# Analysis of defense genes in response to white mold infection in different bean (*Phaseolus vulgaris)* genotypes

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## INTRODUCTION

Understanding the function of quantitative resistance genes and their mode of expression is necessary to enable breeders to select which QTL to deploy in marker assisted selection for resistance (Kelly and Vallejo, 2005).
The objective of this research was to investigate the role of *PGIP, Glucanase,* and *PAL* genes in the defense response of different bean genotypes following infection with *Sclerotinia sclerotiorum*.

## MATERIALS AND METHODS

Four genotypes of dry bean; AN-37, G122, P02630 and Beryl were used based on their different reaction to white mold in the straw test. G122 is cranberry landrace from India (Miklas et al., 2001), AN-37 (Miklas et al., 2006) is pinto line derived from a navy line possessing resistance from Bunsi a source of resistance to white mold. Both of these cultivars are moderately resistant, while Beryl (a great northern) and P02630 (MSU pinto breeding line) are susceptible.

The plants were grown in the greenhouse under the same conditions as when conducting the straw test. Briefly plants were inoculated 21 days after planting as described by Petzoldt and Dickson (1996). Control plants were wounded without infection. All pots were kept at 25°C in the greenhouse.

Tissue sampling was conducted from both the necrotic part and the chlorotic area of each lesion within 2 cm of the lesion edges at 0, 24, 48 hours post inoculation (hpi) and 7 days post-inoculation (dpi) and immediately frozen in liquid nitrogen prior to RNA extraction.

Gene expression levels were analyzed via density analysis of Gel Doc EZ imager and Image Lab™ software. Amplified product intensity was expressed as relative absorbance units.

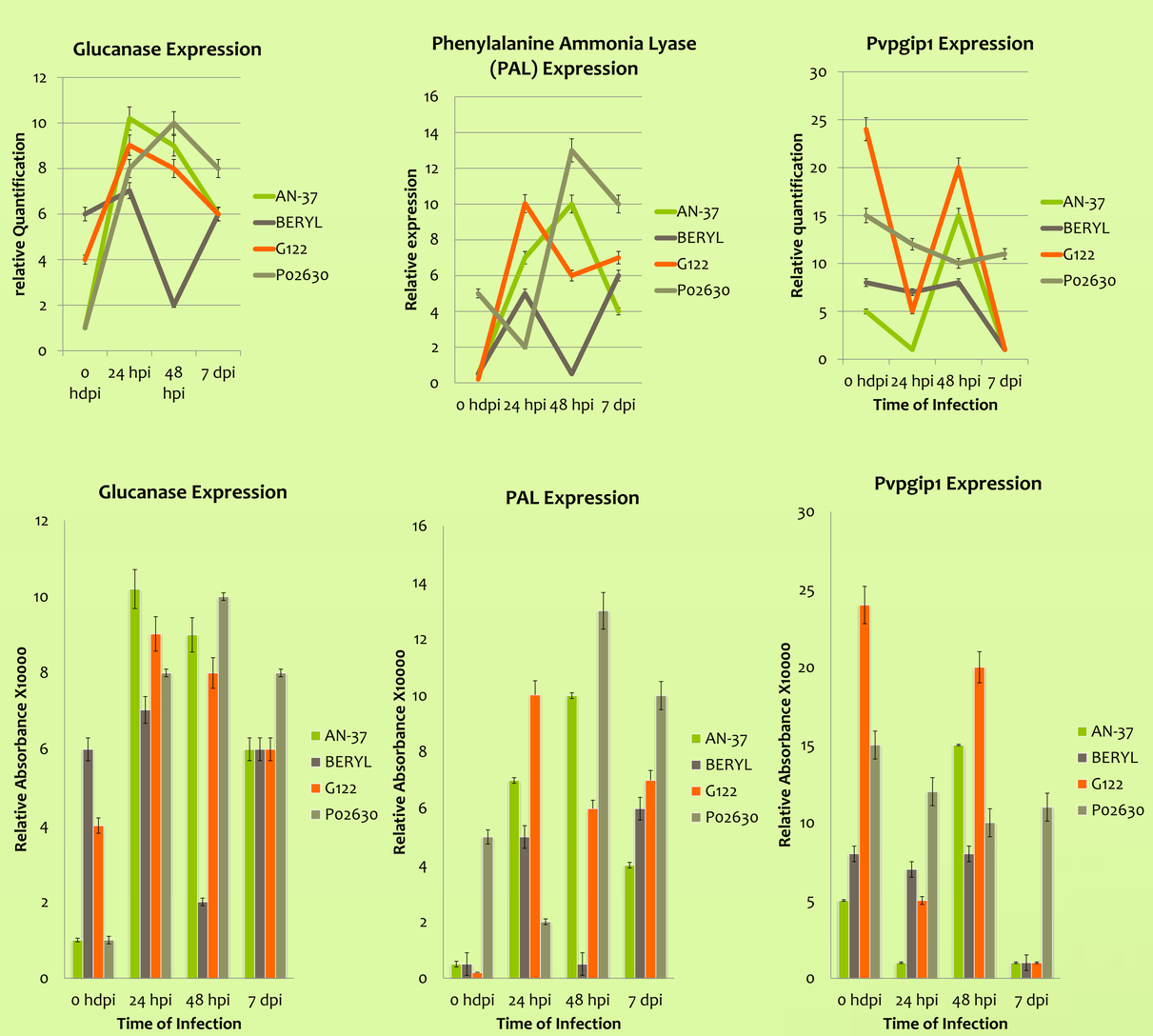
**Table 1:** Effect of inoculation of the genotypes with *Sclerotinia sclerotiorum*

