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# HIGH-THROUGHPUT GENOTYPING AND COMPARATIVE GENOMICS APPROACHES FOR MAP BASED CLONING OF *UNICULME4*, A MENDELIAN LOCUS CONTROLLING BARLEY SHOOT ARCHITECTURE

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Manipulation of plant architectural traits such as the number of tillers can effectively increase grain yield in cereals. *Uniculme (cul)* recessive loci including *cul4* are required for tillering in barley. As participants in the FP7 TriticeaeGenome project (http://www.triticeaegenome.eu/), an objective of our group is the fine mapping and positional cloning of the *cul4* gene. Initial efforts were based on genotyping of six F2 populations deriving from crosses of *cul4.3, cul4.5,* and *cul4.15* mutants with wild-type cultivars using an Illumina GoldenGate assay: 96 EST-derived SNP markers covering a 50 cM interval on 3HL were selected starting from an initial set of 8 SNPs identified by comparison of a *cul4* introgression line and its recurrent parent. As a result, the *cul4.5* x Morex segregating population was selected as the most informative cross and propagated into >4900 F3 plants for positional cloning. The large F3 population was genotyped with tightly linked SNP markers using the KASPar genotyping system resulting in the identification of 179 recombinants around *cul4*. Phenotyping and genotyping of these plants with 8 new markers developed from collinear Brachypodium and rice genomic regions allowed the identification of a candidate gene cosegregating with *cul4* as well as mapping of the two flanking genes in Brachypodium 0.11 cM and 0.12 cM from *cul4,* defining a 0.23 cM interval around the locus. Comparative genomic analysis with these three gene-based markers identified 27 kb and 30 kb

collinear regions in rice and Brachypodium, respectively. Physical mapping of the *cul4* gene region is underway taking advantage of the available barley physical map.