Supplementary Online material

Regulation of two germin-like protein genes during plum fruit development.

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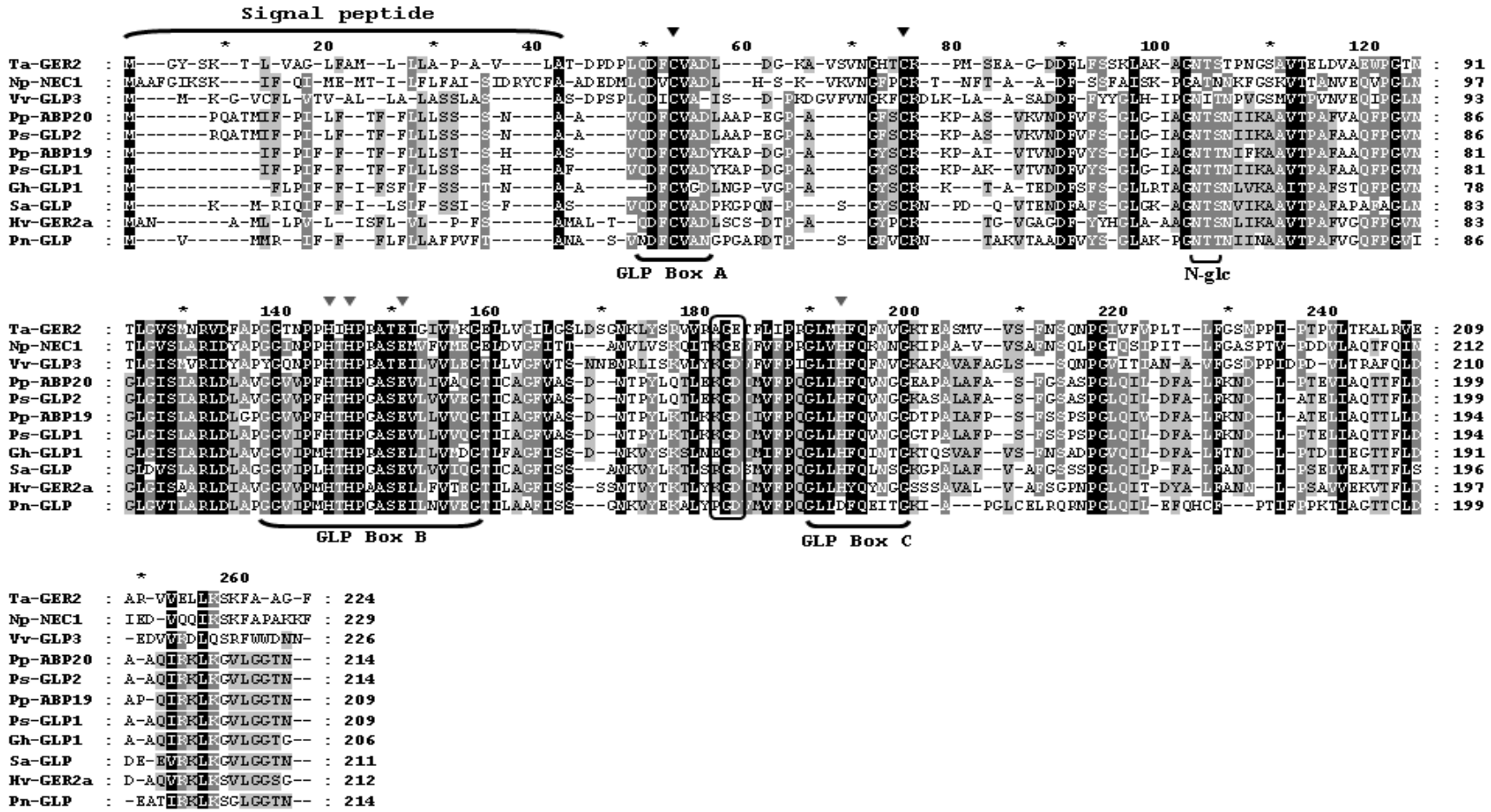
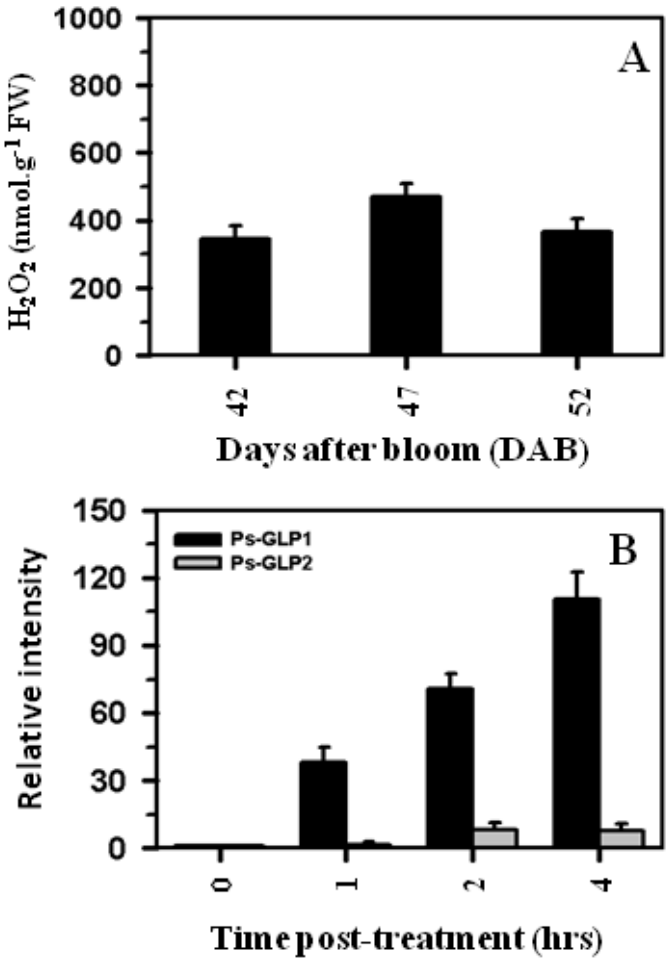
This PDF file includes:

