

Proteomic and phosphoproteomic analysis of polyethylene glycol-induced osmotic stress in root tips of common bean (*Phaseolus vulgaris* L.)

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Supplementary material

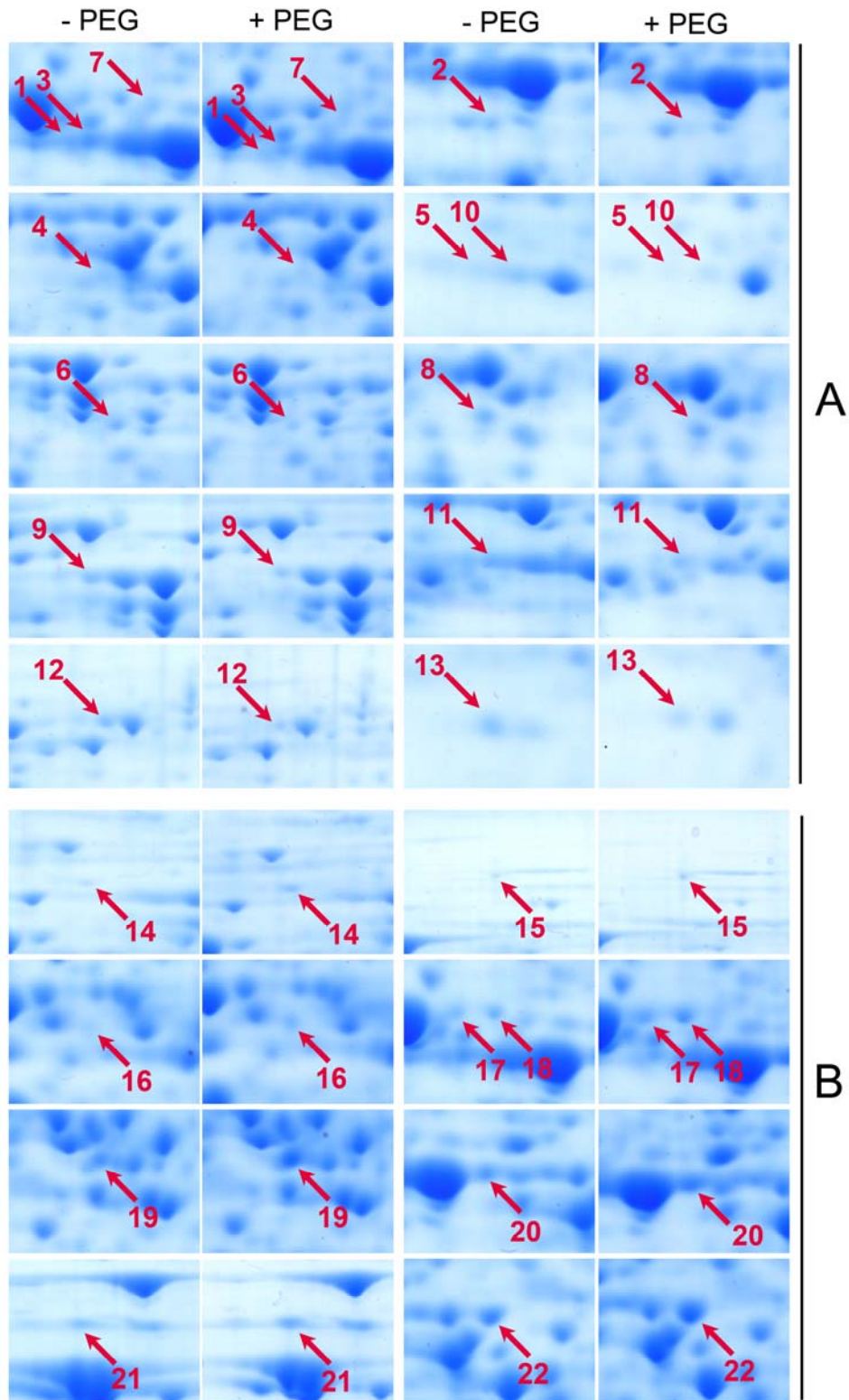


Figure S1 Close-ups of significantly decreased (A) and increased (B) protein spots in response to PEG in the root tips of common bean genotype VAX 1. The Coomassie-stained 2D IEF/SDS-PAGE gels of the total soluble proteins are shown in Fig. 2.

