MOLECULAR MAPPING OF HEXAPLOID OATS (*AVENA SATIVA* L.) USING RFLP MARKERS

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ABSTRACT

Cultivated oat (*Avena sativa* L.) is hexaploid with a basic chromosome number of n=3x=21. It consists of three basic genomes (A, B, and D). Few simply inherited morphological markers and disease resistance genes have been identified and no classical linkage map has been developed for this crop species. As a result, genetic studies of oat have lagged behind those of other crops.

The development of molecular markers, such as RFLP (restriction fragment length polymorphism) and other polymerase chain reaction-based markers, has permitted the development of linkage maps in many crop species. A prerequisite for RFLP mapping is to have a sufficient level of polymorphism between lines. In a preliminary study, we have found that 71% of the probes used detected polymorphisms among 90 oat cultivars grown throughout North America.

The mapping of cultivated oats is complicated by its large genome size and its polyploid nature. To date, two A-genome diploid oat maps have been developed. Also, construction of a molecular linkage map of hexaploid oats has been initiated by several US and Canadian researchers using recombinant inbred lines.

The objective of this study was to construct an RFLP-based linkage map of hexaploid oats using an F_2 population. The mapping population consisted of 173 F_2 plants that were developed from a cross of Cayuse and Froker varieties. F_2 plants were selfed in the greenhouse. F_2 plants were space-planted in the field. Fresh leaf tissue samples were collected from F_2 plants. Analysis of RFLPs included isolation of genomic DNA, digestion with restriction enzymes, Southern blotting, hybridization with labeled probes, and developing autoradiograms. Initially, parents were screened with 256 probes with 110 detecting polymorphisms between parents. These polymorphic probes were then used to analyze RFLPs of F_2 plants. Autoradiograms were read visually using a light box, and presence or absence of polymorphic bands were recorded as '1' and '0', respectively. So far, analysis of 71 probes has been completed. MAPMAKER version 3.0 software was used for linkage analysis. Linkage groups

were obtained using two-point analysis with an LOD score (logarithm of the likelihood ration) of 3.0 and a maximum recombination level of .40 using the "group" command. Multipoint analysis was then used to order the loci within each linkage group. The loci formed 14 linkage groups ranging in size from 5.2 cM (centimorgan) to 92.9 cM and consisted of an average of 4.2 loci. Twenty-seven loci remained unlinked. The current map is 517.7 cM. With the addition of 39 probes (in process), the map size is expected to increase.

This map will provide a tool for quantitative trait loci analysis of several important traits that we are investigating currently, such as hull percent, heading date, and plant height. These data will be used for marker-assisted selection in oat breeding.