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Poster Abstract – D.54

LINKAGE MAPPING OF CANDIDATE GENES FOR APOMIXIS

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Seed is one of the key factors of crop productivity and the comprehension of the mechanisms underlying seed formation is crucial for the quantitative and qualitative progress of agricultural production. In angiosperms two pathways of reproduction through seed exist: sexual, or amphimictic, and asexual, or apomictic. Genetic linkage mapping of apomixis loci in natural apomicts is one of the possible approaches to isolate genes related with the trait and transfer apomixis into crop species. The overall results indicated simple, dominant inheritance either of apomixis as a whole or as a few independent loci. Nevertheless in an increasingly number of species apomeiosis, either apospory or diplospory, and parthenogenesis have recently been found inherited independently. Up to now, no evidence for recombination suppression was found at the locus for parthenogenesis in species such as *Erigeron annuus* and *Poa pratensis* for which mapping data were available. *P. pratensis* (Kentucky bluegrass) is a hardy, persistent, attractive forage and turf grass adapted to a wide range of soils and climates. Its mode of reproduction is extremely variable and can range naturally from nearly obligate apomixis to complete sexuality.

The main goal of the study was to map selected genes (APOSTART, BABY BOOM, PpSERK and PpMET) as well as some 179 ESTs, differentially expressed between sexual and apomictic genotype of *P. pratensis* into a genetic linkage map. By crossing a completely sexual clone (S1/1–7) with a highly apomictic genotype (L4) we developed a segregating population which was characterized for its mode of reproduction. The linkage analysis was carried out following a pseudo-testcross strategy and using molecular data from 88 genotypes of the F1 population. We have applied SAMPL, AFLP and MFDP techniques to generate the framework for mapping the candidate genes and the putative loci for apospory and parthenogenesis with the aim of looking for those co-segregating with the mode of reproduction (apospory/parthenogenesis).

The current map for S1-1/7 covers about 1700 cM and consist of 270 markers distributed in 26 linkage groups, considering just those groups containing EST-derived markers. In the L4 map, 200 markers are distributed in 25 linkage groups for a total of 1400 cM covered.