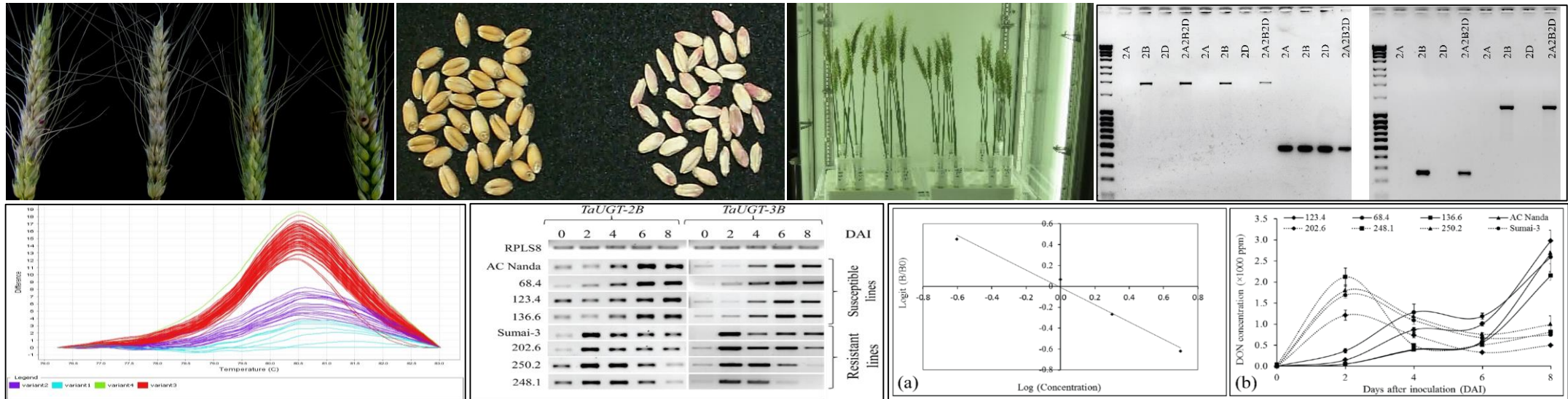


Development and Utilization of Single Nucleotide Polymorphic Markers on *UDP-Glucosyl Transferases* to Develop *Fusarium* Head Blight Resistant Wheat Varieties



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Fusarium head blight (FHB) – New sources of resistance are needed

- Major disease of wheat
- *Fusarium graminearum* Schwabe
– most common species



FHB infected wheat spikes

- FHB reduces wheat yield and grain quality
- Deoxynivalenol (DON) – virulence factor for FHB

