

Transcriptomic analysis for the optimization of transformation of legumes

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Motivation and Aim: Legumes have multiple benefits for agriculture due to their nutritional qualities and ability to fix atmospheric nitrogen. Although there is a need for genetic modification of different legume species, transformation of most of them is hampered by their low regeneration capacity. The aim of this study is to discover new genes which can affect regeneration, unravel the mechanisms of their functioning and check the possibility of their usage for the optimization of regeneration and/or transformation protocols.

Methods and Algorithms: We used *Medicago truncatula* as model leguminous species, because it has small sequenced genome and lines, differing in their regeneration capacity. For that species, somatic embryogenesis, i.e. development of embryo-like structures from somatic cells, is the main regeneration pathway. We apply transcriptomic analysis and ChIP-seq methods to embryogenic and non-embryogenic *M. truncatula* lines to find new potential regulators of somatic embryogenesis.

Results: We found several genes from *WOX* family which are able to affect somatic embryogenesis being overexpressed. Some of them, like the *MtWOX2* gene, induce callus formation, whereas other, like *MtWOX1* or *MtWOX9-1*, stimulate somatic embryogenesis itself. Interestingly, when compared with control, *MtWOX2* and *MtWOX9-1* overexpressing calli have partly opposite transcriptomic changes. We also found several participants of somatic embryogenesis among members of the NF-Y family of transcription factors.

Conclusion: The results obtained on *M. truncatula* allowed us to find several new potential regeneration regulators. Their ability to stimulate regeneration is currently being checked on non-model leguminous species, like *Lens culinaris*, *Pisum sativum* and *Trifolium repens*.

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