SEQUENCE-SPECIFIC AMPLIFIED POLYMORPHISM (S-SAP) MARKERS DISTRIBUTION IN A BARLEY LINKAGE MAP

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barley, retrotransposons, S-SAP markers, molecular mapping

The sequence-specific amplified polymorphism (S-SAP) method is a powerful tool for genetic analyses which exploits the LTR (Long Terminal Repeat) sequences of retrotransposons, common in plant genomes. The advantages of using the S-SAP technique rely on the high levels of polymorphism detected with these markers, related to the retrotransposons features and their major role in plant gene and genome evolution.

Saturated linkage maps are important tools to gain insights of the organisms genetic. For this reason we enriched the coverage of an existing RFLP barley map using the S-SAP markers technology. To study the distribution and inheritance of the S-SAP markers in barley, the Steptoe x Morex (SxM) doubled haploid (DH) population was used.

Ninety polymorphic markers were obtained using only six S-SAP primer combinations with a resulting polymorphism level of 28.1%, and 89 were unambiguously integrated in the linkage map. The S-SAP markers were largely interspersed among the previously mapped markers framework, covering both all the seven barley chromosomes and the total length of chromosomes. The final mapping showed a wide distribution of the S-SAP markers over the barley genome with a tendency to cluster, as justified by the retrotransposons insertion features.

The results obtained in this experiment are consistent with the previous knowledge of retrotransposons organization and confirm the utility of the S-SAP technique for molecular mapping. Moreover, this set of genetically characterized markers can be used for future genetic diversity analyses.