IDENTIFICATION OF NEW QTL FOR NATIVE RESISTANCE TO FHB IN SRW WHEAT

Subas Malla
Virginia Tech

FUSARIUM HEAD BLIGHT OF WHEAT

- Estimated $3 billion in losses due to FHB (McMullen et al., 1997)
- Methods of control
  - Reduction of crop residue – tillage
  - Fungicide application – reduce disease severity
    - Disease prediction models
    - Target fungicide and biocontrol application
- Breeding for resistance

FUSARIUM HEAD BLIGHT OF WHEAT

- Breeding for resistance gives consistent and durable protection (Bai and Shaner, 2004)
- FHB resistance QTL have been mapped on every wheat chromosome
- Complete resistance not identified (Buerstmayr et al., 2009; Dodds and Rathjen, 2010). Putative genes are:
  - *Fhb1* – 3BS ‘Sumai 3’
  - *Fhb2* – 6BS BW278
  - *Fhb3* – 7DS from alien *Leymus racemosus* (wild rye)
  - *Fhb4* – 4BL Chinese landrace Wanshuibai
  - *Fhb5* – 5AS Chinese landrace Wanshuibai
- United States: Becker, Ernie, Freedom, Goldfield, IL94-1653, Massey, Patterson, Patton, SD97060, Stoa, and Truman (Buerstmayr et al., 2009; Liu et al., 2009).

SRW WHEAT CULTIVARS

Jamestown:

- Parents: Roane / Pioneer Brand '2691'
- Resistance to multiple diseases including:
  - FHB (*Fusarium graminearum*)
  - Leaf rust (*Puccinia triticina*),
  - Stripe rust (*Puccinia striiformis*)
  - Hessian fly (*Mayetiola destructor*)

Tribute:

- Parents: VA92-51-39/AL870365

- Jamestown and Tribute are widely used parents in the Mid-Atlantic and Southern states (Griffey et al., 2010).

OBJECTIVES

- 1) Characterize and map quantitative trait loci (QTL) for resistance to Fusarium Head Blight (FHB) in soft red winter wheat cultivars Jamestown (‘Roane’/ Pioneer Brand ‘2691’), Roane, and Tribute.
- 2) Identify tightly linked DNA markers associated with FHB resistance QTL in these cultivars that can be used in marker-assisted selection (MAS) and pyramiding of resistance genes.

MATERIALS & METHODS

Jamestown and Roane Mapping Populations:

- Jamestown Mapping Populations:
  - Pioneer Brand ‘25R47’ x Jamestown (P47/JT): 184 $F_{5:7}$ RILs
  - F/G95195 X Jamestown (FG/JT): 177 $F_{5:7}$ RILs
  - Jamestown X LA97113UC-124 (JT/LA): 77 $F_{5:7}$ RILs
- Roane Mapping Populations:
  - Roane X Allegiance (R/A): 33 $F_{4:7}$ RILs
  - Roane X KY93C-1238-17-1 (R/KY93); 18 $F_{4:7}$ RILs
- Evaluated in 2011 & 2012 Scab nurseries:
  - The FG/JT and JT/LA RILs (southern populations) were grown and evaluated for FHB incidence (Inc) and severity (Sev) in AR, LA, GA and VA scab nurseries in 2011 and 2012.
  - The P47/JT RILs and Roane (R/A and R/KY93) RILs (northern populations), were grown and evaluated for FHB Inc and Sev in 2011 and 2012 scab nurseries. The P47/JT RILs were evaluated in MD, NC, VA, and Roane RILs in MO, MD, NC, VA, and KY.

MATERIALS & METHODS

Jamestown and Roane Mapping Populations:

- Genotyping:
  - Monsanto Company used a 9k platform to run single nucleotide polymorphic (SNP) markers on the population. The following number of RILs from each of the populations:
  - JT/LA -77 $F_{5:7}$ RILs
  - P47/JT – 42 $F_{5:7}$ RILs
  - Additionally, the remaining 142 RILs from P47/JT were genotyped for 90K SNP in collaboration with USDA-ARS Genotyping Centers at Fargo, ND and Raleigh, NC.
  - Bulk Segregant Analysis (BSA) was used to genotype with SSR markers in the populations.
  - Molecular markers associated with stable QTL in the P47/JT population were genotyped in JT/LA and FG/JT populations for QTL validation. Additionally, molecular markers associated with the stable QTL from P47/JT were also genotyped in R/A and R/KY93 populations.

