Dissection of Gene Network Underlying Wheat Baking Characteristics Using a High-Density SNP-Based Linkage Map

Sepehr Mohajeri Naraghi[1], Ajay Kumar[1], Senay Simsek[1], S. M. Hisam Rabbi[1], Elias M. Elias[1], Mohammed S. Alamri[2] and Mohamed Mergoum[3]

[1]Plant Sciences, North Dakota State University, Fargo, ND; [2]Dept. of Food Sciences & Nutrition, King Saud University, Riyadh, Saudi Arabia;
[3]Department of Crop and Soil Sciences, University of Georgia, Griffin, GA 30223 0000.

NDSU PLANT SCIENCES

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important crops consumed by humans in the world. Hard red spring wheat (HRSW) produced in the northern Great Plains of the U.S. is of great importance due to its high protein and bread-baking quality. Improvement of end-use quality traits, such as baking characteristics, in wheat depends on a deep understanding of the genetic basis of these traits.

Previous studies have genetically dissected grain protein content (GPC) and reported the existence of genes associated with this trait on all wheat chromosomes (Kunert et al., 2007; Li et al., 2012; Maphosa et al., 2013). To our knowledge, limited information is available on the genetic control of baking characteristics. Kunert et al., (2007) reported two major QTLs for loaf volume on 6B and 7B chromosomes in a BC2F_3 population. Simons et al., (2012) identified QTLs on the long arm of chromosome 1D for bake mixing time and water absorption traits in a population derived from a cross between BR34 and Grandin.

The present study aimed to dissect the genetics of major end-use quality traits and construct a high-density genetic linkage map of these traits in spring wheat to facilitate the development of improved wheat cultivars.

Material and Methods

Plant Material

A mapping population, consisting of 127 F_{10} recombinant inbred lines (RILs), derived from the cross between Glenn (PI 639273) and Traverse (PI 642780) was used in this study. Glenn was developed by North Dakota State University in 2005 and Traverse from South Dakota State University in 2006.

Field Experiment

The 127 RILs, parents, and 15 checks were planted in a 12 × 12 simple lattice design with two replicates, at three North Dakota locations; Prosper, Casselton and Carrington from 2012 to 2014.

Phenotypic data collection and analysis

For quality evaluations, a single location was considered as a replicate and data from all environments was analyzed as a randomized complete block design using the Statistical Analysis System (SAS 9.3).

Phenotypic data (the means across locations) including for GPC, bake mixing time, baking absorption (percent), loaf volume (cubic centimeter), crumb color, and crust color was measured according to the American Association of Cereal Chemist International (AACCI) methods (AACCI, 2008).

Genetic Map and QTL Analysis

The genetic map for this population contained 8553 SNP markers covering all chromosomes except chromosome 3D with a total coverage of 2955 cM and an average interval of 3.45 cM per marker. The QTL analysis was conducted with inclusive CIM in QTL IciMapping software Version 3.3. The LOD threshold was determined by a 1000 permutation test, and type I error α= 0.05. The P values for entering a variable (PIN) was set at 0.001, and the scanning step was set at 1.0 cM.

Results and Discussion

A total of 20 QTL were detected for all quality traits investigated except crumb color (Figure 1). Among these, two QTL for bake mixing time were mapped on chromosomes 1B, and 3B with phenotypic variation (PV) of 13.48% and 14.50%, respectively. Previous studies however, (Maphosa et al., 2013) found a QTL for bake mixing time using a doubled haploid population, located on chromosome 2B. Seven QTL for baking absorption were mapped on chromosomes 1B, 2B, 3B, 4B, 1D and 4D with PV ranging from 4.97% to 21.15%. Tsilo et al., (2011) also identified a baking absorption QTL on chromosome 1B. Two QTL for loaf volume were mapped on chromosomes 7A, and 4B with PV of 26.43% and 9.82%, respectively. Previous work by Groos et al., (2007) also reported a QTL for loaf volume on chromosome 7A. Seven QTL were mapped for crumb color on chromosomes 6A, 6B, and 7B with phenotypic variation ranging between 10.38 to 61.26%. Similarly, Groos et al., (2007) also reported a QTL for crumb characteristics on chromosome 6B. Two QTL were mapped for GPC on chromosomes 3B, and 4B with PV of 26.80% and 22.56%, respectively. This confirms previous findings by Maphosa et al., (2013) who detected a QTL for GPC on chromosome 3B. A total of 10 QTL that we identified explained more than 15% of PV and were considered as major QTL, while the remaining QTL explained less than 15% of phenotypic variation and were considered as minor QTL (Table 1). Strong correlation between loaf volume and GPC (not reported in this study) and co-location QTL for these traits, suggesting either pleiotropic effects or closely linked genes controlling these traits.

Figure 1. Linkage map of chromosomes carrying major QTL associated with wheat quality traits (grain protein content, baking absorption, loaf volume, and crumb color) of a RIL population derived from the cross between Glenn and Traverse evaluated from 2012 to 2014 over three different locations (Prosper, Casselton, and Carrington) in ND, USA.

