Mapping research continued to provide additional markers, QTL and gene locations in 2008. Potokina et al. (2008) used the Barley GeneChip to map transcript derived markers (TDMs) and expression QTL for 16,000 barley genes in embryo-derived tissue from germinating seed of the Steptoe x Morex mapping population. They added 243 TDMs and 3673 expression QTL to the chromosome 7H map. These gene-specific markers should be useful to define the genetic control behind traits of interest. Kota et al. (2008) sequenced 437 expressed sequence tag (EST)-derived gene fragments in seven cultivars, including the parents of three mapping populations. Single nucleotide polymorphisms (SNPs) and insertion/deletion (InDel) polymorphisms were mapped, including 35 markers on chromosome 7H, and the SNP markers were converted to cleaved amplified polymorphism (CAP) assays. These markers showed 2 to 6 haplotypes and 1 to 28 SNPs from the 35 sequences. Varshney et al. (2008) screened 50 simple sequence repeat (SSR) and 50 SNP markers on six diverse barley genotypes from ICARDA and six parents from mapping populations to identify a core set of highly polymorphic markers. Four SSR and four SNP markers were selected for chromosome 7H. Two of the SNPs could be identified by CAP assays, one by InDel and the final one by pyrosequencing. Each marker identifies a single locus, gives high quality amplification, and was highly polymorphic among the diverse genotypes tested.

Disease resistance QTL were evaluated in a variety of populations. Sato et al. (2008) mapped QTL for FHB resistance in five two-rowed populations derived from crosses with Harbin 2-row as one of the parents. One locus on chromosome 7H was identified in three of the populations, with the Harbin 2-row allele contributing to susceptibility. Wagner et al. (2008) examined scald resistance in two populations, Igri (rrs1) x Triton (Rrs1) and Post x Vixen (both rrs1). Three QTL were present in the first population, including Rrs1 on chromosome 2H and a minor QTL from Triton on the long arm of chromosome 7H that explained about 20% of the variation for scald reaction. This is probably Rrs2. A minor QTL from Vixen was located on the short arm of chromosome 7H that explained about 10% of the variation. Both of these loci are in regions where multiple resistance genes have been located. Grewal et al. (2008a and b) examined markers for both the net and spot forms of net blotch. QTL analysis of a cross between CDC Dolly (susceptible) and TR251 (resistant) located several loci, including one on chromosome 7H that provided resistance to both forms. They also tested markers linked to net blotch resistance in Australian germplasm for their utility in Canadian breeding materials. QTL analysis of a Chebec x Harrington population located a major QTL for seedling resistance on chromosome 7H, in the same position as Rpt4. This QTL is not of much use in Canadian germplasm because it is not effective against the common spot form of net blotch prevalent in Canada.
Lehmensiek et al. (2008) added a covered smut resistance gene, Ruh.7H, to the Alexis x Sloop linkage map, linked to the RFLP marker ABG704. They identified an EST-based codominant PCR marker between Ruh.7H and ABG704. They then used high resolution melting (HRM) procedures to locate two additional SNP markers to the telomere of chromosome 7HS. The HRM technique allowed mapping of single base changes without sequencing. Schmalenbach et al. (2008) developed a set of 59 introgression lines in Scarlett, each containing a chromosomal segment of Hordeum vulgare ssp. spontaneum accession ISR42-8. They tested the lines for reaction to powdery mildew and leaf rust. A powdery mildew resistance QTL was located on chromosome 7H in three potentially overlapping introgression lines. A QTL for leaf rust resistance was located in one of the introgression lines. Both QTL were previously identified in the BC2DH population used to derive the introgression lines (von Korff et al. 2008b).

Mirllohi et al. (2008) examined allelic variability of the Rpg1 stem rust resistance locus in eight Swiss landraces and eight wild barley accessions compared to the Morex allele to investigate diversity and possible origins of the gene. Only one Swiss landrace contained an intact and functional Rpg1. The other lines had a GTT InDel, evidence of unequal recombination, or lacked all or part of the locus which resulted in susceptibility to stem rust. No other functioning alleles were found at the locus. Jafari et al. (2008) mapped genes for non-host resistance to four leaf rust pathogens that infect wall barley, meadow barley, wheat grass or wheat, in a cross between SusPtrit x Cebada Capa and the Oregon Wolfe barley DH population. These were compared to locations of non-host resistance genes identified in SusPtrit x Vada. Chromosome 7H contained QTL for immunity to Puccinia triticina, P. hordei-murini, and P. persistens, from both Vada and SusPtrit. The locations often corresponded to map positions of defense gene homolog-based markers.