MATERIALS & METHODS

Tribute Mapping Population:

- Pioneer Brand ‘26R46’ x Tribute (P46/Tribute): 115 DH Lines

Evaluated in 2013 & 2014 Scab nurseries:

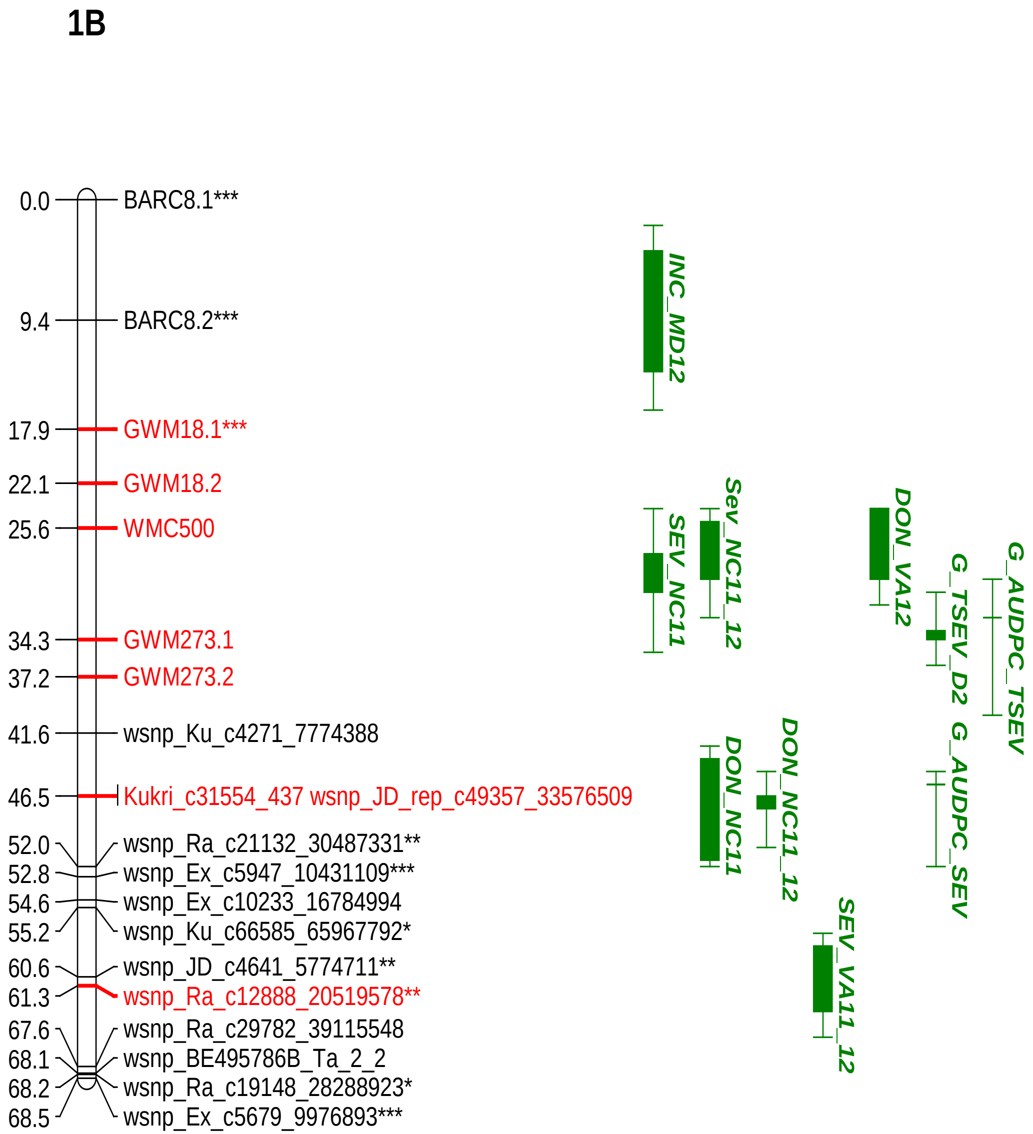
- The DH lines were evaluated for FHB incidence, severity, Fusarium damaged kernel (FDK), and morphological traits in scab nurseries at two locations in AR [Fayetteville, AR (AR_F), Newport, AR (AR_N)], and one location each in KY, MD, NC, and VA in 2013 and 2014 except MD in 2014. Deoxynivalenol (DON) content of the DH population has been analyzed for tests from all locations in 2013 and for VA in 2014.

Genotyping:

