



 @vasuakshaya15

Gene expression dynamics upon allopolyploidization: Global transcriptome analysis reveals large-scale repression of the 'D'- subgenome in synthetic hexaploid wheat

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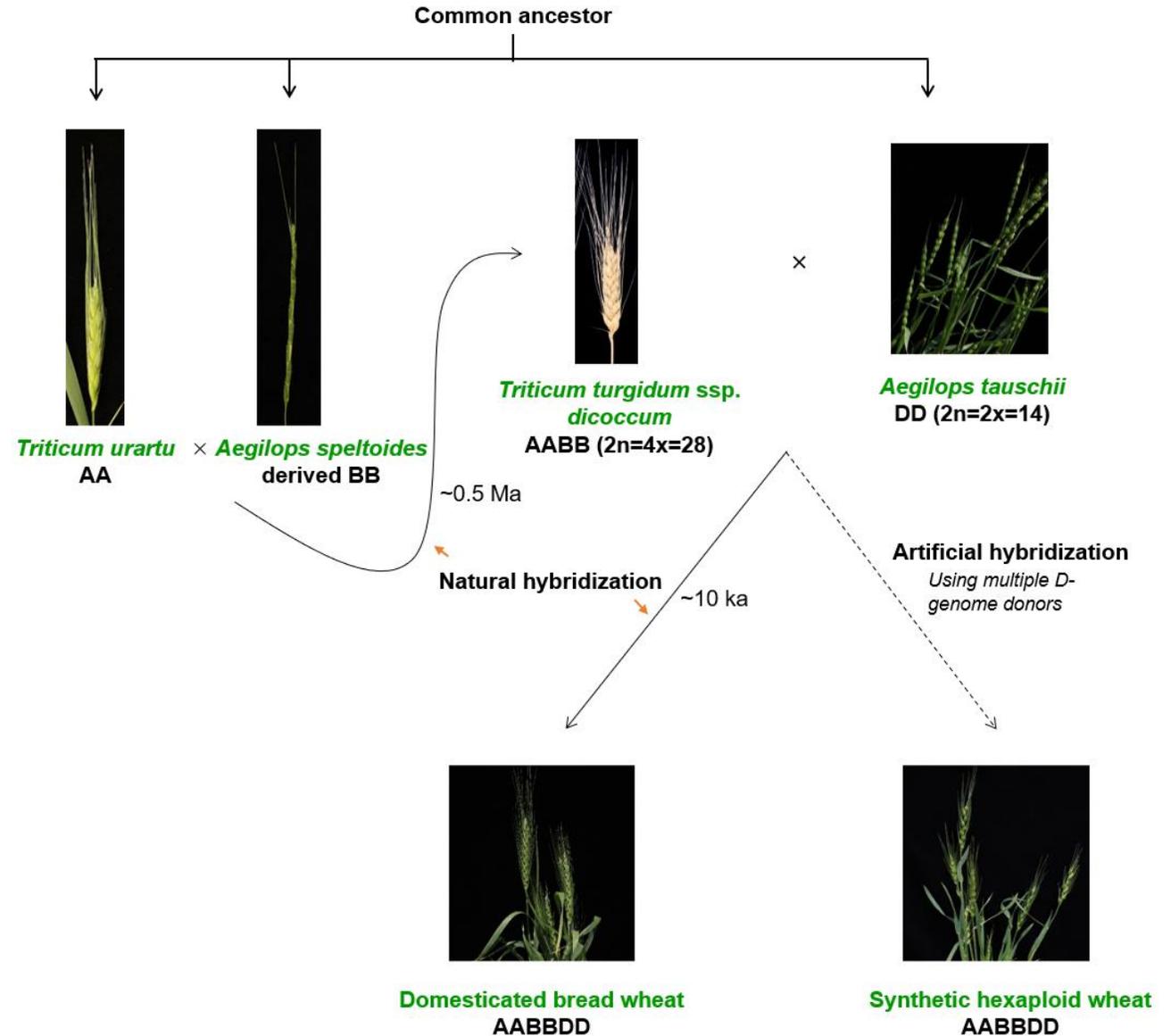