↓
Toxic to humans

2 ppm – Food	} Health Canada
1 ppm – Baby food	



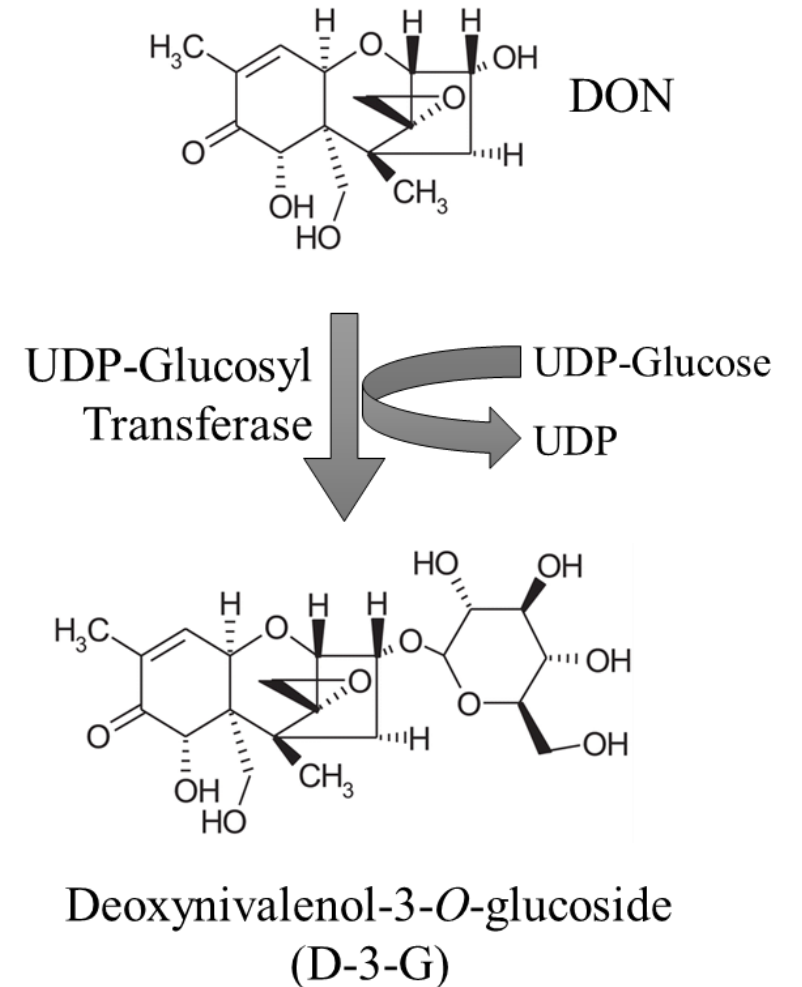
Healthy grains

FHB infected grains

- Mutagenesis can be followed to induce variation in the trait

FHB resistance in wheat

- FHB resistance – Quantitative trait
- B-genome of wheat (AABBDD) participates predominantly in FHB resistance
- *FHB1* - major QTL (Quantitative Trait Loci)
 - Present on 3BS
- *UGT* gene - Encodes UDP-glucosyl transferase
 - Present in close vicinity of *Fhb1*



Hypothesis

- Ethylmethane sulfonate can induce variation for FHB resistance using *in vitro* spike culture technique.
- Candidate genes for FHB resistance on B-genome of wheat can be targeted to find single nucleotide polymorphic (SNP) markers.

Objectives

- To study FHB resistance in the mutant population.
- To identify SNP markers associated with FHB resistance.
- To utilize FHB resistant genotypes and SNP markers in a breeding program.

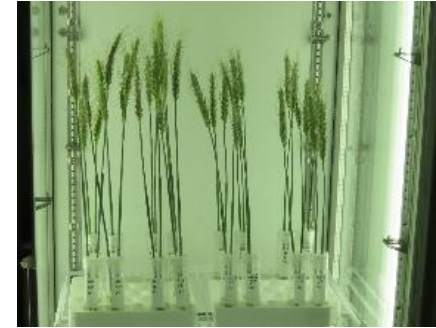
Workflow of the project



Spike Culture Derived Variants (SCDV) of AC Nanda - EMS



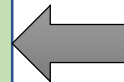
A population of 134 SCDV lines was developed



Identification of FHB resistant and susceptible lines – *in vitro* spike culture

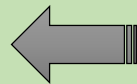


Wheat spikes of resistant and susceptible SCDV lines
AC Nanda – FHB susceptible control
Sumai3 – FHB resistant control

