

GENETIC DIVERSITY STUDIES IN SOME CHILI HYBRIDS FROM KHANDESH REGION USING SDS - PAGE

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ABSTRACT

Present study was undertaken to estimate genetic diversity in 12 hybrids of chili (*Capsicum annum L.*) from Khandesh region, using SDS-PAGE. Storage seed protein banding pattern studied. Total seed storage protein were extracted and separated on 10 % polyacrylamide gel using standard protocol. The data generated from scoring of bands of proteins separated in 12 chili hybrids were analyzed using NTSys & UPGMA dendrogram developed. Dendrogram analysis provide 2 major clusters. Hybrid 12 (Pikato green) & Hybrid 1 (ARCH-82) Shows maximum similarity, indicates probable origin from same parent. Hybrids from cluster I & II shows considerable genetic distance.

Keywords: *Capsicum annum L.*, Seed storage protein, SDS-PAGE, UPGMA dendrogram

INTRODUCTION

Chili (*Capsicum annum L.*) is the most important vegetable cum spice crop because of their pungency, flavor, color and aroma. This is belonging to the family Solanaceae. Number of capsicum species has been known as part of human diet since the beginning of civilization. There is little recorded genetic diversity among cultivated chili. However, general knowledge is that commercial varieties and particularly hybrids varieties of vegetable crops are based on increasingly narrower genetic base (Padma J and Shiva K. 2013). Previously the data like color, shape, size, pungency, flavor and physiological traits are generally used to estimate the magnitude of genetic diversity present in chili germplasm. However with the increase in the number of varieties in each crop, it is difficult to distinguish varieties/ hybrids on the basis of data from morphological characters alone. Such data may not provide an accurate indication of genetic diversity because of environmental influences upon the expression of observed traits. This has led to the development of new stable parameter such as use of genetic material (Nucleic acid and Proteins) as a tool to estimate genetic diversity. Recently genetic diversity in capsicum has been studied using cytological and biochemical system (Gopinath et al., 2006.) Seed storage protein used as genetic markers in the study of genetic variation because any change in coding sequence of a gene generally reflects the corresponding change in the primary structure of a protein (Srivill et al., 1999). Genetic and taxonomic relationship in the genus capsicum have been investigated with electrophoresis of seed storage protein banding patterns (Valdova et al., 2000; Zubiada et al., 2006).

The present work was carried out on total 12 chili hybrids. The 12 chili hybrids from Khandesh region of Maharashtra state were taken to evaluate seed storage protein variability and for their exploitation in successful crossing programs.

MATERIALS AND METHODS

Seed Material: Seed material used for present study includes 12 accessions (Hybrids) which were locally available in Khandesh region of Maharashtra. 10 seeds of each accession were taken for total seed storage protein extraction.

EXTRACTION OF SEED STORAGE PROTEIN

10 seeds of each accession were powdered separately. 10 mg seed powder of each line along with 5 ml of 0.01M Tris.HCL buffer (pH 7.5) were taken & vortex thoroughly to homogenize. The resulting homogenate was centrifuged at 15,000 rpm for 10 min. at 4°C. The supernatant was collected and used as soluble protein for SDS-PAGE.

SDS-PAGE analysis: Extracted soluble protein were separated by one dimension SDS-PAGE. Percent of running and stacking gel was kept 10% & % respectively. Electrophoresis was conducted at a constant current 85mA until the tracking dye reached the bottom of the gel. After electrophoresis the gel was stained overnight in 0.25% Coomassie Brilliant blue R-250, followed by de-staining in Methanol and Acetic acid solution for 45 min. The gel was further de-stained until the background was clear enough for band scoring. Protein marker of Hi-Media was used as standard to score the sample bands. Molecular weight of protein band were estimated by their relative mobility. After de-staining the gel were photographed using gel documentation system 'UVtech'.

Data analysis: For Genetic diversity analysis, every scoreable band was considered and scored 1 for presence and 0 for absence. The bivariate 1-0 data was used to estimate the pair-wise genetic distance following UPGMA procedure for dendrogram (Nei and Li., 1979).