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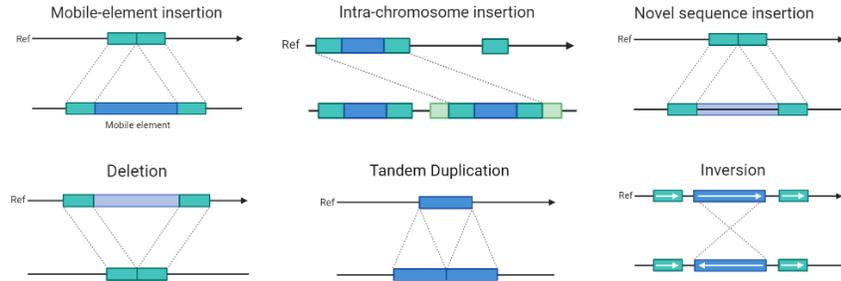
Wheat genome evolution: Polyploidization

- Whole genome duplication has strong association with plant speciation
- Bread wheat is an allohexaploid crop ($2n = 6x = 42$; AABBDD)
- Genetic diversity of D genome in bread wheat is lesser than the A and B genomes

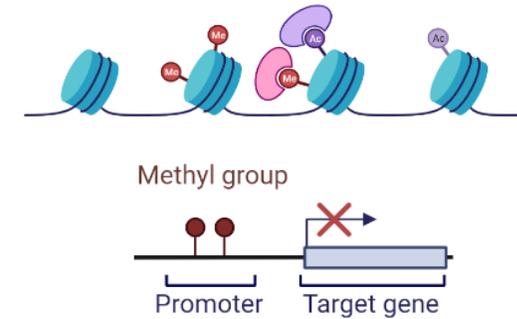


Consequences of polyploidization: Genomic shock

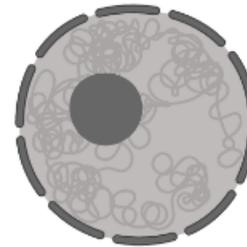
Genetic changes



Epigenetic modifications



Alterations in three-dimensional chromatin architecture



All these potentially trigger changes in **transcriptome**.

Objective: To understand the influence of genome interactions at various ploidy levels on gene expression in SHW lines

Materials

Plant material

		Male parent	
		AS2386 (DD) <i>Ae. tauschii</i>	AS2399 (DD) <i>Ae. tauschii</i>
Female parent	PI377655 (AABB) <i>T. turgidum</i> ssp. <i>dicoccum</i>	C66* (AABBDD)	C65* (AABBDD)
	Langdon (AABB) <i>T. turgidum</i> ssp. <i>durum</i>	C44* (AABBDD)	C45* (AABBDD)

* SHW – Synthetic Hexaploid Wheat

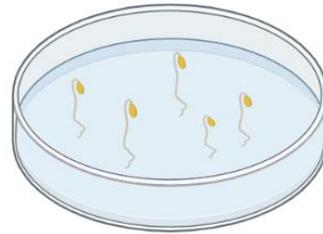
Sequencing data

- mRNA-sequencing data from above eight genotypes
- 10 different tissues
- Three biological replicates

Tissues used in the study



1. Shoot (below rachis)



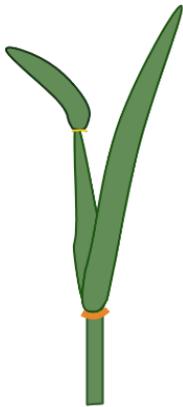
2. Root
3. Hypocotyl



4. Lemma and Palea



5. Glume



6. Head at boot stage

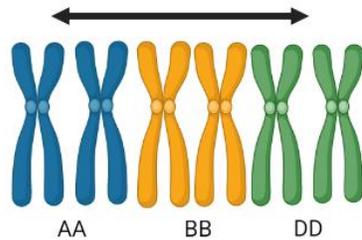


7. Pistil - when anthers are at immature stage
8. Mature anthers
9. Pistil - when anthers are at mature stage
10. Pistil - one day after anthesis

