Molecular Mapping of Fusarium Head Blight Resistance in 'Glenn' Spring Wheat Cultivar

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Abstract

Fusarium head blight (**FHB**) is a major disease that affects both wheat yield and quality in many wheat-growing regions, including the US Northern Plains. Therefore, developing wheat cultivars with high resistance to FHB is crucial. Successfully, North Dakota State University's spring wheat breeding program has released several FHB-resistant cultivars including the high yielding 'Glenn' and 'Parshall'. Based on Glenn's pedigree, its resistance is based on 'Sumai3'. However, molecular analysis showed that Glenn does not possess any molecular markers associated with the major QTL Sumai3-*Fhb1* locus (including the Umn10). In this study we attempted to understand the genetics of FHB-resistance in 'Glenn'. To achieve this goal, a (**GM**) RIL population developed from a cross between the resistant parent (Glenn) and the susceptible parent (MN00261-4). The population was assessed for different FHB variables (incidence (**INC**), severity (**SEV**), and deoxynivalenol (**DON**) level) and plant height (**HGT**) in several field and greenhouse experiments in the states of ND, MN using artificial inoculation. Besides, GM population was genotyped using Diversity Array Technology (**DArT**). Linkage map generated and used in QTL analysis for FHB traits. Total QTL identified were 15 (SEV); 15 (INC); 7 (DON) and 8 (HGT). One major QTL (located on 5B) for SEV was detected in 4 environments. Six QTL (located on 1B, 5B, 6B, 7A, 7D) for SEV and 1 QTL for INC (located on 1A) were all detected in 2 environments. The study did not identify consistent QTL with Sumai3 background, suggesting that the resistance source in Glenn is something other than Sumai3.

FHB Screening

Population:

- 112 (**GM**) RILs developed from Glenn (FHB-resistant) × MN00261-4 (FHB-susceptible).

Phenotyping:

- **FHB Severity (SEV):** percentage of diseased spikelets on the infected spick (Disease spread)➔**for 6-environments.**
- **FHB Incident (INC):** percentage of infected spikes per entry ➔ **for 4-environments.**
- **FHB DON Analysis:** DON concentration is run by gas chromatography and/or mass spectroscopy methods ➔ **for 2-environments.**
- **Plant heights (HGT):** measured by inch scale from ground to spikes tip excluding awns ➔ **for 2-environments.**

Mapping

Genotyping:

- **DArT** analysis http://www.triticate.com.au.

Genetic map and QTL analysis:

- **645** DArT markers mapped to **37** linkage groups belonging to **19** chromosomes (excluding **4D** and **5D**).
- Total genetic distance=2,229 cM (4.87cM/marker loci).
- Composite interval mapping (**CIM**) carried out using QTL CARTOGRAPHER.

Table 1. Important QTL repeated in more than 2 environments for FHB traits (SEV, INC, DON and HGT).

