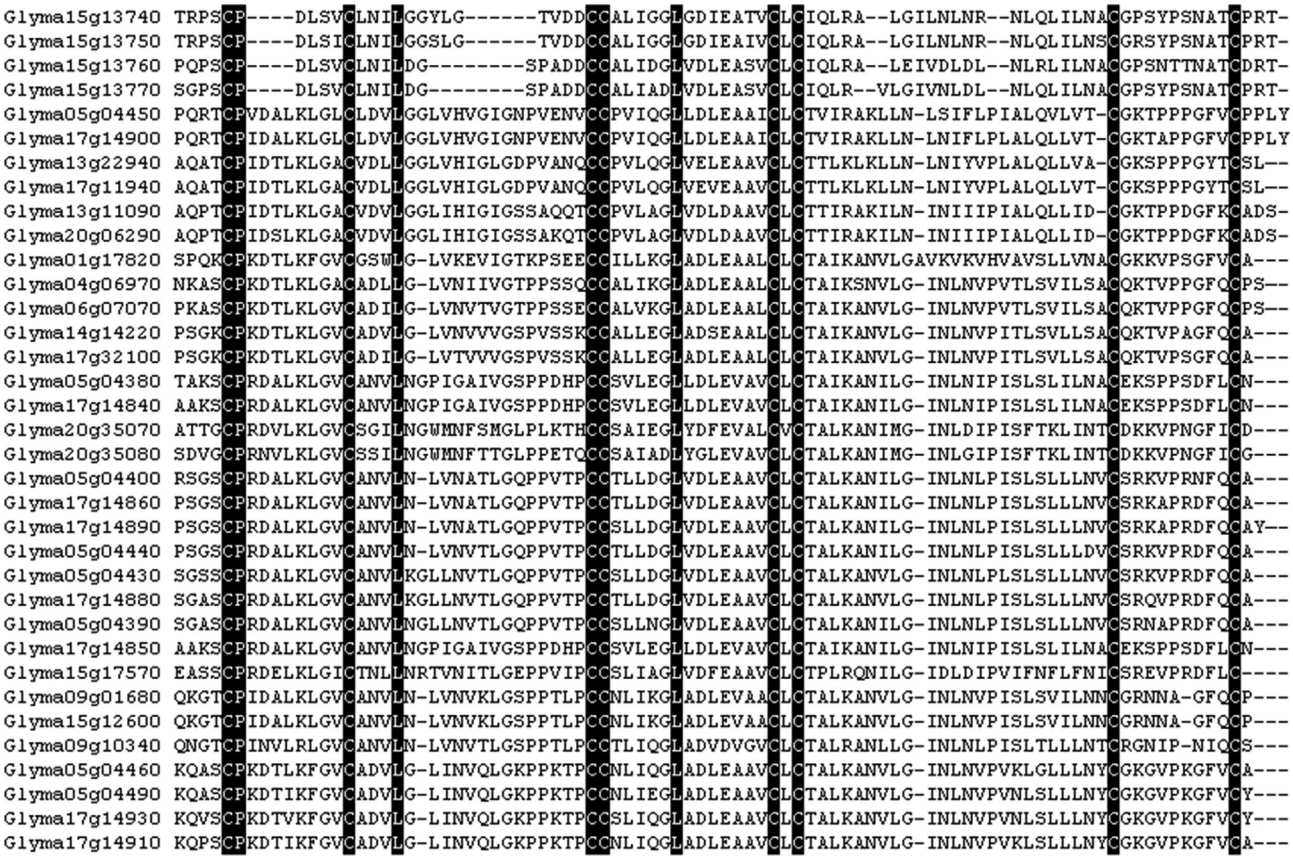

Figure S1 - Alignment of the conserved C-terminal domains of soybean HyPRPs using Muscle software.

