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Functional analysis of the soybean genes related to natural products for human and animal health

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Objectives

In an attempt to examine function of the sequence linked to the molecular markers for functional metabolites in soybean, a transgenic hairy root of soybean with various candidate genes either over-expressed or repressed will be generated and analyzed.

Materials and Methods

1. Materials

Plant Sinpaldalkong2ho, SS2-2

Agrobacterium strain *Agrobacterium rhizogenes* K599

2. Methods

RNAi Gateway system, Hairy root transformation

Results and Discussion

As a first step toward that, the genes for isoflavone and anthocyanin pathways are being obtained from the soybean EST collections or cloned directly from soybean.

The functional analysis of the genes will be performed by RNAi construction following transformation of soybean hairy root with *Agrobacterium rhizogenes* K599. The transgenic hairy root will be analyzed by HPLC or 2D IEF/SDS-PAGE for any changes in profile of metabolites or proteomes. For a high throughput functional analysis of various target genes and sequence pENTR/D-TOPO and gateway vector system will be used to construct RNAi vector in pB7GWIWG2(I). The introduction of a gene expressing hpRNAs into roots by *A.rhizogenes*-mediated hairy root transformation induces efficient silencing of the target gene in the roots of soybean.

As a preliminary result a hairy root transformation was stably performed in soybean and RNAi construction of a soybean gene MDH, for a metabolic pathway was completed using the proposed procedure. The *A.rhizogenes*-transformed roots and its nodules showed the same genetic traits and as the parent root morphology as normal.

A high-throughput system for functional analysis of a large number of the genes involved in synthesis of soybean functional metabolites is about to launch.

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