Registration of the OS9XQ36 Mapping Population of Wheat (*Triticum aestivum* L.)

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ABSTRACT

The OS9XQ36 wheat (*Triticum aestivum* L.) mapping population (Reg. No. MP-2, NSL 465170) is a set of 164 F_6–derived recombinant inbred lines (USDA–ARS Germplasm Resources Information Network [GRIN] accession no. GSTR 11903 through GSTR 12066) from the cross between OS9A (PI 658243), a single plant selection from the cultivar Stephens (CI 17596), and QCB36 (PI 658244), a single plant selection from the elite breeding line OR9900553. This population was developed to investigate the consistently lower grain hardness and superior end-use quality of OR9900553 compared with Stephens. This population has also been genotyped with diversity array technology (DArT) and simple sequence repeat (SSR) markers resulting in the construction of a 270-marker linkage map covering 1785 cM at a density of one marker per 7 cM. This F_6–derived population is one of 20 mapping populations being used by the WheatCAP consortium (http://maswheat.ucdavis.edu/) for extensive quantitative trait locus analysis and forms part of a publicly available long-term genetic resource to map complex traits in wheat.

The OS9XQ36 wheat (*Triticum aestivum* L.) mapping population (Reg. No. MP-2, NSL 465170) is a set of recombinant inbred lines from the cross between two elite soft white genotypes, OS9A (PI 658243) and QCB36 (PI 658244). OS9A is a single-plant selection from 'Stephens' (CI 17596; 'Nord Desprez'/Pullman Sel. 101, CI 13438) (Kronstad et al., 1978), a widely adapted, high-yielding semidwarf (*Rht-B1b Rht-D1a*) variety with durable high-temperature adult-plant (HTAP) resistance to stripe rust (*Puccinia striiformis* Westend f. sp. *tritici* Ericks.) (Chen and Line, 1995a; Chen and Line, 1995b). QCB36 is a single-plant selection from OR9900553 ('Arminda'/3/VPM/'Moisson 951'//2*'Hill'/5/'Kavkaz'/3/'Hybrid Delhi'/'Olesen'//'Bluebird'/4/Pullman 101//'Omaha'/178383//'Riebsel'/3/'Riebsel 1744'//'Suweon'/'Gaines'/5/'Stephens'//'Aurora'/'Yamhill'), a high-yielding, facultative (*vrn-A1 Vrn-B1 vrn-D1*) semidwarf (*Rht-B1a Rht-D1b*) soft white wheat breeding line.

OR9900553 and Stephens were evaluated in the USDA–ARS Western Regional Nurseries in 2003 and 2004. End-use quality assessments of these nurseries showed that OR9900553 had consistently lower grain kernel hardness (texture) and had superior end-use quality with respect to Stephens (Western Wheat Quality Laboratory, http://www.wsu.edu/~wwql/php/index.php; verified 9 Oct. 2009). These observations suggested that a population from the cross between OS9A and QCB36 could be used to determine the genetic basis of differences in kernel characteristics and related aspects of soft wheat end-use quality. For these reasons, we contributed this population to the collection of populations that are part of WheatCAP consortium's (http://maswheat.ucdavis.edu/; verified 9 Oct. 2009) effort to perform extensive quantitative trait locus (QTL) analysis and to establish publicly available genetic resources to map complex traits in wheat.

Materials and Methods

The cross between OS9A (Stephens) and QCB36 (OR9900553) was made in 1999 at Oregon State University. Subsequently, F_2 plants were inbred to the F_6 generation by single seed descent. In 2006 164 F_6 plants, each tracing to an independent F_2 plant, were grown in the greenhouse to produce the source seed of each recombinant inbred line.

For the development of a linkage map, the OS9XQ36 population and parents were grown for DNA extraction following the protocol described by Riera-Lizarazu et al. (2000). A collection of approximately 1320 simple sequence

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Abbreviations: DArT, diversity array technology; DH, doubled haploid; GRIN, USDA–ARS Germplasm Resources Information Network; QTL, quantitative trait locus/loci; RIL, recombinant inbred line; SSR, simple sequence repeat.

