

Mean performance of F₃ population for yield and yield attributing characters in chilli (*Capsicum annuum* L.)

ABSTRACT

In the current experiment, 256 test treatments and four control treatment (checks) were assessed in augmented block design for analyzing yield and yield attributing traits. F₃ population of chilli were assessed for yield and yield components during kharif, 2018-19. The analysis of variance showed significant mean sum of squares for all characters for different sources of variation. The number of genotypes that exceeded the best check was 47 (plant height), 45 (number of primary branches), 42 (days to 50% flowering), 37 (number of fruits per plant), 34 (fruit length), 36 (fruit width), 39 (fruit weight), 33 (fruit shape index), 48 (pedicel length), 33 (yield per plant), 37 (dry yield per plant) and 32 (dry recovery %). Plant number 91 was the best genotype among the test treatments for all traits except fruit width and pedicel length. Among the checks, B-HP-143 was observed to be best for plant height, days to 50% flowering, number of fruits per plant, yield per plant, dry yield per plant and dry recovery %, whereas B-HP-144 was found to be superior over all the checks for rest of the traits.

Keywords- Chilli, check, evaluation, yield, yield attributing traits, Augmented block design

Introduction

Chilli, (*Capsicum annuum* L.), which is an important spice cum vegetable crop widely cultivated both as rainfed and irrigated crop in India. It belongs to the genus *Capsicum* and family solanaceae. This crop was native to Mexico, Southern Peru and Bolivia. There are generally five commercial *Capsicum* spp. viz., *C. annuum*, *C. baccatum*, *C. chinense*, *C. frutescens* and *C. pubescens*. Among these species, *Capsicum annuum* is the principal species all through the world and is mostly categorized into non-pungent i.e. sweet pepper and pungent i.e. chilli or hot pepper (Bosland and Votava, 2000). Chilli is a main constituent in daily cuisine of India and also a major constituent of vitamin A, E, C and potassium. Oleoresin extracted from chilli fruits has noble export potential.

India ranks first in chilli production, consumption and export with an area of 3,63,000 ha., production of 4027000 MT and productivity of 11.09 MT/ha. (Agricultural Statistics, 2019-20). In Odisha, this is cultivated in area of 65.50 (000 ha) with a production of 64.50 (000) MT (NHB, 2016-17). Telangana, Maharashtra, Andhra Pradesh, Karnataka Odisha and Tamil Nadu accounts for more than 75% of area and production in chilli in India.

Capsaicin is the pungent principle existing in placenta of chilli fruits and it has various prophylactic and beneficial usages in Allopathic and Ayurvedic medicine (Sumathy and Mathew, 1984) and directly scavenge various free radicals (Kogure *et al.*, and 2002; Bhattacharya *et al.*, 2010). Chilli is a rich source of vitamin C (ascorbic acid) used in food and beverage industries (Bosland and Votava, 2000). Oleoresin allows good supply of colour

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and flavour in foods. It is important to survey the kind and amount of variability present in the available materials which is the pre-requisite of any breeding programme. The selection and development of variety will be much effective if the nature and amount of variability present in the available germplasm is more. In chilli breeding programme, the major goal is to develop varieties with high yield and good qualitative characters. The significance of genetically different genotypes with required combinations has also been understood by several workers. Considering the above details, the present analysis was followed to know the performance of genotypes of chilli for different quantitative traits and to find out the best performing genotype for application in further breeding programme.

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Comment [K29]: Taking into account the foregoing information, the current study was carried out to determine the performance of chilli genotypes for various quantitative traits and to identify the best performing genotype for future breeding programs.

Materials and Methods

The experiment was carried out with 256 test treatments and four control treatments (2018-19) in an augmented block design (Federrer, 1956) with eight blocks, consisting of 32 test entries and four checks in each. The crop was grown with standard package of practices. Ten plants were selected at random for recording the observations on 12 characters viz., plant height (cm), number of primary branches, days to 50% flowering, number of fruits per plant, fruit length (cm), fruit width (cm), fruit shape index, fruit weight (g), pedicel length (cm), yield per plant (g), dry yield per plant (g) and dry recovery %. The recorded data was statistically analyzed through statistical software.

