Toward a better understanding of a major FHB resistance QTL in tetraploid wheat.

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Fusarium head blight (FHB), mainly caused by the fungus *Fusarium graminearum*, is a destructive disease of wheat and poses a serious threat to wheat production and health of wheat consumers worldwide. Partial resistance to FHB has been identified in common wheat (*Triticum aestivum*). A source of effective resistance to FHB, however, has not been found in durum wheat (*T. turgidum* L. subsp. *durum*). A major FHB resistance QTL, *Qfhs.ndsu-3AS,* was identified and mapped to chromosome 3A of *T. turgidum* L. subsp. *dicoccoides*, a wild relative of durum wheat, in a previous study. This QTL explains 42% of the phenotypic variation for FHB resistance and is not homoeologous to *Qfhs.ndsu-3BS*, a major FHB-resistance QTL identified in the Chinese common wheat cultivar Sumai 3. We have saturated the genomic region harboring the QTL using EST-derived TRAP (target region amplified polymorphism), STS (sequence tagged site), and SSR (simple sequence repeat) markers and are developing a high-resolution map of this FHB-resistance QTL. We used the genomic sequences from 10 PACs on the short arm of rice chromosome 1, which are collinear with the chromosomal regions harboring *Qfhs.ndsu-3AS*, to search the wheat EST pool and identified 404 unmapped wheat ESTs for marker development. To date, a total of 58 new molecular marker loci have been detected on chromosome 3A. Five new EST-derived STS markers mapped to a chromosomal interval of 10.7 cM harboring the QTL in a population of 83 recombinant inbred chromosome lines (RICLs). One of the STS markers was derived from the EST of a gene from which expression was induced by the FHB pathogen *F. graminearum* in the common wheat cultivar Frontana. This STS marker mapped 0.6 cM proximal to *Xgwm2*, an SSR marker closely linked to the QTL peak. Frontana also contains a major FHB-resistance QTL on chromosome 3A. In addition, we have been genotyping a large F_2 population (>2,000 individuals) derived from the cross between Langdon durum and a RICL that has a small *T. turgidum* subsp. *dicoccoides* chromosomal fragment (10.7 cM) harboring *Qfhs.ndsu-3AS* for fine mapping of the QTL. This research facilitates the use of *Qfhs.ndsu-3AS* in wheat breeding and germ plasm development through marker-assisted selection and map-based cloning of the QTL.

Linkage disequilibrium and association mapping for wheat improvement.

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Knowledge of the level of genetic diversity and historical relationships among elite wheat germ plasm is very useful for association mapping (AM) and the exploitation of genetic variation in wheat. Linkage disequilibrium (LD), or nonrandom association of alleles at adjacent loci throughout the genome within a population forms the basis for AM strategies. The power of association analysis is affected by the patterns of LD, the extent of LD in the genome, and the variation in LD from one population to another. Linkage disequilibrium is affected by mating system, recombination rate, population structure, population history, genetic drift, directional selection, and gene fixation. Linkage disequilibrium estimates for cultivated wheat and barley have indicated that LD decays over 5 to 40 cM, a much slower rate than reported for outcrossing species. Germ plasm can be broadly classified into three categories: exotic accessions from germ plasm bank collections, intermating populations, and elite lines. These classes of germ plasm can be used for different purposes according to their genetic expectations. A core collection from a germ plasm bank may be used to screen high heritability traits, whereas elite lines are usually evaluated for low heritability traits in replicated, multi-environment trials. Intermated progenies of a segregating population are evaluated in different ways depending on the recurrent selection method and traits. The genetic expectations for an exotic core collection are low LD, low to medium population structure, and high allelic diversity. Linkage disequilibrium is high in the early generations of a segregating population and declines with additional cycles of intermating and selection. Elite lines have high LDs and population structure. Exotic germ plasm is typically used as a source of novel alleles in a marker-assisted backcross scheme, whereas elite lines are intermated and marker-assisted selection is used in the segregating progenies in a forward-breeding strategy. Intermated segregating populations offer a favorable balance of power and precision for association analysis and would allow mapping of quantitative traits with increasing resolution through cycles of intermating.