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repeat (SSR) markers (Somers et al., 2004) were screened, in house, for polymorphism between OS9A and QCB36. This screen yielded 380 polymorphic SSR markers that we used to genotype the mapping population. We also genotyped the population with allele-specific markers for the semidwarfing genes *Rht-B1* and *Rht-D1* and the vernalization response gene, *Vrn-B1*. Simple sequence repeat marker assays were performed as described by Leonard et al. (2008) and assays for gene-specific markers followed protocols described by Ellis et al. (2002) and Fu et al. (2005). In addition, DNA from the mapping population and parental lines was sent to Triticarte Pty Ltd. (Yarralumla ACT, Australia) for genotyping with diversity arrays technology (DArT) markers (Jaccoud et al., 2001; Wenzl et al., 2004). The linkage map was constructed using Jointmap 4 (van Ooijen, 2006) with the regression mapping method and the Kosambi mapping function.

For phenotypic assessments and seed increase, the OS9XQ36 mapping population was first planted in Corvallis, OR, in 2007. Subsequently, in 2008, the population was planted in five additional field environments in the U.S. Pacific Northwest (Corvallis, Pendleton, and Moro, OR; Pullman, WA; and Moscow, ID). In all cases, 164 recombinant inbred lines (RILs) and the two parents were planted in randomized complete blocks with two replications.

Field evaluations included measurements of plant height and heading date. Plant height was determined by measuring the height (cm) of the stem to the tip of the spike excluding awns measured between maturity and harvest. Days to heading was determined by counting the numbers of days from 1 January until 50% of the spikes in a plot had completely emerged. Upon harvest, kernel hardness, kernel weight, kernel diameter, break flour yield, flour yield, test weight, and whole grain protein were measured. Kernel hardness (hardness index), kernel weight (mg), and kernel diameter (mm) were determined using a SKCS 4100 single kernel characterization system (Perten Instruments AB, Huddinge, Sweden). Break flour yield (the proportion of flour from break rolls by weight of total products) and potential flour yield (the proportion of break flour and unground middling stock by weight of total products) were measured on grain samples (15 g) equilibrated to 13% moisture using a short flow micromill custom-designed at the USDA–ARS Western Wheat Quality Laboratory (Pullman, WA). Test weights (kg m^{-3}) were measured using a GAC2100 GI analyzer (DICKEY-john Corporation, Auburn, IL).Whole grain protein (%) was determined using an Infratec 1241 grain analyzer (FOSS, Eden Prairie, MN).

Analyses of variance were performed on phenotypic data of 164 RILs and two parents grown in six environments. These analyses were performed using the general linear model (GLM) procedure of SAS version 9.1 (SAS Institute, Cary, NC). For multiple mean comparisons, we used Fishers' *F*-protected LSD tests using a 0.05 probability value to declare significance.

Characteristics

The OS9XQ36 population was genotyped with 360 polymorphic DArT and 341 polymorphic SSR markers. A robust (LOD 3) framework map based on the OS9XQ36 population was constructed with 229 SSR, 38 DArT, and three gene-specific markers (Table 1) arranged in 34 linkage groups corresponding to all 21 wheat chromosomes. The total distance of the genetic map is 1785 cM, with an average intermarker distance of 7 cM. While genotyping the mapping population, QCB36 (OR9900553) was found to carry the $2N^{v}S$-2AS.2AL and 5B:7B chromosome translocations. These chromosome translocations have also been found in other VPM1-derived lines (Badaeva et al., 2008; Bariana and McIntosh, 1994; Bonhomme et al., 1995). QCB36 was also found to carry the 1BS.1RL translocation (Zeller, 1973).

Phenotypic assessments showed significant variation for the traits that were measured (Table 2). Although genotype × environment interactions were observed, OS9A had significant ($P < 0.05$) and consistently greater kernel hardness, kernel diameter, potential flour yield, and plant height.

Table 1. Description of map distances and maker distribution for 34 linkage groups that constitute the framework linkage map based on the OS9XQ36 wheat mapping population.

Chromosome	Number of linkage groups	Map distance	Total no. of markers	Number of markers		
				SSR†	DArT	Gene-specific‡
		cM				
1A	1	111	15	12	3	
2A	1	91	11	11		
3A	2	43	10	7	3	
4A	2	12	6	4	2	
5A	1	88	11	10	1	
6A	2	58	10	8	2	
7A	2	118	17	11	6	
1B	2	30	5	5		
2B	1	103	11	10	1	
3B	2	104	17	14	3	
4B	1	73	19	14	4	1
5B	1	149	18	10	7	1
6B	1	110	14	12	2	
7B	1	53	8	7	1	
1D	2	82	10	8	2	
2D	2	74	13	13		
3D	3	55	13	13		
4D	3	70	18	17		1
5D	1	132	14	14		
6D	1	53	5	5		
7D	2	176	25	24	1	
Total	34	1785	270	229	38	3

†SSR, simple sequence repeat; DArT, diversity array technology.

