Mean Performance of F₃ Genotypes for Yield and Yield Attributing Characters in Chilli (*Capsicum annuum* L.)

Meenakshi Badu [a,b*], Ponnam Naresh [c], Gouri Shankar Sahu [a], Pradyumna Tripathy [a], Niranjan Das [d] and Usha Rani Veera [a]

[a] *Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Odisha, India.*
[b] *Faculty of Agriculture, Sri Sri University, Cuttack, Odisha, India.*
[c] *Indian Institute of Horticultural Research, Bangalore, India.*
[d] *Department of Nematology, College of Agriculture, Odisha University of Agriculture and Technology, Odisha, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

In the current experiment, 256 test treatments and four control treatments (checks) were assessed in an augmented block design for studying yield and yield-attributing traits. F₃ population of chilli was assessed for yield and yield components during *kharif* in the year 2018-19. The analysis of variance showed a 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, dry recovery %, whereas B-HP-144was found to be superior over all the checks for the rest of the traits.

_____

Corresponding author: E-mail: meenakshi.b@srisriuniversity.edu.in;

1. INTRODUCTION

Chilli, (*Capsicum annuum* L.), which is an important spice cum vegetable crop widely cultivated both as a rainfed and irrigated crop in India. It belongs to the genus *Capsicum* and the family solanaceae. This crop was native to Mexico, Southern Peru, Bolivia. There are generally five commercial *Capsicum* spp*. viz., C. annuum, C. baccatum, C. chinense, C. frutescens, 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 [1]. Chilli is a main constituent in the 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, export with an area of 3,63,000 ha., a 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 the area and production of chilli in India.

Capsaicin is the pungent principle existing in the placenta of chilli fruits and it has various prophylactic and beneficial usages in allopathic and ayurvedic medicine [2] and directly scavenges various free radicals [3,4]. Chilli is a rich source of vitamin C (ascorbic acid) used in food and beverage industries [1]. Oleoresin allows a good supply of colour 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 varieties will be much more effective if the nature and amount of variability present in the available germplasm is greater. In the chilli breeding program, the major goal is to develop varieties with high yield and good qualitative characteristics. The significance of genetically different genotypes with required combinations has also been understood by several workers. 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.

2. MATERIALS AND METHODS

The experiment was carried out with 256 test treatments and four control treatments (2018-19) in an augmented block design [5] with eight blocks, consisting of 32 test entries and four checks in each. The crop was grown with a 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 percent. The recorded data was statistically analyzed through statistical software [6].

3. RESULTS AND DISCUSSION

Augmented block design [5] is a statistical method of choice to start an 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 the 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 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 % are mentioned in Table 1. 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. [7] evaluated 53 germplasm genotype of chilli and observed substantial variability for the 12 quantitative traits studied.

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 material and substantial opportunity for their development [8]. These outcomes are in trend with earlier reports of Farhad et al. [9], Gupta et al. [10], Suryakumari et al. [11] and Kumar et al. [12] in chilli. Twenty outstanding genotypes for different characters in F_3 population are mentioned in Table 2.

The plant number 91 was found to have a maximum height (100.7cm), while plant number 105 had a minimum height (47.1cm) among the population from F_3 generation. The general mean was observed to be 69.4 cm. For plant height, 47 genotypes were found significantly superior to 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 the lowest number of primary branches (2.6) among the population from F_3 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 F_3 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. [13] and Litoriya et al. [14]. 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 F_3 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 F_3 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. [15], Yatagiri et al. [16], Ajith and Manju [17] in chilli.

Among the population from F_3 generation, the plant number 149 was found to have a 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. [18], Mishra et al. [19] and Farwah et al. [20]. The range for dry yield per plant of F_3 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. [21], Nahak et al. [15], Jyothi et al. [22] and Pujar et al. [23]. 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 [24].

Table 1. Mean, range and least significant differences in Augmented Block Design for various characters of F$_3$ population among chilli genotypes

SI 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	Pedicel 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

