Introgression and characterization of climate-adaptive alleles from wild relatives

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Outline

- Why are wild relatives important in wheat breeding?
- Sources of climate adaptive allelic (CAA) variation from crop wild relatives (CWR).
- Approach for introgressing climate adaptive alleles from CWR for wheat improvement.
- Pipeline for detecting introgression and evaluation of climate adaptive introgressions.
- Prioritization of climate adaptive introgression haplotypes for deployment in wheat breeding programs.
- Practical considerations for effective utilization of wild relative allelic diversity in wheat breeding.

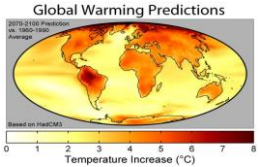
- Why are wild relatives important in wheat breeding?

Biotic factors

Pests and diseases

- Stem rust (Ug99)
- Stripe rust
- Leaf rust
- FHB
- WSMV
- Hessian Fly
- Wheat stem sawfly

Abiotic factors



www.themightyearth.com

Climate change

- Drought stress
- Heat stress
- Floods

Reduced wheat yield

~8 billion people to feed

Stock image. *(iStock/Getty)*

No access to food

- Millions are hungry
- Malnourished
- Poor

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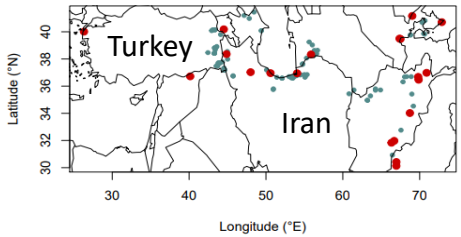
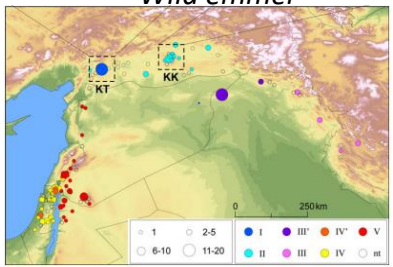
Sources of climate adaptive allelic variation from CWR

A. tauschii



Wild emmer



Özkan et al. 2011

Distribution of *A. tauschii* and wild emmer in the fertile crescent

1. Landraces
   - Contain historical introgressions
   - Due to gene flow between domesticated and wild species
   - Hard to determine the exact source of introgression

2. Introgression populations
   - Derived by crossing wild relatives with elite wheat cultivars or via synthetic hexaploids
   - Capture more climate adaptive alleles
   - Source of adaptive variation is traceable

