

**0203-CR-120 Microsatellite Marker Development and Mapping.**

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PROJECT ABSTRACT

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To date, the genetic approach that has resulted in increased resistance to *Fusarium* head blight has been the discovery of a quantitative trait locus (QTL) that provides partial resistance to this devastating disease. Microsatellite or simple sequence repeat (SSR) markers were the resource that made this QTL discovery possible and which have permitted subsequent marker assisted selection to move the resistance QTL to adapted genetic backgrounds. Despite this initial achievement, additional resistance QTL need to be discovered and moved into productive cultivars with high grain quality. Successful QTL analysis is dependent upon the availability of a robust and informative set of genetic markers with good marker density and even distribution across the target genome. As compared to other major U.S. crops such as maize and soybean, the number and density of SSR markers available to U.S. wheat breeders is low. Here, we propose a final year of work aimed at developing SSR markers from genomic libraries. Thus, it is the objective of this proposal to develop and map an additional 400 -500 SSR markers to bring the total number available to U.S. wheat geneticists and breeders to approximately 1200. This will create the genetic marker and map resource needed to expedite the discovery and molecular marker tagging of additional *Fusarium* head blight resistance QTL. QTL marker associations enable indirect selection for those QTL via marker-assisted selection. Equally as important, the reconstitution of the elite cultivar background can be accelerated through background selection with a set of molecular markers that is well distributed throughout the wheat genome. Thus, scab resistant cultivars with current levels of productivity and grain quality can reach the producer as rapidly as possible. We anticipate that essentially all of the A and B genome markers developed will be completely functional in durum wheat. Newly developed markers will be assayed initially for polymorphism among 'Chinese Spring', 'Opata 85' and M6. Those that are polymorphic in the Opata x M6 ITMI mapping population will be mapped on 83 lines of that population. The remaining markers will be positioned in the genome via physical mapping using nullisomic-tetrasomic lines. Approximately 150 loci generated in this final granting period will be examined on a panel of 45 elite hexaploid and five durum wheats as well as on a group of scab resistant genotypes. The database of allele sizes developed from this panel of genotypes, when added to the loci genotyped in the FY2001 granting cycle, will permit selection of SSR loci that distinguish locally adapted cultivars from scab resistant sources and will expedite the reconstitution of elite parent backgrounds. The primer sequence data and PCR conditions, map positions, and the information relating to allele size in the panel of elite and scab resistant genotypes will be made available to the U.S. research community via the USWBSI website and GrainGenes, the USDA-ARS Genome Database.