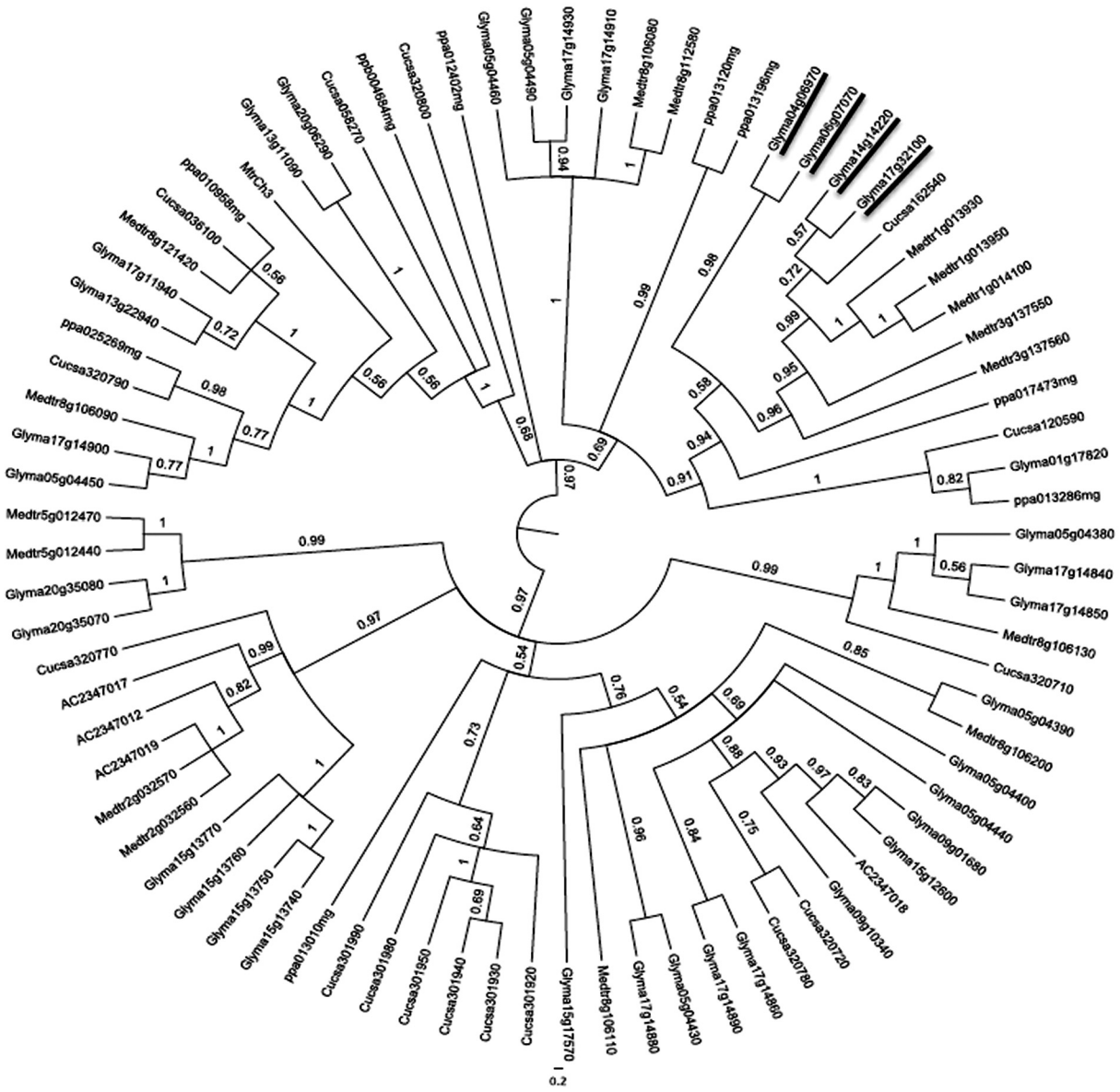

Figure S2 - Bayesian phylogenetic tree of 81 HyPRPs from soybean and three other plant species. The Bayesian analysis was done using MrBayes v.3.1.2 after alignment of the conserved 8CM domain of HyPRPs using Muscle software, as described in Material and Methods, except for two independent runs of 5,000,000 generations each. The unrooted cladogram was edited using FigTree v.1.3.1. Nodal support is given by the posteriori probability values shown next to the corresponding nodes. Bootstraps from neighbor-joining analysis have been omitted since they were less reliable than the Bayesian method. The scale bar indicates the estimated number of amino acid substitutions per site. The soybean pathogen responsive genes analyzed in a time-course real time RT-qPCR experiment are underlined in black. The names of the HyPRP-encoding genes are identified by their locus ID in Phytozome: Cucsa - *Cucumis sativus*, Glyma - *Glycine max*, AC or Medtr - *Medicago truncatula* and ppa - *Prunus persica*.

