Original Research Paper

Breeding potential of multi-parent derived populations in chilli (*Capsicum annuum* L.)

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ABSTRACT

Selection from multi-parent (MP) derived populations is most likely to fix a greater number of alleles governing complex traits compared to two parents'-derived populations which result in fixation of only two alleles. It is hypothesized that more than two-parents'-derived populations harbour greater variability than those derived from two-parents'. To test this hypothesis, ten multi-parents' (MP) populations (8 parents) were field evaluated for average fruit length and fruit weight, fruits plant^{-1} and green fruit yield plant^{-1}. Breeding potential of these ten MP populations was assessed in terms of means, standardized range (SR), phenotypic coefficient of variation (PCV) and frequency of transgressive segregants (TS). The MP populations with greater trait mean, SR, PCV and TS are interpreted as those with high breeding potential (BP). When each statistical criteria considered separately, the results suggested that BP of the MP populations differed. Hence, a rank-sum method, which combines all the statistical criteria into one criterion was used to identify MP populations with high BP. MP populations designated as D5×D2, D4×D2 and D6×D2 with lower rank-sum were considered to possess high BP. These MP populations are suggested for preferential use to isolate new inbred lines to develop new hybrids.

Keywords: Breeding potential, MP populations, pure-line cultivar, rank-sum, transgressive segregants

INTRODUCTION

Hot pepper or chilli pepper (*Capsicum annuum* L.) family Solanaceae, is one of the most important economic spice-cum-vegetable crops worldwide (Poulos, 1992). Globally chilli was cultivated with an area of 18.03 lakh hectares, with a production of 58.22 lakh tonnes and an average productivity of 3,229 kg per hectare (Sharma et al., 2024). Being a high value crop, chilli offer commercial benefits to smallholders and farmers. It significantly contributes to increased family income and socio-economic status (Weinberger & Lumpkin, 2007). It has been an indispensable ingredient in Indian cuisines and preparations due to its pungency, appealing colour, taste and flavour. It is widely found garnished on dishes (Rao et al., 2020). Among the 5 cultivated species of the genus *Capsicum*, *C. annuum* is the most widely cultivated in India for its pungent (chilli syn. hot pepper) and non-pungent (sweet pepper syn. capsicum, bell pepper) fruits. (Reddy, 2014).

Commercial cultivars of chilli are either open pollinated varieties (OPV) or F_1 hybrids. These OPVs and parents of F_1 hybrids, are routinely developed from segregating populations derived from bi-parental crosses. Such bi-parental segregating populations not only harbour narrow genetic base but also often lack all the desired combination of traits due to restricted recombination events and fewer combination of genotypes driven by two alleles at locus.

Further, selection from bi-parental populations is likely to result in possible fixation of only two alleles controlling target traits in segregating populations. In contrast, selection in multi-parent (MP) derived populations is likely to fix more than two alleles at each or most loci governing economically important quantitative traits. Selection from MP populations also assembles greater number of combinations of desirable alleles from multiple parents compared to bi-parental populations. Considering these advantages, there has been increased interest to develop and use MP populations for development of cultivars in many crops including chilli. However, even with moderate number (8) of founder parents, a large number of MP populations are possible. Very often breeders are constrained to work with limited resources. Selection

and handling of only a few productive MP population is therefore critical for efficient use of limited resources (Krishnappa et al., 2009; Suresh et al., 2017; Bernardo, 2020). An objective method of identification of such only a few productive MP populations is therefore necessary. Assessment of breeding potential of segregating populations is suggested as a dependable method of selection of best MP population. Breeding potential of segregating populations can be assessed based on statistical parameters such as quantitative trait means, standardized range (SR), phenotypic coefficient of variation (PCV) and frequency of transgressive segregation (TS) and their combination. These parameters can serve as useful predictors of breeding potential of segregating population including those of MP population/s. Under these premises, the present study was implemented to assess the breeding potential of MP populations.