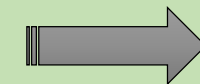


Identification of SNPs by comparing gene sequences from AC Nanda and Sumai3

SNPs validation in SCDV population



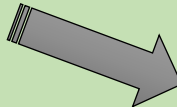
Expression and DON accumulation study



Transcriptome analysis



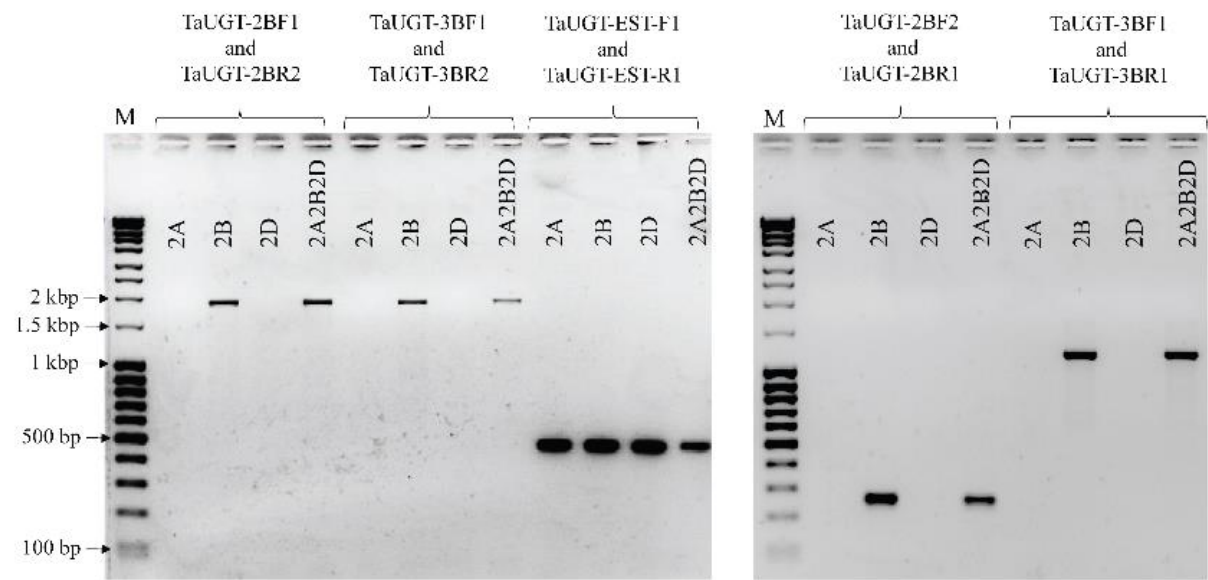
Field experiments



Breeding program

Genome specificity of the primers

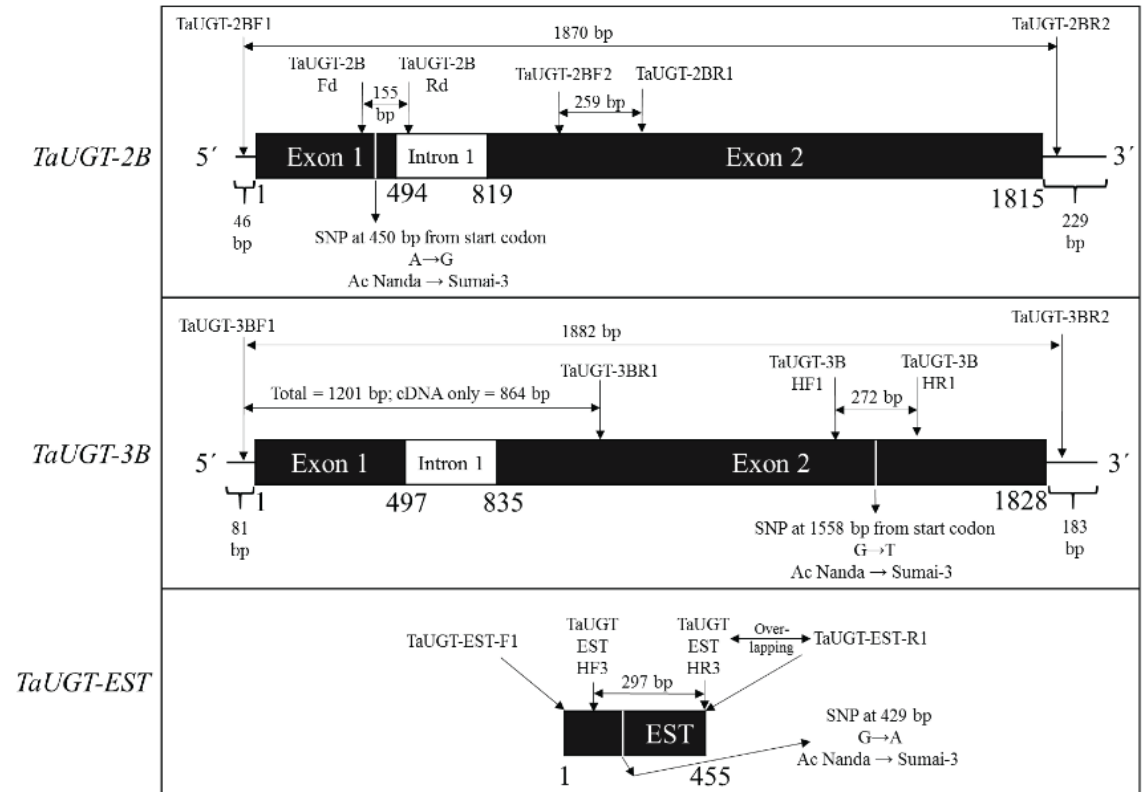
2A = *Triticum monococcum*
 2B = *Aegilops speltoides*
 2D = *Aegilops Tauschii*
 2A2B2D = Hexaploid Wheat



