

## Genomic and Proteomic Variation in Glycine Max Genotypes towards Salinity

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**Abstract :** In order to investigate the influence of genetic background on salt tolerance in Soybean (Glycine max) ten soybean genotypes released/notified in India were selected. (Pusa-20, Pusa-40, Pusa-37, Pusa-16, Pusa-24, Pusa-22, BRAGG, PK-416, PK-1042, and DS-9712). The 10-day-old seedlings were subjected to 0, 25, 50, 75, 100, 125, and 150 mM NaCl for 15 days. Plant growth, leaf osmotic adjustment, and RAPD analysis were studied. In comparison to control plants, the plant growth in all genotypes was decreased by salt stress, respectively. Salt stress decreased leaf osmotic potential in all genotypes however the maximum reduction was observed in genotype Pusa-24 followed by PK-416 and Pusa-20. The difference in osmotic adjustment between all the genotypes was correlated with the concentrations of ion examined such as Na<sup>+</sup> and the leaf proline concentration. These results suggest that the genotypic variation for salt tolerance can be partially accounted for by plant physiological measures. The genetic polymorphisms between soybean genotypes differing in response to salt stress were characterized using 25 RAPD primers. These primers generated a total of 1640 amplification products, among which 1615 were found to be polymorphic. A very high degree of polymorphism (98.30%) was observed. UPGMA cluster analysis of genetic similarity indices grouped all the genotypes into two major clusters. Intra-clustering within the two clusters precisely grouped the 10 genotypes in sub-cluster as expected from their physiological findings. Our results show that RAPD technique is a sensitive, precise and efficient tool for genomic analysis in soybean genotypes.

**Keywords :** glycine max, NaCl, RAPD, proteomics

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