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Evaluation of F_2 generation of Mundu chilli (*Capsicum annuum* L.) for yield and quality

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Abstract
An experiment was carried out at the western farm of Department of Vegetable Science Horticultural College and Research Institute, TNAU, Periyakulam to study the Genetic Variability, Heritability and Genetic Advance in F_2 population of Mundu Chilli. In this study four F_2 populations derived from the F_1 crosses *viz.*, PKM CA 20 X PKM CA 08 (C1), PKM CA 32 X PKM CA 33 (C2), PKM CA 32 X PKM CA 20 (C3), PKM CA 38 X PKM CA 33 (C4) were tested. Among the four F_2 crosses studied the PKM CA 32 X PKM CA 33 and PKM CA 38 X PKM CA 33 showed high PCV, GCV, high heritability estimates and high genetic advance of per cent of mean for plant height, fruit length, single fresh fruit weight, single dry fruit weight, ripened fruit yield per plant and dry fruit yield per plant.

Keywords: Mundu chilli, variability, GCV, PCV, heritability, genetic advance

Introduction
Chilli (*Capsicum annuum* L.) is a widely grown and consumed vegetable in almost many countries. It is an annual crop that belongs to the Capsicum genus in the Solanaceae family. It is native to the New World's tropics and subtropics. The most common chilli species found in India are *Capsicum annuum*, *Capsicum frutescens*, and *Capsicum chinensis*. In terms of area and production of chillies, India is one of the leading countries with the production and productivity of 35.92 lakhs tonnes and 4.74 tonnes per hectare respectively with a total area of about 3.09 lakh hectares. Andhra Pradesh led all states in chilli farming, followed by Karnataka, West Bengal, Madhya Pradesh, Orissa, and Tamil Nadu (NHB, 2020) [7].
Mundu chilli is mostly grown as a rainfed crop in Tamil Nadu's coastal saline belt districts, such as Ramanathapuram, Viruthunagar, and Tuticorin, where soils are moderate to high in alkalinity (pH 7.5-9.5) and yearly rainfall is low (460.00 mm). It has a thick pericarp (0.24 mm) and measures 0.5-1.4 inches long and 2.4-5.10 inches in diameter.
Crop improvement is primarily determined by the extent to which desired traits are inherited and the magnitude of genetic variability. All conceivable variations are available in F_2 generation, which is obtained by selfing of F_1 hybrid. As a result, selection with specific goals in F_2 generation is particularly effective, and selfing of those genotypes generation after generation aids in the development of inbred lines (similar to the parental lines of the exotic hybrids). While starting the breeding programme, a breeder should be aware that the selection for the desired traits may be influenced by the environment, i.e., the variability in the population may be environmental instead of genetic, and thus the selection may not yield positive results in the next generation; Hence the concentration of breeder should discuss on the genetic variability (Reddy *et al.*, 2013) [12]. Genetic variability study is necessary since individual plant selection is entirely dependent on it. The mean and heritability estimations of the quantitative character are effective in projecting the selection process and a single plant-based estimate is most dependable (Johnson *et al.*, 1955) [3]. In addition to determining the extent and heritability of genetic variability, genetic advance is also a very valuable parameter to conformit must be estimated. Estimation of the variability coefficient helps to determine variability in a population.
In mundu chilli also lot of variation are available *viz.*, "oosi mundu", "chatti mundu" etc, because of no systematic breeding procedure have been followed with an objective to select/develop genetically pure type of mundu chilli all the available variants from the cultivable area are followed and purified through systematic breeding programme at Department of Vegetable Science, Horticultural College and Research Institute, TNAU, Periyakulam. To arrangement the performance of selected genotypes, crossing work with

superior identified types were taken to develop F_1 hybrids. From the F_1 hybrids four promising hybrids were selected and raised to F_2 generation selection to confirm the hybridity and to develop a hybrid derivative.

Materials and Methods

Experimental location

The present study was carried out in the western farm of Department of Vegetable Science, Horticultural College and Research Institute, TNAU, Periyakulam during 2020-21, which is situated at 10 ^{0}N latitude and 77 ^{0}E longitude with an altitude of 300 m above mean sea level.

Experimental material

The experimental material comprised of four F_2 generations *viz.*, PKM CA 38 X PKM CA 33, PKM CA 20 X PKM CA 08, PKM CA 32 X PKM CA 33, PKM CA 32 X PKM CA 20 which were maintained at the Department of Vegetable Science Horticultural College and Research Institute, Periyakulam, Tamil Nadu.