QTL	Chrom. (group)	Environments*	LOD	QTL effect	R^2(%)	Other associated traits
FHB severity (SEV)						
QSEV.GM.ndsu-1B.2	1B.1	Pros-2010, MN-2010	3.21	3.44	10.26	INC
QSEV.GM.ndsu-2B.2	2B.2	Pros-2011	5.79	3.27	17.12	
QSEV.GM.ndsu-2D	2D.1	Pros-2012	3.7	-4.74	13.78	
QSEV.GM.ndsu-5B.2	5B.1	Carr-2011, Pros-2012	4.09	-4.47	12.09	DON
QSEV.GM.ndsu-5B.3	5B.1	GH-2011, Pros-2010, Pros-2012, Carr-2011	7.86	6.21	20.49	INC
QSEV.GM.ndsu-6B.1	6B.2	GH-2011, Pros-2011	4.29	-6.29	12.1	
QSEV.GM.ndsu-7A.1	7A.1	Carr-2011, MN-2010	2.6	-3.09	8.61	INC, HGT
QSEV.GM.ndsu-7D.1	7D.1	MN-2010,Pros-2010	2.86	7.23	10.44	
QSEV.GM.ndsu-7D.2	7D.1	Pros-2010, MN-2010	4.04	-8.27	12.39	INC
FHB incidence (INC)						
QINC.GM.ndsu-1A.1	1A	MN-2010	3.37	-4.1	9.03	HGT
QINC.GM.ndsu-3B.2	3B	MN-2010	2.04	-2.95	4.94	DON
QINC.GM.ndsu-7A	7A.1	MN-2010	2	-3.05	5.17	SEV-HGT
QINC.GM.ndsu-7D	7D.1	MN-2010	5.58	-16.59	16.34	SEV
QINC.GM.ndsu-1B.2	1B.1	Carr-2011	2.72	-1.56	10.12	Sev
QINC.GM.ndsu-4B	4B.2	Pros-2011	3.99	-1.22	12.82	
QINC.GM.ndsu-5B	5B.1	Pros-2011	2.3	0.84	6.9	SEV
QINC.GM.ndsu-1A.3	1A	Pros-2012	3.05	-3.7	8.32	DON
QINC.GM.ndsu-1B.1	1B.1	Pros-2012	3.27	3.65	8.9	Sev
QINC.GM.ndsu-3B.1	3B	Pros-2012	3.24	3.81	8.96	Sev
Deoxynivalenol (DON)						
QDON.GM.ndsu-1A	1A	Pros-2010	2.4	-0.09	10.19	INC
QDON.GM.ndsu-2B.2	2B.3	Pros-2010	4.52	-0.17	13.88	
QDON.GM.ndsu-5B	5B.1	Pros-2010	3.24	-0.1	12.61	SEV
QDON.GM.ndsu-7B	7B.1	Pros-2010	3.93	0.1	12.07	
QDON.GM.ndsu-3B	3B	Pros-2011	2.61	-0.34	9.06	INC
Plant height (HGT)						
QHGT.GM.ndsu-5B	5B.2	GH-2011	3.03	-1.55	8.02	SEV
QHGT.GM.ndsu-6A	6A.2	GH-2011	4.38	-1.87	13.31	SEV
QHGT.GM.ndsu-1A	1A	GH-2012	2.12	1.42	5.89	INC
QHGT.GM.ndsu-2A	2A.1	GH-2012	4.39	2.52	18.65	
QHGT.GM.ndsu-2B	2B.1	GH-2012	3.15	-1.98	11.84	SEV-DON
QHGT.GM.ndsu-7A.2	7A.1	GH-2012	3.03	1.79	9.65	INC-SEV

*Environments: Pros=Prosper, ND; Carr=Carrington, ND; GH=Greenhouse; MN= Minnesota State

