

Utility of genetic and genomic resources from *L. japonicus* to cultivated species of *Lotus*

[NIELS SANDAL](#)*, NIELS JØRGENSEN, SVEND DAM, GITTE NAUTROP, JAKOB FREDSLUND, BIRGIT K. HOUGAARD, SIMONA RADUTOIU, LEILA TIRICHINE, LENE H. MADSEN, ESSEN B. MADSEN, KEISUKE YOKOTA, PALOMA ROMERO, ANNA JURKIEWICH, ANITA ALBREKTSSEN, ESSEN M.H. QUISTGAARD, EIGO FUKAI, JENS STOUGAARD

Department of Molecular Biology, University of Aarhus, Gustav Wieds Vej 10, DK-8000 Aarhus C, Denmark

* Corresponding author

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 as well as EMS mutagenesis have all been used in *Lotus japonicus*. 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.*, 2007). At Kazusa DNA Research Institute, Japan 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 Affymetrix 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

- TIRICHINE, L., SANDAL, N., MADSEN, L.H., RADUTOIU, S., ALBREKTSSEN, A.S., SATO, S., ASAMIZU, E., TABATA, S., STOUGAARD, J. 2007. A Gain-of-Function Mutation in a Cytokinin Receptor Triggers Spontaneous Root Nodule Organogenesis. *Science*, **315**, 104-107.
- FREDSLUND J., MADSEN L.H., HOUGAARD B.K., NIELSEN A.M, BERTIOLI D., SANDAL N., STOUGAARD J. and SCHAUSER L. 2006. A general strategy for the development of anchor markers for comparative genomics in plants. *BMC Genomics*, **7**, 207.