Nursery raising and cultivation practices

Twenty-four hours before sowing, the seeds were treated with *Trichoderma viride* @ 4 g kg^{-1} of seeds and planted in protrays. To facilitate quick germination and healthy seedling development, the nursery beds were watered twice a day with rosecan. To avoid the damping-off of seedlings, the beds were kept moist but not wet. Seedlings that were 35 days old were transplanted to the main field at a 45 cm x 30 cm spacing.

All the cultural practices followed were outlined in TNAU Agri Portal (https://agritech.tnau.ac.in/horticulture/horti_vegetables_chilli_index.html).

Observations recorded

For each of the F_2 populations, observations were made on a single plant. Ten quantitative characteristics were recorded for each plant in the population., which includes plant height (cm), number of primary branches per plant, days to 50% flowering, number of fruits per plant, fruit length (cm), fruit girth (cm), fresh fruit weight (g/fruit), dry fruit weight (g/fruit), fresh fruit yield per plant (g/plant), dry fruit yield per plant (g/plant).

Statistical Analysis

For each character, the mean values from all F_2 progenies were collated and analysed using analysis of variance (Panse and Sukhatme, 1957) [10]. Genotypic and phenotypic coefficient of variance was estimated using the following formula.

The phenotypic and genotypic coefficients of variation were estimated using the method advocated by Burton, 1952 [1].

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean}} \times 100$$

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Mean}} \times 100$$

Heritability in the broad sense was measured using Lush's (1940) [6] approach and expressed in percentage.

$$h^2 \text{ in a broad sense} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Genetic advance (GA) was proposed by the method suggested by Johnson *et al*. (1955) [3].

$$\text{Genetic advance} = \frac{\sigma^2_g}{\sigma^2_p} \text{ x k x } \sqrt{\sigma^2_p}$$

The following formula was used to express genetic adavance as a percentage of the mean (Johnson *et al*., 1955) [3].

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Results and Discussion

The mean, range, variability estimates including phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (GAM) of F_2 population are presented in Table 1.

The selection of superior genotypes is the most important criteria to consider in the breeding programme for the segregating generations. The F_2 generation should be used as a preliminary step for the selection. Choosing desirable combination and choosing the best progeny from those crosses are also important considerations in F_2 generation. By using this technique, may be explanted the advantage of the transgressive diversity that exists within a cross (Lerner, 1958) [5].

Among the four crosses studied in F_2 generation, PKM CA 32 X PKM CA 33 revealed a wide range of variability for plant height and it ranged from 30.75 to 92.24cm. This was followed by PKM CA 32 X PKM CA 20. The dwarf plant was observed in PKM CA 38 X PKM CA 33 with an average height of 57.69 cm whereas the tallest plant height is observed in PKM CA 32 X PKM CA 33 with an average height of 62.16 cm. In the F_2 population phenotypic coefficient of variation is ranged from 7.03 (PKM CA 20 X PKM CA 08) to 21.06 (PKM CA 38 X PKM CA 33). The genotypic coefficient of variation is ranged from 6.39 (PKM CA 20 X PKM CA 08) to 18.06 (PKM CA 38 X PKM CA 33). The F_2 population had high heritability in all four crosses. PKM CA 32 X PKM CA 33 and PKM CA 38 X PKM CA 33 exhibited in high genetic advance of per cent of mean, while the other three crosses had a moderate genetic advance of per cent of mean. High heritability and high genetic advance of per cent of the mean are observed in PKM CA 32 X PKM CA 33 and PKM CA 38 X PKM CA 33 and all other crosses had high heritability and moderate genetic advance of per cent of mean. Segregating population PKM CA 32 X PKM CA 33 revealed a wide range of variability in the number of primary branches per plant. The mean ranged from 4.83 (PKM CA 32 X PKM 33) to 5.11 (PKM CA 32 X PKM CA 20). The phenotypic coefficient of variation is moderate in PKM CA 32 X PKM CA 33 and all other three crosses exhibited in high, while a genotypic coefficient of variation is high in PKM CA 38 X PKM CA 33 remaining all three crosses exhibited in moderate genotypic coefficient of variation. The high heritability and moderate genetic advance of per cent of the mean are observed in PKM CA 32 X PKM CA 20 and often three crosses had high heritability and high genetic advance of per cent of mean. In F_2 population PKM CA 32 X PKM CA 20 revealed a wide range of days to 50 % flowering and it ranged from 42 to 58 days. The early flowering was observed in PKM CA 32 X PKM CA 33 with average days to 50 % flowering of 47.66 days, while the late flowering is observed in PKM CA 38 X PKM CA 33 with average days to 50 %

