QTL MAPPING OF MALTING QUALITY TRAITS AND CHARACTERIZATION OF DOUBLED HAPLOID LINES BY MEANS OF MOLECULAR MARKERS


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malting quality traits, quantitative trait loci, barley

In order to study the genetic regions important for malting quality traits in the 'winter' by 'spring', and 'feeding' by 'malting' barley cross 'Nure' x 'Tremois', a barley genetic map based on a doubled-haploid (DH) population of 136 genotypes had been developed. Doubled haploid lines have thus been tested for their malting quality related traits by means of a micromalting machine. After harvest 2002 QTLs have been mapped on four chromosomes for malt extract, friability, protein content, viscosity of extract and for a synthetic score of malting quality. The QTLs of malting quality have been then validated in the following season 2002/2003 in different locations in Italy. By means of couples of markers flanking each QTL of quality, additional 90 DH lines have been genotyped. Lines with best haplotypes at all QTLs have then been selected for high grain yield and malting quality. Finally, the best performing line is being tested in a Multi-Locational Yield Trial (MLYT).