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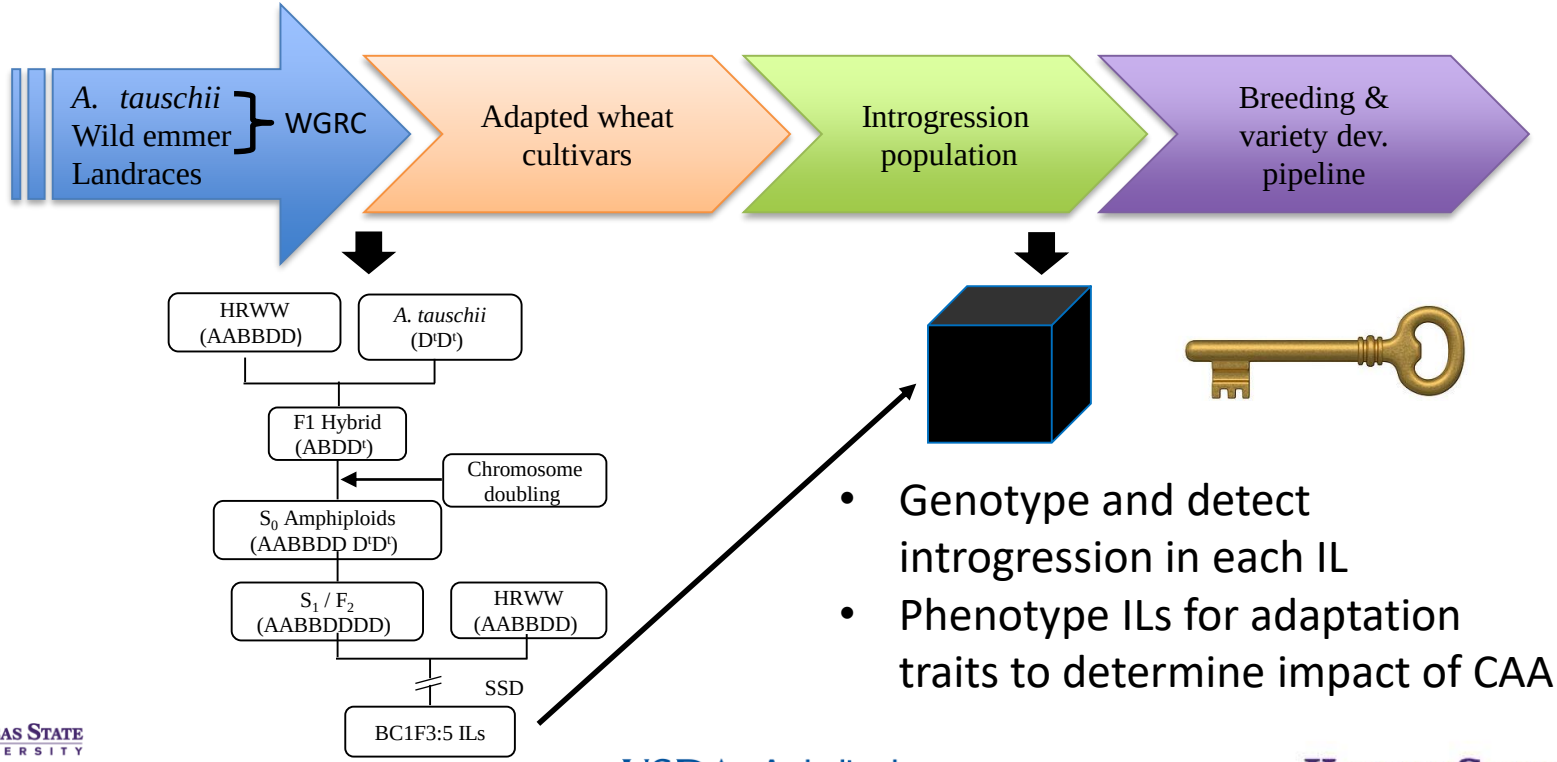
Approach for introgressing climate adaptive alleles from CWR for wheat improvement



- Genotype and detect introgression in each IL
- Phenotype ILs for adaptation traits to determine impact of CAA

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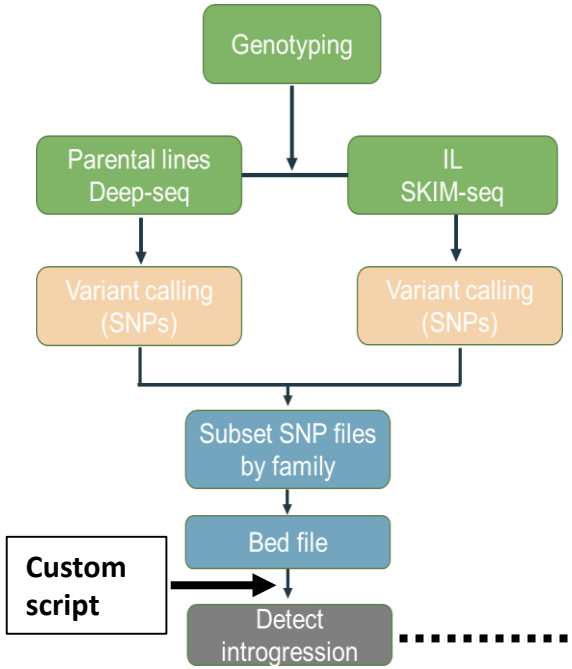
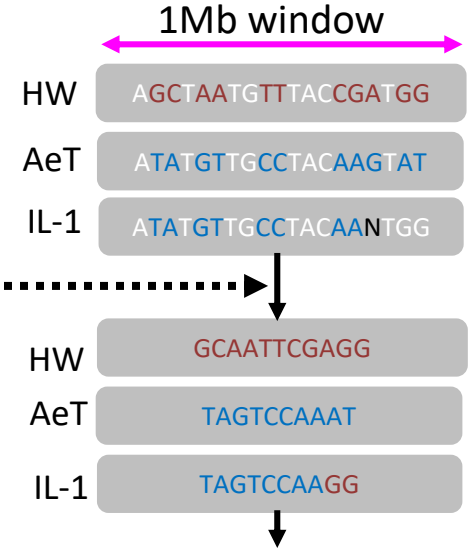
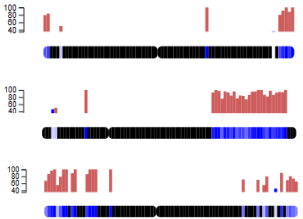
Pipeline for detecting introgressions in adapted hexaploid wheat background



