

# Association Analyses for Yield Components and End-use Quality in Synthetic Derived and Advanced Winter Wheat Breeding Lines and Model Selections for Genomic Prediction

Zhen Wang<sup>1,2#</sup>, Xiaoxiao Liu<sup>1</sup>, Chenggen Chu<sup>1</sup>, Shichen Wang<sup>3</sup>, Smit Dhakal<sup>1</sup>, Yan Yang<sup>1</sup>, Qingwu Xue<sup>1</sup>, Jackie C. Rudd<sup>1</sup>, Amir M.H. Ibrahim<sup>2</sup>, Dirk Hays<sup>2</sup>, Jason Baker<sup>1</sup>, Kirk Jessup<sup>1</sup>, Ravindra Devkota<sup>1</sup>, Shannon Baker<sup>1</sup>, Kele Hui<sup>1</sup>, Geraldine Opena<sup>2</sup>, Charlie Johnson<sup>3</sup>, Rich Metz<sup>3</sup>, Shuyi Liu<sup>1\*</sup>

<sup>1</sup>Texas A&M AgriLife Research, Amarillo, TX; <sup>2</sup>Soil and Crop Science, Texas A&M University, College Station, TX; <sup>3</sup>Genomic and Bioinformatic Service Center, Texas A&M AgriLife Research, College Station, TX. #Presenting, \*Corresponding.

## ABSTRACT

- Synthetic derived lines (SDLs) from hard red winter wheat backcrossing has been reported having a higher yield potential.
- 298 SDLs derived from the crosses between 21 primary synthetic hexaploid spring wheat lines and TAM 111 or TAM 112.
- Yield and end-use quality traits of 298 SDLs and 356 advanced lines were collected, and all the lines were genotyped by genotyping-by-sequencing, ddRADseq.
- Genetic loci for yield and end-use quality traits were identified through genome-wide association study (GWAS) using GAPIT.
- Using the 298 SDLs and 99 lines from 2019 to build two training models with rrBLUP.
- Genomic estimated breeding values (GEBV) of 152 SDLs and 105 lines from 2020 yield trials were calculated from the training models.
- Correlation between GEBV and the actual trait data collected were calculated to estimate reliability of training models.

## INTRODUCTION

- Genetic improvement is an important method to increase wheat yield, which is important for ensuring global food security.
- Synthetics derived lines were artificially developed using multiple durum wheat and diverse *Ae. tauschii* lines that could provide genetic diversity and variations for yield related traits.
- Synthetic derived lines contains high-diversity D genomes, which have potentials as genetic resources for novel yield genes for breeding programs.
- Whole genome SNPs of wheat lines can be easily acquired by GBS, which provide genetic information for GWAS and training model construction.
- Training model can be used for genomic prediction and selection, which only require genotyping data and could save labor in trait data collection.

## OBJECTIVES

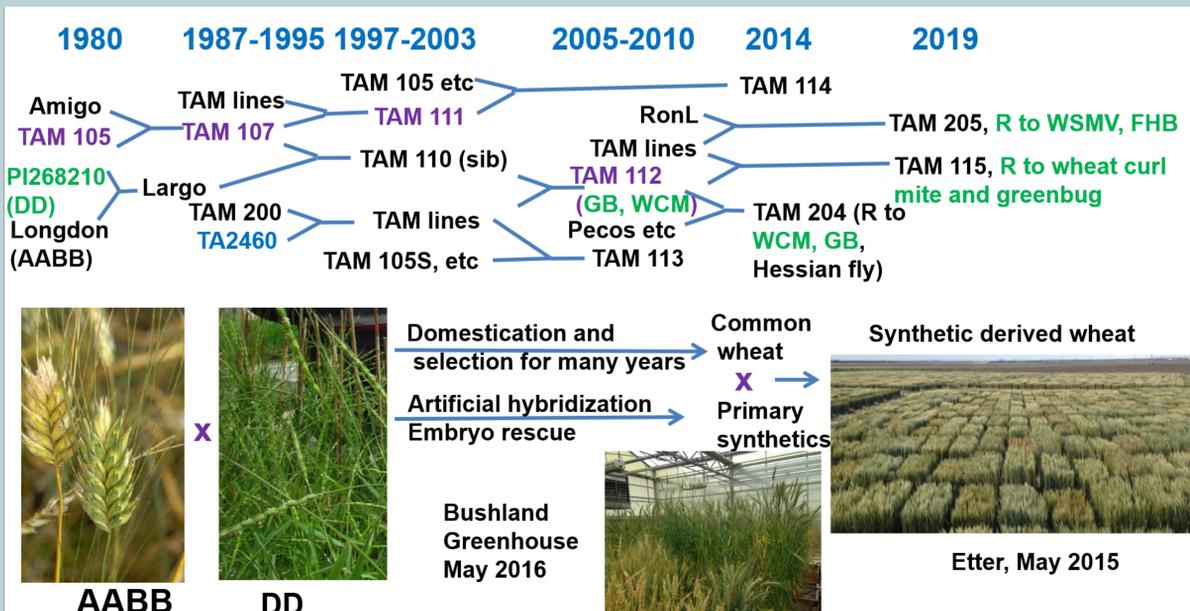
- Identify superior alleles in synthetic-derived lines and adapted bread wheat and employing them in breeding programs.
- Build genomic selection training model and verify the reliability for breeding value prediction.
- Incorporate the genomic prediction into a real breeding program to increase select efficiency and genetic gains.

