

# Transcriptome Profiling of the Shoot and Root Tips of *S562L*, a Soybean *GmCLAVATA1A* Mutant

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## Abstract

Plant shoot apical meristems (SAM) and root apical meristems (RAM) contain stem cells that form overall-plant architecture. Mechanisms acting in these regions keep a balance between the stem cell population and differentiation. These mechanisms are well-studied in *Arabidopsis*, but little is known in the legume soybean (*Glycine max* (L.) Merr.). In *Arabidopsis*, the Leucine-rich repeat (LRR) Receptor kinase *CLAVATA1* (*CLV1*) is a crucial regulator of this process in the SAM. In soybean, the receptor most similar to *ATCLV1* is *GmNARK*, which is involved in nodulation control. In contrast, the homeologous partner of *GmNARK* in soybean, called *GmCLV1A*, appears to have no function in 'Autoregulation of nodulation' (AON) a role in regulating shoot architecture in the SAM. Here, the transcriptome of the shoot and root tip areas of a chemically induced and TILLING-selected *GmCLV1A* missense mutant, *S562L*, and its wild type, cultivar Forrest, were analysed to identify genes which are affected by impaired function of *GmCLV1A*. Among the differentially expressed genes identified, many were categorised as having a role in receptor kinase activity, transcription or defense/stress-response. Molecular categories over-represented in the shoot tip of the mutant include those involved in hormone biosynthesis/activity and secondary metabolism, signalling, photosynthesis, and transport. Functional categories including those involved in polyamine metabolism, nucleotide metabolism, RNA regulation, protein targeting and protein degradation were under-represented in the shoot tip of the mutant. In the root tip, categories associated with signal

ling, transport, protein synthesis and metabolism were over-represented in the mutant, while categories associated with cell wall degradation, stress, RNA regulation, protein degradation and targeting were under-represented in the mutant. Factors similar to *Arabidopsis* regulatory components are most likely functioning in specialised shoot structures in legumes. Furthermore, *GmCLV1A* may have an unexpected role in the regulation of flavonoid biosynthesis in soybean.

**Keywords:** *Glycine max*, legume, plant development, RAM, receptor kinase, RNAseq, SAM, symbiosis.

## Introduction

Soybean (*Glycine max* (L.) Merr.), garden pea (*Pisum sativum*), common bean (*Phaseolus vulgaris*) and alfalfa/lucerne (*Medicago sativa*) are some of the important crops belonging to the legume family, which are second to the grasses in providing food for the world's population. One-third of all dietary protein and one-third of processed vegetable oil for human consumption are provided by grain legumes (Gepts et al., 2005; Graham and Vance, 2003).

Nitrogen is the most required nutrient of plants and enters into many biological molecules such as amino acids, proteins and nucleic acids. Although dinitrogen gas ( $N_2$ ) forms a main part of the earth's atmospheric gas (78.1%), it cannot be used by most of the plants, generating a global need for nitrogen-containing fertiliser. Leguminous plants, however, are able to use dinitrogen gas through a symbiotic association with soil bacteria, collec-

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