

Laboratory of Structural Genomics

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Research topics:

- Genetic mapping of the *Lupinus angustifolius* (narrow-leaved lupin) genome using sequence defined molecular markers designed based on data bases of the sequences of model species *Medicago truncatula* and *Arabidopsis thaliana*,
- The use of the BAC library of the nuclear narrow-leaved lupin genome (constructed within the framework of the national research project No. 3 P06A 009 24) to analyse the structure of genes involved in the nodulation process, genes responsible for the expression of important agricultural traits (disease resistance, flowering earliness, pod shattering) as well as genes coding enzymes of the phenylpropanoid synthesis pathway,
- Physical mapping of the *L. angustifolius* genome regions involved in the expression of genes of resistance to pathogenic fungi,
- Cytogenetic analysis of the *Lupinus* genome by FISH (fluorescence *in situ* hybridization) with the use of BAC clones from the nuclear genome library as molecular probes (BAC-FISH aimed at assigning linkage groups to chromosomes),
- Localization of short sequences in plant chromosomes by PRINS (primed *in situ* labelling),
- Idiogram construction of the narrow-leaved lupin on the basis of chromosome measurements with computer software and localization of chromosome specific markers,
- Plant transformation (tobacco, lettuce) to produce proteins of bio-pharmaceutical importance and obtain materials derived from transgenic lettuce and tobacco containing HBV surface antigens (S-HBs, M-HBs, L-HBs) for the 3rd generation vaccine against hepatitis B,
- Research, conducted in co-operation with Institut Pasteur (Paris) and INRA (Versailles), on obtaining of transgenic tobacco lines expressing antigens of HBV and HIV-1 as initial materials for an oral bivalent vaccine against hepatitis B and AIDS.

Main research achievements:

- Construction of a genetic map of the pea genome; localization and genetic characteristics of QTL loci responsible for the expression of agricultural traits connected with yield structure and protein content in pea seeds.
- Estimation of nuclear genome size and relationships of Old and New World taxa within the genus *Lupinus*.
- Cytogenetic localization of 18S-25S and 5S rDNA in 12 Old World species of the genus *Lupinus*.
- Construction of the nuclear genome BAC library of *L. angustifolius*; analysis of structure and organization of genome regions containing genes of resistance to pathogenic fungi.
- Elaboration of pea *in vitro* regeneration and *Agrobacterium*-mediated transformation protocols.
- Expression of S-, M- and L-HBs antigens as well as core antigen Hbc of HBV in herbicideresistant transgenic lettuce and tobacco plants as materials for the preparation of an oral or injection 3rd generation vaccine against hepatitis B.
- Elaboration of a plant-derived tablet-form prototype vaccine containing the S-HBs antigen against HBV.