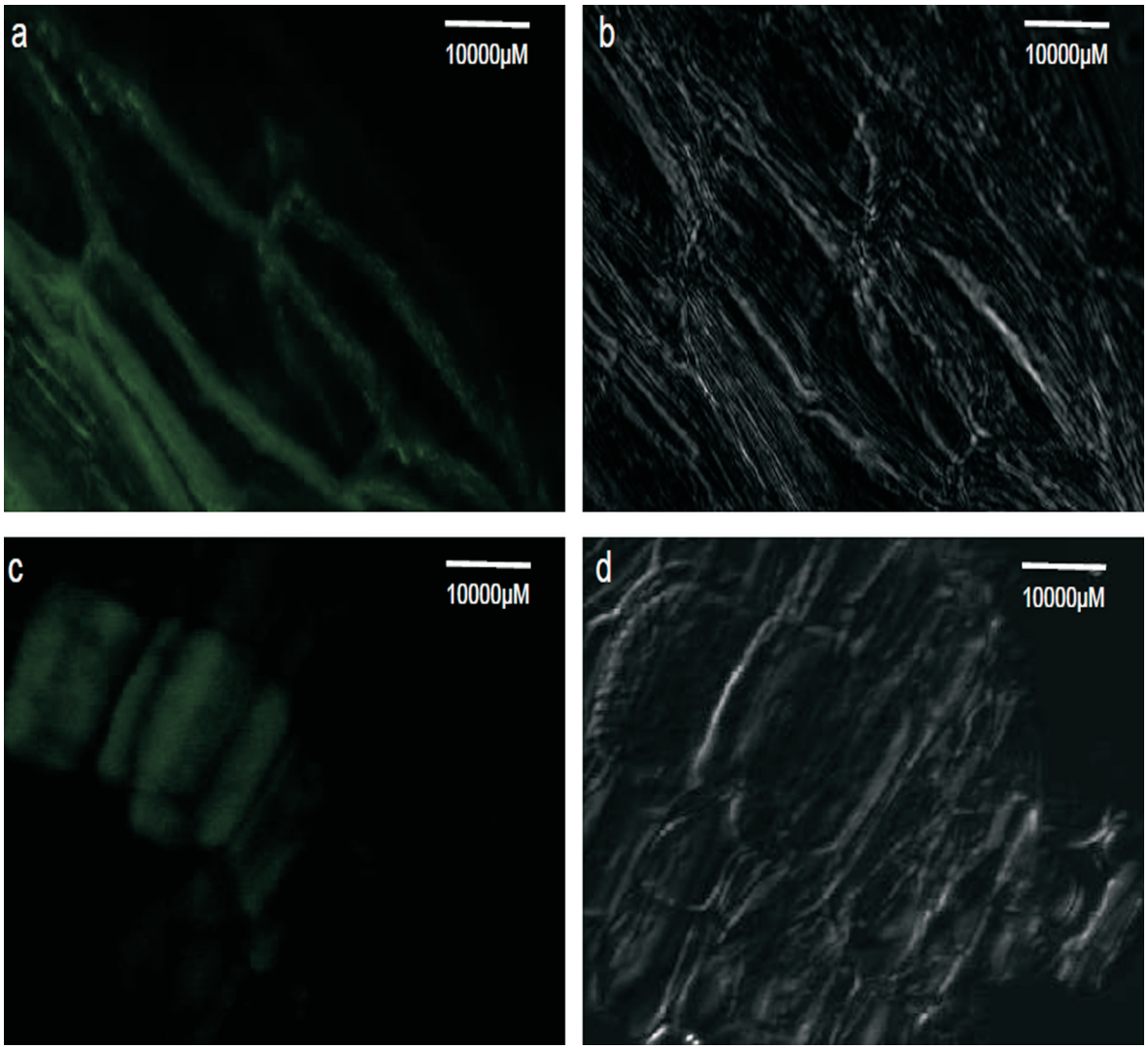

Figure S3 - Subcellular localization of GmHyPRP16 (Phytozome gene model: Glyma14g14220; GenBank accession no. EV274235.1) in soybean root cells after dehydration. The recombinant pCAMBIA1300-(CaMV) 35S promoter-GFP+GmHyPRP16-(CaMV) 35S terminator plasmid was confirmed by DNA sequencing and inserted into *Agrobacterium rhizogenes* strain K599 by electroporation. This is the first time that the *A. rhizogenes*-mediated root transformation system has been used to obtain transgenic soybean root cells. **(A)** Confocal microscopy image showing the fluorescence of GmHyPRP16-GFP protein in transgenic soybean root cells expressing 35S::SbPRP-GFP. **(C)** Confocal microscopy image of wild-type soybean roots cell; **(B)** and **(D)** Bright field images of the cells shown in **(A)** and **(C)**, respectively.