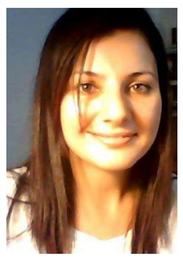
Precise Mapping of Hessian Fly Resistance Gene from variety 'WA8076' via 90K SNP Assay and development of high density genetic map of broad utility

Alwan[1], E.A., N.A. Bosque-Pérez[2], D.R. See[1], and M. Pumphrey[1]

[1]Dept.Crop & Soil Science, P.O. Box 646420, Washington State University, Pullman, WA, 99164-6420, [2]Dept. Plant, Soil & Entomological Sci., P. O. Box 442339, University of Idaho, Moscow, ID 83844-2339



Introduction

Hessian fly (HF), Mayetiola destructor (Say) is an important pest of spring wheat in the Pacific Northwest (PNW). Breeding for resistance is the most effective and economical control strategy to reduce yield losses (1).

The objective of this research is to identify DNA markers for selection of the Hessian fly resistance gene in Washington breeding line WA8076, which may be used for routine breeding efforts.

Hessian fly adults

http://www.ianrpubs.unl.edu/pages/publicationD.jsp?publicationId=1142

Materials and Methods

A mapping population was developed via doubled haploid (DH) approach (wheat by maize method) with WA8076 as the resistant parent and HT080158LU as the susceptible parent, with 300 progeny produced.

Phenotypic evaluation of the double haploid population for fly resistance was conducted in the laboratory in 2014 using the method by Schotzko and Bosque-Pérez (2). Chi square analysis was used to test segregation ratios.

Genotypic Analysis: The DH population was genotyped with 90K SNP markers using the Illumina Infinium platform. Genotype calling of the raw SNP data, allele clustering were completed using methods described by Wang et al (2014).

Genetic Mapping: A genetic map was constructed using the multipoint software v3.2 (3). Recombination fraction of 0.25 and LOD threshold of 3.0 were used for distance determination and markers sorting. Kosambi mapping function was applied to estimate the map distance.

Results

Hessian fly Phenotyping The Chi-square result confirms the segregation ratio of 1:1, which is indicative of a single gene.

The genotyping efforts resulted in15,236 SNP markers were polymorphic in the mapping population, of which 3769 SNP loci detected unique recombination events. Twenty-three linkage groups were obtained representing all 21 wheat chromosomes (Figure.1). The total combined map length was 3952.07 cM, with an average SNP distance of 1.05 cM/marker across chromosomes (Table.1). High coverage and relatively even spread of markers on most of the 21 chromosomes was achieved. In addition, sufficient marker coverage of the D genome was obtained compared to previous studies (Figure.2)

Chromosome	# of loci	Chrom length(cM)	Marker density
A	1306	1,287.06	0.99
B	1821	1,769.19	0.97
D	627	895.8	1.43
Total	3769	3952.07	1.05

Table 1. Chromosome length, marker number, and marker distance

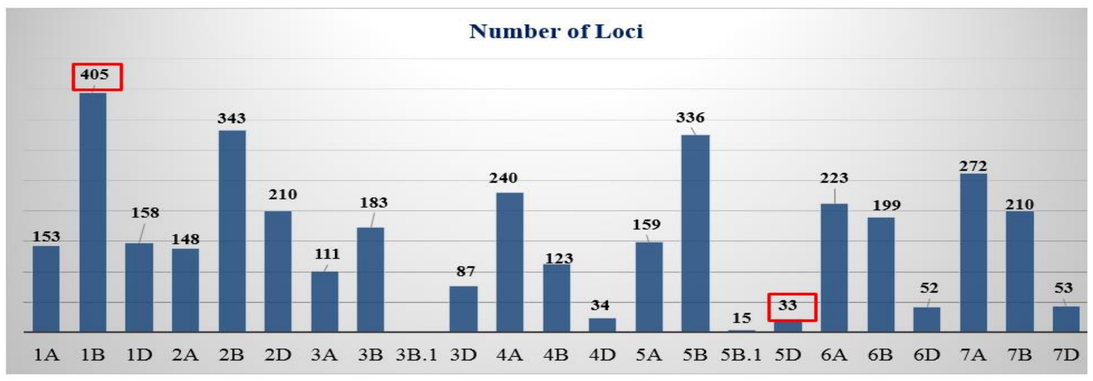


Figure 2. Marker distribution across the 21 wheat chromosomes

Results:

The HF resistance gene was mapped at 12.42 cM on the distal region on the short arm of chromosome 6B (Figure.3). The HF resistance gene was flanked by two markers, IWB71431and IWB61175, which spanned 8.3 cM and were 2.8 and 5.4 cM from the HF resistance gene, respectively.

