Broadening the Genetic Base of Wheat Using Primary Hexaploid Synthetics

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Introduction

Wheat (*Triticum aestivum* L.) improvement from intercrosses of existing elite materials has narrowed the genetic diversity of the crop resulting in a slower genetic gain. The potential use of synthetic hexaploid wheat to enhance breeding outcomes is well known.

However, the success of synthetic hexaploid wheat utilization in breeding could have been much higher if they were guided by the knowledge of genes controlling biotic (diseases) and abiotic (drought and cold) stresses.

Objectives

- Identify superior primary synthetics possessing resistance to diseases, drought, and cold
- Identify respective genetic regions and develop molecular markers
- Evaluate the variation for improved grain quality and mineral content

Materials and Methods

Research Sites

Fig. 1. Location of experimental sites (six locations in Turkey and Mead, Nebraska, USA) shown by a star symbol.

Experimental Design

- Augmented Row-Column Design
- Replications: Two checks (Gerek and Karahan)
- Synthetic hexaploid wheat: 126

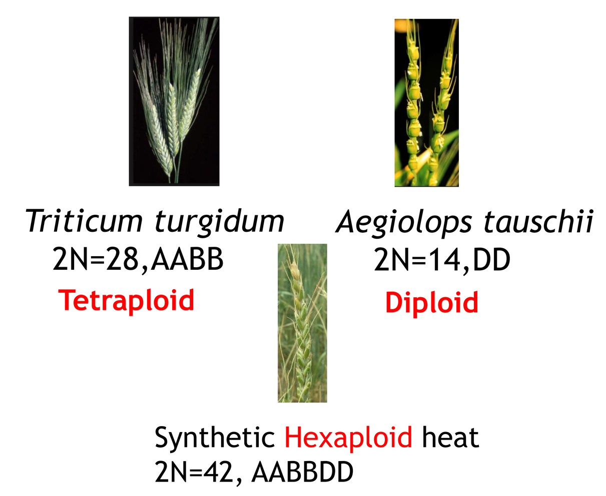
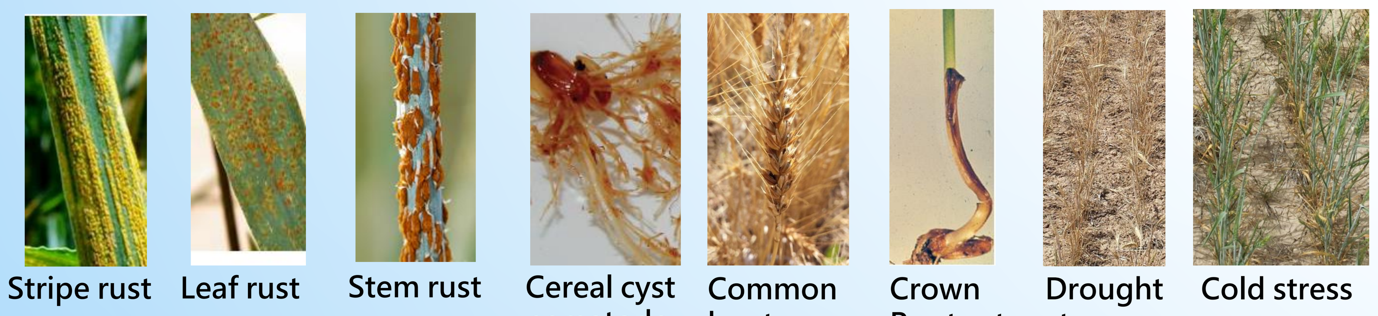


Fig 2. Synthetic wheat development

Data collected



Preliminary Results

Fig. 3. Seven synthetic hexaploid wheat had significantly higher grain yield and comparable flour protein concentration to checks (Gerek and Karahan) in Konya, Turkey under drought in 2016.