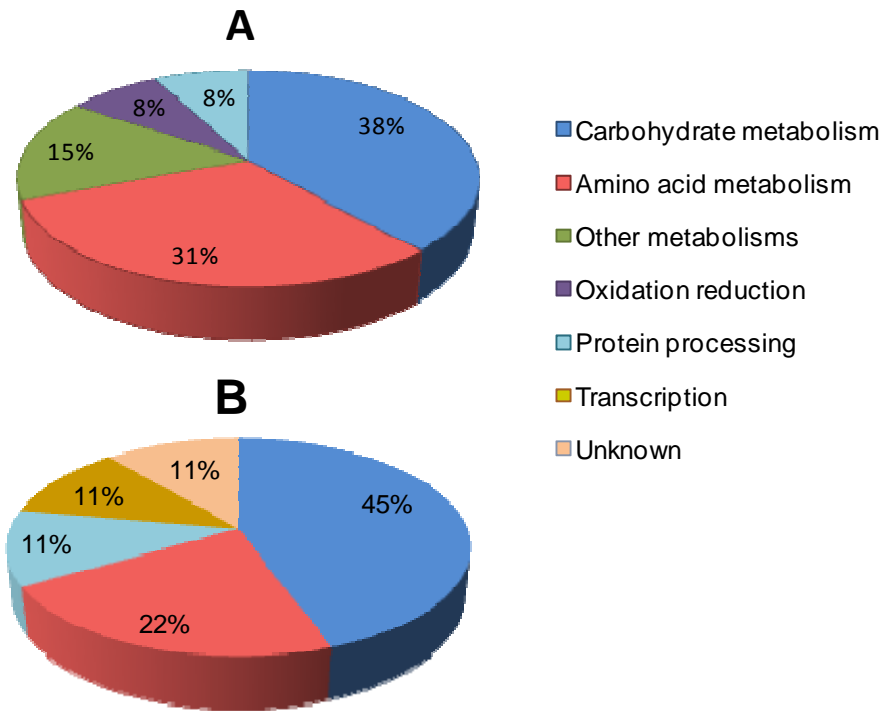


Figure S2 Functional categories of the 22 significantly decreased (A) and increased (B) proteins in response to PEG-induced osmotic stress in the root tips of common bean genotype VAX 1. The identifications of these 22 proteins by nano LC-MS/MS are shown in Table 1.

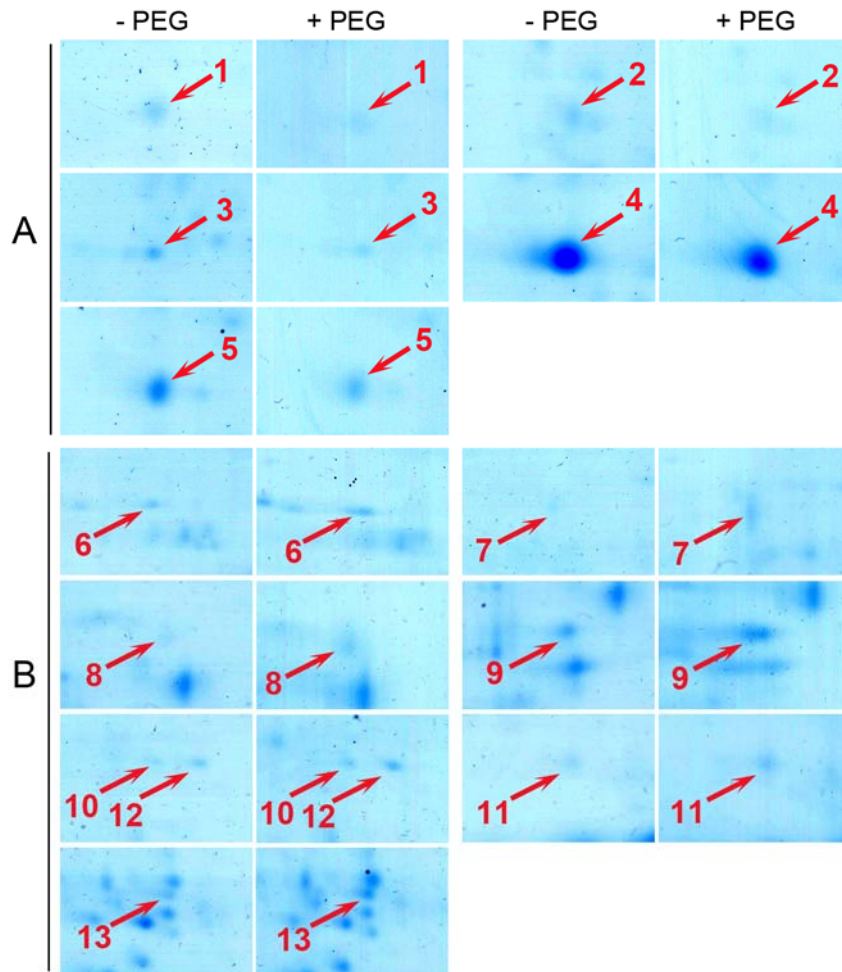


Figure S3 Close-ups of significantly decreased (A) and increased (B) apoplastic protein spots in response to PEG in the root tips of common bean genotype VAX 1. The Coomassie-stained 2D IEF/SDS-PAGE gels of the apoplastic proteins are shown in Fig. 4.