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Results and Discussion

Augmented block design (Federrer, 1956) is a statistical method of choice to start initial assessment of a large set of germplasm to choose genotypes suitable for diverse parts of crop breeding. This is the most vital in cases where primary seed is limited in amount to start replicated experiments. The strategy makes use of a technique wherein a large number of test entries to be estimated along with standard checks, with the checks being replicated randomly in all blocks. The data from checks is used to adjust mean values of test entries to make them comparable and also provide a guess of experimental error. In the present study, 256 test entries along with four checks were evaluated in an augmented block design for yield and yield component traits. The mean values (Table 1) of plant height (cm), number of primary branches, days to 50% flowering, number of fruits per plant, fruit length (cm), fruit width (cm), fruit shape index, fruit weight (g), pedicel length (cm), yield per plant (g), dry yield per plant (g) and dry recovery % were 69.4, 3.5, 84.9, 367.8, 5.2, 1.34, 3.4, 4.3, 2.9, 798.4, 151.2 and 17.6 respectively. The range for these traits were 47.1-100.7, 2.6-5.3, 78.6-104.4, 138.8-663.6, 2.2-9.0, 0.7-1.9, 1.7-6.2, 1.4-7.2, 1.3-4.4, 321.2-1798.2, 92.5-343.0 and 15.8-30.0 respectively. Co-efficient of variation (CV) was highest in case of fruit width (19.4 %) followed by dry recovery % (17.9 %) while fruit length (7.1%) had lower co-efficient of variation. Mopidevi *et al.*, (2018) evaluated 53 germplasm genotype of chilli and observed substantial variability for the 12 quantitative traits studied.

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The analysis of variance discovered significant changes amongst the plants for all the twelve characters studied representing the presence of genetic variability in the breeding

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material and substantial opportunity for their development. These outcomes are in trend with earlier reports of Farhad *et al.*, (2008), Gupta *et al.*, (2009), Suryakumari *et al.*, (2010) and Kumar *et al.*, (2012) in chilli. Twenty outstanding genotypes for different characters in F₃ population are mentioned in table number 2.

The plant number 91 was found to have maximum height (100.7cm), while plant number 105 had minimum height (47.1cm) among the population from F₃ generation. The general mean was observed to be 69.4 cm. For plant height 47 genotypes were found significantly superior than best check B-HP-143 (79.6 cm). The highest number of primary branches was recorded in the plant number 91 (5.3), while plant number 189 had minimum number of primary branches (2.6) among the population from F₃ generation. The general mean was observed to be 3.5. 45 genotypes were found significantly superior than the best check B-HP-144(4.4) for number of primary branches. The plant number 185 was found to have late flowering (104.4days), while plant number 91 earliest to flower (78.6 days) among the population from F₃ generation. The general mean was observed to be 84.9 days. For days to 50% flowering 42 genotypes were found significantly superior over best check B-HP-143 (76.9days). Similar results were also reported by Janaki *et al.* (2015) and Litoriya *et al.* (2014). The plant number 91 had maximum number of fruits per plant (663.6), while plant number 111 had minimum number of fruits per plant (138.8) among the population from F₃ generation. The general mean was 367.8. For number of clusters, 37 genotypes were found significantly higher than the best check B-HP-143 (357.6). The plant number 91 was found to have maximum fruit length (9.0cm), while plant number 131 had minimum fruit length (2.2 cm) among the population from F₃ generation developed. The general mean was observed to be 5.2 cm. 34 genotypes were found to be significantly superior to the best check B-HP-144(7.1cm) for fruit length. Similar observations were also reported by Nahak *et al.* (2018), Yatagiri *et al.* (2017), Ajith and Manju (2006) in chilli.