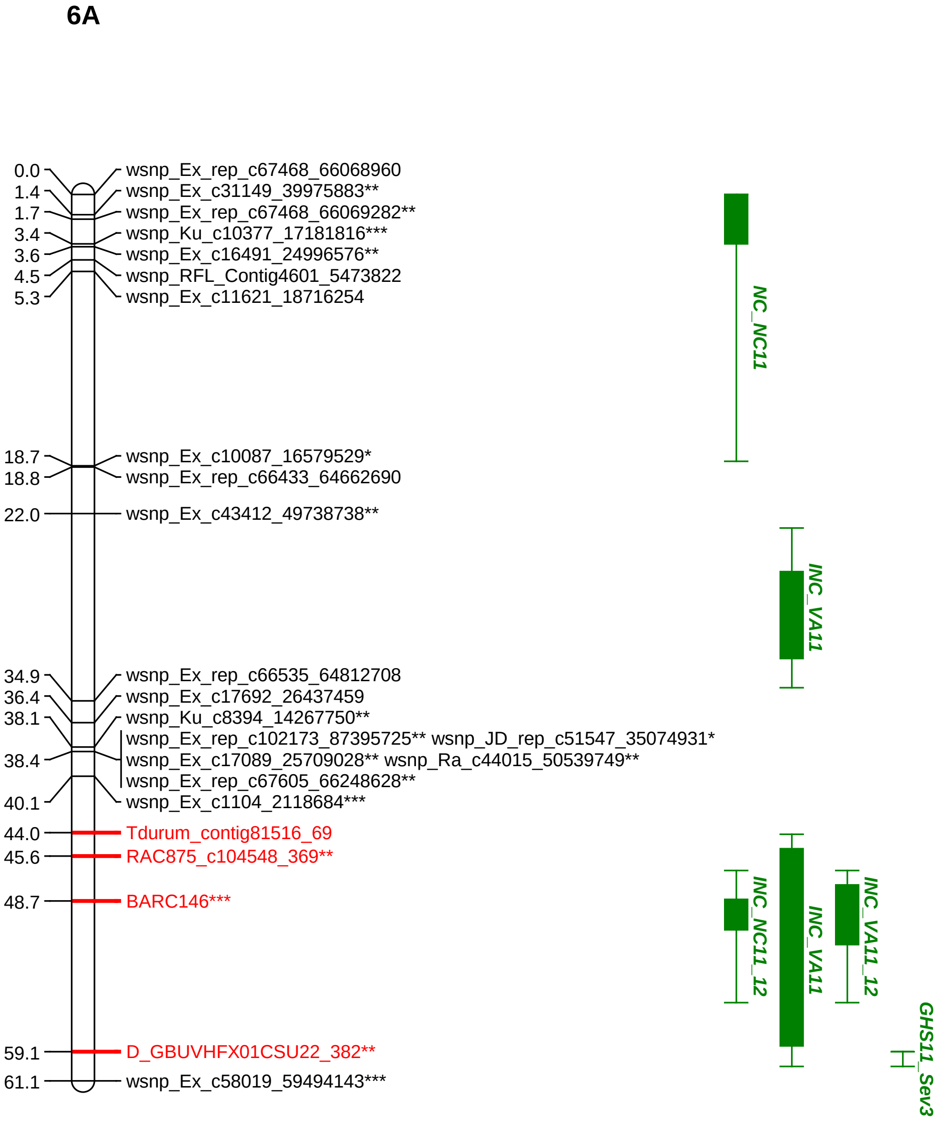
- Selected SSR markers were used to genotype the population.

