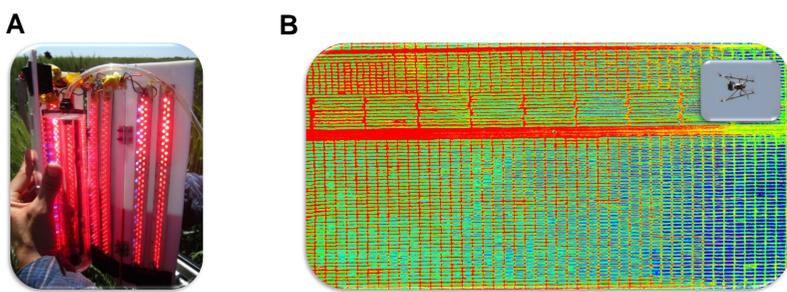


Fig. 2 (A) Spike photosynthesis measurement chamber (B) UAVs to measure NDVI, CT, and spectral reflectance parameters; a mosaic of canopy temperature.

Understanding the physiology and genetics for key traits

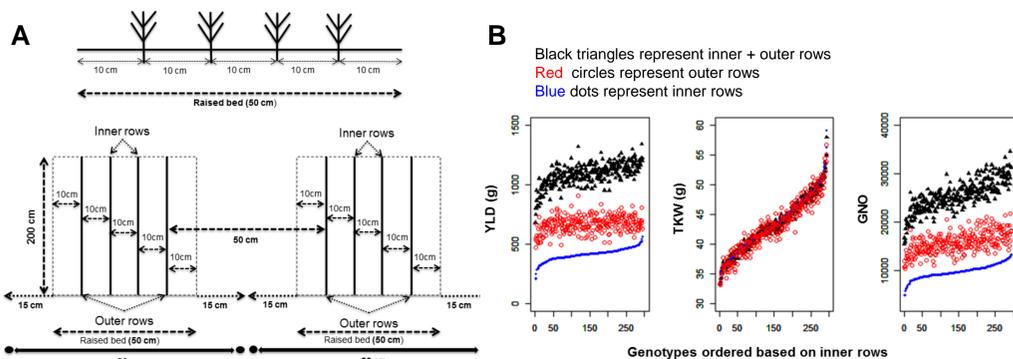


Fig. 3 (A) An experimental design to phenotype for adaptation to density (B) grain yield and grain number affected by adaptation to density, whereas grain weight is stable (Sukumaran et al. 2016 *Crop Sci.*).

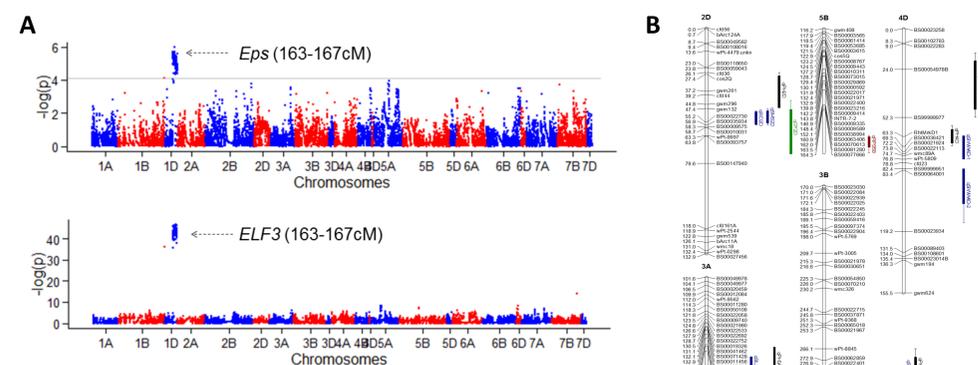


Fig. 4 (A) Identification of *Ta-ELF3* as a marker for *earliness per se* (*Eps*) flowering time locus in spring wheat (Sukumaran et al. 2016 *Crop Sci.*) (B) QTLs for lodging resistance (Piñera-Chavez et al. unpublished).

Development of genomic selection and pedigree based prediction models

We fitted seven different models (M1-M7) with different components including E=environments, L=line, A=pedigree, G=genomic, AE=pedigree × environment interaction, GE=genomic × environment interaction, and e=residual error on a 287 lines wheat association mapping initiative (WAMI) population phenotyped in 15 environments. The genomic prediction models with interaction terms-genotype × environment (G×E)- had the highest average prediction ability (Fig. 5).

