

Molecular approaches in Barley Improvement

Molecular approaches have been taken as tools for number of applications ranging from localization of a gene to improvement of plant varieties by marker-assisted selection in barley.

Localization of corn leaf aphid (CLA) resistance in barley

A study was conducted to determine the inheritance of resistance and to identify molecular markers of resistance in the barley (*Hordeum vulgare* L.) line EB921. A RIL population of cross Alfa93/EB921 was used to identify molecular markers linked to the genomic region that provides resistance against corn leaf aphid (CLA) in barley. STS marker KV1/KV2 (1H) retained significance during chi square test and was found closely linked when recombination fractions were calculated with the MAP MANAGER version QTXb20 using the Kosambi mapping function. This suggested that CLA resistance was conferred by a single dominant gene on 1H chromosome in barley.



Localization of Genomic Regions for Leaf blight resistance in barley

Leaf blight resistant (DWR49) and susceptible (RD 2503) lines were crossed to investigate inheritance of resistance and to identify QTLs associated with resistance. 283 SSR and STS primers specific to the seven chromosomes were used to screen the parental lines, of which 50 showed polymorphism over resistant and susceptible bulks and used for genotyping of 142 RILs (Recombinant Inbred Lines) of the cross DWR49 x RD2503. Total three, two major and one minor QTLs were identified during

Composite interval mapping (CIM). QTL Rcs-qt1-1H-1 at proximal end (0.0 cM) on 1H near Bmac 213 with LOD score 9.1, QTL Rcs-qt1-1H-2 identified near 9.0 cM with LOD score 4.3 flanked by markers ABG059 and Bmag872 and QTL Rcs-qt1-5H-1 on 5H chromosome at 92 cM with LOD score 12.3 flanked by markers SCIND16991-GMS1. These three QTLs explained total 52% phenotypic variance.



Developing Molecular Profiles of Indian Barley lines for Varietal Registration

The molecular information (molecular profiles) has become requisite as per the recommendation of CVRC guidelines for varietal registration. Taking this into account, molecular information of recently released barley varieties was generated for registration purpose. A set of Advanced Varietal Trials entries for barley sowing zones (North-Western Plains, North-Eastern Plains, Central zone and Northern Hills) were characterized at molecular level using STS/SSR markers for registration of identified entries and evaluation of genetic diversity among the test entries under all India coordinated wheat & barley improvement program (AICW&BIP). In total 68 marker alleles were scored for 17 lines and 1156 data points were generated. 22 markers were found polymorphic and number of alleles ranged from 0 to 2 with an average of 1.48 alleles per locus. The band fragment size varied from 110 bp to 1200 bp with PIC values ranging from 0 to 0.4160 for AVT of crop season 2011-12. In total 66 alleles were scored in selected 16 genotypes and 1041 data points were generated. The number of alleles ranged from 0 to 3 with an average of 1.43 alleles per locus. The band fragment size varied from 108 bp to 1200 bp with PIC values ranging from 0 to 0.4360. 21 markers were found polymorphic for the entries and checks for AVT. This information is further validated by developing similarity matrices and constructing dendrograms to infer genetic relationships among test entries of AVTs. This suggested that genetic variability of barley genotypes remained at par in last two years for major barley sowing regions of India.