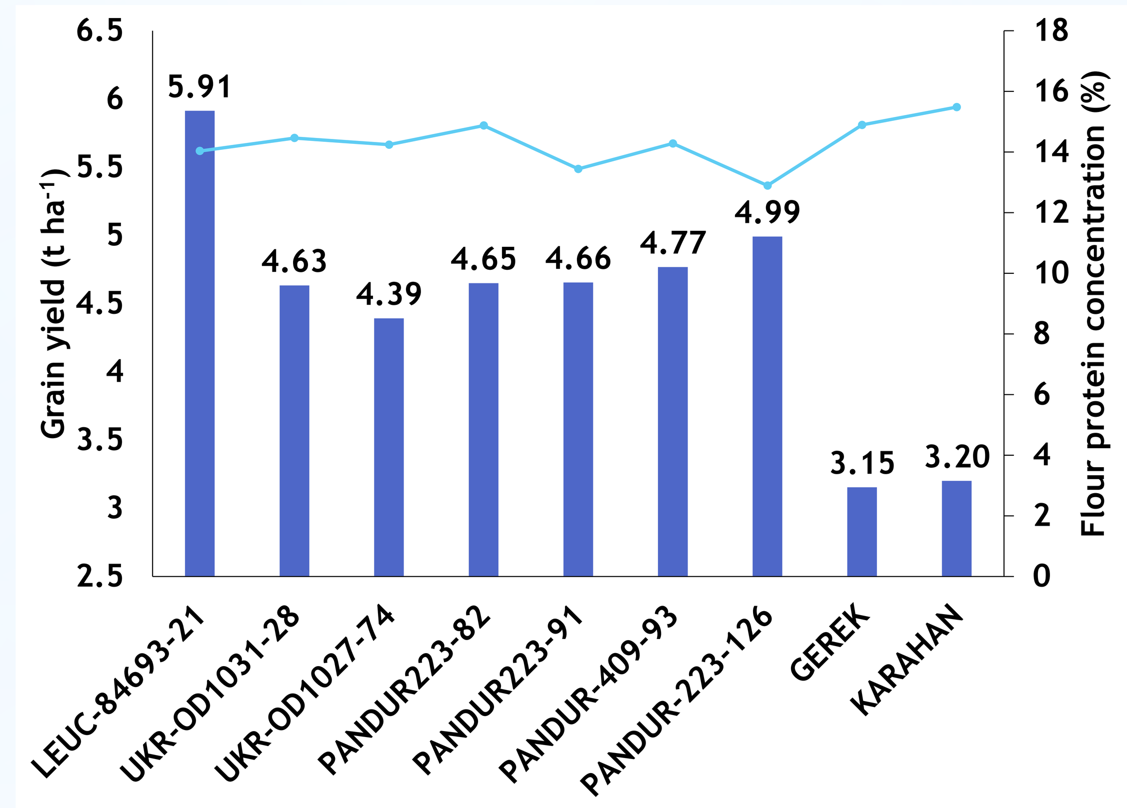


Fig. 4. Venn diagram presents the number of rust resistant and drought tolerant entries.