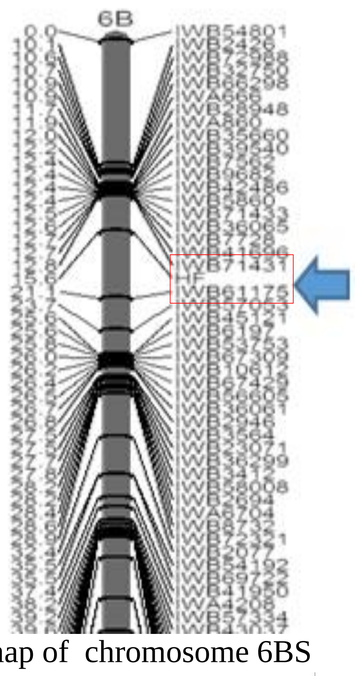


Figure 3. Genetic map of chromosome 6BS

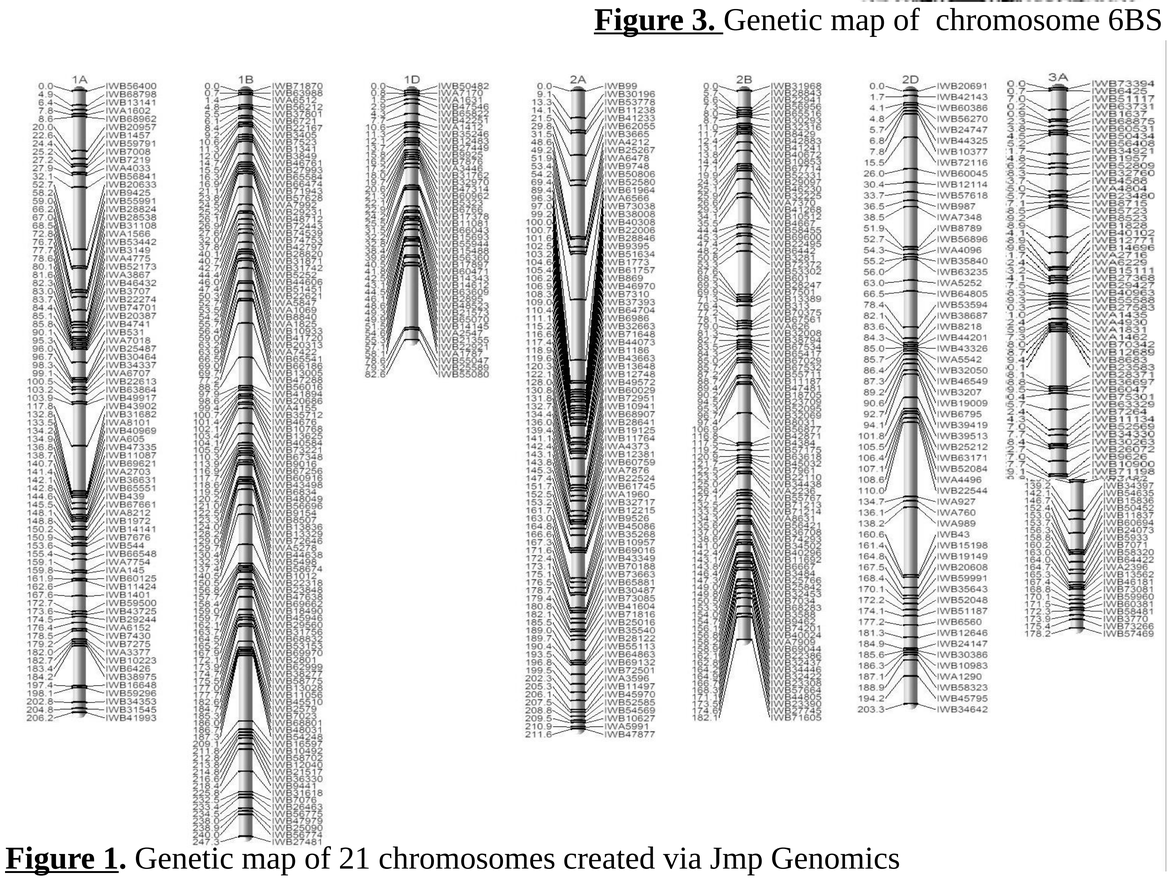


Figure 1. Genetic map of 21 chromosomes created via Jmp Genomics

Conclusion and Future Directions

The elite line 'WA008076' provides a novel source of resistance not yet exploited by breeding programs in the PNW. Additional GBS markers will be integrated into the genetic map in an attempt to obtain higher markers coverage and maximize the likelihood of developing markers diagnostic for the resistance gene. SNP markers will be converted to PCR-based markers & validated on an array of diverse wheat materials from the WSU breeding program. Further, the diagnostic molecular markers will facilitate marker-assisted selection and assist identifying Hessian fly resistance genes as well as identifying genes related with other important agronomic traits in the PNW spring wheat cultivars.

References

1. Ratcliffe, R.H., S.E. Cambron, K.L. Flanders, N.A. Bosque-Pérez, S.L. Clement, and H.W. Ohm. 2000. Biotype composition of the Hessian fly populations from the southeastern, midwestern, and northwestern United States and virulence to resistance genes in wheat. J. Econ. Entomol. 93: 1319-1328.
2. Schotzko, D.J., and N.A. Bosque-Pérez. 2002. Relationship between Hessian fly infestation density and early seedling growth of resistant and susceptible wheat. J. Agric. Urban Entomol. 19: 95-107.
3. http://www.multiqtl.com/
4. Wang S, Wong D, Forrest K, et al (2014) Characterization of polyploid wheat genomic diversity using a high-density 90 000 single nucleotide polymorphism array. Plant Biotechnol J 12:787–796. Doi: 10.1111/pbi.12183

Acknowledgements

We thank the Washington Grain Commission, the University of Idaho and Washington State University for funding our research.