## MATERIALS AND METHODS

- A set of 298 synthetic derived lines from 21 different synthetics and two popular cultivars, TAM 111 and TAM 112.
- A set of 356 advanced breeding lines tested in 2019 and 2020 yield trials with trait data collected from multiple years and locations.
- Genome-wide association study (GWAS) used for identify significant SNP-trait associations.
- rrBLUP was used to build the training model for genomic prediction.
- Genomic estimated breeding values of important agronomic traits will be used by breeders to increase selection efficiency and genetic gains.

## RESULTS AND DISCUSSIONS

### I. TAM cultivars and synthetic derived lines.



### II. Manhattan plot of yield and end-use quality traits.

Fig. 1a/1b Significant SNP for yield of 99 advanced breeding lines in 2019 yield trials

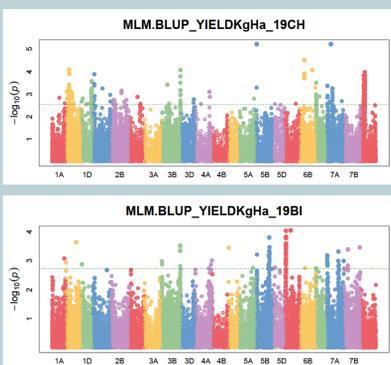


Fig. 2a/2b Significant SNP for test weight of 105 advanced breeding lines in 2020 yield trials

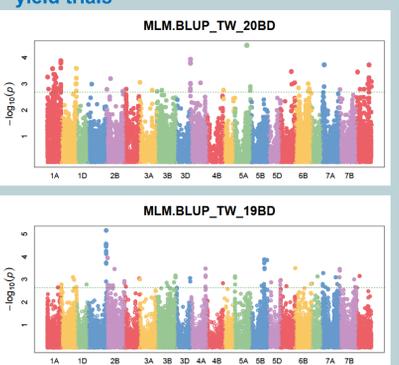
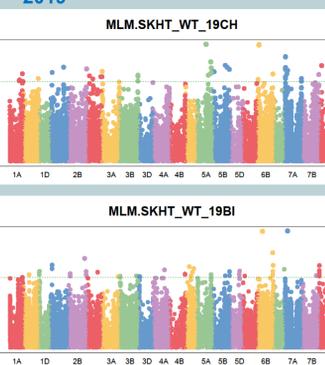


Fig. 3a/3b Single kernel weight of 99 advanced breeding lines in 2019



### III. Phylogenetic tree of 356 breeding lines with 79K SNPs in 2019 and 2020 yield trials.

Green colored are those derived from synthetics that are clustered together.

### IV. Genomic prediction using the 298 synthetic derived lines for 156 lines in preliminary yield trials that were derived from the same set of synthetics. Using 99 lines in 2019 elite and advanced yield trials to predict the 2020 elite and advanced lines with the same set of SNPs.

Trait	Correlations
Yield	0.37 (Irrigated)
Test weight	-0.1 (Irrigated)
Height	-0.12 (Dryland)
Yield	-0.16 (Dryland)