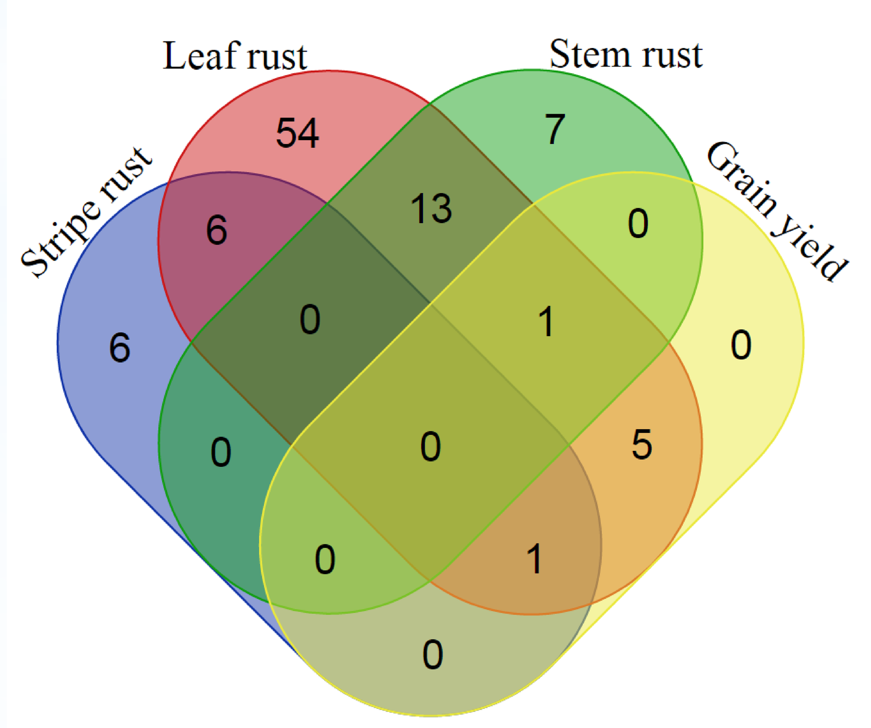


Fig. 5. Venn diagram presents the number of Cereal Cyst Nematode (CCN), Crown Root Rot (CCR), Common Bunt (C.BUNT) resistant, and drought tolerant entries.