TYPE II SCREENING IN GREENHOUSE

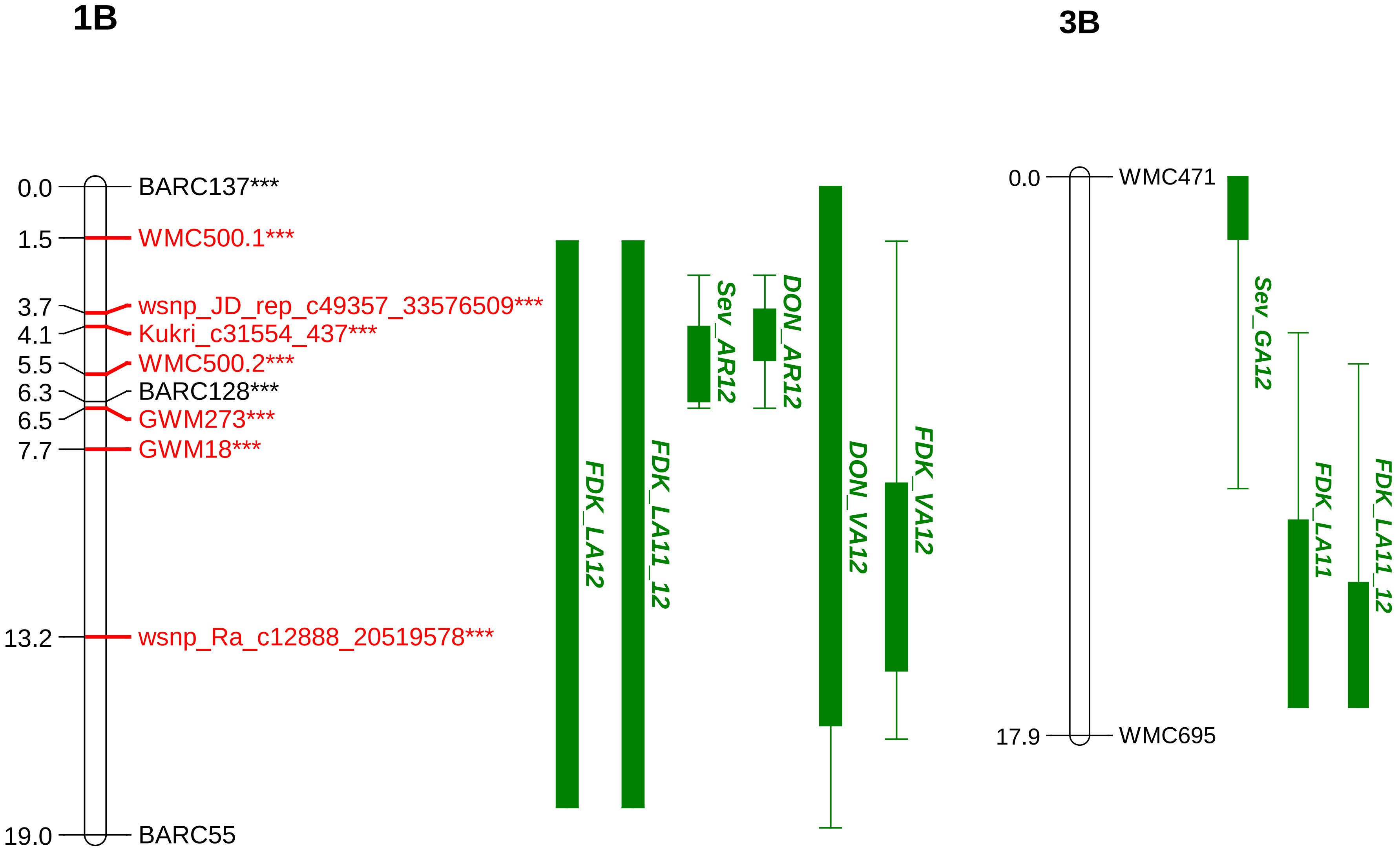
RESULTS: P47 / JT Stable QTL



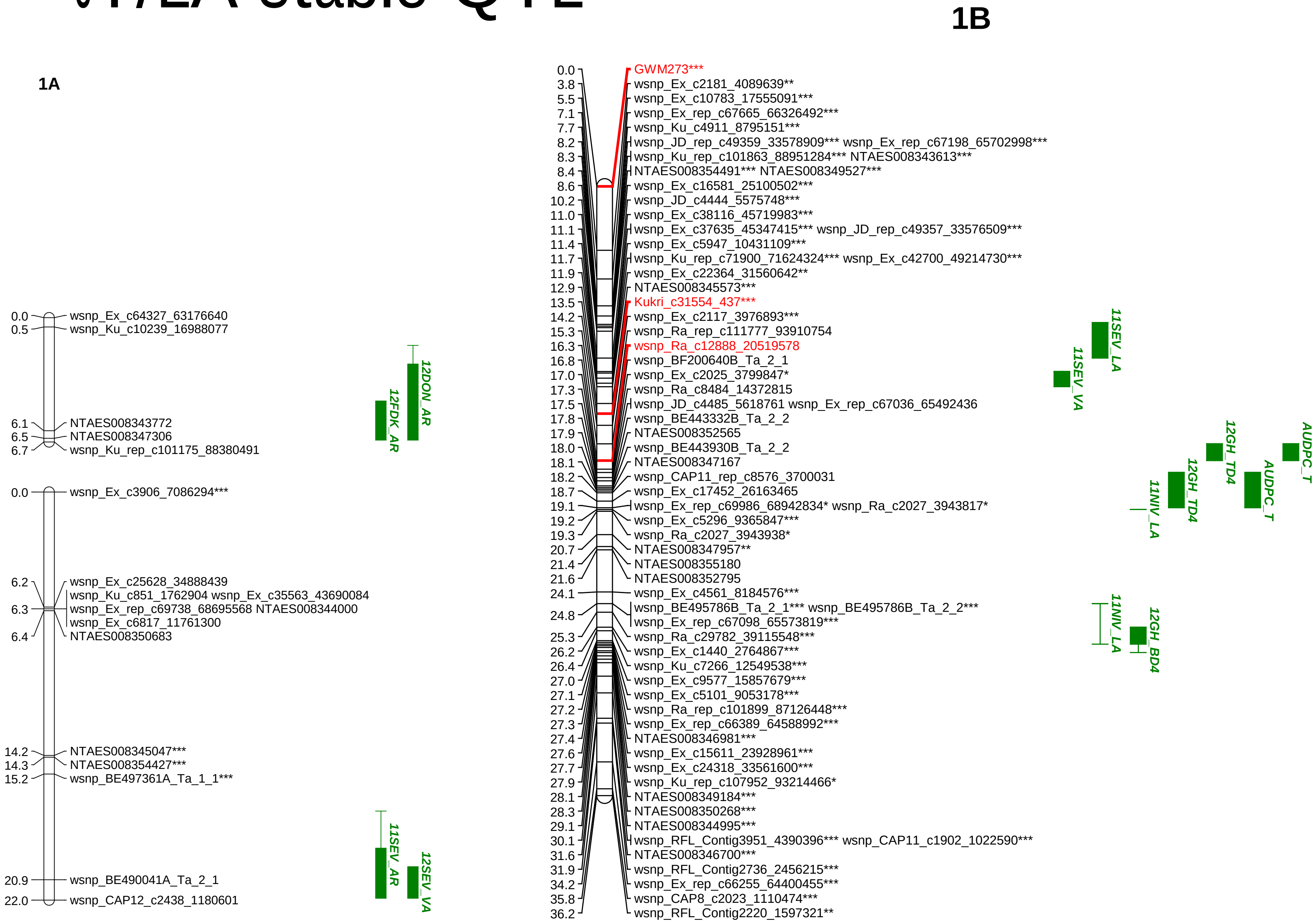
P47 / JT Stable QTL (Contd.)