- Supplementary figures and figure legends online.



Supplementary Fig.1 online. Amino acid sequence alignment of the *P. salicina* genes, Ps-GLP1 and Ps-GLP2 with closely related sequences *P. persica* Pp-ABP19, Pp-ABP20, *G. hirsutum* Gh-GLP1, *S. alba* Sa-GLP, *H. vulgare* Hv-GER2a, *I. nil* Pn-GLP, *N. plumbaginifolia* Np-NEC1, *V. vinifera* Vv-GLP3, and *T. aestivum* Ta-GER2, using ClustalX program. Conserved residues are shaded in black. Dark grey shading indicates similar residues in nine out of eleven of the sequences and clear grey shading indicates similar residues in eight out of eleven of the sequences. Putative N-terminal signal sequences are indicated by “Signal peptide”. The three conserved germin/GLP motifs are signed GLP Box A, B, and C (Bernier and Berna, 2001). The conserved two cysteine residues are pointed with two black arrows. The three histidines and the glutamate amino acid residues involved in metal binding are pointed with four gray arrows. The predicted N-glycosylation sites of Ps-GLP sequences are indicated by “N-glc”. RGD-like tripeptides (KGD) is outlined.



Supplementary Fig.2 online. **[A]** The evolution of H_2O_2 levels during stage 2 of fruit development using the whole fruit. The experiments were carried out in triplicate. The *x*-axis represents the developmental stage indicated by number of days after bloom (DAB). The y-axis represents the concentration of detected H_2O_2 (nmol.g^{-1} FW). **[B]** Expression of *Ps-GLP1* and *2* in response to H_2O_2 treatment. Fruit from early stage 2 (42 DAB) were treated with 1µM H_2O_2 for 15 min. After that the fruits were dried and incubated at room temperature for 0, 1, 2, and 4 hrs post-treatment. The expression of both transcripts has been assessed by QRT-PCR. The experiments were carried out in triplicate. The *x*-axis represents the time of incubation after treatment (hours). Relative intensity in the y-axis refers to the fold difference in gene expression relative to the control (time zero).