flowering of 50.51 days. The phenotypic coefficient of variation is ranged from 7.02 (PKM CA 20 X PKM CA 08) to 16.88 (PKM CA 38 X PKM CA 33). The genotypic coefficient of variation is ranged from 4.71 (PKM CA 20 X PKM CA 08) to 13.66 (PKM CA 38 X PKM CA 33). Heritability estimates were high in PKM CA 38 X PKM CA 33 and the other three crosses had moderate heritability. The low genetic advance of per cent of mean was observed in PKM CA 20 X PKM CA 08 and PKM CA 32 X PKM CA 33 whereas high genetic advance of per cent of mean is observed in PKM CA 38 X PKM CA 33. High heritability and high genetic advance of per cent of mean are observed in PKM CA 38 X PKM CA 33, moderate heritability and low genetic advance of per cent of mean is observed in PKM CA 20 X PKM CA 08 and PKM CA 32 X PKM CA 33. These results were in agreement with findings of Pandit *et al.* (2014), Janaki *et al*. (2015) [8, 2].

PKM CA 38 X PKM CA 33 revealed a wide range of variability for the number of fruits per plant. The mean ranged from 57.43 (PKM CA 38 X PKM CA 33) to 70.45 (PKM CA 20 X PKM CA 08). The phenotypic coefficient of variation is high in PKM CA 32 X PKM CA 20 remaining all other crosses exhibited in moderate, while the genotypic coefficient of variation is also high in PKM CA 32 X PKM CA 20 remaining other three crosses exhibited moderate genotypic coefficient of variation. High heritability combined with high genetic advance of per cent of mean was registered in all four crosses. In F_2 population variability in fruit length was found to be maximum in PKM CA 38 X PKM CA 33 (1.19 cm to 2.01 cm) and minimum in PKM CA 32 X PKM CA 20 (1.23 cm to 1.76 cm). The phenotypic and genotypic coefficient of variation was high for all crosses except PKM CA 20 X PKM CA 08, which was observed in moderate Phenotypic and genotypic coefficient of variation. All the crosses performed high heritability and high genetic advance of per cent of mean except PKM CA 20 X PKM CA 08, which was observed in moderate heritability and moderate genetic advance of per cent of mean. In fruit girth variability was found to be maximum in PKM CA 32 X PKM CA 20 (3.97 cm to 6.21 cm) and minimum in PKM CA 20 X PKM CA 08 (3.50 cm to 5.24 cm). The phenotypic coefficient of variation was high in PKM CA 20 X PKM CA 08 and PKM CA 38 X PKM CA 33 often crosses exhibited moderate, while the genotypic coefficient of variation is also high in PKM CA 38 X PKM CA 33 when other crosses recorded moderate genotypic coefficient of variation except for PKM CA 32 X PKM CA 20., which was observed in low genotypic coefficient of variation. High heritability and high genetic advance of per cent of mean are observed in PKM CA 20 X PKM CA 08, moderate heritability with the moderate genetic advance of per cent of mean is observed in PKM CA 32 X PKM CA 33 and PKM CA 38 X PKM CA 33. Similar results were reported earlier by Sharanappa and mogali (2014), Ullah *et al.* (2015), Rai *et al.* (2016) [13, 15, 11].