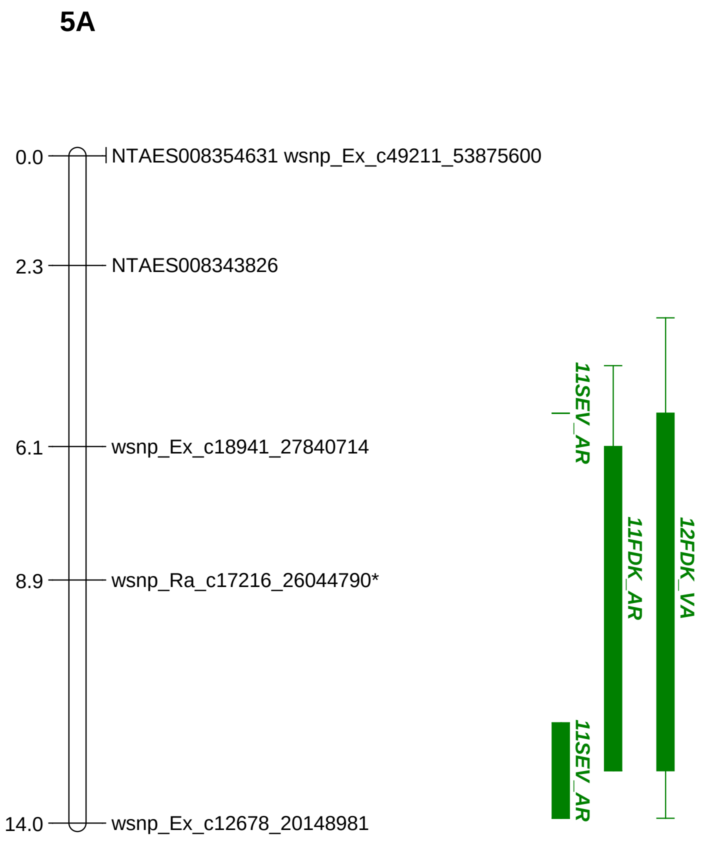
FG / JT Stable QTL

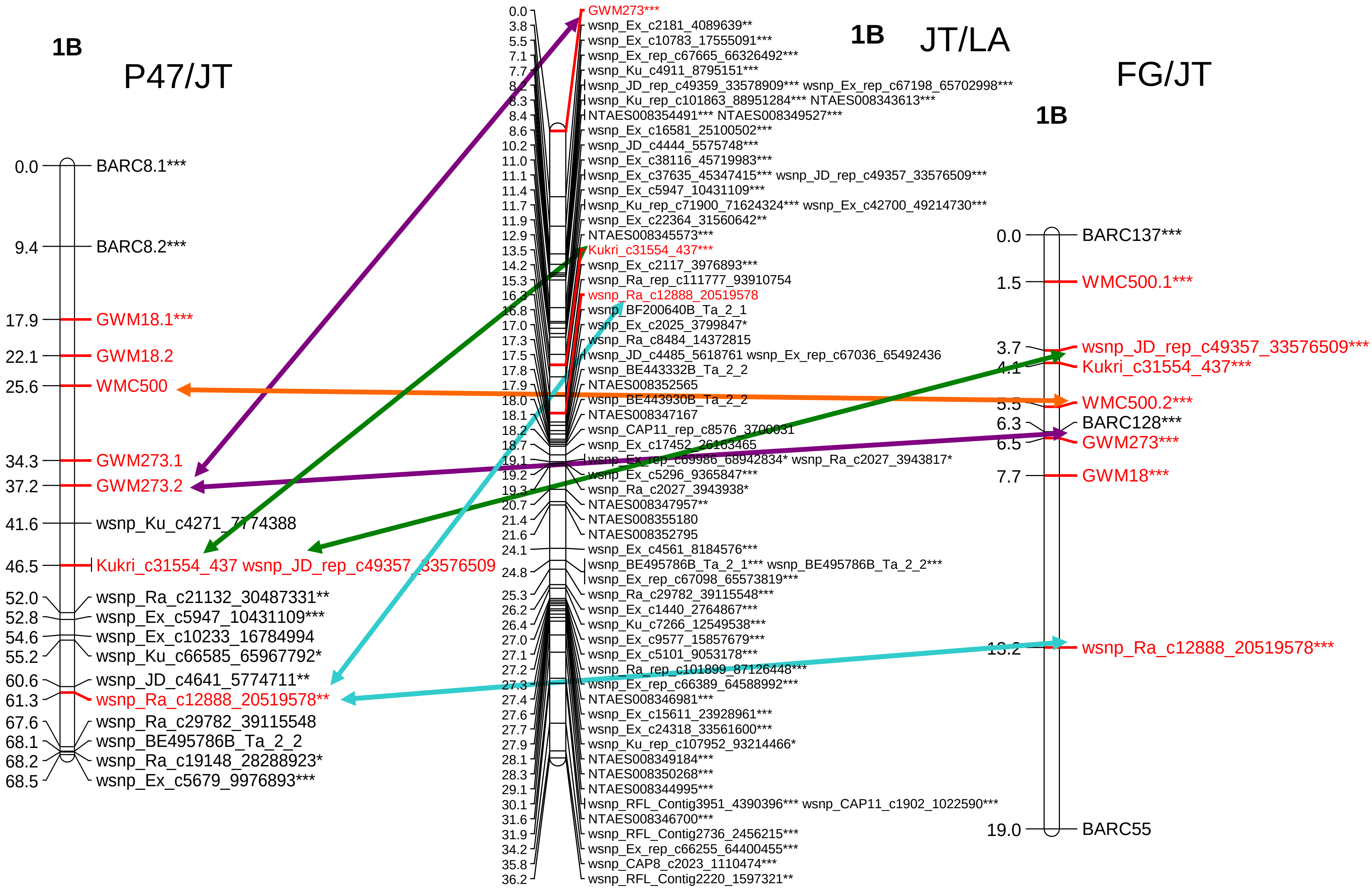


JT/LA Stable QTL



JT/LA Stable QTL (Contd.)





Marker	Marker Type	Population	LOD	R2	Additive	Basepair Size
Kukri_c31554_437	SNP	P47/JT	3.1 to 6.8	6.7 to 11.8	-1.1 to -2.6;AUDPC:-83.7	
Kukri_c31554_437	SNP	JT/LA	2.4 to 3	10 to 12.5	-7.1 to -7.5;AUDPC:-99.5	
Kukri_c31554_437	SNP	FG/JT	3.05 to 5.7	7.6 to 14.1	-0.7 to -2.9	
Wmc500	SSR	P47/JT	3 to 8.2	6.7 to 23.4	-6.0 to -7.5	Jamestown=188
Wmc500	SSR	FG/JT	3.4 to 6.2	8.2 to 14.5	-0.7 to -3.1	Jamestown=188

QTL PREVIOUSLY IDENTIFIED ON CHROMOSOME 1B

Table 1.2: QTL Identified on Wheat Chromosome 1B for Resistance to Fusarium Head Blight and Deoxynivalenol (DON)

Resistance Trait	**Original Source**	**Molecular Markers Associated with QTL**	**References**
Severity†	Alondra¶	*XeTCG-mAGC.7 - XeACCGmCT-C.7*	Zhang et al., 2004
Incidence‡	Cansas¶	*XE38M52.378 - Xgwm131*	Klahr et al., 2007