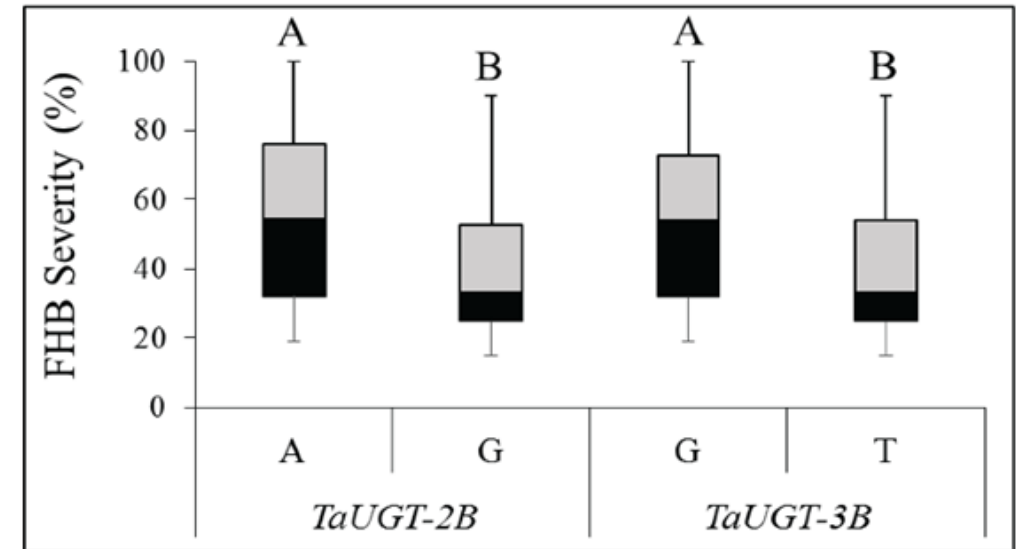
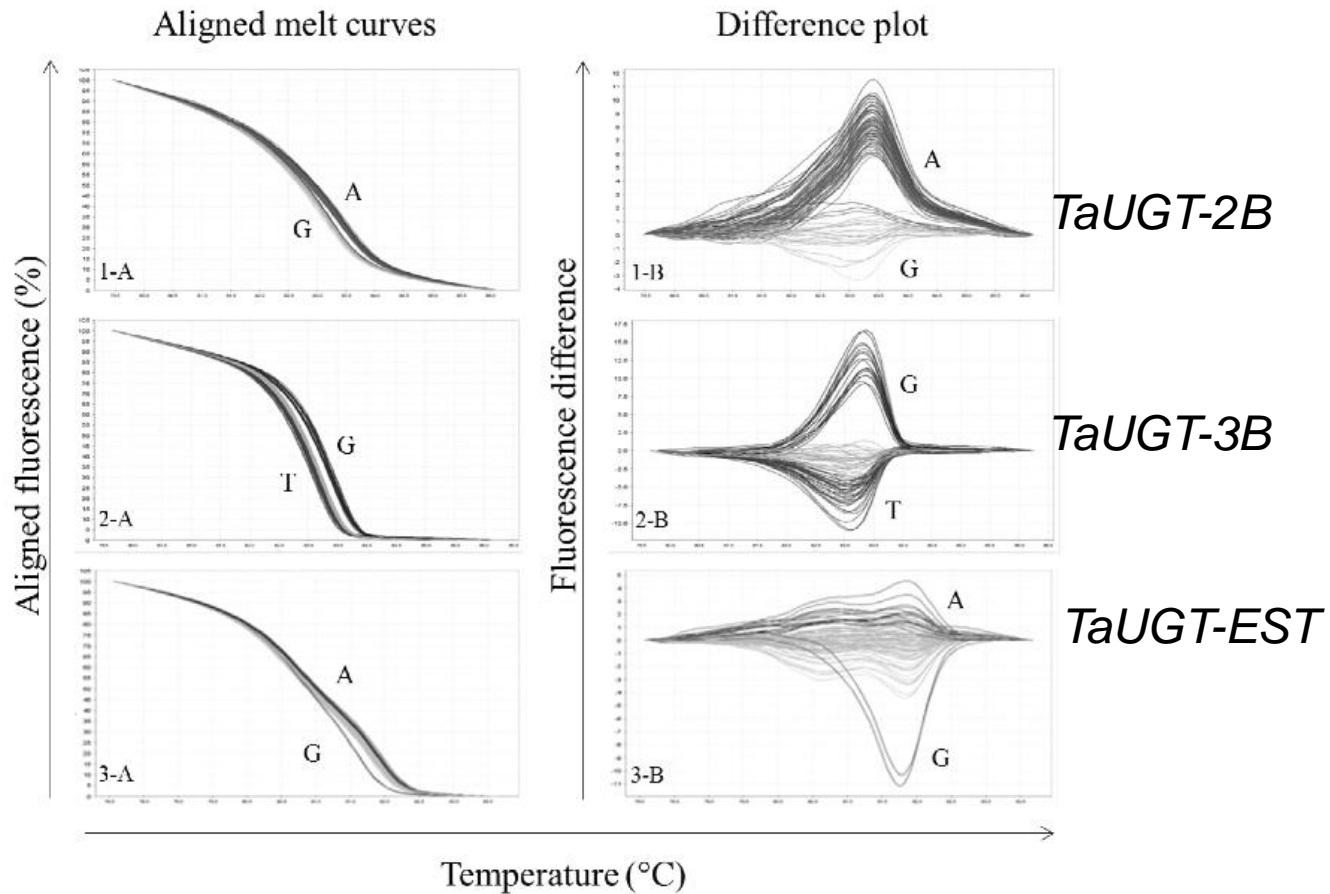
Schematic representation of B-genome specific *UGT* genes