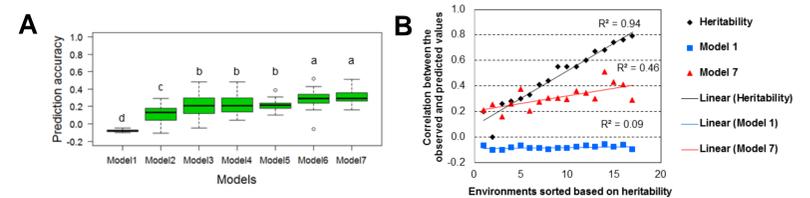


Fig. 5 (A) comparison of boxplot distributions of prediction accuracy for each model (M1-M7) for trait grain yield (GY); Models: M1 $Y=E+L+e$; M2 $Y= E+L+A+e$; M3 $Y= E+L+G+e$; M4 $Y= E+L+A+AE+e$; M5 $Y= E+L+G+GE+e$; M6 $Y= E+L+G+A+e$; M7 $Y= E+L+G+A+GE+AE+e$, (B) Comparison between heritability values and the correlation between observed and predicted values for the best and worst models in predicting trait grain yield. (Sukumaran et al. 2017. *G3: Genes, Genomics, Genetics Vol 7*)

Development and evaluation of international nurseries

Three nurseries developed under irrigated conditions to increase yield potential (Wheat yield collaboration Yield Trials (WYCYTs) and four abiotic stresses—drought and heat—Stress adapted traits yield nurseries (SATYNs), were grown in several major wheat growing countries (altogether 120 environments) in South Asia, North Africa, Western Asia, and Mexico. We used spring wheat yield data from these environments to evaluate the predictive ability (PA) of different models by modelling G×E using the pedigree-derived additive relationship matrix (A matrix). Results on the PA for the intra and inter population analyses indicated that best predictive model (model 6 = E+L+A+AE+e), always included the G×E denoted as the interaction between the pedigree derived matrix (A) with environments (Fig. 6).

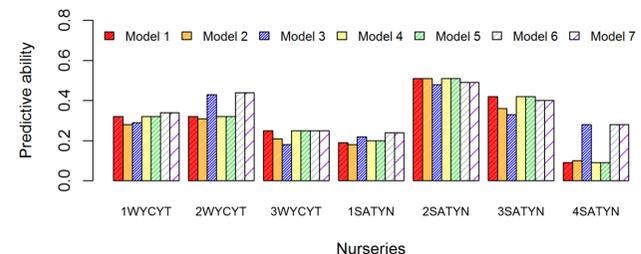


Fig. 6 Comparison of seven different pedigree based prediction models (model 1 = E+L+e, model 2 = E+A+e, model 3= E+A+AE+e, model 4= E+L+A+e, model 5= E+L+A+LE+e, model 6 = E+L+A+AE+e, and model 7 = E+L+A+LE+AE+e). Sukumaran et al., 2017. *Crop Sci.*

The physiological trait (PT) lines have shown increased grain yield compared to checks in most environments where WYCYT and SATYN nurseries were evaluated (Fig. 7)

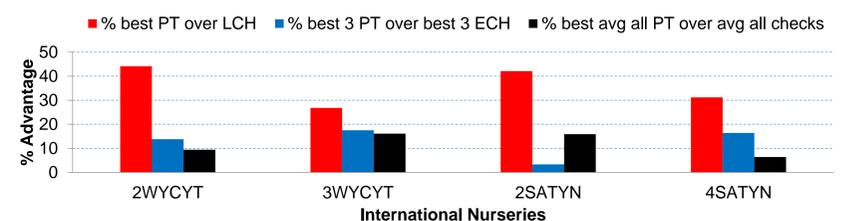


Fig. 7. Percent genetic gains expressed for the best PT line over the local check (LCH), the best 3 PT lines over the best 3 elite checks (ECH), and of the average of all PT lines over the average of all checks, for the largest cluster of low G x E sites of each international nursery. Reynolds et al. *Euphytica* (submitted)

Conclusions

An integrated approach including physiology, genetics, genomics, and breeding is needed to provide genetic gains in spring wheat. Conventional breeding combined with marker-assisted selection approaches will complement the present physiological breeding approach.

Acknowledgements