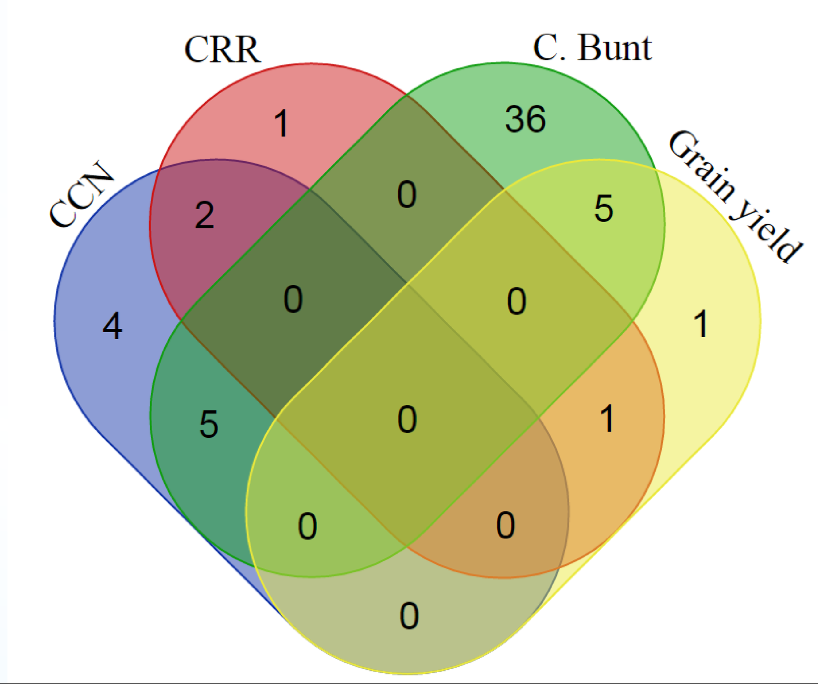
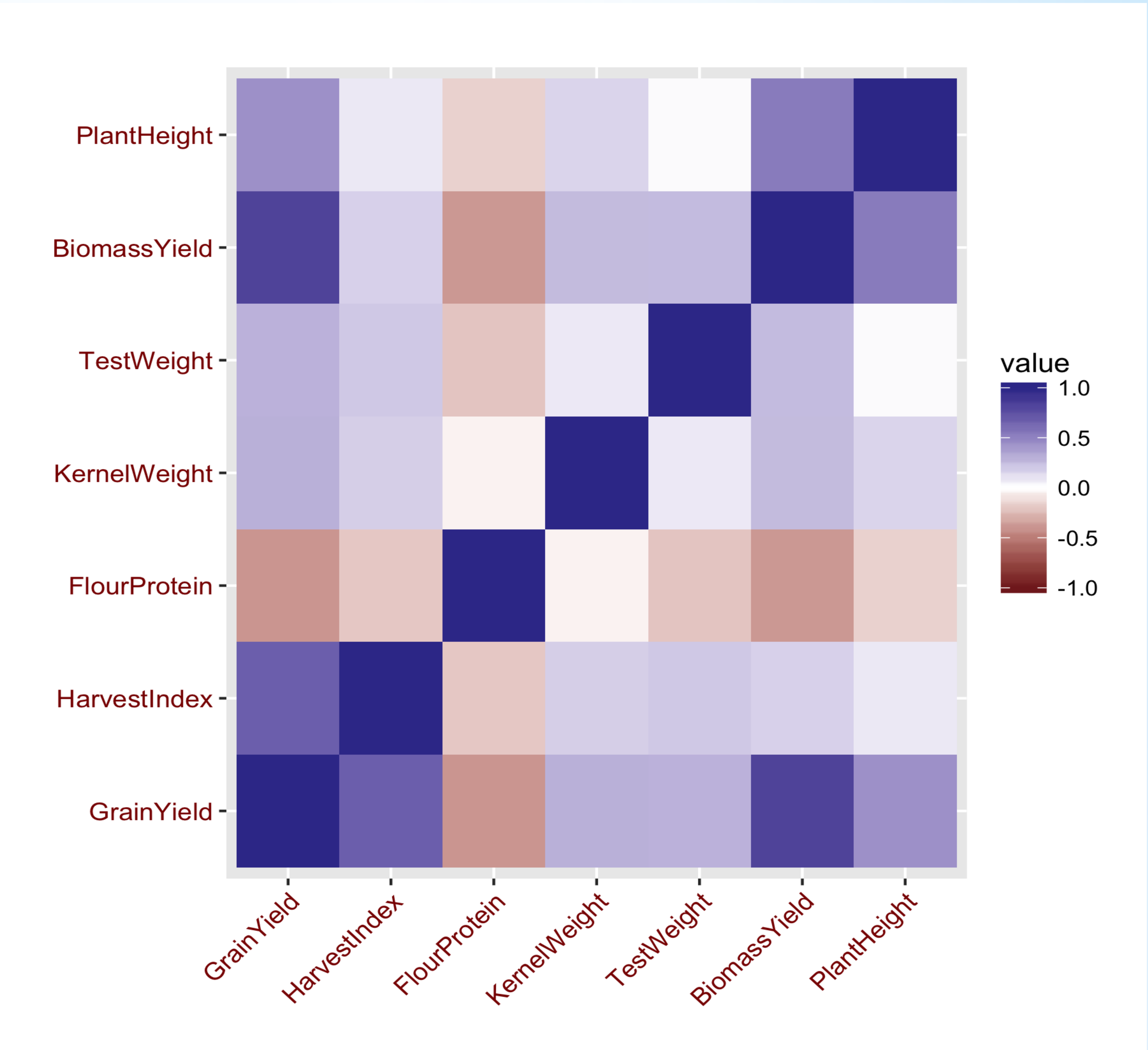


Fig. 6. Correlation heat map between phenotypic traits under drought conditions in Konya, Turkey in 2016.



Conclusions

- Abundant variations for biotic and abiotic stresses
- Potential for new sources of resistance
- May be used in elite wheat breeding program to broaden the genetic base

Future Directions

- Continue phenotypic data collection
- QTL and gene discovery from GWAS using GBS derived SNP markers
- Winter hardiness experiment in 2017 & 2018
- Mineral content analysis

References

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Acknowledgements

We would like to acknowledge Monsanto Beachell-Borlaug International Scholarship Program for funding this project. Germplasm evaluation in Turkey by the following institutions is highly appreciated: Bahri Dagdas International Agricultural Research Institute, Konya (yield and related traits), Central Field Crop Research Institute, Ankara (stripe and stem rust), Maize Research Station, Adapazari (leaf rust), Transitional Zone Agric. Research Institute, Eskesehir (common bunt and crown root rot), and CIMMYT-Turkey (cereal cyst nematode and crown root rot) for collaborating with University of Nebraska Lincoln to conduct this research.