

Article title	Root proteome analysis of soybean under phosphorus starvation reveals the genotypic variation in organic acid exudation potential
Keywords	Soybean
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Abstract	<p>Experiments were performed to evaluate a diverse soybean panel for total carbon exudation potential employing shoot labeling with $^{14}\text{CO}_2$. Traits contributed to maximum genotypic variability were total ^{14}C exudation, P uptake and total dry weight. The proportion of organic acids was highest among root exuded compounds induced by low P stress. Efficient soybean genotypes exhibited superior growth and P acquisition efficiency under low soil P availability attributed to its higher root exudation potential aiding in mining fixed soil P. To understand the molecular mechanism governing differentially regulating root exudation potential in contrasting genotypes, root proteome analysis at low P stress was carried out. Among the total proteins visualized by 2D-gel electrophoresis, 105 (32%) were differentially expressed between sufficient and low P levels. A total of 44 (14%) proteins were down regulated by more than two-fold under low P while 61 (15%) proteins were up-regulated by more than two-fold at low P. Several key enzymes in organic acid synthesis and glycolytic bypass pathways were differentially regulated under low P stress in the P efficient soybean genotype, EC-232019. Alterations at the metabolite and protein level of EC-232019 suggest the cross talk between various metabolic pathways conferring higher P acquisition efficiency to plants under stress. Characterization of 17 proteins with unknown function might reveal roles of novel genes under low P stress. The identified genotypes have potential to be used as donors in crop improvement programs to develop high yielding P efficient cultivars, which may be an asset to low input sustainable agriculture.</p>
Publication date	2016-08
Link to the actual article	Root proteome analysis of soybean under phosphorus starvation reveals the genotypic variation in organic acid exudation potential Request PDF (researchgate.net)