

Lotus genetics and genomics: Resources and approaches

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The molecular genetics of *Lotus* is focused on three diploid species: *Lotus japonicus*, *Lotus filicaulis* and *Lotus burttii*. In addition to the inbred germplasm of these species a resource of recombinant inbred lines has also developed from *L. filicaulis* x *L. japonicus* ecotype Gifu, from *L. japonicus* ecotype Gifu x *L. burttii* and from *L. japonicus* ecotype Gifu x *L. japonicus* ecotype MG20. In parallel several methods for genetic analysis of gene function have been established within the *Lotus* community. Insertion mutagenesis with T-DNA, transposable elements and retrotransposons have all been used in *Lotus japonicus* and an EMS mutagenesis machine for reverse genetics has been established at the John Innes Centre. To enable map-based cloning genetic maps are constructed and different methods for positional cloning of symbiotic loci are currently applied in order to clone genes involved in nodule initiation, nodule function as well as autoregulation (Tirichine *et al.*, 2006). At the Kazusa DNA Research Institute the genome of the model *Lotus japonicus* is under sequencing and the complete sequence of substantial parts of the genome is already available in public databases. The sequencing program is focused on gene rich regions and an approach using seed points anchoring sequences onto the genetic map has been developed. Taking advantage of the available genome and EST sequences a proteomic program has been initiated on seed proteins and a transcriptome analysis based on Affymetix will soon be available. A summary of the structural and functional genomics within the *Lotus* community and the future perspectives will be given together with a discussion of the possibilities for transfer of information into cultivated legumes (Fredslund *et al.*, 2006).

References

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