

Construction and comparison of genetic linkage maps of four F1 populations of Italian ryegrass (*Lolium multiflorum* Lam.)

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Introduction The objective of this work was to integrate genetic maps and QTL-positions within 4 two-way pseudo-testcross F1 populations (each 110 genotypes) of Italian ryegrass (*Lolium multiflorum*). To integrate genetic maps and QTL-positions within the 4 populations and to the ILGI reference map, the maps used for initial QTL-analysis and marker assisted selection for yield and for different quality traits were further evaluated.

Materials and methods Four two-way pseudo-testcross F1 populations (each 110 genotypes) of Italian ryegrass (*Lolium multiflorum*) were generated by pair-crosses between non-related promising clones of our breeding pool. Genetic linkage maps based on microsatellites, STS and AFLPs were constructed for each population. These preliminary maps, generated by straightforward mapping of all types of markers under the “cross-pollinator” option of Joinmap, were used for QTL-analysis and marker assisted selection for yield and for different quality traits. Preliminary results will be available after evaluation in yield plots in 2005. This strategy was used due to meet the strict time schedule for plant selection, selfing and installation of polycrosses. To integrate genetic maps and QTL-positions within the 4 populations and to the ILGI reference map, the maps used for the initial analysis were evaluated further. The construction of parental maps followed by their integration was performed for each of the four crosses.

Results and discussion The integrated maps were aligned with the original maps. Most aligned linkage groups did not show major changes in length, number of markers or markers order. Some linkage groups presented changes in order and number of markers. Other groups could not be aligned. The integration or not of the less informative AFLP markers segregating as <hkxhk> has also been evaluated. Without the <hkxhk> type of markers, parental maps could not be aligned to build an integrated map within each cross. When mapping together markers of both parental origins using the cross-pollinator option in Joinmap, a map without the less informative markers could be calculated. Alignment to the original maps was possible showing in most groups a reduction of marker numbers. Other linkage groups appeared divided while they were originally grouped or the other way around. A new integrated map is being constructed.