Single Nucleotide Polymorphic (SNP) Markers on the genes



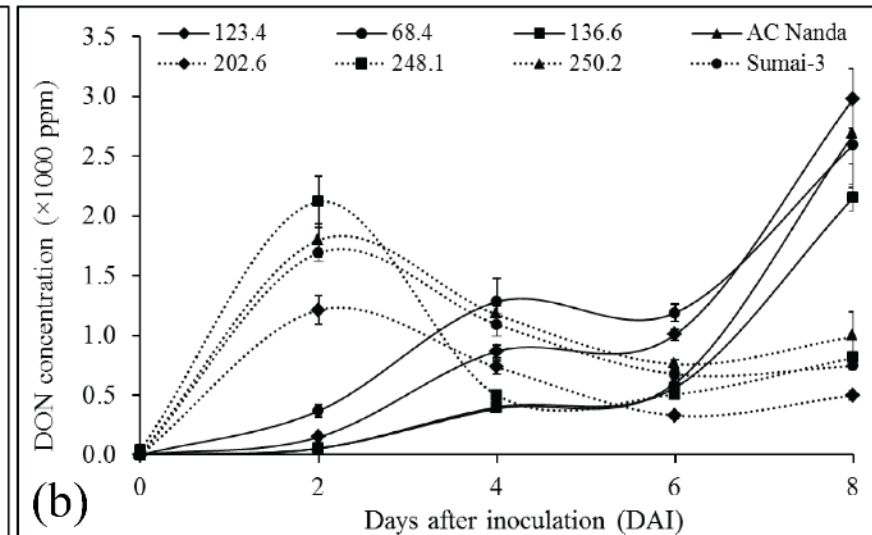
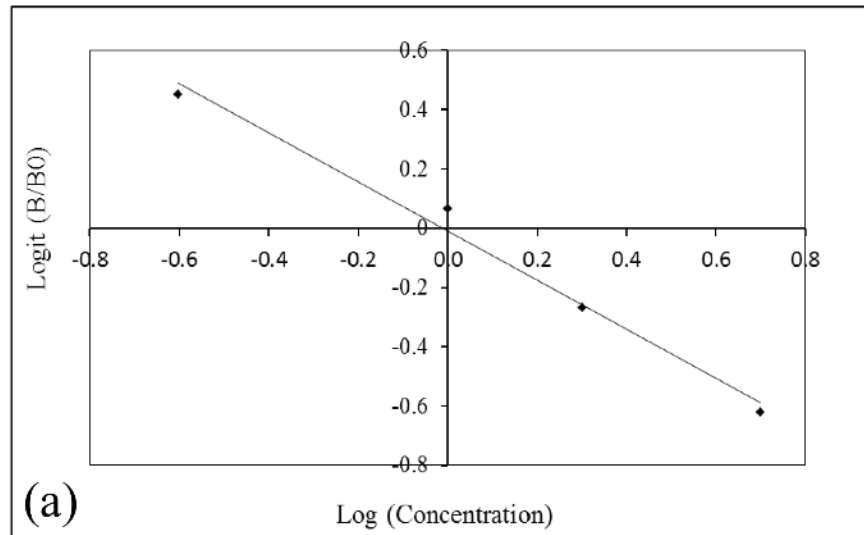
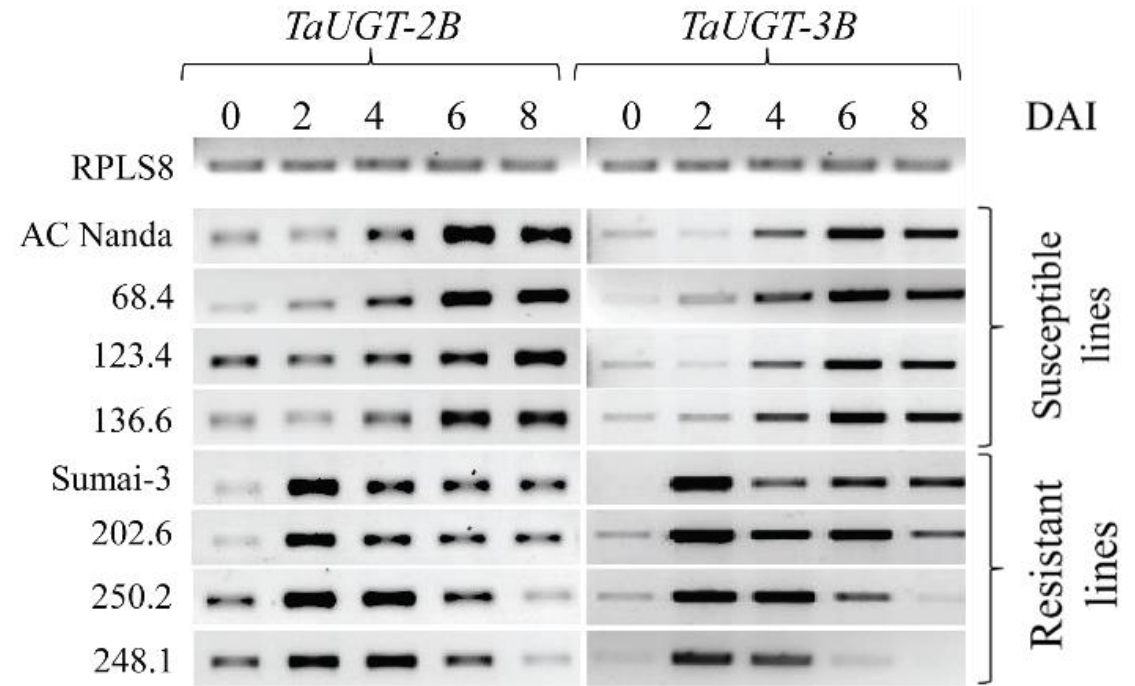
SNP markers on *UGTs* can significantly differentiate between FHB -resistant and -susceptible genotypes



Box plot analysis of *UGTs* and FHB severity

High resolution melt curve (HRM) analysis

Expression of *UGTs* correlates with accumulation of Deoxynivalenol



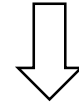
FHB rating in field experiments confirms the reliability of *in vitro* spike culture technique

Location and Trait	Mean Sum of Squares	
	Genotype	Replication
Carmen		
Incidence	260.5***	13.3ns
Severity	285.5*	40.8ns
Visual rating index (VRI)	265.1**	29.5ns
FHB Nursery (University of Saskatchewan)		
Incidence	651.0**	175.2ns
Severity	76.2**	200.2ns
VRI	72.9***	93.2ns

***, ** and * are significant at $P \leq 0.001$, 0.01 and 0.05, respectively whereas, ns represents non-significant values.