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Table 1: Mean, range and least significant differences in Augmented Block Design for various characters of F₃ population among chilli genotypes

Sl No.	Characters	Genotypes		Checks				CV	CM	AVSB	AVDB	AVAC
		Mean	Range	B-HP-143	IIHR-B-HP-142	G4	G5					
1	Plant height (cm)	69.4	47.1-100.7	79.6	77.4	73.3	75.9	13.4	2.3	6.7	8.2	6.1
2	Number of primary branches	3.5	2.6-5.3	3.3	4.4	3.3	3.5	15.6	0.7	2.0	2.4	1.8
3	Days to 50% flowering	84.9	78.6-104.4	76.9	81.2	80.4	85.8	12.2	2.2	6.2	7.7	5.7
4	Number of fruits per plant	367.8	138.8-663.6	357.6	301.7	248.7	186.5	14.7	6.2	17.7	21.7	16.3
5	Fruit length (cm)	5.2	2.2-9.0	6.6	7.1	6.8	5.3	7.1	0.5	1.5	1.9	1.4
6	Fruit width (cm)	1.34	0.7-1.9	1.15	1.55	1.35	1.1	19.4	0.3	0.8	1.0	0.8
7	Fruit weight (g)	3.4	1.7-6.2	4.4	4.6	2.9	4.4	16.4	0.8	2.4	3.0	2.2
8	Fruit shape index	4.3	1.4-7.2	4.2	4.9	4.4	3.7	16.9	0.3	0.9	1.1	0.8
9	Pedicle length (cm)	2.9	1.3-4.4	3.1	3.6	3.5	3.3	12.2	0.4	1.3	1.7	1.2
10	Yield per plant (g/plant)	798.4	321.2-1798.2	1307.4	1073.5	438.2	589.1	16.4	6.1	7.3	21.2	15.9
11	Dry yield per plant (g)	151.2	92.5-343.0	272.4	209.8	85.4	99.8	12.3	6.2	17.6	21.5	16.1
12	Dry recovery %	17.6	15.8-30.0	23.2	20.8	21.2	20.6	17.9	2.0	5.8	7.1	5.3

CM= least significant difference between the means of two check varieties, AVSB = least significant difference between adjusted values of two selections in the same block, AVDB = least significant difference between adjusted value of two selection in different blocks, AVAC = least significant difference between an adjusted selection value and a check mean