Table 1 : Parentage of 10 multi-parent (MP) derived populations

MP population code	Parentage	Population size
D4 × D2	[(LG 174×BD) × (Vang×CA14)] × [(PC1×CMS 10B) × (JL×CMS 8B)]	119
D2 × D1	[(PC1×CMS 10B) × (JL×CMS 8B)] × [(LG 174×BD) × (Ti×CA14)]	112
D3 × D2	[(UA×PJ) × (PS×CMS 6B)] × [(PC1×CMS 10B) × (JL×CMS 8B)]	82
D5 × D2	[(LG 174×BK) × (Vang×CA14)] × [(PC1×CMS 10B) × (JL×CMS 8B)]	110
D1 × D3	[(LG 174×BD) × (Ti×CA14)] × [(UA×PJ) × (PS×CMS 6B)]	145
D6 × D3	[(GB×BK) × (Vang×LG 181)] × [(UA×PJ) × (PS×CMS 6B)]	155
D5 × D3	[(LG 174×BK) × (Vang×CA14)] × [(UA×PJ) × (PS×CMS 6B)]	110
D4 × D3	[(LG 174×BD) × (Vang×CA14)] × [(UA×PJ) × (PS×CMS 6B)]	99
D6 × D2	[(GB×BK) × (Vang×LG 181)] × [(PC1×CMS 10B) × (JL×CMS 8B)]	122
D7 × D2	[(GB×CA14) × (Vang×LG 181)] × [(PC1×CMS 10B) × (JL×CMS 8B)]	153

Table 2 : Salient features of founder lines used in the development of MP populations

Founder lines	Salient features
Byadgi Dabbi (BD)	High oleoresin/colour
Gouribidanur (GB)	High pungency
Tiwari (Ti)	Tolerant to sucking pest
Utkal Awa (UA)	Resistance to bacterial wilt
Byadgi Kaddi (BK)	High oleoresin
Japani Long (JL)	Tolerant to sucking pest
Phule Jyothi (PJ)	Resistance to CMV
Pusa Sadabahar (PS)	Tolerant to sucking pest & ChiLCV
Vangara (Vang)	High fruit yield & combining ability
CMS 6B (6B)	High oleoresin & early maturing
CMS 8B (8B)	High yield with good combining ability
CMS 10B (10B)	High yield with good combining ability
Pant C_1 (PC$_1$)	Tolerant to sucking pest & ChiLCV
CA 14	High yielding
LG 174	Tolerant to Anthracnose
LG 181	Tolerant to Anthracnose

MATERIALS AND METHODS

The material consisted of ten eight-parent MP populations (Table 1) derived from 16 trait specific founder lines (Table 2). The seeds of these 10 MP populations were procured from hot pepper improvement unit, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Bangalore, India. The seeds of these 10 MP populations along with 16 founder lines were sown in nursery bed of size 10 m × 1.5 m. Sufficient care was taken to raise healthy plants and to maintain adequate population size (Table 1).

Forty-day old seedlings of the each of the ten MP populations were planted separately in contiguous blocks with a spacing of 75 cm between rows and 45 cm between plants within a row during 2019 rainy season at experimental plots. These seedings of 10 MP populations were planted in a row of length 4.5 m. The number of rows varied from 7 to 15 depending on nursery population size at the time of transplanting. The 16 parental (founder) lines were planted in a randomized complete block design with two replications. The seedlings were planted in a single row of 4.5 m with a spacing of 0.75×0.45 m^2. Recommended agronomic practices were followed to maintain a healthy population in the field.

Data on four quantitative traits (average fruit length and weight, fruits plant[1] and green fruit yield plant^{-1}) on each plant from each of the 10 MP population and 20 plants (10 in each replication) of founder lines were recorded.

Statistical analysis

The data recorded on individual plants of MP populations were used to estimate different statistical parameters such as mean, standardized range [(highest-lowest)/mean] and phenotypic coefficient of variance (PCV) = (phenotypic standard deviation/

mean × 100) (Snedecor & Cochran, 1967). The parental data used to calculate non-genetic source of variance for estimating PCV. The MP population plants that surpassed their higher scoring parent for four quantitative traits in each of the ten MP population were counted and were considered as transgressive segregants.

Criteria to assess the breeding potential of MP populations

The population/s with high quantitative trait's mean, standardized range (SR), PCV and frequency of transgressive segregation (TS) among ten MP populations were considered as those with better breeding potential (BP). As BP of MP populations differed with the criteria and with trait, a rank-sum method (Kang, 1988) which takes care of all the traits and all the criterion was used to assess the BP of MP populations. For each trait, each MP population was ranked from 1 to 10 (rank 1 and 10 were assigned to the population that expressed highest and lowest estimate of each statistical parameter, respectively). Further, ranks were summed across the traits and parameter (Kang, 1988). The population with lower rank-sum was considered as the most productive MP population.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) is a diagnostic step to quantify the variability attributable to different sources of variation. Significant mean sum of squares attributable suggested significant variability among founder lines for all the four traits (Table 3). Breeding populations with high mean and a large variance for trait (s) of interest is considered as ideal ones for the recovery of superior RILs in advanced segregating generations. Starting with a high mean increases the likelihood that selected progeny will have a high mean, even when the selection is not precise (Bernardo,