Severity	Fundulea201R¶	*Xbarc8*	Shen et al., 2003
Severity	Lynx¶	*Xp78m51.237- Xs26m23.356 (Xgwm18.iag95)*	Schmolke et al. 2005
Severity	Rialto¶	*XwPt-0705*	Srinivasachary et al., 2008
Severity	Seri82¶	*Xe38m50_10*	Mardi et al., 2006
Severity	Sincron¶	*Gli-R1*	Ittu et al., 2000
Severity	Arina_1	*XS16M14.400*	Draeger et al., 2007
Severity	Romanus	*XP70M56.308*	Holzapfel et al., 2008
Severity	CM82036	*XgluB1*	Buerstmayr et al., 2002
Severity	Wangshuibai_1	*Xgwm018- Xbarc181*	Lin et al., 2004
Severity	Wangshuibai_2	*Xwms759*	Zhou et al., 2004
DON§	Wangshuibai_3	*Xwms759*	Yu et al., 2008
Severity	Arina_2	*XP43/M62-400 - XwPt-3475*	Semagn et al., 2007
Severity	History	*XP64M51.190*	Holzapfel et al., 2008
Severity	Biscay	*XP64M51.190*	Holzapfel et al., 2008
Severity	Pirat	*XP64M51.190*	Holzapfel et al., 2008
Incidence & Severity	Remus	*Xs12m25.14 - Xs24m17.2*	Steiner et al. 2004

