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# Genetic Studies in Chilli (*Capsicum annuum* L.)

**Ashish Kumar Maurya**
Ph. D. Research Scholar, Department of Horticulture, Institute of Agriculture Science, BHU, Varanasi, India
**M. L. Kushwaha**
Professor, Department of Vegetable Science, G.B. Pant University of Agriculture and Technology, Pantnagar (U. S. Nagar), Uttarakhand, India
**B. K. Singh**
Professor, Department of Horticulture, Institute of Agriculture Science, BHU, Varanasi, India

***Abstract:***
*Knowledge of the magnitude of genetic variability for marketable fruit yield and quality traits is needed to improve quality breeding in chilli (Capsicum annuum L.). Thirty genotypes of chilli were evaluated in a field study to assess genetic variability, heritability and genetic advance. Higher phenotypic and genotypic coefficients of variation were observed for days to 50 % flowering, number of fruits per plant, fruit body length, number of seeds per fruit, weight of seeds per fruit, seed husk ratio, average dry fruit weight and dry fruit yield per plant. High heritability coupled with high genetic advance were observed for seed husk ratio, average dry fruit weight and dry fruit yield per plant, so these characters imply the potential for crop improvement through selection.*

***Keywords:*** *Genetic variability, heritability, genetic advance, chilli.*

## 1. Introduction

Chilli (*Capsicum annuum* L.) is one of the commercial vegetable cum spice crops at the global level. It finds its place in spice as well as condiments. Particularly in India, there is no home which does not consume chilli. It is used both at green and dry stage and is used and marketed as whole as well as ground form. India is the major producer, consumer, and exporter of chilli, contributing about one fourth of the world production. Chilli contributes about 33% of the total spice export from India and share about 16% of the world spice trade. It finds a place in pharmaceuticals also. Maximum diversity can be noticed among different cultivars available in India and outside with respect to shape, size, yield, quality and other traits. Identification of a variety better suited for a particular region and its improvement is of immediate task to exploit its potential. The successful of selection depends on the amount of genetic variation present in a population. Larger amount of variability increases the chance of selecting desired genotypes (Vavilov, 1951). The improvement can be brought out after confirming the variability in different characters among different genotypes. The potential for improvement in any crop is proportional to the magnitude of genetic variability present in the germplasm. A wide range of variability is available in chilli due to its ability to cross pollinate, which provides possibilities to improve fruit yield through a breeding program. Hence, an experiment was conducted at Pantnagar with the aim of estimating genetic variability, heritability and genetic advance and identification of yield contributing traits for genetic improvement of chilli (*Capsicum annuum* L.).

## 2. Material and Methods

Thirty genotypes of chilli were evaluated at Vegetable Research Centre, Pantnagar during spring summer season of 2014. The genotypes were raised in Randomized Block Design with three replications, having 18 plants per plot, under irrigated conditions, per local management recommendations. Six plants were selected randomly from each genotype and growth, quality and yield observations on plant height, number of primary branches per plant, canopy width, days to 50% flowering, days to 50% ripening, fruit body length, perimeter of fruit, number of fruits per plant, average dry fruit weight, dry fruit yield per plant, number of seeds per fruit, weight of seeds per fruit, 100 seed weight, seed husk ratio and dry matter percent were recorded. Analysis of variance was performed to test variations among different genotypes. The data obtained was statistically analyzed following the standard procedure as given by Gomez and Gomez (1984) to test the significance of genotypes to arrive at valid conclusions. Variability, heritability and expected genetic advance at 5% intensity of selection for different quantitative characters were calculated as per Burton and De Vane (1952), Hanson *et al.* (1956) and Robinson *et al.* (1949), respectively.

