

NF-Y genes in the somatic embryogenesis

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Motivation and Aim: NF-Y are conserved transcription factors of eukaryotes, consisting of three subunits, NF-YA, B and C. In plants, each subunit is encoded by a family of genes, and combinations of different subunits are able to regulate various processes in plant development. One of the *NF-YB* genes in *Arabidopsis thaliana*, the *LEC1* gene, regulates many processes, most of which are associated with embryogenesis [1]. For example, it is involved in the morphogenesis of the embryo, the accumulation of storage substances in the seed, and can also stimulate the development of somatic embryos.

Somatic embryogenesis – the embryo development from vegetative tissues – is an important process for biotechnology. As a regeneration process, it is used for reproduction and for obtaining transgenic plants. For most leguminous plants, despite their importance for agriculture, protocols for obtaining somatic embryos have not been developed and their regeneration, as well as transformation, is not always possible. We hypothesized that, since the *LEC1* protein is involved in embryogenesis in *A. thaliana*, its orthologues in legumes can also stimulate somatic embryogenesis functioning in combination with specific NF-YA and C subunits. The aim of our study was to find new somatic embryogenesis regulators among *NF-Y* genes in legumes

Methods and Algorithms: We used *Medicago truncatula* as model species and applied qPCR analysis, as well as transcriptomic databases analysis, to find *NF-Y* genes with high expression levels during somatic embryogenesis. We also used yeast two-hybrid system to find potential partners among *M. truncatula* NF-Y proteins.

Results: We found several genes from *NF-Y* family which are expressed during somatic embryogenesis and during seed development. T0 calli with overexpression of *LEC1* orthologues did not demonstrate increased somatic embryogenesis capacity, but overexpression of one of *NF-YA* genes increased callus weight.

Conclusion: The data about *NF-Y* genes participating in the somatic embryogenesis can be used for the search of NF-Y complexes involved in this process. We are planning to investigate the effect of co-overexpression of *NF-YA*, *B* and *C* genes on the regeneration processes.

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References

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