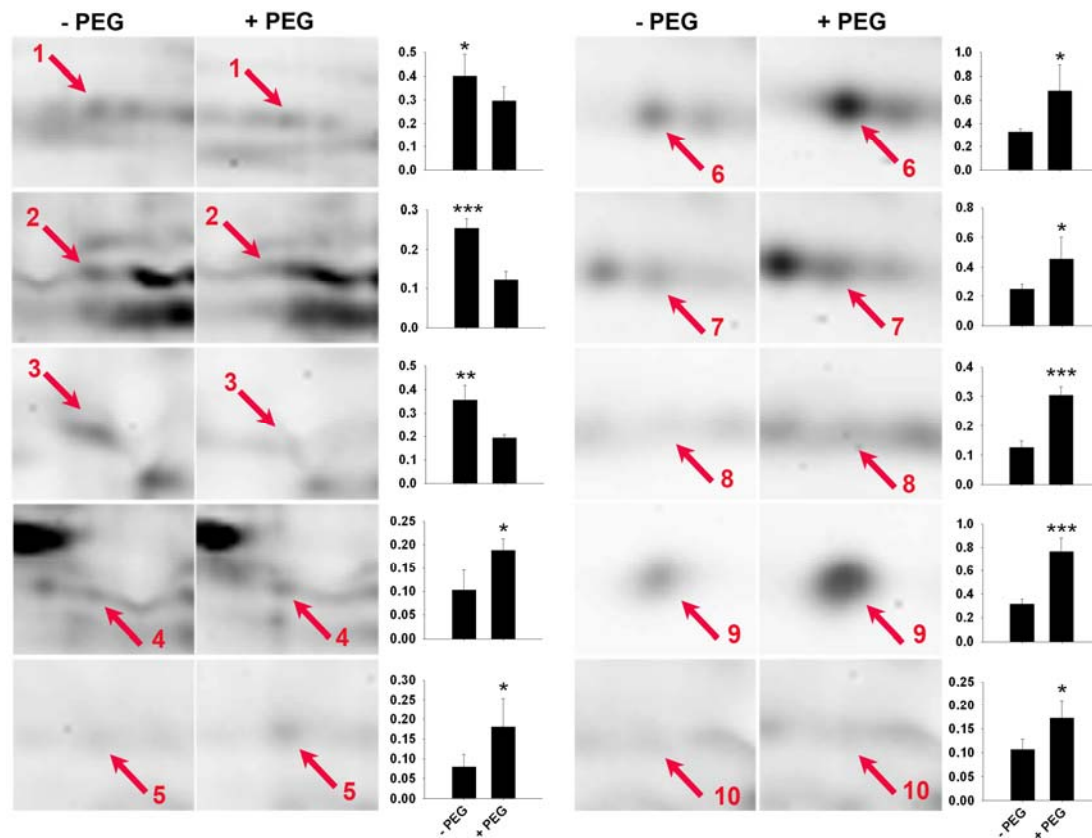


Figure S4 Close-ups and the relative volume of the 10 significantly decreased and increased phosphorylated protein spots in response to PEG in the root tips of common bean genotype VAX 1. The Pro-Q DPS-stained 2D IEF/SDS-PAGE gels of the phosphorylated proteins are shown in Fig. 5A.

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AAB00554 MAEETQNKYE TAESSEVEVQ DRGVDFDLGK KKEEEKPQEE VIVTEFEKIT VSEKKKEEG 60
Spot 6 -AEETQNKYE TAESSEVEVQ DRGVDFDLGK --EEEKPQEE VIVTEFEK-- -----
Spot 7 -AEETQNKYE TAESSEVEVQ DRGVDFDLGK ----- ----- -----
Spot 9 -AEETQNKYE TAESSEVEVQ DR----- ----- ----- -----
AAB00554 EKKHSLLEKL HRSDSSSSSS SEEEGEDGEK KKKKKKEKKE KKKIEEKIEG YHKEDTSPVP 120
Spot 6 ---HSLLEK- ----- ----- ----- -----IEG YHKEDTSPVP
Spot 7 ----- ----- ----- ----- ----- -----
Spot 9 ----- ----- ----- ----- ----- -----
AAB00554 EKVEVVESEE KKGFLLEKI KLPGHKKSEE AAAPPPPPPA ATSSHEGEA KEKKGILEKI 180
Spot 6 EKVEVVESEE K----- -KSEE AAAPPPPPPA ATSSHEGEA K-----
Spot 7 --VEVVESEE K----- -KSEE AAAPPPPPPA ATSSHEGEA K-----
Spot 9 ----- ----- ----- ----- ----- -----
AAB00554 KEKLPGYHSK TEEKEKESG GH 202
Spot 6 ----- ----- ----- ----- ----- -----
Spot 7 ----- ----- ----- ----- ----- -----
Spot 9 ----- ----- ----- ----- ----- -----

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Figure S5 Prediction of potential phosphorylation sites of the dehydrin protein. The phosphorylation sites were analyzed with KinasePhos 2.0 software (<http://kinasephos2.mbc.nctu.edu.tw/index.html>, Wong et al., 2007) online. Highlighted are peptides which may undergo phosphorylation.