| Genotype | Disease score[1] |
|---|---|
| AN-37 | 3a |
| BERYL | 8b |
| G122 | 1c |
| P02630 | 4a |

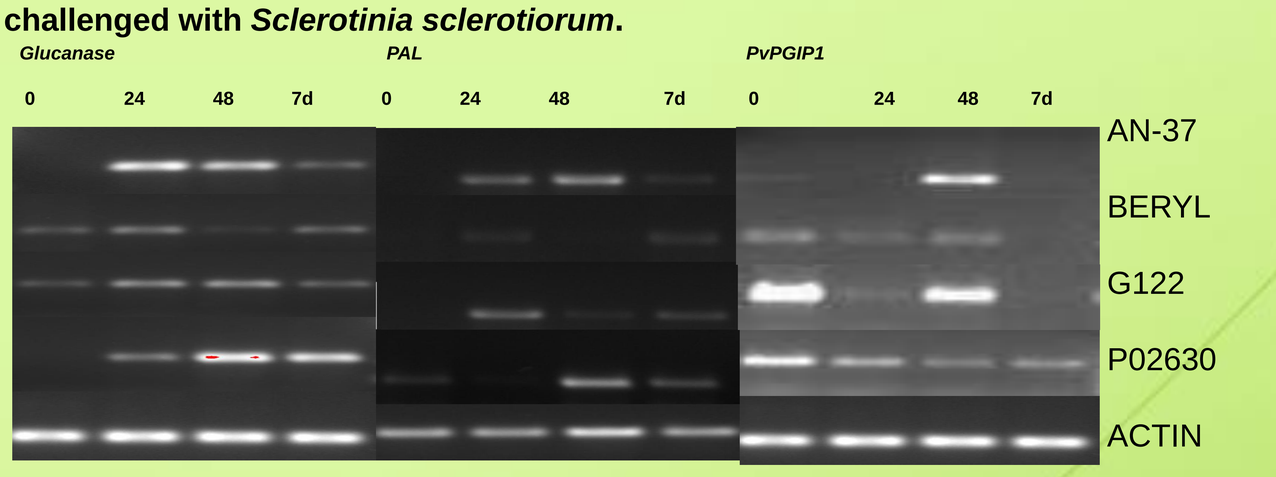
[1] 1=no disease; 9=highly susceptible; Genotypes followed by the same letter are not significantly different from each other.

## RESULTS

**Figure 1. Gene Expression Analysis**




**RT-PCR product analysis for the *Glucanase, PAL and PvPGIP1* genes, indicating the differences in signal strength at four different time points in four bean genotypes challenged with *Sclerotinia sclerotiorum*.**




## DISCUSSION AND CONCLUSION

The expression patterns exhibited by the three genes confirm that they have a role in defense response following infection with *Sclerotinia sclerotiorum*.

Glucanase expression indicates that its effectiveness is enhanced when expressed beyond 24 hpi especially at 48hpi. The most temporal expression was in the intermediate pinto genotypes AN-37 and P02630 suggesting that it is a distinct defense response however the availability of transcripts in the other genotypes at 0 hpi indicates that the gene also responds to wounding.

The induction of PAL at 24-48 hrs suggests that some phytoalexins play a role in plant defense following *Sclerotinia sclerotiorum* infection. However based on relative amounts of transcripts in comparison to the other two genes this pathway may only offer generalized defense response.
PvPGIP1 seems to be activated in response to wounding as it could not be detected at 24 hpi in the resistant genotypes.
These results confirm the quantitative nature of different levels of resistance to white mold infection observed in different bean cultivars. The use of the straw test could be confounding resistance mechanisms and the interpretation of disease ratings because it also induces genes involved in wounding.

## CONT ACT

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