†Severity = resistance to spread of FHB in the wheat spike

‡Incidence = resistance to initial infection of FHB

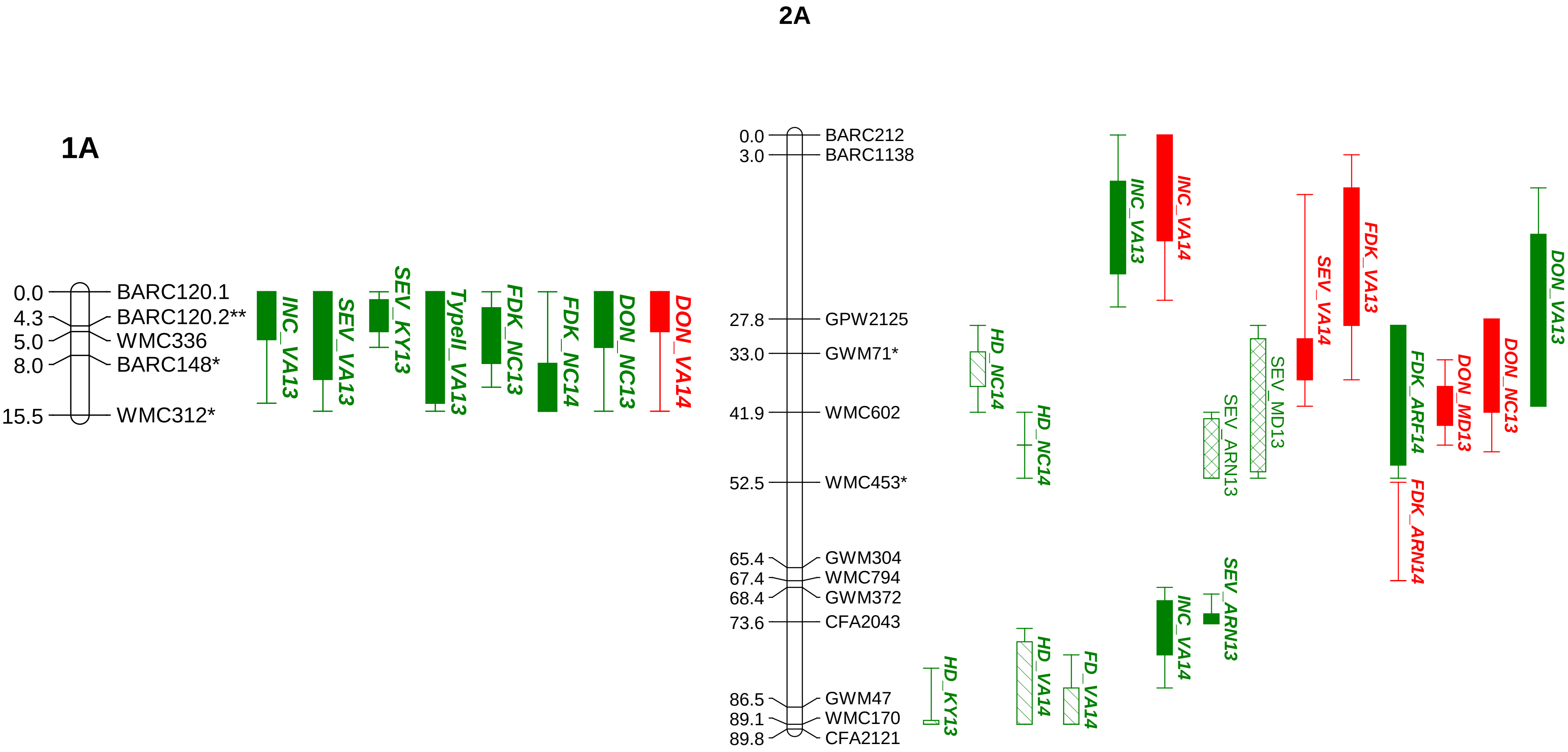
§ DON = resistance to deoxynivalenol accumulation in the seed

¶ T1BL.1RS translocation

Validation in Roane Populations

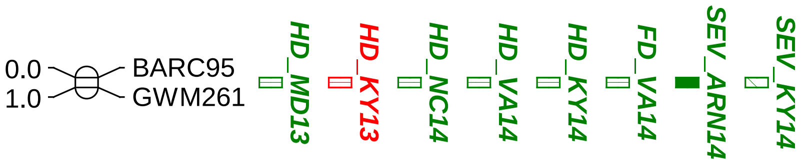
- Six SNP molecular markers, three each from 1B and 6A, associated with the stable resistance QTL from P47/JT population were not significant ($P < 0.001$) in single marker analysis in the Roane (R/A and R/KY93) populations.
- This suggests that these QTL for FHB resistance in Jamestown were not derived from Roane; although, this needs to be further validated.

