

Biochemical and Molecular Approaches to Overcome Salt- stress Constraint in Pigeon Pea (*Cajanuscajan* L.)

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Abstract—Salinity being a critical factor to sustainable pigeon pea production addresses limitations to meet the demands of resource-poor people where pigeon pea is grown. Pigeon pea (*Cajanuscajan* (L.) Millsp), a short-lived perennial shrub, commonly known as 'Arhar' or 'Tuhr' is one of the major grain legume (pulse) crops of the Indian subcontinent, has a diploid genome with 11 pairs of chromosomes and a genome size estimated to be 858 Mbp. Total 160 pigeon pea genotypes with reference to salt responsiveness were screened based on % germination, vigor and salt tolerance. Based on morphological and biochemical expressions - antioxidant potential, lipid peroxidation and total phenolic contents, most salt- susceptible (ICP1071) and salt- tolerant (ICP7) genotype were selected. Protein profile of control as well as salt stressed shoot region of selected pigeon-pea genotypes showed differential variation. Biochemical expressions were more prominent in the shoot as compared to the roots with reference to phenol content and lipid peroxidation but in the case of antioxidant potential it was more or less same. Three selected pigeon pea stress- responsive genes, viz., CcHyPRP, CcCDR and CcCYP affording explicit tolerance against multiple abiotic stresses were isolated, cloned and sequenced from the pigeon pea salt- tolerant (ICP7) genotype and their relative expression analysis is under way. These findings shall go a long way not only in understanding the important molecular and biochemical mechanisms underlying the salinity tolerance of the pigeon but also can be utilized in providing important leads to the breeders to evolve improved varieties of pigeon pea with higher salinity tolerance levels.