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Genomic and Proteomic Variability in Glycine Max Genotypes in Response to Salt Stress

Authors : Faheema Khan

Abstract : To investigate the ability of sensitive and tolerant genotype of Glycine max to adapt to a saline environment in a field, we examined the growth performance, water relation and activities of antioxidant enzymes in relation to photosynthetic rate, chlorophyll a fluorescence, photosynthetic pigment concentration, protein and proline in plants exposed to salt stress. Ten soybean genotypes (Pusa-20, Pusa-40, Pusa-37, Pusa-16, Pusa-24, Pusa-22, BRAGG, PK-416, PK-1042, and DS-9712) were selected and grown hydroponically. After 3 days of proper germination, the seedlings were transferred to Hoagland's solution (Hoagland and Arnon 1950). The growth chamber was maintained at a photosynthetic photon flux density of 430 μmol m−2 s−1, 14 h of light, 10 h of dark and a relative humidity of 60%. The nutrient solution was bubbled with sterile air and changed on alternate days. Ten-day-old seedlings were given seven levels of salt in the form of NaCl viz., T1 = 0 mM NaCl, T2=25 mM NaCl, T3=50 mM NaCl, T4=75 mM NaCl, T5=100 mM NaCl, T6=125 mM NaCl, T7=150 mM NaCl. The investigation showed that genotype Pusa-24, PK-416 and Pusa-20 appeared to be the most salt-sensitive. genotypes as inferred from their significantly reduced length, fresh weight and dry weight in response to the NaCl exposure. Pusa-37 appeared to be the most tolerant genotype since no significant effect of NaCl treatment on growth was found. We observed a greater decline in the photosynthetic variables like photosynthetic rate, chlorophyll fluorescence and chlorophyll content, in salt-sensitive (Pusa-24) genotype than in salt-tolerant Pusa-37 under high salinity. Numerous primers were verified on ten soybean genotypes obtained from Operon technologies among which 30 RAPD primers shown high polymorphism and genetic variation. The Jaccard's similarity coefficient values for each pairwise comparison between cultivars were calculated and similarity coefficient matrix was constructed. The closer varieties in the cluster behaved similar in their response to salinity tolerance. Intra-clustering within the two clusters precisely grouped the 10 genotypes in sub-cluster as expected from their physiological findings.Salt tolerant genotype Pusa-37, was further analysed by 2-Dimensional gel electrophoresis to analyse the differential expression of proteins at high salt stress. In the Present study, 173 protein spots were identified. Of these, 40 proteins responsive to salinity were either up- or down-regulated in Pusa-37. Proteomic analysis in salt-tolerant genotype (Pusa-37) led to the detection of proteins involved in a variety of biological processes, such as protein synthesis (12 %), redox regulation (19 %), primary and secondary metabolism (25 %), or disease- and defence-related processes (32 %). In conclusion, the soybean plants in our study responded to salt stress by changing their protein expression pattern. The photosynthetic, biochemical and molecular study showed that there is variability in salt tolerance behaviour in soybean genotypes. Pusa-24 is the salt-sensitive and Pusa-37 is the salt-tolerant genotype. Moreover this study gives new insights into the salt-stress response in soybean and demonstrates the power of genomic and proteomic approach in plant biology studies which finally could help us in identifying the possible regulatory switches (gene/s) controlling the salt tolerant genotype of the crop plants and their possible role in defence mechanism.

Keywords : glycine max, salt stress, RAPD, genomic and proteomic variability
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