Principle



Acc	Chr	Start	End	HW allele count	AeT allele count	HW prop	AeT prop
IL-1	1D	1	1e6	4	16	0.2	0.8



Chromosome plots showing the proportion of wild relative alleles (red bars) in the introgression lines.

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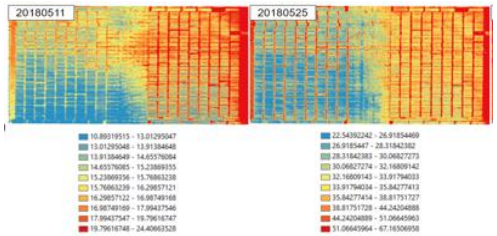
Phenotyping of the introgression population



UAS Thermal image from irrigated and non-irrigated trials

Brittle rachis (*Btr*), Watanabe et al. 2005

- Evaluate ILs under optimal and extreme conditions such as drought and heat stress to identify lines with climate adaptive introgressions.
- Look out for ILs with improved yield under extreme conditions.
- End-use quality, agronomic and domestication traits such as *Tg and Btr* are important considerations for variety development pipeline.
- Remote sensing is critical for traits complex to phenotype such as canopy temperature and vegetation indices.
- Reduce the genetic load by limiting the CWR introgressions to beneficial alleles.

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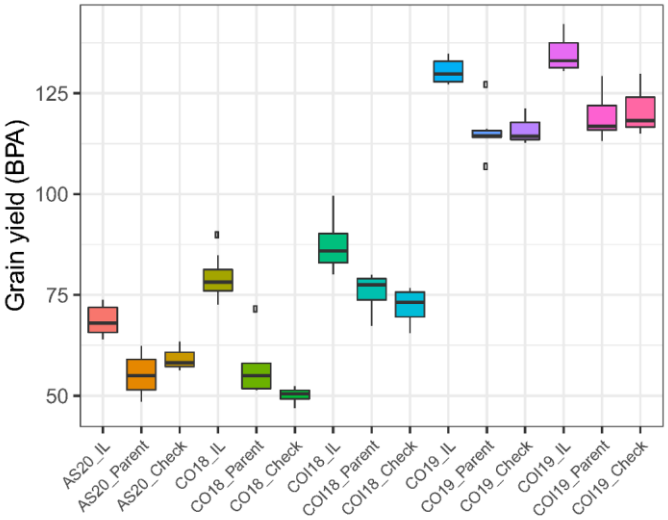
Evaluating the potential of CAA from *A. tauschii* introgressed in winter wheat background



Nyine *et al*. 2021

Group ID	No. of IL	Mean yield IL	Mean yield controls	% yield diff.
AS20_ILP	6	68.6	55.2	24.3
AS20_ILC	6	68.6	59.3	15.8
CO18_ILP	21	78.7	57.1	37.8
CO18_ILC	21	78.7	50.1	57.1
COI18_ILP	94	86.9	75.7	14.8
COI18_ILC	94	86.9	72.1	20.6
CO19_ILP	11	130.5	115.5	13.0
CO19_ILC	11	130.5	116.1	12.4
COI19_ILP	6	134.2	119.2	12.6
COI19_ILC	6	134.2	121.0	10.9

AS: Ashland non-irrigated trial, **CO:** Colby non-irrigated trial, **COI:** Colby irrigated trial**, ILP:** introgression lines by parents' grain yield comparison and **ILC:** introgression lines by checks grain yield comparison.