The range of variability in F_2 population for single fresh fruit weight was maximum in PKM CA 32 X PKM CA 20 (3.67g to 5.98) and minimum in PKM CA 20 X PKM CA 08 (3.89g to 6.21g). The phenotypic coefficient of variation ranged from 12.16 per cent (PKM CA 20 X PKM CA 08) to 27.01 per cent (PKM CA 32 X PKM CA 33). The genotypic coefficient of variation ranged from 11.94 per cent (PKM CA 20 X PKM CA 08) to 22.76 per cent (PKM CA 32 X PKM CA 33). All four crosses exhibited high heritability and high genetic advance of per cent of mean. Among the four crosses studied, PKM CA 38 X PKM CA 33 revealed the maximum range of variability in single dry fruit weight. The mean number of single dry weights was high in PKM CA 32 X PKM CA 33 (1.18g). The phenotypic coefficient of variation is high in all four crosses, while the genotypic coefficient of variation is high in all crosses except PKM CA 20 X PKM CA 08 and PKM CA 32 X PKM CA 20, which was observed in moderate genotypic coefficient of variation. High heritability combined with high genetic advance of per cent of mean was observed in PKM CA 32 X PKM CA 33 and PKM CA 38 X PKM CA 33, while moderate heritability combined with high genetic advance of per cent of mean was observed in PKM CA 20 X PKM CA 08 and PKM CA 32 X PKM CA 20. A wide range of ripened fruit yields per plant was observed in PKM CA 32 X PKM CA 33 (115.56g to 502.35g). The mean ranged from 236.74g (PKM CA 38 X PKM CA 33) to 324.47g (PKM CA 20 X PKM CA 08). The phenotypic coefficient variation was ranged from 11.12 per cent (PKM CA 20 X PKM CA 08) to 20.62 per cent (PKM CA 32 X PKM CA 20). The genotypic coefficient variation ranged from 10.01 per cent (PKM CA 38 X PKM CA 33) to 20.52 per cent (PKM CA 32 X PKM CA 20). The high heritability with the high genetic advance of per cent of mean was noticed in PKM CA 20 X PKM CA 08, PKM CA 32 X PKM CA 33 and PKM CA 32 X PKM CA 20. The high heritability with the moderate genetic advance of per cent of mean was observed PKM CA 38 X PKM CA 33. The range of variability for dry fruit yield was maximum in PKM CA 32 X PKM CA 33 (29.47g to 102.41g) and minimum in PKM CA 38 X PKM CA 33 (27.67g to 81.64g). The mean for this trait ranged from 51.26g (PKM CA 32 X PKM CA 20) to 75.65g (PKM CA 32 X PKM CA 33). The phenotypic coefficient variation is high in PKM CA 32 X PKM CA 33, PKM CA 32 X PKM CA 20 and PKM CA 38 X PKM CA 33 remaining cross PKM CA 20 X PKM CA 08 is observed in moderate phenotypic coefficient variation. The genotypic coefficient variation is high in PKM CA 32 X PKM CA 33 and PKM CA 38 X PKM CA 33 often all two crosses showed moderate genotypic coefficient variation. All four crosses exhibited high heritability with a high genetic advance of per cent of mean. Similar results were also reported by Sharma *et al.* (2010) [14], Reddy *et al.* (2013) [12], Pandit *et al.* (2014) [9].

High heritability with a high genetic advance of per cent of mean might be due to additive gene effect. So, these characters could be considered as reliable selection indices and selection based on these characters might be rewarding. The results agreed with Varkey *et el.* (2005), Vani *et al.* (2007), Jyothi *et al.* (2011) [17, 16, 4]. Low heritability coupled with low genetic advance of per cent of mean indicates the influence of non-additive gene action and considerable influence of environment on expression. These traits could be exploited through the manifestation of dominance and epistatic components through heterosis breeding (Verma *et al.*, 2014) [18].

Table 1: Range, mean, variability, heritability, genetic advance and genetic advance as per cent of mean in four F_2 population cross

Characters	Cross	Mean	Range		Co-efficient of variation		Heritability (BS)	GAM
			Minimum	Maximum	Phenotypic	Genotypic		
Plant Height (cm)	C1	59.42	35.14	86.47	7.03	6.39	82.64	11.97
	C2	62.16	30.75	92.24	10.23	10.05	96.61	20.36
	C3	59.26	32.74	89.74	10.40	8.33	64.11	13.74
	C4	57.69	38.47	82.65	21.26	18.06	72.16	31.61
Number of primary branches per plant	C1	4.90	3.00	6.00	20.92	17.32	68.54	29.54
	C2	4.83	2.00	7.00	19.85	16.03	69.04	29.95
	C3	5.11	4.00	6.00	20.90	11.77	31.74	13.65
	C4	5.02	3.00	7.00	28.20	24.90	77.98	45.30
Days to 50 % Flowering (Days)	C1	50.05	45.00	56.00	7.02	4.71	45.07	6.52
	C2	47.66	40.00	52.00	9.51	5.62	34.91	6.84
	C3	49.76	42.00	58.00	16.75	11.91	50.53	17.44
	C4	50.51	46.00	61.00	16.88	13.66	65.52	22.78
Number of fruits per plant	C1	70.45	42.00	138.00	12.01	10.83	81.33	20.13
	C2	66.56	35.00	122.00	10.77	10.69	98.39	20.96
	C3	60.28	32.00	118.00	22.21	20.79	87.59	40.09
	C4	57.43	29.00	135.00	12.51	11.36	82.51	21.27

