Volume 48(1-4):51, 2004
Acta Biologica Szegediensis
http://www.sci.u-szeged.hu/ABS

DISSERTATION SUMMARY

Construction of a linkage map for *Medicago truncatula* RIL population and its comparative analysis with other *Medicago* genetic maps

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The Fabaceae, better known as the legume family, is the second most important family of crop plants. From agronomical point of view, legume crops are valuable source of vegetable protein for humans and livestock, and as green manure in the field. It is mostly due to the special capacity of legumes to form symbiotic relationship with nitrogen-fixing bacteria.

Medicago truncatula (M.t.) species is an important model system for legume molecular biology, which is closely related with alfalfa (*Medicago sativa, M.s.*). There is a multilateral international Medicago Genome project that encompasses four general categories of activities: cDNA sequencing and hybridization arrays for gene-expression studies, knock-out mutant collections and categorizing plant phenotypes, structural genomics with a goal of reconciling physical and genetic maps, and comparative and evolutionary analysis of gene families or genomes.

Our work is closely related to the last two activities of the genome program. A detailed genetic map of the diploid *M.s.* has been constructed by our laboratory (Kaló et al. 2000, Kiss et al. 1993). Based on the expertise of our lab in genetic mapping, one of our aims was to develop an improved genetic map for a *M. t.* RIL (Recombinant Inbred Line) population in cooperation with a French laboratory. The second aim was to compare the genetic maps of the *M. t.* and alfalfa. The individuals of the RIL population are the seventh generation of the cross between Jemalong 6 and DZA 315 lines (Thoquet et al. 2002). Other two *M. t.* populations, resulted from the cross of A17xA20 (D. Cook's laboratory) and J6xDZA (T. Huguet's group), were also used for the comparative mapping analysis.

PCR based markers were used for mapping. Gene-specific primers were designed by intron targeting method or single sequence repeats were taken into consideration. The genotypes of the individuals in the mapping populations were determined after agarose gel electrophoresis for those markers that showed either length polymorphism or dominant inheritance. The non polymorphic PCR fragments in agarose gels were subjected for further analysis to detect polymorphism; either SSCP experiments were performed or the sequence of the amplified products were determined for different alleles. Based on the sequence information, restriction enzyme digestion (CAPS) was performed to identify polymorphism, where it was possible.The genotypes of the individuals of the RIL population were determined for 250 genetic markers. Newly and previously mapped RFLP and PCR based markers corresponding to genes with known functions or sequences were used for the comparison. The comparative analysis of linkage maps revealed high level of correlation of the marker order between the two *Medicago* species. Only a few differences in the marker position and allele numbers were detected between the maps. The results of this syntenic analysis allow us to create an integrated *Medicago* map and to use the mapping data mutually for further genetic experiments.

References

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