RESULT & DISCUSSION

Genetic diversity among cultivars are pre-requisite to identify high performing parents (Padma J. and Shiva S. 2013). Similarity matrix was subjected to UPGMA clustering to generate dendrogram. Cluster analysis of UPGMA is extensively used for genetic diversity studies in important plants. Electrophoresis analysis of 12 chili genotypes reveal not much more variation in the banding pattern of proteins (Figure 1). Twelve *Capsicum* hybrids were characterized on the basis of seed storage protein using SDS-PAGE (Figure 2). Studied cultivars were grouped into 2 major clusters. Cluster I corresponding 4 genotypes whereas cluster II includes 8 genotypes. Dendrogram depicted by UPGMA shows low genetic diversity as most of varieties belong to single cluster. This may be due to genotype homozygosity (Odeigah P.G.et.al., 1999) which causes the narrow genetic base. Valdova et.al., (2000) and Zubiada et.al., (2006) also studied chili varieties of India using seed storage protein. Our results show less variability in among the studied samples except for some lanes (L1,L4,L8) where considerable variation observed. There line specific bands shows variation between 12 chili genotypes and themselves. This observation suggests that SDS-PAGE technique can be used to differentiate this genotypes from the rest of the genotypes. Pikato green and ARCH 82 were found to be closely similar. This may attributed to the same genetic background of them. Whereas Sizzling hot, Shama, Shimla red, Omega, Sitara and Local genotypes formed separate cluster in cluster II. This may due to their morphological differences between them. Also, cluster pattern of these genotypes revealed that these genotypes may be developed from same parental genotypes.

CONCLUSIONS

The present study exploited seed storage protein for identification of better parents. Hybrid 12 (Pikato green) and Hybrid 1 (ARCH-82) shows maximum similarity indicates probable origin from same parents. Parents of cluster I & cluster II hybrids can be used to produce improved hybrid from Khandesh region.

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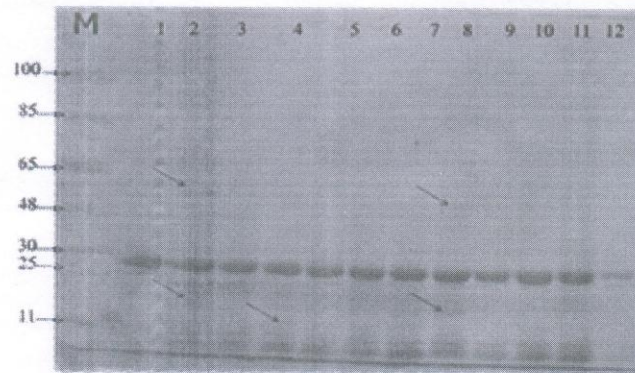


Figure - 1: Total seed storage protein profile of 12 Chili hybrids. M= Molecular weight marker; 1-12 chili hybrids.

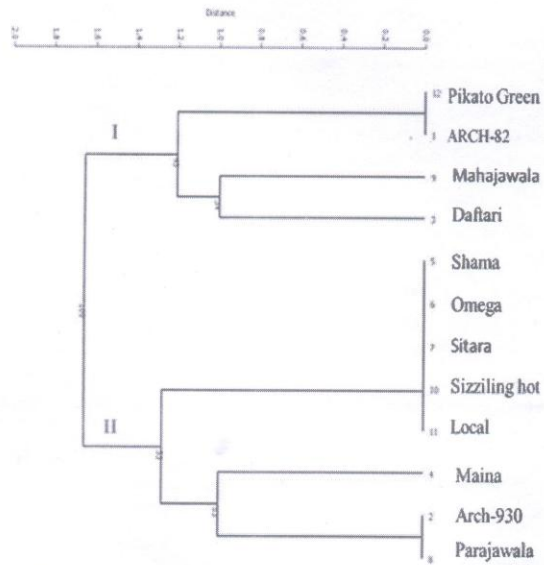


Figure - 2: UPGMA dendrogram of 12 Chili hybrids based on seed storage protein.