Positional cloning was used by Taketa et al. (2008) to identify the gene responsible for hull adherence at the nud locus. Markers that cosegregated or were closely linked to nud were used to identify overlapping BAC clones containing the locus. Nud was identified as an ethylene response factor family transcription factor that controls lipid biosynthesis and thus hull adherence. Lines without hull adherence (nud) had a 17 kb deletion in the transcription factor and lack a lipid layer between the hull and developing caryopsis. Evidence from their study indicates a single mutation deleting Nud was selected and spread across the world to domesticate barley. Jestin et al. (2008) identified QTL for aleurone thickness and cell layer number from a cross between Erhard Frederichen (3-4 cell layers) and Criolla Negra (2 cell layers). One of the three QTL located near the center of chromosome 7H explained 12-15% of the variation in cell layer number and thickness. As the aleurone is rich in minerals and vitamins, a thicker aleurone may provide improved nutrition for barley consumers. Burton et al. (2008) located seven members of the cellulose synthase-like (CslF) genes which are involved in β-glucan biosynthesis in barley. One of these genes, HvCslF6, was located on chromosome 7H, near locations where QTL for grain β-glucan have been found. HvCslF6 mRNA was more abundant than transcripts of the other CslF genes in barley in most tissues examined, but especially in the developing barley coleoptile and endosperm.

Several studies examined traits that affect quality. QTL for preharvest sprouting were located on most chromosomes by Ullrich et al. (2008). One of these was on chromosome 7H, between the Brz and Amy2 loci. This QTL influenced preharvest sprouting and germination percent in both
the greenhouse and field. Von Korff et al. (2008a) located QTL for malting quality from *H. vulgare* ssp. *spontaneum* advanced backcrosses. On chromosome 7H, they found one QTL for fine-grind malt extract, three for friability and one for Hartong 45°C. Only one of the favorable alleles on chromosome 7H came from the wild parent. QTL involved in β-glucan levels were examined by Li et al. (2008) in a cross between CDC Bold and TR251. A major QTL near the centromere of chromosome 7H was detected in all three years of the study, which explained up to 39% of the variation for β-glucan. Another chromosome 7H QTL was detected on the long arm in one year which explained 12.7% of the variation. Both low β-glucan alleles came from CDC Bold.

Three studies verified QTL in locations previously reported for heading and anthesis dates on chromosome 7H (Cuesta-Marcos et al. 2008a and b; Castro et al. 2008). Most of these QTL had minor effects, except for one major QTL located by Cuesta-Marcos et al. (2008a) which explained up to 14% of the variation in heading date.

With drought conditions becoming more prevalent in many barley growing areas, several studies mapped QTL associated with adaptation to dry conditions. Takahashi et al. (2008) located QTL for elongation of the coleoptile and first internode of deep-seeded barley. A major QTL was found for first internode elongation on chromosome 7H. Four QTL with small effects were also located on chromosome 7H, two for coleoptile elongation and two for first internode elongation. Von Korff et al. (2008c) examined QTL associated with dryland adaptation in a cross between Tadmor and ER/Apm. A main effect QTL for grain yield was located on the end of the long arm of chromosome 7H. They also found three QTL x environment interactions on chromosome 7H, two for grain yield and one for heading date. A set of 192 genotypes were grown in wet and dry environments in seven countries for two years in a study by Comadran et al. (2008). They identified a large number of marker-grain yield associations, including nine potential QTL on chromosome 7H. These three studies provide linkages for marker-assisted selection and a start at identifying candidate genes to define pathways involved in drought tolerance.

Two studies examined marker allele changes in breeding programs over time. Condon et al. (2008) tested regional ancestors, parental lines and cultivar candidates from the University of Minnesota breeding program with 71 markers, 12 of which were on chromosome 7H. In most cases, allele number decreased over time, especially around Rpg1, a spot blotch locus from NDB112 and the major malt quality QTL on the short arm of 7H. Three of the chromosome 7H loci were fixed in the cultivar candidate group from 1988-1998. Pswarayi et al. (2008) examined allele frequencies at marker loci linked to QTL in 188 landraces and old and modern cultivars mostly from the Mediterranean area. Three of the chromosome 7H markers were associated with yield QTL. For each of these loci, alleles associated with higher yield were present at a higher frequency in modern cultivars than in the landraces. Both of these studies emphasize the concerns about reduced genetic variability in modern cultivars and the need to examine older germplasm for traits that can improve adaptation.
References:


Integration of molecular and morphological marker maps

No report received

Barley Genetic Stock Center

No report received

Trisomic and aneuploid stocks

No report received