‡Gene-specific markers correspond to *Rht-B1* and *Rht-D1* on chromosomes 4B and 4D, respectively, and *Vrn-B1* on chromosome 5B.

On the other hand, QCB36 showed significant and consistently greater grain protein content, break flour yield, and days to heading. OS9A and QCB36 did not differ for kernel and test weight. Phenotypic values for the OS9XQ36 RILs had continuous distributions, and significant ($P < 0.05$) transgressive segregants were observed for all traits measured. Consequently, quantitative trait analysis using these data showed the presence of QTL for these traits. Specific QTL analyses are currently ongoing and results from these studies will be published elsewhere.

Table 2. Trait means and ranges for wheat selections OS9A ('Stephens'), QCB36 (OR9900553), and 164 F_6–derived recombinant inbred lines (RILs).

Trait	Environment†	OS9A (Stephen)	QCB36 (OR9900553)	RILs‡			CV
				Mean	Range	SD	
Kernel hardness	Corvallis, OR, 2007	36.2a§	22.7b	34.2	17.5–52.3	6.67	12.45
	Corvallis, OR, 2008	28.5a	11.4b	25.9	6.0–42.3	6.39	4.82
	Moro, OR, 2008	27.7a	15.2b	25.4	7.0–44.3	7.23	8.80
	Pendleton, OR, 2008	23.5a	15.9b	23.2	4.9–38.1	6.27	15.75
	Pullman, WA, 2008	23.4a	11.3b	21.9	3.6–44.7	6.95	9.44
	Moscow, ID, 2008	5.9a	–1.6b	7.1	–10.6–27.5	6.78	29.93
	Combined	24.0a	12.4b	23.0	5.4–40.6	10.47	12.09
Kernel weight (mg)	Corvallis, OR, 2007	47.6a	43.9a	46.8	38.9–58.4	3.78	4.64
	Corvallis, OR, 2008	57.2a	46.5b	51.9	43.0–61.4	3.81	2.77
	Moro, OR, 2008	40.3a	39.5a	39.6	31.7–47.7	3.93	6.19
	Pendleton, OR, 2008	33.2a	31.2a	37.9	27.8–46.8	4.07	11.40
	Pullman, WA, 2008	38.6a	37.0a	38.4	30.5–48.7	3.67	7.31
	Moscow, ID, 2008	47.8a	38.8b	44.3	34.5–54.5	4.29	5.43
	Combined	44.3a	39.5a	42.4	35.2–49.2	6.44	5.55
Kernel diameter (mm)	Corvallis, OR, 2007	3.0a	2.7b	3.1	2.6–3.6	0.17	3.18
	Corvallis, OR, 2008	3.2a	2.7b	3.0	2.7–3.4	0.16	3.09
	Moro, OR, 2008	2.7a	2.4b	2.6	2.2–2.9	0.18	1.93
	Pendleton, OR, 2008	2.4a	2.1a	2.5	2.0–3.0	0.20	8.65
	Pullman, WA, 2008	2.6a	2.4a	2.5	2.1–2.9	0.17	6.73
	Moscow, ID, 2008	3.0a	2.4b	2.8	2.4–3.3	0.20	5.42
	Combined	2.8a	2.4b	2.7	2.3–3.0	0.27	4.15
Break flour yield (g kg^{-1})	Corvallis, OR, 2008	138b	165a	142	102–185	15.9	7.43
	Moro, OR, 2008	130b	164a	135	95–172	18.7	3.36
	Pendleton, OR, 2008	140b	180a	148	108–194	17.5	3.50
	Pullman, WA, 2008	135b	174a	138	112–174	15.6	8.19
	Combined	134b	171a	141	112–178	17.7	8.54
Potential flour yield (g kg^{-1})	Corvallis, OR, 2008	767a	739b	739	687–780	16.8	0.90
	Moro, OR, 2008	728a	707a	713	665–763	23.0	2.08
	Pendleton, OR, 2008	728a	709a	726	672–764	20.6	2.18
	Pullman, WA, 2008	735a	709b	719	679–762	17.1	1.50
	Combined	740a	717b	725	689–764	21.9	1.74
Plant height (cm)	Corvallis, OR, 2007	84a	74b	90	47–128	16.7	4.45
	Corvallis, OR, 2008	96a	85b	102	54–135	17.58	3.57
	Moro, OR, 2008	64a	58b	65	43–81	7.43	1.72
	Pendleton, OR, 2008	90a	87a	97	54–123	15.04	7.04
	Pullman, WA, 2008	63a	63a	72	41–97	10.62	10.57
	Moscow, ID, 2008	75a	64b	78	47–110	11.43	4.57
	Combined	79a	72b	83	48–105	18.96	6.43
Days to heading (d)	Corvallis, OR, 2007	143b	146a	144	140–151	2.45	0.74
	Corvallis, OR, 2008	146b	151a	149	143–154	2.65	0.41
	Moro, OR, 2008	151b	157a	155	149–162	2.58	1.75
	Pendleton, OR, 2008	154b	158a	156	151–163	2.40	0.85
	Pullman, WA, 2008	168a	169a	171	166–174	1.97	3.16
	Moscow, ID, 2008	174a	177a	175	171–180	1.83	1.03
	Combined	156b	160a	161	151–166	11.33	1.00

