P0096 Positional Cloning of the Barley Tillering Gene *uniculme4*

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Manipulation of plant architectural traits such as the number of tillers can effectively increase grain yield in cereals. Within the frame of the TriticeaeGenome project (*www.triticeaegenome.eu), the* objective of our group was the fine mapping and positional cloning of *uniculme4* (*cul4),* a gene required for tillering in barley. Based on initial medium resolution mapping of the locus, a segregating population including 4900 F3 plants was developed and genotyped with three tightly linked SNP markers (Tavakol et al., abstract P321, PAG XIX). The locus was further resolved through mapping of 8 synteny-derived markers allowing the identification of a candidate gene that co-segregates with the *cul4* phenotype. The two genes that flank the candidate gene in Brachypodium and rice were positioned 0.11 cM and 0.12 cM from *cul4,* respectively: development of new markers is underway using sequence information from two BACs anchored to the physical map and spanning this region. The intron-exon structure of the candidate gene was determined from a cDNA isolated from wild-type plants. Resequencing of independent *cul4* stocks identified three distinct mutations within the candidate gene, including a deletion of the 5’ region. Comparison of expression levels and patterns in mutant and wild-type plants is underway.

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