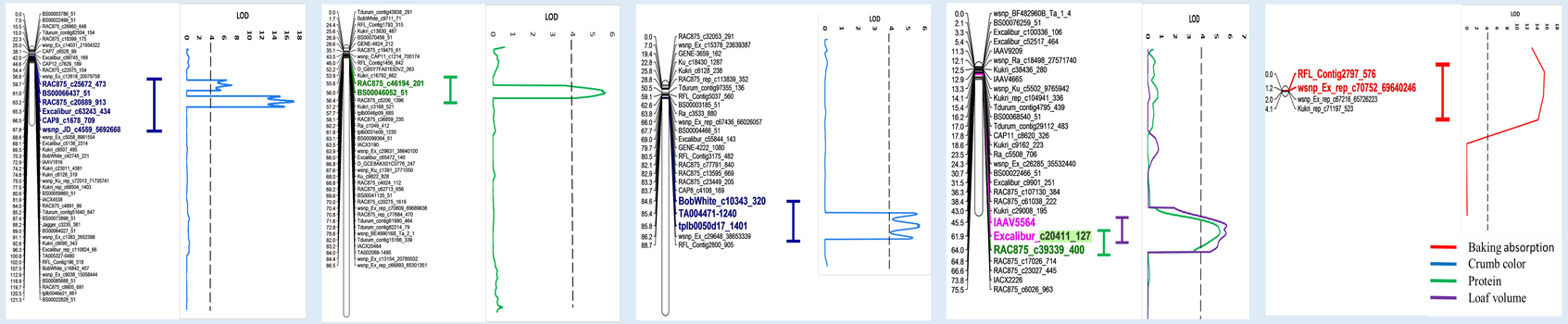

Table 1. Summary of information for QTL identified in a RILs population derived from the cross between Glenn and Traverse evaluated from 2012 and 2014 over three different locations (Prosper, Casselton, and Carrington) in ND, USA.

Trait	Chromosome	Flanking markers		LOD	Phenotypic variation (PV) (%)	Add*
Baking absorption	1B3	RFL_Contig785_1700	wsnp_BG274687B_Ta_2_1	8.73	10.79	-0.4
Bake Mixing Time	1B5	Excalibur_c56657_282	Tdurum_contig288_253	5.05	13.48	0.13
Baking absorption	1D3	CAP8_c1305_148	BS00104199_51	4.64	5.11	-0.27
Baking absorption	2B1	Kukri_c898_328	RAC875_c21405_591	4.3	4.97	0.27
Bake Mixing Time	3B1	RAC875_c7158_687	BS00063711_51	5.95	14.49	0.13
Grain protein content	3B3	RAC875_c46194_201	BS00046052_51	5.64	26.79	0.37
Baking absorption	3B4	Kukri_c60633_121	TA006289-1238	4.68	5.12	0.28
Baking absorption	3B5	TA005743-0552	Kukri_c20199_83	8.44	12.55	0.44
Grain protein content	4B1	Excalibur_c20411_127	RAC875_c39339_400	5.26	22.56	-0.33
Loaf volume	4B1	IAAV5564	Excalibur_c20411_127	5.76	26.43	-4.08
Baking absorption	4B2	IAAV8848	wsnp_Ex_c15490_23776560	7.28	8.41	-0.35
Baking absorption	4D	RFL_Contig2797_576	wsnp_Ex_rep_c70752_69640246	15.49	21.15	-0.56
Crust color	6A1	BobWhite_c10343_320	TA004471-1240	5.7	21.17	0.12
Crust color	6A1	TA004471-1240	tplb0050d17_1401	5.29	22.57	0.12
Crust color	6B2	RAC875_c25672_473	BS00066437_51	6.37	15.54	-0.1
Crust color	6B2	BS00066437_51	RAC875_c20889_913	7.24	17.38	-0.11
Crust color	6B2	Excalibur_c63243_434	CAP8_c1678_709	14.98	61.21	0.2
Crust color	6B2	CAP8_c1678_709	wsnp_JD_c4559_5692668	17.13	61.25	0.2
Loaf volume	7A1	Ku_c554_1239	IACX8453	4.23	9.83	2.51
Crust color	7B1	wsnp_BM134363B_Ta_2_7	BobWhite_rep_c66630_331	4.58	10.38	0.08

* Additive effect indicate the source of QTL contributed by the allele from the parental lines.

Conclusion

- Several novel and major (PV>15%) QTL were identified for most quality characteristics studied.
- Other minor (PV<15%), but also novel, QTL detected may play a an important role in wheat quality traits.
- QTL detected in this study could be useful for breeders and geneticists to improve end-use quality traits of wheat.
- Further studies to confirm/validate the novel QTL are warranted.

Literature Cited

Groos, C., E. Bervas, E. Chanliaud, · G. Charmet. 2007. Genetic analysis of bread-making quality scores in bread wheat using a recombinant inbred line population. Theor. Appl. Genet. 115:313–323

Kunert A., A.A. Naz, O. Dedeck, K Pillen, J. Léon. 2007. AB-QTL analysis in winter wheat: I. Synthetic hexaploid wheat (T. turgidum ssp. dicoccoides T. tauschii) as a source of favorable alleles for milling and baking quality traits Theor. Appl. Genet. 115:683–695.

Li, Y., R. Zhou, J. Wang, X. Liao, G. Brandland, and J. Jia. 2012. Novel and favorable QTL allele clusters for end-use quality reveled by introgression lines derived from synthetic wheat. Mol. Breed. 29:627-643.

Maphosa L, P. Langridge, H. Taylor, K.J. Chalmers, D. Bennett, H. Kuchel, D.E. Mather. 2013. Genetic control of processing quality in a bread wheat mapping population grown in water-limited environments. J Cereal Sci. 57:304-311.

Simons, K., J.A. Anderson, M. Mergoum, J.D. Faris, D.L. Klindworth, S.S. Xu, C. Sneller, J-B. Ohm, G.A Hareland, M.C Edwards, S Chao. 2012. Genetic mapping analysis of bread-making quality traits in spring wheat. Crop Sci. 52:2182-2197.

Tsilo, T.J, S. Simsek, J-B. Ohm, G.A. Hareland, S. Chao, and J.A. Anderson. 2011. Quantitative trait loci influencing endosperm texture, dough-mixing strength, and bread-making properties of the hard red spring wheat breeding lines. Genome 54:460-470.