Abstract

Pigeon pea (*Cajanus cajan* (L.) Millsp.), a potential legume as an economic source of protein, is commonly cultivated in tropical and subtropical regions of the world. It possesses medicinal properties and acts as a cash crop, benefiting low-income farmers economically. The identification of pigeon peas exhibiting drought tolerance has become crucial in addressing water scarcity issues in the agriculture sector. In addition, exploring the genetic diversity among genotypes is important for conservation, management of genetic resources, and breeding programs. The aim of this study was to evaluate the morpho-physiological and biochemical responses of selected pigeon pea genotypes under pot-induced water stress conditions through different field capacities as well as the genetic diversity using start codon targeted (SCoT) markers. A significant variation was observed for the physiological traits studied. The accumulation of fresh weight (FW) and dry weight (DW) was significantly reduced in moderate and severe drought stress conditions. The lowest % DW decrease was found in LM (35.39%), KAT (39.43%), and SM (46.98%) than other genotypes at severe drought stress. Analyses of physiological responses including the photosynthetic efficiency (Phi2), the chlorophyll content (SPAD), and the relative water content (RWC) revealed positive and negative correlations with various parameters, reflecting the impact of drought stress on the chlorophyll content. The results revealed that biochemical traits including the total phenolic content, soluble sugars, proline, total protein, total amino acids, and free amino acids were variably and significantly increased under water stress. Antioxidant enzyme activity levels, specifically ascorbate peroxidase (APX) and catalase, varied among the genotypes and in response to severe water stress, offering further insights into adaptive responses. The eight genotypes analysed by use of 20 SCoT markers revealed 206 alleles and an average of 10.3 alleles per locus. Genetic similarity ranged from 0.336 to 0.676, clustering the pigeon pea genotypes into two major groups by the unweighted pair group method of arithmetic averages (UPGMA) cluster analysis. Principal coordinate analysis (PCoA) explained 43.11% of genetic variation and based on analysis of molecular variance, a high genetic variation (80%) within populations was observed, emphasizing the potential for genetic improvement. Among the eight genotypes studied, LM and KAT were drought tolerant and genetically diverse and therefore could be used as parents for developing drought tolerance in pigeon pea.