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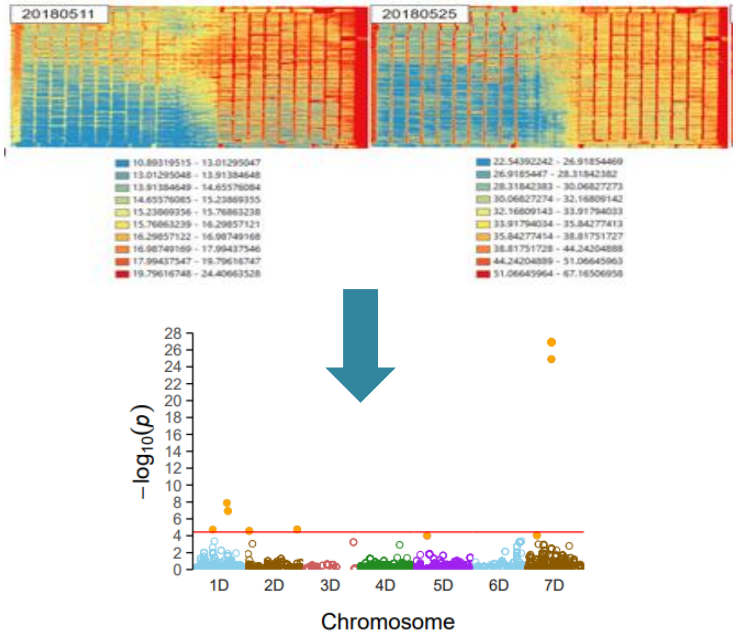
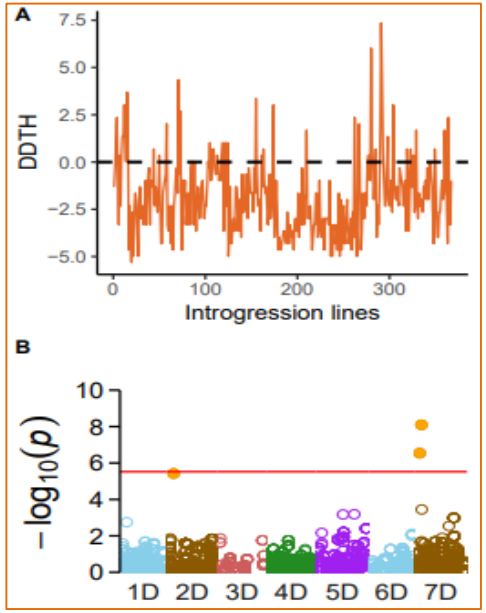
Prioritization of climate adaptive introgression haplotypes for deployment in wheat breeding programs



Canopy temperature



Heading date

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Practical considerations for effective utilization of wild relative allelic diversity in wheat breeding

- Climate adaptive alleles from wild relatives must be introgressed in the best but also diverse adapted hexaploid backgrounds to reduce the breeding cycle and genetic load.
- Whole genome introgressions must be detected and catalogued for efficient allele mining.
- Retention of genome-wide climate novel alleles is necessary for improving quantitative traits like yield and abiotic stress tolerance.
- Linkage drag between climate adaptive alleles and deleterious alleles must be minimized.
- In-depth analysis of adaptive variation and traceability through cost-effect high throughput genotyping platforms e.g. KASP markers, MIPs or SNP-chip is necessary.

Summary

- We developed a pipeline for detecting introgression which is a key step toward novel allele mining in the introgression population.
- Introgression of wild relative climate adaptive alleles in adapted wheat background generated introgressions lines that can either go into variety development pipeline or the breeding pipeline as donor parents.
- Field evaluation of the introgression population suggests the potential of wild relative adaptive alleles for improving wheat yield under water limiting conditions.

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