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DISSERTATION SUMMARY

The enrichment of the genetic map of alfalfa (*Medicago sativa*) and its comparison with other Fabaceae and *Arabidopsis thaliana* genetic maps

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Alfalfa (*Medicago sativa)* is one of the most important cultivated forage legume in the world. The high nutrition level and the capacity to estabilish symbiotic nitrogen fixing interaction with the *Rhizobium meliloti* made alfalfa an important subject for molecular genetic studies. To analyze the genes involved in the control of the nitrogen fixing pathway it was important to construct a detailed genetic map of alfalfa. In our group at the begining of the '90s, a basic genetic map was constructed for alfalfa using 98 RFLP, RAPD, isozyme and morphological markers which could be ordered in eight linkage groups (LG; Kiss et al. 1993). Later an improved version of the genetic map was made on the basis of 1800 PCR-based (CAPS, RAPD, SSCP), RFLP and isozyme markers (Kaló et al. 2000).

The aim of our work was to increase the number of markers with known function on the genetic map of alfalfa and using this information to compare this map with the genetic map of other species from the Fabaceae family and model plant *Arabidopsis thaliana.* The intron-targeting method was used to design new primers using cDNA*s* of the model legume *M. truncatula* aligned to *A. thaliana* genomic sequences. Since intron sequences are less conserved during evolution by amplification of these segments there is a better chance to detect length polymorphism. Following PCR amplification agarose gel electrophoresis was made to detect length polymorphism or dominant inheritance. The non polymorphic PCR fragments in agarose gels were subjected for further analysis to detect polymophism; either SSCP experiments were performed using polyacrylamid gel electrophoresis or the sequences of the amplified products were determined for the two alleles. In the case of amplification products where no polymorphism could be detected with the above mentioned methods, the sequence of the fragments were determined and possible CAPS sites were identified. The new markers were positioned on the 8 LGs of alfalfa by using the colormap method developed in our laboratory (Kiss et al. 1998). The genetic map of alfalfa was then compared with three different genetic maps of the model legume *M. truncatula*, *Pisum sativum* and *Arabidopsis thaliana.*

The comparison of the genetic maps of the two *Medicago* species (the maps of one *M. sativa* and 3 *M. truncatula* population) was made on the basis of 157 markers with known function or sequence. As expected the alignment of the four genetic maps shows a high degree of conservation in marker order. The few detected differences were mostly due to distinct loci number of some markers. One major difference could be observed concerning the position of the rDNA location. On the genetic map of *M. truncatula* the rDNA marker could be found on the LG5 while on alfalfa is located on the LG6.

M. sativa and *P. sativum* are two related species both belonging to the Fabaceae family. The genetic map of pea contains seven LGs. By comparing the genetic maps of pea and alfalfa a high degree of synteny in the marker order could be detected. Four LGs could be completely aligned to the corresponding alfalfa LGs while in the case of three LGs cromosomal rearrangements could be seen. The information obtained from the comparison of these two genetic maps can be used to enhance the genome analysis of pea which is hindered by its big genome size.

In order to test the degree of synteny between unrelated species the genetic map of alfalfa was compared with that of the *A. thaliana.* For this comparison we selected mapping data for *A. thaliana* from the official webpage www.arabidopsis.org. For a reasonable comparison 268 low copy number ortholog genes were used for our work. From the comparison of the two maps we concluded that no macrosynteny could be detected between the marker order of the genetic map of alfalfa and *A. thaliana.*

References

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