Methods

Alignment to **IWGSC RefSeq v2.1** using STAR v2.7.1a

Comparison of homoeo-allele expression within the same genomic background



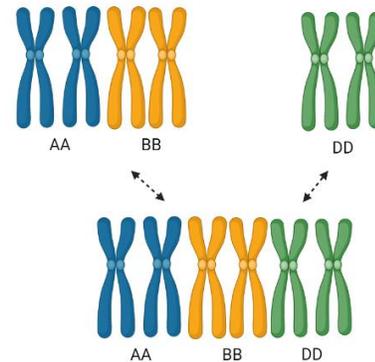
18,357 triads (IWGSC 2018; Zhu et al. 2021)

Homoeolog expression bias (HEB) estimation

$$HEB = \log_2 \left(\frac{RPKM_a}{RPKM_b} \right)$$

HEB analysis of triads using likelihood ratio test (Smith et al. 2019)

Comparison of expression differences between different genomic backgrounds



106,913 high confidence gene models

Differential expression analysis between SHWs and their parents:

With all high confidence models using edgeR (Robinson et al. 2010)

Qualitative changes in transcripts



SHW vs parents comparison of differentially spliced isoforms

rMATS (Shen et al. 2014)

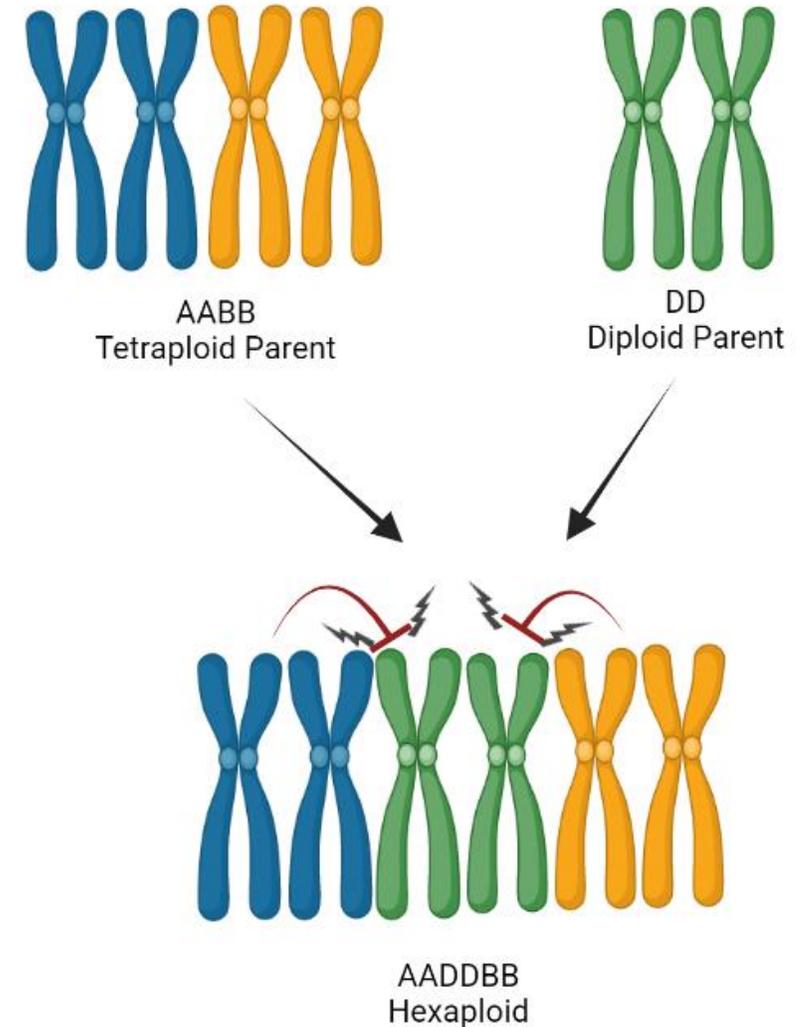
1. Mutually exclusive exons
2. Alternative 3' splicing site
3. Alternative 5' splicing site
4. Retained intron
5. Skipped exon

Results

Manuscript under preparation, hence removed from this slide deck.

Summary

- Within genome comparison of homoeo-allele expression:
 - The repression of D-genome specific homoeologues in synthetic hexaploid background
- Between genome comparison at different ploidy level:
 - Majorly impact on expression of genes in the D-subgenome
- Qualitative differences:
 - Differences in mRNA splicing between parents and the SHW lines
 - Retained intron was the predominantly detected event



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Thank You
நன்றி (in Tamil)