C1-PKM CA 20 X PKM CA 08 C2-PKM CA 32 X PKM CA 33 C3-PKM CA 32 X PKM CA 20 C4-PKM CA 38 X PKM CA 33

Table 2: Mean, range, variability, genetic advance and genetic advance as percent of mean for Number of fruits per plant, Fruit length (cm), Fruit girth (cm) and Single fresh fruit weight (g)

Characters	Cross	Mean	Range		Co-efficient of variation		Heritability (BS)	GAM
			Minimum	Maximum	Phenotypic	Genotypic		
Fruit length (cm)	C1	1.68	1.20	1.98	22.82	14.19	38.70	18.19
	C2	1.53	1.15	1.84	23.32	21.43	84.40	40.56
	C3	1.42	1.23	1.76	23.47	21.25	82.02	39.65
	C4	1.65	1.19	2.01	29.93	27.12	82.10	50.63
Fruit girth (cm)	C1	4.10	3.50	5.24	22.65	19.82	76.55	35.72
	C2	4.55	3.80	5.56	17.15	12.16	50.30	17.77
	C3	4.77	3.97	6.21	17.59	8.66	24.28	8.79
	C4	4.17	3.12	4.97	29.46	23.47	39.41	13.98
Single fresh fruit weight (g)	C1	4.53	3.89	6.21	12.16	11.94	96.41	24.16
	C2	4.22	3.49	5.74	27.01	22.76	70.98	39.50
	C3	4.43	3.67	5.98	18.04	17.66	95.92	35.65
	C4	4.09	3.12	4.98	21.35	19.63	84.60	37.21
Single dry fruit weight (g)	C1	0.91	0.54	1.01	28.37	19.81	48.77	28.50
	C2	1.18	0.78	1.87	37.45	32.68	76.16	58.75
	C3	0.76	0.45	1.56	24.29	16.36	45.36	22.70
	C4	0.75	0.35	1.48	25.96	21.83	70.72	37.82

C1-PKM CA 20 X PKM CA 08 C2-PKM CA 32 X PKM CA 33 C3-PKM CA 32 X PKM CA 20 C4-PKM CA 38 X PKM CA 33

Table 3: Mean, range, variability, genetic advance and genetic advance as percent of mean for Single dry fruit weight (g), Ripened fruit yield per plant (g), Dry fruit yield per plant (g) and Dry fruit recovery (%)

Characters	Cross	Mean	Range		Co-efficient of variation		Heritability (BS)	GAM
			Minimum	Maximum	Phenotypic	Genotypic		
Ripened fruit yield per plant (g)	C1	324.47	128.14	495.74	11.12	10.42	87.80	20.12
	C2	302.99	115.56	502.35	17.70	14.50	67.15	24.48
	C3	243.91	107.54	487.17	20.62	20.52	99.06	42.08
	C4	236.74	128.34	459.64	12.52	10.01	63.93	16.49
Dry fruit yield per plant (g)	C1	64.30	23.14	89.74	19.86	19.31	94.56	38.68
	C2	75.65	29.47	102.41	23.47	22.78	93.48	37.42
	C3	51.26	25.40	78.64	20.25	19.00	88.01	36.73
	C4	53.31	27.67	81.64	26.85	25.80	89.45	37.02

C1-PKM CA 20 X PKM CA 08 C2-PKM CA 32 X PKM CA 33 C3-PKM CA 32 X PKM CA 20 C4-PKM CA 38 X PKM CA 33

Conclusions

Analysis of variance revealed the presence of considerable amount of genetic variability for yield and yield attributing characters of chilli genotypes. The genotypes expressed high genotypic and phenotypic coefficient of variation, heritability and genetic advance for plant height, fruit length, single fresh fruit weight, single dry fruit weight, ripened fruit yield per plant and dry fruit yield per plant. revealed these traits are under the control of additive gene action. This indicated high response to selection for genetic improvement of chilli genotypes under study.

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