Table 2. Continued.

Trait	Environment†	OS9A (Stephen)	QCB36 (OR9900553)	RILs‡			CV
				Mean	Range	SD	
Test weight (kg m^{-3})	Corvallis, OR, 2007	766a	766a	772	721–803	16.31	1.23
	Corvallis, OR, 2008	796a	778b	789	741–819	14.38	0.79
	Moro, OR, 2008	768a	761a	769	707–808	22.79	1.50
	Pendleton, OR, 2008	699a	697a	757	651–802	32.13	10.41
	Pullman, WA, 2008	757a	762a	785	713–823	20.77	2.12
	Moscow, ID, 2008	731a	739a	745	710–777	15.21	1.08
	Combined	757a	750a	770	719–797	26.06	1.63
Grain protein content (g kg^{-1})	Corvallis, OR, 2007	87b	110a	101	88–139	7.9	2.43
	Corvallis, OR, 2008	101b	112a	107	82–160	11.6	4.94
	Moro, OR, 2008	111a	112a	119	101–147	11.4	15.95
	Pendleton, OR, 2008	131a	142a	130	111–154	9.3	7.95
	Pullman, WA, 2008	107a	123a	120	103–144	9.3	6.89
	Moscow, ID, 2008	113b	122a	131	102–155	10.8	3.21
	Combined	109b	121a	118	104–146	15.0	6.41

†The combined values represent averages across all field environments.

‡Mean, range, and standard deviation for values of 164 RILs of the OS9XQ36 mapping population.

§Mean trait values for the parental lines OS9A and QCB36 followed by the same letter are not significantly different at the 0.05 probability level using Fisher's *F*-protected LSD test.

Discussion

Quantitative trait locus mapping is used to identify genetic determinants that underlie quantitative traits (Paterson et al., 1988; Tanksley, 1993). This approach also yields marker-trait associations that may be exploited for marker-assisted selection (Paterson et al., 1991). Basic prerequisites of this approach are the availability of a linkage map and a mapping population. In this regard, populations based on RILs or doubled haploids (DH) are of particular interest because these constitute permanent mapping populations where multiple groups can contribute to additional genetic mapping and subsequent QTL analysis (Burr et al., 1988). Thus, a collection of publicly available DH or RIL mapping populations and their linkage maps may be viewed as permanent resources to study quantitative traits and to develop markers for indirect selection.

The OS9XQ36 RIL population is one of about 20 mapping populations being used for QTL analysis under the WheatCAP consortium. Genotypic, phenotypic, and QTL data collected in the course of this project will be deposited and will be publicly available in the GrainGenes 2.0 database (http://wheat.pw.usda.gov/GG2/index.shtml; verified 9 Oct. 2009). Although the OS9XQ36 RIL population was originally developed to investigate the genetic basis of grain hardness and related soft wheat end-use quality, our preliminary analyses suggests that this population will be useful in studying other traits of agronomic importance.

Availability

Seeds of OS9A (GRIN accession no. GSTR 11901), QCB36 (GRIN accession no. GSTR 11902), and the OS9XQ36 population (GRIN accession nos. GSTR 11903 through GSTR 12066) have been deposited in the USDA–ARS National Small Grains Collection in Aberdeen, ID. Small amounts of seed of the OS9XQ36 mapping population are available from the corresponding author. We request that the source of this mapping population is acknowledged and that this registration is cited when referring to these materials and when these materials contribute to marker development, research publications, or cultivar development.

