

USE OF BIOCHEMICAL MARKERS FOR GENETIC DIVERSITY AND DETERMINING QTLs IN *VIGNA MUNGO* GERMPLASM

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One hundred and eleven genotypes of blackgram from diverse origin were evaluated for agronomic traits for 2 years to determine the extent of genetic diversity. Seed proteins were analyzed using Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis (SDS-PAGE) through vertical slab type unit. High genetic variance was observed for days to flowering, days to maturity, number of branches/plant, number of pods/plant, biomass/plant, grain yield/plant and harvest index, whereas low genetic variance was observed for pod length, seeds/pod and 100-seed weight during both the years. On the basis of SDS-PAGE, a low level of inter-collection diversity was observed and no clear differentiation on the basis of origin or source was observed. The genotypes in one cluster with similar agronomic characters were not necessarily belonging to the same source or origin. The indifferent clustering pattern of germplasm collected from Pakistan might be due to exchange of germplasm between the neighbouring regions, and perhaps with same ancestors. Clustering of advanced breeding lines and approved variety in one group revealed that only a portion of genetic diversity has been exploited for blackgram improvement, and it is suggested to broaden the genetic base of cultivated blackgram involving diverse parents in breeding programme. Screening analysis for marker bands to QTLs revealed significance in determining QTLs in blackgram through SDS-PAGE markers. The factors affecting quantitative traits may occur as individual genes or gene clusters scattered throughout the genome, therefore, quantitative trait were expected differently at several loci. Variation in seven quantitative traits out of ten was significantly associated with 9 protein peptides, however, the actual number of QTL might be fewer because several of these traits were correlated. Variation at protein peptides in the vicinity of QTL in blackgram may be an indication of genetic variation potentially available to breeding programmes. Expansion of genetic base for blackgram breeding might be accomplished by systematic use of germplasm that differ from common banding pattern and known to be associated with variation in quantitative traits.