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Authors: Kalidas Pati (/browse?type=author&value=Kalidas+Pati)

Advisor: Ravinder Kumar (/browse?type=author&value=Ravinder+Kumar)

Title: STUDIES ON GENETIC VARIABILITY OF CUCUMBER (*Cucumis sativus* L.) BASED ON MORPHOLOGICAL TRAITS AND MOLECULAR MARKERS

Type: Thesis

Abstract: Genetic variability of cucumber (*Cucumis sativus* L.) based on morphological traits and molecular markers Abstract The present investigation was carried out at the Division of Vegetable Science, I.A.R.I., New Delhi during March to June, 2007 to study the genetic variability of cucumber (*Cucumis sativus* L.) by utilizing 36 genotypes based on morphological traits and molecular marker systems. The genetic parameters viz genotypic and phenotypic coefficient of variation, heritability, genetic advance, correlation, path coefficient and genetic divergence were studied with respect to 12 quantitative traits. PCR based marker, Sequence Tagged Microsatellite Site (STMS) markers had been utilized for better understanding of variability at molecular level. Highly significant differences were observed among the genotypes for all the characters studied. Yield per plant followed by fruit index exhibited the highest phenotypic and genotypic coefficient of variation. The high heritability estimates coupled with high genetic advance for characters like fruit index, yield per plant and fruit weight may attributed to additive gene effects and could be improved through selection. Characters like number of fruits per plant and fruit weight had a highly significant positive correlation with yield per plant at genotypic and phenotypic level. Path analysis at genotypic level revealed that fruit weight had the maximum direct effect on yield per plant followed by days to opening of first female flower, total number of fruits per plant. All the 36 genotypes were grouped into 7 clusters based on D² values, which exhibited no association between clusters and geographical distributions of the genotypes. Out of 40 Sequence Tagged Microsatellite Site (STMS) markers screened to study molecular diversity, 17 primers showed polymorphism. Morphological diversity of 36 genotypes based on 12 quantitative traits and molecular diversity based on 17 STMS primers were not similar and the grouping pattern was different in the two systems, which indicated the role of environment in the expression of phenotypic traits. Results obtained from variability studies and diversity analysis through morphological basis and molecular markers, suggested the utilization of promising genotypes in the breeding programme for the development of high yielding varieties and F₁ hybrids.

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