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References

Badaeva, E.D., O.S. Dedkova, J. Koenig, S. Bernard, and M. Bernard. 2008. Analysis of introgression of *Aegilops ventricosa* Tausch. genetic material in a common wheat background using C-banding. Theor. Appl. Genet. 117:803–811.

Bariana, H.S., and R.A. McIntosh. 1994. Characterisation and origin of rust and powdery mildew resistance genes in VPM1 wheat. Euphytica 76:53–61.

Bonhomme, A., M.D. Gale, R.M.D. Koebner, P. Nicolas, J. Jahier, and M. Bernard. 1995. RFLP analysis of an *Aegilops ventricosa* chromosome that carries a gene conferring resistance to leaf rust (*Puccinia recondita*) when transferred to hexaploid wheat. Theor. Appl. Genet. 90:1042–1048.

Burr, B., F.A. Burr, K.H. Thompson, M.C. Albertson, and C.W. Stuber. 1988. Gene mapping with recombinant inbreds in maize. Genetics 118:519–526.

Chen, X.M., and R.F. Line. 1995a. Gene action in wheat cultivars for durable, high-temperature, adult-plant resistance and interaction with race-specific, seedling resistance to *Puccinia striiformis*. Phytopathology 85:567–572.

Chen, X.M., and R.F. Line. 1995b. Gene number and heritability of wheat cultivars with durable, high-temperature, adult-plant (HTAP) resistance and interaction of HTAP and race-specific seedling resistance to *Puccinia striiformis*. Phytopathology 85:573–578.

Ellis, M.H., W. Spielmeyer, K.R. Gale, G.J. Rebetzke, and R.A. Richards. 2002. "Perfect" markers for the Rht-B1b and Rht-D1b dwarfing genes in wheat. Theor. Appl. Genet. 105:1038–1042.

Fu, D., P. Szucs, L. Yan, M. Helguera, J.S. Skinner, J. von Zitzewitz, P.M. Hayes, and J. Dubcovsky. 2005. Large deletions within the first intron in VRN-1 are associated with spring growth habit in barley and wheat. Mol. Genet. Genomics 273:54–65.

Jaccoud, D., K. Peng, D. Feinstein, and A. Kilian. 2001. Diversity arrays: A solid state technology for sequence information independent genotyping. Nucleic Acids Res. 29:E25.

Kronstad, W.E., C.R. Rohde, M.F. Kolding, and R.J. Metzger. 1978. Registration of Stephens wheat. Crop Sci. 18:1097.

Leonard, J.M., C.J.W. Watson, A.H. Carter, J.L. Hansen, R.S. Zemetra, D.K. Santra, K.G. Campbell, and O. Riera-Lizarazu. 2008. Identification of a candidate gene for the wheat endopeptidase *Ep-D1* locus and two other STS markers linked to the eyespot resistance gene *Pch1*. Theor. Appl. Genet. 116:261–270.

Paterson, A.H., E.S. Lander, J.D. Hewitt, S. Peterson, S.E. Lincoln, and S.D. Tanksley. 1988. Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. Nature 335:721–726.

Paterson, A.H., S.D. Tanksley, and M.E. Sorrells. 1991. DNA markers in plant improvement. Adv. Agron. 46:39–90.

Riera-Lizarazu, O., M.I. Vales, E.V. Ananiev, H.W. Rines, and R.L. Phillips. 2000. Production and characterization of maize chromosome 9 radiation hybrids derived from an oat-maize addition line. Genetics 156:327–339.

Somers, D.J., P. Isaac, and K. Edwards. 2004. A high-density microsatellite consensus map for bread wheat (*Triticum aestivum* L.). Theor. Appl. Genet. 109:1105–1114.

Tanksley, S.D. 1993. Mapping poygenes. Annu. Rev. Genet. 27:205–233van Ooijen, J.W. 2006. JoinMap, software for the calculation of genetic linkage maps. Version 4. Kyazma BV, Wageningen, the Netherlands.

Wenzl, P., J. Carling, D. Kudrna, D. Jaccoud, E. Huttner, A. Kleinhofs, and A. Kilian. 2004. Diversity arrays technology (DArT) for whole-genome profiling of barley. Proc. Natl. Acad. Sci. USA 101:9915–9920.

Zeller, F.J. 1973. 1B/1R wheat-rye chromosome substitutions and translocations. p. 209–221. *In* E.R. Sears and L.M.S. Sears (ed.) Proceedings of 4th International Wheat Genetics Symposium, Columbia, MO. 6–11 Aug. 1973. Univ. of Missouri, College of Agriculture, Columbia.