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Finding genes for nodulation

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Summary

Characterization of nodule-specific genes in *Medicago truncatula* will enhance our understanding of nodule development

Significance and context

Leguminous plants interacting with symbiotic nitrogen-fixing bacteria (for example, the plant *Medicago truncatula* with the bacterium *Sinorhizobium meliloti*) develop new organs, called nodules, on their roots. These nodules contain differentiated bacteria (bacteroids) that fix atmospheric nitrogen into ammonium, which is subsequently provided to the host plant, a process known as symbiotic nitrogen fixation. Nodule development is a complex process that probably involves a large set of genes. So far, not many genes have been described and proved to be required for nodule development. Fedorova *et al.* analyzed an expressed sequence tag (EST) database of the model legume *M. truncatula* and determined and characterized putative gene products or tentative consensus sequences (TCs) specifically expressed in root nodules.

Key results

The *M. truncatula* EST database used in this study contained 140,000 sequence entries from 30 non-normalized cDNA libraries representing a set of vegetative and reproductive organs. Those included five libraries prepared from mRNA of *M. truncatula* root nodules at different developmental stages. The entire EST collection was screened for TCs that were exclusively present in the latter five libraries and not in the others. This revealed 340 nodule-specific entries. A database search showed that 7% of the TC-encoded proteins were leghemoglobins, 17% were nodulins (for example, homologs to plant defense proteins, probable peroxisomal proteins, possible plasma membrane proteins, and possible integral membrane proteins), 9% were involved in metabolism, 7% in transport, 19% in signal transduction, 11% in cell structure and maintenance, 2% were growth factors, 19% were hypothetical, unknown, or putative proteins, and 9% had an unknown function. Of the nodule-specific TCs, 91 were analyzed by DNA macroarray to confirm their enhanced expression in nodules. The expression level of all TCs was at least twofold higher in nodules compared to roots, and when compared to leaves, the expression level of as many as 72 of those TCs was at least twofold higher, supporting their assignment as nodule-specific.

Links

The large-scale EST database of *M. truncatula* can be accessed at the [TIGR%20Medicago%20truncatula%20Gene%20Index%20\(MtGI\)](#). Nodule-specific TCs can be viewed at the [Medicago%20truncatula%20Consortium](#).

Reporter's comments

Fedorova *et al.* determined a large collection of TCs that are specifically expressed in nodules of the model legume *M. truncatula*, and may, therefore, act in nodulation and/or nitrogen fixation. It will be interesting to see whether these nodule-specific TCs are present in non-nodulating plants such as *Arabidopsis thaliana*, and in agronomically important crops such as rice, wheat and maize. This study may help in engineering such crops to carry out symbiotic nitrogen fixation.

Table of links

[Plant%20Physiology](#)

[TIGR%20Medicago%20truncatula%20Gene%20Index%20\(MtGI\)](#)

[Medicago%20truncatula%20Consortium](#)

References

1. Fedorova M, van de Mortel J, Matsumoto PA, Cho J, Town CD, Vandenbosch KA, Gantt JS, Vance CP: Genome-wide identification of nodule-specific transcripts in the model legume *Medicago truncatula*. *Plant Physiol.* 2002, 130: 519-537.