4. CONCLUSION

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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Bosland PW, Votava EJ. Peppers: Vegetable and spice capsicums. CABI Publishing, CAB International, Walingfort, U.K.; 2000.
2. Sumathy KMA, Mathew AG. Chilli processing. Indian Cocoa, Arecanut and Spice J. 1984;7:112-113.
3. Kogure K., Goto S, Nishimura M, Yasumoto M, Abe K, Ohiwa L. Mechanism of potent antiperoxidative effect of capsaicin. Biochimicaet Biophysica Acta. 2002;1573:84-92.
4. Bhattacharya A, Chattopadhyay A, Mazumdar D, Chakravarty A, Pal S. Antioxidant constituents and enzyme activities in chilli peppers. Intl. J. Veg. Sci. 2010;16(3):201-211.
5. Federer W. Augmented designs. Hawaiian Planter Recorder. 1956;55:191-208.
6. FAOSTAT, Food and Agriculture Organization Corporate Statistical Database; 2020.
Available:http://faostat.fao.org/site/339/default.aspx
7. Mopidevi MN, Reddy RVSK, Reddy KM, Naidu LN, Rani AS, Krishna KU. Performance of chilli (*Capsicum annuum* L.) genotypes for yield and yield attributing traits. Int. J. Curr. Microbiol. App. Sci. 2018;7(12):2252-2260.
8. Peter KV, Rai B. Heterosis as a function of genetic distance in tomato. Ind. J. Genet. Plant Breeding. 1978;38(2):173-178.
9. Farhad M, Hasanuzzaman M, Biswas BK, Azad AK, Arifuzzaman M. Reliability of yield contributing characters for improving yield potential in chilli (*Capsicum annum* L.). Intl. J. Sustain. Crop Prod. 2008;3:30-38.
10. Gupta AM, Singh D, Kumar A. Genetic variability, genetic advance and correlation in chilli (*Capsicum annuum* L.). Indian. J. Agr. Sci. 2009;79:221-223.
11. Suryakumari, S, Umajyothi K, Srihari D, Sankar AS, Sankar CR. Variability and genetic divergence in paprika (*Capsicum annuum* L.). J. Spi. Arom. Crops. 2010; 19:71-75.
12. Kumar D, Bahadur V, Rangare SB, Singh D. Genetic variability, heritability and correlation studies in chilli (*Capsicum annuum* L.). Hort. Flora Res. Spectrum. 2012;1:248-252.
13. Janaki M, Naram Naidu L, Venkataramana C, Paratpararao M. Performance of chilli (*Capsicum annuum* L.) genotypes for yield and yield attributing traits. Plant Archives. 2015;15(2):661-666.
14. Litoriya NS, Gandhi K, Talati JG. Nutritional composition of different chilli (*Capsicum annuum* L.) varieties. Indian Journal of Agricultural Biochemistry. 2014; 27(1):91-92.
15. Nahak SC, Nandi A, Sahu GS, Tripathy P, Dash SK, Patnaik A, Pradhan SR. Studies on variability, heritability and genetic advance for yield and yield contributing characters in chilli (*Capsicum annuum* L.). Journal of Pharmacognosy and Phytochemistry. 2018;7(1):2506-2510.
16. Yatagiri N, Telugu RK, Shafiqurrahaman M, Sanap PB. Evaluation of chilli genotypes for yield attributing and incidence of leaf curl and white fly traits in Coastal Maharashtra, India. International Journal of Current Microbiology and Applied Sciences. 2017;6(9):3140-3148.
17. Ajith PM, Manju P. Genetic variation for yield and anthracnose resistance in chilli (*Capsicum annuum* L.). Indian Journal of Genetics and Plant Breeding. 2006; 66(2):161-162.
18. Jogi MY, Madalageri MB, Pujari RJ, Mallimar MS, Bawoor S, Mangi V, Porika H. Genetic variability studies in chilli (*Capsicum annuum* L.) for growth and early yield. International Journal of Pure & Applied Bioscience. 2017;5(5):858-862.
19. Mishra TS, Chaturvedi A, Tripathi AN. Genetic analysis of agroeconomic traits in chillies (*Capsicum annuum*). Progressive Horticulture. 2015;47(2):322-332.
20. Farwah S, Hussain K, Rizvi S, Hussain SM, Rashid M, Saleem S. Genetic variability, heritability and genetic advance studies in chilli (*Capsicum annuum* L.) genotypes. Journal of Chemical Studies. 2008;8(3):1328-1331.

21. Sushmitha A, Allolli TB, Ganiger VM, Ajjappalavar PS, Evoor S, Gopali JB, Kareem A. Assessment of genetic variability, heritability and genetic advance for growth, yield and quality traits of Byadgi Dabbi genotypes of chilli (*Capsicum annuum* L.). Journal of Pharmacognosy and Phytochemistry. 2019;8(5):944-947.

22. Jyothi KU, Kumari SS, Ramana CV. Variability studies in chilli (*Capsicum annuum* L.) with reference to yield attributes. Journal of Horticultural Science. 2011;6(2):133-5.

23. Pujar UU, Shantappa T, Jagadeesha RC, Gasti VD, Sandhyarani N. Genetic variability, heritablity, correlation and path analysis in chilli (*Capsicum annuum* L.). International Journal of Pure & Applied Bioscience. 2017;5:579-586.

24. National Horticulture Board. Data Base of Horticultural crops. Gurgaon, New Delhi. 2017-18.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/89700