P46 / Tribute Stable QTL

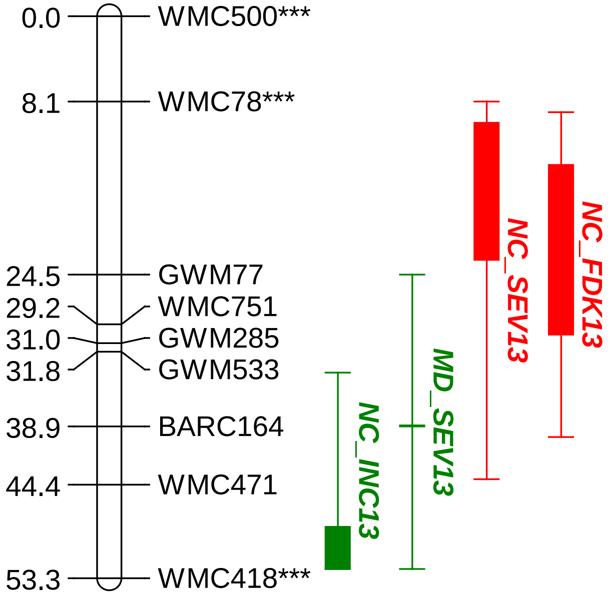


P46 / Tribute Stable QTL (Contd.)

2D



3B



CONCLUSIONS

Jamestown:

- A stable FHB resistance QTL was identified and validated on 1B in Jamestown.
    - Dignostic molecuar markers: *Wmc500* (SSR; 188 bp for Jamestown), *Kukri_c31554_437* (SNP)

Tribute:

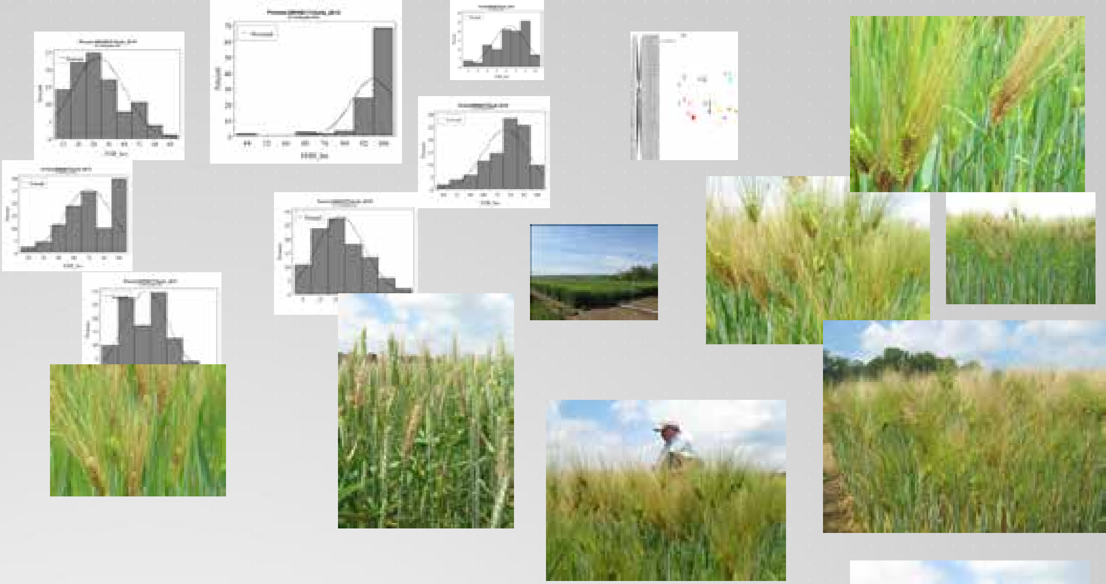
- Stable resistance QTL were found on chromosomes 1A, 2A, and 3B. The QTL on 1A and 3B could be utilized in marker assisted selection (MAS) for FHB resistance in wheat breeding programs. The QTL on 2A could be utilized in MAS for FHB resistance in wheat breeding programs where earlier heading and flowering dates are preferred.

Future Work

- Validation of QTL from the populations:
  - FG95195/Jamestown
  - Jamestown/LA97113UC-124
- SNP Markers: 90K platform in Pioneer 26R46 / Tribute Population
- Identify tightly linked markers for use in MAS and gene pyramiding in Jamestown and Tribute

ACKNOWLEDGEMENTS

- Dr. C. Griffey
- VA Tech Small Grains Breeding Group
- Dr. P. Murphy, Dr. J. Costa, A. Cooper, Dr. E. Milus, Dr. J. Johnson, Dr. S. Harrison, Dr. D. Van Sanford, A. Clark, Dr. McKendry
- Dr. D. Schmale and N. McMaster
- USDA-ARS Regional Genotyping Centers at Fargo, ND and Raleigh, NC
- U.S. Wheat and Barley Scab Initiative
- Virginia Small Grain Board
- Monsanto SNP genotyping group



Questions?