

GENETIC VARIABILITY, CHARACTERS ASSOCIATION AND THEIR DIRECT AND INDIRECT CONTRIBUTIONS IN DIVERSE CHILLI (CAPSICUM ANNUUM) GENOTYPES

MUKESH MEENA, T.K. SINGH* AND SUNIL PRAJAPATI

Department of Horticulture, College of Agriculture, Rewa Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur-482004 (Madhya Pradesh) India *Corresponding author: tapanvns1@gmail.com

ABSTRACT: The analysis of variance revealed that sufficient variability was present in the experimental material. The mean dry fruit yield plant¹ was found the highest in genotypes BVC-37 followed by Pant C-1, BVC-1, HO-413, LCA-960, IC119455 and IC112109 superior genotypes had high mean value for dry fruit yield plant¹. High genotypic and phenotypic coefficient of variations were observed for dry fruit yield plant¹, test weight, leaf area, fresh ripe fruit weight, dry weight of red ripe fruits, number of fruits plant¹, fruit flesh thickness, number of seeds fruit¹, fruit width, fresh green fruit weight, fruit length, pedicel length, number of primary branches plant¹. The very high heritability with high genetic advance as per cent of mean was manifested by dry fruit yield plant¹ and test weight. The positive association of dry fruit yield plant¹ was observed with fresh ripe fruit weight, number of fruits plant¹, fresh green fruit weight, test weight, stem girth, plant height, number of seeds fruit¹, dry weight of red ripe fruits, fruit flesh thickness, number of primary branches plant¹, days to flower initiation, days to 50% flowering, fruit length, fruit width, days to maturity, leaf area and number of secondary branches plant¹. The study found positive direct effect of number of fruits plant¹ on fresh ripe fruit weight, green fruit weight, stem girth, plant height, test weight, fruit flesh thickness, dry weight of red ripe fruits, days to flower initiation, days to 50% flowering, fruit length, fruit width and leaf area and pedicel length. However, number of primary branches plant¹, days to maturity, number of seeds fruit¹, pedicel length and number of secondary branches plant¹ expressed negative direct effect on dry fruit yield plant¹.

Key words: Chilli, genetic variability, association, path co-efficient analysis, fruit yield

Citation: Meena M, Singh TK, Prajapati S (2016) Genetic variability, characters association and their direct and indirect contributions in diverse chilli (*Capsicum annuum*) genotypes. Indian J Trop Biodiv 24(1): 27-38

Received on: 20 Jan. 2016 Accepted on: 14 Mar. 2016 Published on: 30 Jun. 2016

Chilli (*Capsicum annuum* L.) belong to family Solanaceous (2n=24), it is native of tropical America and occupies a prominent place in dietary habits of the people of nation, the five cultivated species and twenty wild species grown in India. It is a rich source of vitamin C and Vitamin A in its fresh state. The capsaicin alkaloid is responsible for pungency, at ripening stage, fruits become red in colour because of capsanthin pigment. In India, the major Chilli growing states are Andhra Pradesh, Karnataka, Maharashtra, Odisha, Tamil Nadu, Madhya Pradesh and Rajasthan. In India, Chilli occupies 0.805 (Mha) area and annual production 1.276 (MT), while, in Madhya Pradesh it occupies 0.054 (Mha) area and produce 0.093 (MT) (National Horticulture Board, data base 2012-13).

The exploration of genetic variability in the available germplasm is a pre requisite in a breeding

programme for effective selection of superior genotype. The partitioning of total variability into heritable and non heritable components by using suitable design will enable the breeder to know whether the superiority of selection is inherited by the progenies. Since natural genetic variation for most of the yield attributes is considerably high in Chilli, there is an urgent need for information on the nature and magnitude of variation available in the material and part played by environment in expression of different characters.

Chilli is an often cross pollinated crop with high natural cross pollination and this also contributes to its variability, the aim of any breeding program depends on genetic diversity, characters association and direct and indirect effects on yield and its component characters. Before going to breeding programme through selection it is essential to know the importance