Transcriptome analysis during FHB progression

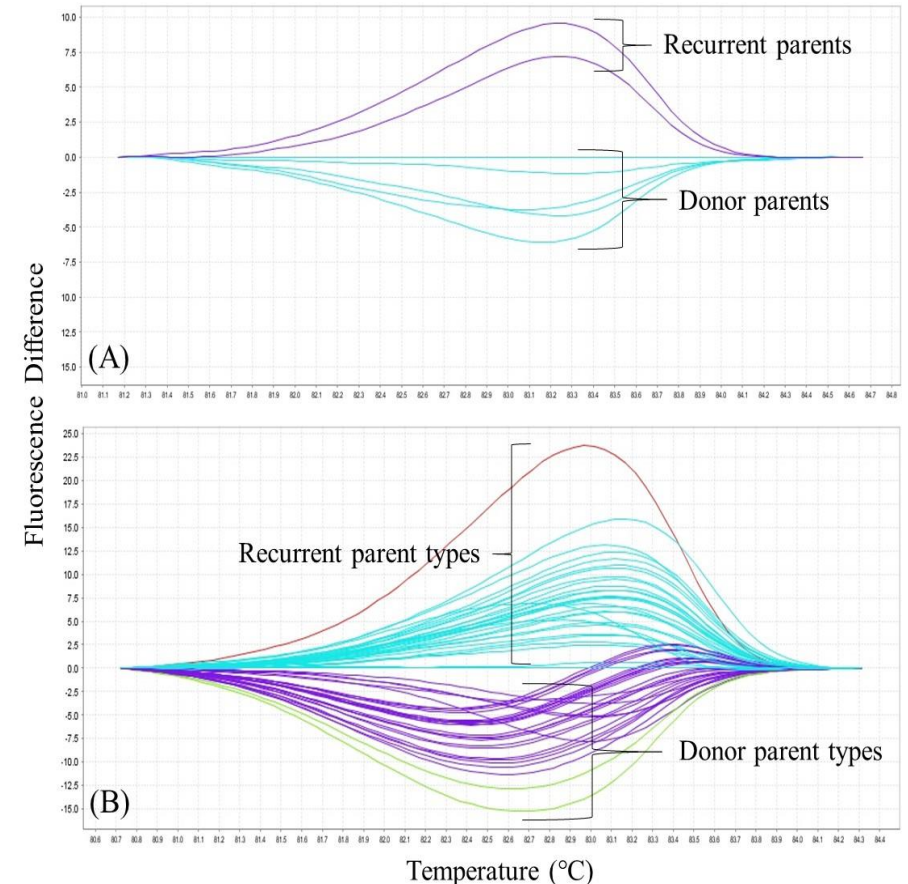
RNA-seq was performed in FHB resistance (5) and susceptible (3) wheat genotypes



New candidate genes and markers will be identified

Breeding Program

- FHB resistant SCDV lines are being crossed with Saskatchewan elite cultivars.
- SNP markers are being utilized to screen the population.



Conclusions and Future Directions

- An *in vitro* spike culture method was optimized to evaluate FHB resistance in wheat.
- New genetic resources of FHB resistance and associated SNP markers were identified that are being used in the breeding program to develop FHB resistant wheat variety.
- To understand the FHB resistance mechanism, transcriptomics has been done on FHB resistant and susceptible lines and the data is being analyzed.

Acknowledgements

- Ravindra N. Chibbar
- Seedhabadee Ganeshan
- H. Randy Kutcher
- Pierre J. Hucl
- Pallavi Sharma
- Chen Huang



Canada Research
Chairs



NSERC
CRSNG

