

IDENTIFICATION AND VALIDATION OF CANDIDATE GENES FOR BARLEY MUTANTS ALTERED IN PLANT ARCHITECTURE: A SYNTENY-BASED APPROACH

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barley, synteny, candidate gene (CG), Single Nucleotide Polymorphism (SNP)

In our laboratory, a collection of barley mutants affected in plant height (*brachytic, brh; slender dwarf, sld4*), shoot and inflorescence branching (*absent lower laterals, als; branched 1, brc1; unicum, cul; double seed 1, dub1; many noded dwarf, mnd6; six rowed-spike 1, vrs1*), development of leaves (*liguleless, lig*) and leaf-like organs (*calcaroides, cal; short awn, lks; suppressors of Hooded, suK; third outer glume, trd; triple awned lemma, trp*), has provided a starting point for genetic dissection of plant development.

Linkage analysis led to locate 40 of the corresponding loci in a molecular map of the barley genome. Based on map position, rice syntenous regions were revealed for 23 of these loci and their annotation led to the identification of candidate genes (CGs) for the mapped barley mutants. This analysis was conducted especially for those rice mutants which are phenotypically similar to our barley mutants. There are evidences that the barley genomic regions hosting the *liguleless* and *branched 1 (brc1, lig)* loci are colinear with the rice regions containing the *Liguleless* and *frizzy panicle* genes, respectively. The *branched 1* mutant is of particular interest because additional ears develop from the main inflorescence and the rachilla is converted into rachis. This phenotype has similarities with *branched silkless1 (bd1)* of maize, and *frizzy panicle (fzp)* of rice which are affected in the transition from spikelet to floral meristem identity.

Partial sequence of the gene putatively controlling the *brc 1* locus (HvFZP) was obtained by PCR from genomic DNA using degenerate primers designed on the *BD1* and *FZP* genes. To confirm that the barley orthologous of *FRIZZY PANICLE* is the CG of the barley *brc 1* locus, a single nucleotide polymorphism (SNP) analysis is being conducted on populations derived from the cross between the mapping parents of the PxN map and the mutant: homozygous recessive and dominant F2 plants are being used to investigate cosegregation between the *brc-1* phenotype and the *HvFZP* gene.