



Screening of Cowpea (*Vigna unguiculata* L. Walp) genotypes for salinity tolerance using field evaluation and molecular analysis

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Abstract:

Abstract Salinity is one of the major abiotic stress which seriously affect cowpea yield production. Thus, developing of new salinity tolerant lines is one important factor to face the harmful effect of salinity. In this study five cowpea genotypes were evaluated for their response to salinity stress using field characterization and inter simple sequence repeat (ISSR) molecular marker analysis. The behavior of some agronomic traits was screened under both normal and saline water irrigation conditions. The results revealed the presence of highly significant differences among all genotypes in both normal and salinity stress conditions whereas saline water reduced the performance of all evaluated traits. The genotypes, Sudany and Chinese red were the most salinity tolerant although they had the lowest yield production. On the other hand, Cream7 was the highest for yield performance with low salinity tolerance. The genetic distance among genotypes was measured by ISSR marker, the percentage of polymorphism was 82.08%. while, genetic similarities ranged from 0.48 to 0.67. Moreover, seven out of nine primers were able to produce many salinity specific unique bands which would be used as salt tolerance markers. The dendrogram separated the genotypes into two main clusters, the first one only consisted of the lowest salinity tolerant genotype while the two highest salinity tolerant genotypes were coupled in one group. The high capacity of some genotypes for salinity tolerance suggested that these genotypes could be used in breeding programs to produce more salinity tolerant varieties having a higher yield production.

Keywords:

Cowpea, salinity stress, ISSR, dendrogram.

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