

The functional role of *GM-RLK3* in soybean growth and response to biotic and abiotic stresses

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ARTICLE INFO

Article history:

Received 31 March 2015

Accepted 19 May 2015

Keywords: Receptor-like kinase; Biotic stress, Abiotic stress, RNA-Seq, Transgenic

ABSTRACT

Soybean *GM-RLK3* is a receptor-like kinase gene, which shares high similarity with the *Arabidopsis thaliana* BAM family gene suggesting a similar functional role in promoting meristem size and cell differentiation. While the functional role of RLK3 has been heavily investigated in models as well as in some agronomic crops, no studies have been conducted in soybean. The aim of this study was to examine the functional role of *GM-RLK3* in soybean growth and development, in addition to assessing the response of transgenic soybean to biotic and abiotic stresses under greenhouse conditions. Stable transgenic plants for overexpression of *GM-RLK3* were developed using immature cotyledon explants. Real time-PCR demonstrated the overexpression of this transgene in different tissues, and showed that GM-RLK3 was overexpressed in unifoliate tissues (52 fold increase) with lower expression in pod tissues (7.7 fold increase). Results showed that overexpression of GM-RLK3 did not improve soybean resistance to necrotrophic pathogens and abiotic stress. Furthermore an enhanced resistance to *Pseudomonas syringae* pv. *glycinea*, as an example of biotrophic pathogens, was observed. This finding reflects activation of soybean signaling pathways involved in resistance to biotrophic pathogens. Additionally, overexpression of GM-RLK3 altered soybean growth and development by enhancing shoot biomass and number/weight of pods. Data analysis from RNA-Seq showed that overexpression of GM-RLK3 altered the transcription of other members of RLK and also of different signaling pathways involved in phosphorus, nitrogen and carbon assimilation. This study demonstrated the importance of GM-RLK3 as a regulator gene in soybean and the overexpression provides a potential insight to improving the efficiency of soybean through manipulation of this protein.

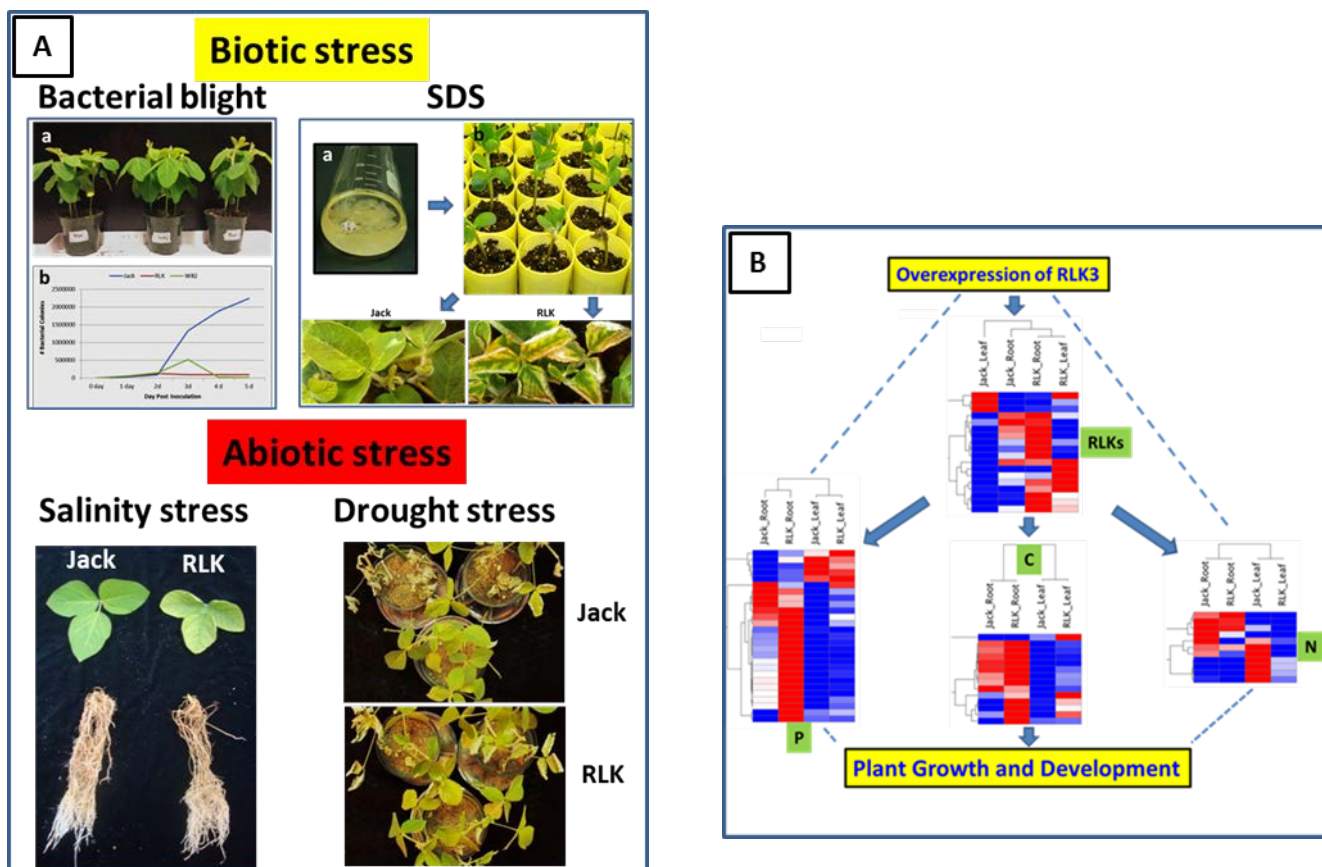


Figure 1. Response of transgenic soybean (RLK) and wild type plants (Jack) to biotic and abiotic stresses (A) and important signaling pathways regulated during overexpression of Gm-RLK3 in soybean using RNA-Seq (B). Sudden death syndrome (SDS) disease caused by a necrotrophic pathogen (*Fusarium virguliforme*) while bacterial blight (BB) disease caused by Psg, *Pseudomonas syringae* pv. *glycinea*, a biotrophic pathogen. In SDS disease, the fungal pathogen (a) was used to inoculate soybean seedlings (b). Three weeks after inoculation, the foliar symptoms appeared. For the BB disease test, the resistant check Williams 82 (W82) was included in addition to transgenic (RLK3) and wild type (Jack) lines. These three soybean lines were inoculated by Psg using vacuum infiltration method (a). Results (b) showed that transgenic soybean (RLK3) reduced the bacterial colonies compared with the wild type (Jack). The response to salinity and drought are two examples of abiotic stress. Figure 1 (B) summarizes data analysis from RNA-Seq profiling the transcriptome of both transgenic and wild type plants. Overexpression of *Gm-RLK3* triggered the transcription of other members of RLK, in addition to different signaling pathways involved in phosphorus (P), nitrogen (N) and carbon (C) assimilation, which have implications on plant growth and development. In figure 1 (B), red color indicates up regulated and blue color indicates down regulated.