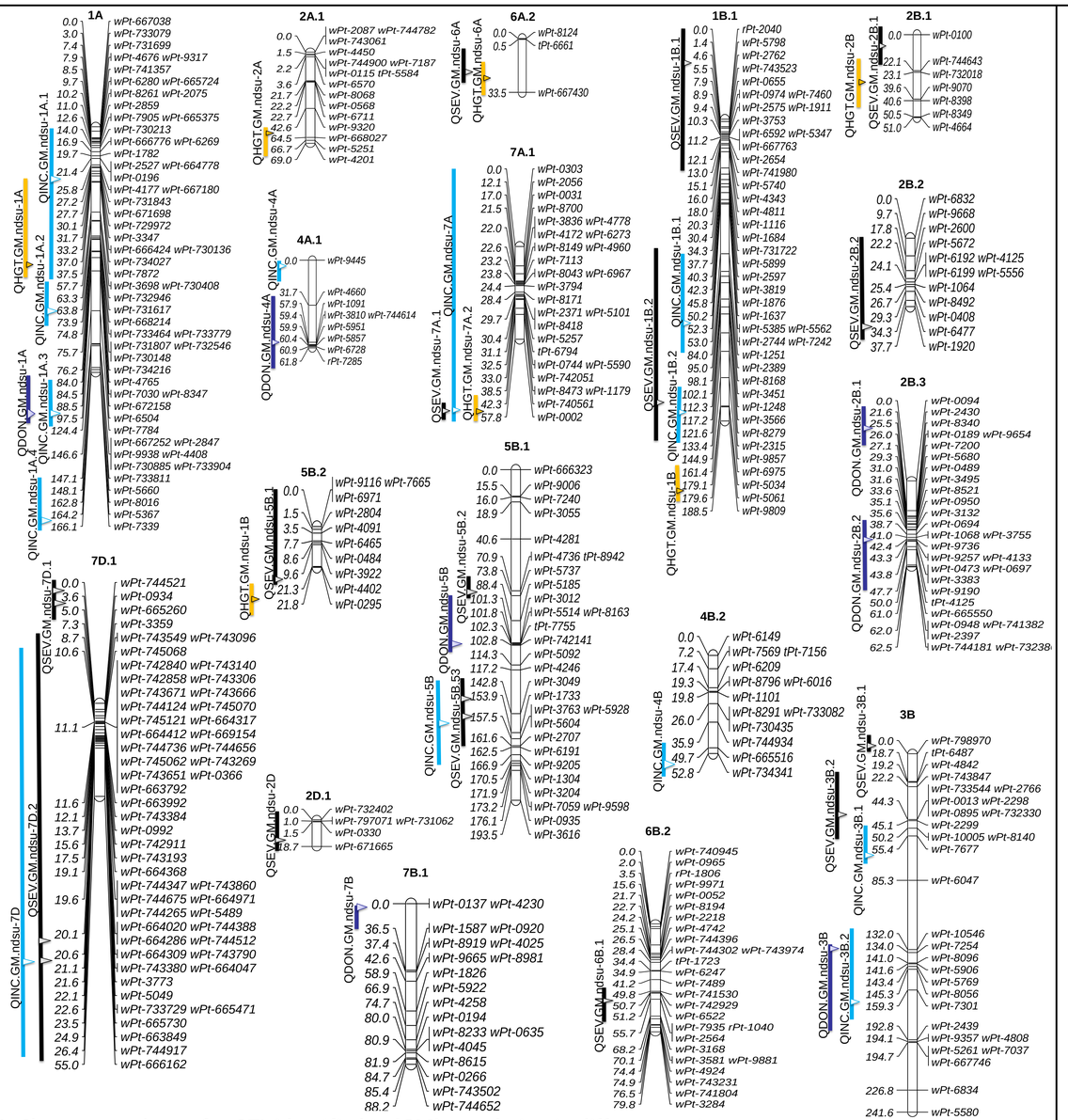

Fig.1. Chromosomal map for QTL identified in (GM) population in different environments. QTL intervals shown as (lines); QTL positions shown as (Triangles); QTL for SEV, INC, DON, and HGT were shown in (Black, Blue, Purple and Brown) respectively.

Results

QTL analysis for FHB severity, incidence, DON and plant height :

- Total **QTL** identified = 15 (FHB-SEV); 15 (FHB-INC); 7 (FHB-DON); 8 (FHB-HGT).
- The phenotypic variance (PV%) explained by individual QTL = 6.41-20.49% (FHB-SEV); 4.94-16.34% (FHB-INC); 7.26 to 13.88% (DON); 5.35-18.65% (FHB-HGT).
- **Major QTL** (PV>10%) = 8 (FHB-SEV); 3 (FHB-INC); 4 (FHB-DON); 3 (FHB-HGT).
- One **major QTL** (located on **5B**) for **SEV** was detected in **4** environments.
- **Six** QTL (located on 1B, 5B, 6B, 7A, 7D) for **SEV** and **1** QTL for **INC** (located on 1A) were all detected in **2** environments.

Conclusions

- The study **did not identify any** consistent **major QTL on** chromosome **3BS**, **suggesting** that the **resistance** source **in Glenn is something other than Sumai3.**
- **Markers associated with** the novel **QTL in Glenn (Table 1)** could be **useful** for **markers assisted introgression** of **new resistant** alleles into other wheat germplasm.
- **Comparison** of map locations, of identified **QTL, assigned** several genomic regions conferring **common loci for different traits** (**Fig. 1**).

REFERENCES

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