**3. Results and Discussion**

The present investigation revealed considerable amount of variation for all the characters studied. The extent of variability in respect of mean, heritability, genetic advance, phenotypic and genotypic coefficients of variation is given in Table.

| Characters | Mean | SEm ± | Heritability (%) | Genetic Advance as % of mean | GCV | PCV |
|---|---|---|---|---|---|---|
| Plant height (cm) | 75.09 | 4.43 | 75.77 | 32.39 | 18.06 | 20.75 |
| Canopy width (cm) | 52.70 | 2.44 | 65.49 | 18.44 | 11.06 | 13.67 |
| Primary branch | 12.00 | 0.42 | 88.48 | 32.60 | 16.82 | 17.89 |
| Days to 50 % flowering | 46.67 | 0.71 | 98.32 | 41.25 | 20.20 | 20.37 |
| Days to 50 % ripening | 87.01 | 1.21 | 91.34 | 15.42 | 7.83 | 8.20 |
| Number of fruit per plant | 89.61 | 7.64 | 84.36 | 64.92 | 34.31 | 37.35 |
| Fruit body length (cm) | 6.84 | 0.24 | 91.64 | 39.75 | 20.16 | 21.06 |
| Fruit periphery width (cm) | 3.29 | 0.11 | 85.88 | 26.24 | 13.75 | 14.83 |
| Number of seed per fruit | 44.94 | 2.03 | 87.40 | 39.65 | 20.59 | 22.02 |
| Weight of seed per fruit (mg) | 197.16 | 8.16 | 89.93 | 41.85 | 21.42 | 22.59 |
| 100 seed weight (mg) | 442.98 | 5.22 | 97.49 | 25.89 | 12.73 | 12.89 |
| Seed husk ratio | 2.11 | 0.04 | 99.23 | 84.57 | 41.21 | 41.37 |
| Dry matter % | 14.67 | 0.49 | 91.43 | 36.89 | 18.73 | 19.58 |
| Average dry fruit weight (mg) | 594.83 | 27.56 | 92.94 | 57.83 | 29.12 | 30.21 |
| Dry fruit yield per plant (g) | 52.99 | 3.26 | 93.24 | 78.71 | 39.57 | 40.98 |

*Table 1: Mean, Heritability, Genetic Advance and Coefficients of Variation for Different Characters*

Such wide variation among the genotypes for all the traits indicating presence of significant variability in the genotypes which can be exploited through selection. Similar findings were also observed earlier with the reports of Singh and Singh (2011), Krishnamurthy *et al*. (2013) and Janaki *et al*. (2015). High values of genotypic and phenotypic coefficient of variations were observed for days to 50 % flowering, number of fruits per plant, fruit body length, number of seeds per fruit, weight of seeds per fruit, seed husk ratio, average dry fruit weight and dry fruit yield per plant. Kumari *et al*. (2010) also reported high phenotypic and genotypic coefficient of variation for number of fruits per plant, dry fruit yield per plant, and number of seeds per fruit.

High heritability estimates have been found to be helpful in making selection of superior genotypes on the basis of phenotypic performance with respect to quantitative characters (Singh and Chaudhary, 2010). High heritability were observed for most of the characters studied and, in particular days to 50 % flowering, days to 50 % fruit ripening, fruit body length, seed husk ratio, dry matter percent, average dry fruit weight and dry fruit yield per plant. This is consistent with the reports of Munshi *et al*. (2010) for days to flowering, fruit length and average fruit weight; Sandeep *et al*. (2013) for fruit yield per plant. High heritability for different traits indicated that large proportion of phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. For estimating the real effects of selection, heritability alone is not sufficient and genetic advance along with heritability is more useful.

The expected genetic advance was high for number of fruits per plant, weight of seeds per fruit, seed husk ratio, average dry fruit weight and dry fruit yield per plant. Similar finding was also reported earlier by Kumari *et al*. (2010) for number of fruits and dry fruit yield per plant; Datta and Das (2013) for fruit yield per plant. High heritability coupled with high genetic advance observed in the present study for seed husk ratio, single dry fruit weight and dry fruit yield per plant, it can be considered as favourable attributes for crop improvement through selection. Likewise, the high heritability combined with high genetic advance could be regarded as an indication of additive gene action and the consequent high-expected genetic gain from selection for these characters.

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