Table 2: List of outstanding genotypes for different characters in F₃ population

Sl No.	RIL number	Plant height (cm)	Number of primary branches	Days to 50% flowering	Number of fruits per plant	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Fruit shape index	Pedicel length (cm)	Yield per plant (g)	Dry yield per plant (g)	Dry recovery percent
1	91	100.7	5.3	78.6	663.6	9.0	1.8	6.2	7.2	4.2	1798.2	343.0	30.0
2	149	97.9	5.1	79.4	509.9	8.8	1.9	6.1	7.1	4.3	1780.5	327.2	29.3
3	173	97.7	4.9	80.2	500.0	8.0	1.6	5.8	6.8	4.2	1644.0	324.2	29.2
4	174	97.4	4.8	80.2	494.9	7.7	1.6	5.8	6.7	4.4	1608.4	315.5	29.1
5	276	97.3	4.7	80.6	493.0	7.6	1.6	5.6	6.7	4.1	1596.4	285.9	28.4
6	66	97.1	4.7	80.7	490.0	7.4	1.6	5.6	6.3	4.1	1554.8	285.5	27.8
7	16	96.4	4.7	81.4	485.2	7.3	1.6	5.6	6.1	4.0	1412.7	275.4	27.1
8	29	95.6	4.7	82.0	476.8	7.2	1.6	5.4	6.1	4.0	1391.3	274.5	26.6
9	40	95.0	4.3	82.4	476.0	7.2	1.6	5.4	6.1	3.9	1390.3	273.1	26.0
10	41	95.0	4.3	82.5	474.1	7.2	1.6	5.3	6.0	3.7	1359.0	271.6	26.0
11	45	92.2	4.3	82.6	471.1	7.0	1.6	5.3	5.8	3.7	1300.8	270.5	25.9
12	98	91.9	4.2	82.6	460.2	7.0	1.6	5.3	5.8	3.7	1278.6	266.8	25.9
13	110	90.4	4.2	82.7	460.1	7.0	1.6	5.2	5.8	3.7	1252.8	265.7	25.9
14	121	90.3	4.2	83.2	458.3	6.9	1.5	5.2	5.8	3.7	1245.1	264.9	25.9
15	125	90.3	4.2	83.2	456.9	6.9	1.5	5.2	5.8	3.6	1213.7	257.0	25.7
16	241	89.9	4.2	83.4	456.3	6.9	1.5	5.2	5.7	3.6	1203.7	254.9	25.3
17	134	89.9	4.2	83.4	452.2	6.8	1.5	5.2	5.7	3.6	1200.8	252.5	25.0
18	154	89.3	4.2	83.4	447.1	6.8	1.5	5.1	5.4	3.6	1198.2	251.6	24.8
19	163	89.3	4.1	83.5	446.3	6.7	1.5	5.1	5.4	3.6	1194.8	248.7	24.7
20	196	89.2	4.1	83.5	441.8	6.7	1.5	5.1	5.4	3.5	1192.3	248.6	24.7

Among the population from F₃ generation, the plant number 149 was found to have maximum fruit width (1.9 cm), while plant number 185 had minimum fruit width (0.7 cm). The general mean was observed to be 1.34 cm. 36 genotypes were found to be significantly superior to the best check B-HP-144(1.55 cm) for fruit width. Fruit weight was recorded highest in plant number 91 (6.2 g) and lowest in plant number 131 (1.7 g) among the plants. The general mean was observed to be 3.4 g. 39 genotypes were found significantly superior over the best check B-HP-144(4.6 g) for fruit weight. The plant number 91 observed to be highest (7.2) and the plant number 131 (1.4) observed to be lowest for fruit shape index. The general mean was observed to be 4.3. 33 genotypes were found significantly superior over the best check B-HP-144(4.9) for fruit shape index. For the character pedicel length plant number 174 (4.4 cm) and 152 (1.3 cm) were found to be highest and lowest respectively. The general mean was recorded to be 2.9 cm. 48 genotypes were found significantly superior over the best check B-HP-144(3.6 cm) for fruit shape index. The plant number 91 was found to have maximum yield per plant (1798.2g), while plant number 185 had minimum yield per plant (321.2g) and the general mean was observed to be 798.4. 33 genotypes were found significantly superior over the best check B-HP-143 (1307.4 g) for yield per plant. The results obtained are in agreement with the findings of Jogi *et al.* (2015), Mishra *et al.* (2015) and Farwah *et al.* (2020). The range for dry yield per plant of F₃ population varied from 343.0 g (plant number 91) to 92.5 g (plant number 194) and the general mean was 151.2 g. 37 genotypes were found significantly superior over the best check B-HP-143 (272.4 g) for dry yield per plant. The plant number 91 was found to have maximum dry recovery percentage (30.0 %), while plant number 185 had minimum dry recovery percentage (15.8 %). The general mean was observed to be 17.6 %. 32 genotypes were found significantly superior over the best check B-HP-143 (23.2%) for dry recovery. Sushmitha *et al.* (2019), Nahak *et al.* (2018), Jyothi *et al.* (2011) and Pujar *et al.* (2017). The characters presenting varied range of difference provide plentiful opportunity for choosing higher types and the particular genotypes can be used in advance crop improvement programme.

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It is concluded in the present study as, a high degree of variability was observed for all the traits. The genotypes which execute better for various yield traits may be further assess to find the best one at other place to use in breeding programme.

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