Table 3 : Analysis of variance for four traits among 16 founder lines

Source of variation	Degrees of freedom	Mean sum of squares			
		Average fruit length	Average fruit weight	Fruits plant^{-1}	Green fruit yield plant^{-1}
Replication	01	3.15	8.34*	6.94*	11.34*
Genotypes	15	28.96**	83.23**	152.56**	232.67**
Residual	15	1.23	6.72	36.01	77.96

* significance at P=0.05, ** significance at P=0.01

Table 4 : Trait wise rank and rank-sum for average fruit length, average fruit weight, fruits plant⁻¹ and green fruit yield plant⁻¹ in MP populations in chilli

Multi parent population code	Mean														Standardized range							
	Average fruit length (cm)	Rank (a)	Average fruit weight (g)	Rank (b)	Fruits plant⁻¹	Rank (c)	Green fruit yield plant⁻¹ (g)	Rank (d)	Average fruit length (cm)	Rank (e)	Average fruit weight (g)	Rank (f)	Fruits plant⁻¹	Rank (g)	Green fruit yield plant⁻¹ (g)	Rank (h)
D4 × D2	11.34	1	5.10	2	88.27	7	432.36	1	0.56	10	2.35	1	2.36	8	2.06	8
D2 × D1	10.63	3	4.19	3	88.79	6	366.41	4	0.62	8	1.39	4	2.21	10	2.04	10
D3 × D2	9.97	9	3.38	8	94.65	4	313.73	8	0.64	5	1.35	6	2.52	6	2.18	6
D5 × D2	11.12	2	4.06	5	109.22	1	425.99	2	0.62	7	1.54	3	2.80	4	2.42	5
D1 × D3	9.97	8	3.85	6	92.78	5	345.58	5	0.81	2	1.03	10	2.25	9	2.16	7
D6 × D3	9.71	10	3.30	9	102	3	333.35	3	0.72	4	1.23	7	2.80	5	2.74	4
D5 × D3	10.42	4	4.09	4	84.09	8	341.48	6	0.63	6	1.05	9	2.81	3	2.87	3
D4 × D3	10.04	7	5.39	1	74.93	10	382.04	3	0.85	1	1.38	5	2.42	7	2.05	9
D6 × D2	10.07	6	3.00	10	102	2	294.65	10	0.58	9	2.09	2	3.29	2	4.63	1
D7 × D2	10.21	5	3.78	7	81.98	9	299.20	9	0.79	3	1.21	8	3.86	1	3.12	2

D1 = [(LG 174 × BD) × (Ti × CA14)], D2 = [(PC$_1$ × 10B) × (JL × 8B)], D3 = [(UA × PJ) × (PS X 6B)], D4 = [(LG 174 × BD) × (Vang × CA14)], D5 = [(LG 174 × BK) × (Vang × CA14)], D6 = [(GB × BK) × (Vang × CA14)], D7 = [(GB × CA14) × (Vang × LG 181)]

Table 4. continued…

MP populations	Phenotypic coefficient of variation								Frequency of transgressive segregants								RANK SUM (a+b+c+d+ e+f+g+h +i+j+k+l+m+ n+o+p)
	Average fruit length (cm)	Rank (i)	Average fruit weight (g)	Rank (j)	Fruits plant⁻¹	Rank (k)	Green fruit yield plant⁻¹ (g)	Rank (l)	Average fruit length (cm)	Rank (m)	Average fruit weight (g)	Rank (n)	Fruits plant⁻¹	Rank (o)	Green fruit yield plant⁻¹ (g)	Rank (p)	
D4 × D2	12.06	6	30.65	1	51.68	7	47.91	8	2.52	2	1.68	2	45.38	4	64.71	1	69
D2 × D1	10.74	10	23.03	6	41.06	10	41.99	10	0.89	4	0	5	59.82	1	58.93	4	98
D3 × D2	11.95	7	25.92	3	53.80	5	53.75	4	0	7	0	6	35.37	6	58.54	5	95
D5 × D2	12.94	3	22.06	8	54.77	3	50.23	6	0	5	0.91	3	58.18	2	62.73	2	61
D1 × D3	13.41	2	22.81	7	45.37	9	43.03	9	2.76	1	0	7	33.79	8	49.66	7	102
D6 × D3	11.69	8	22.03	9	51.56	8	52.92	5	0	9	0	8	43.23	5	58.06	6	107
D5 × D3	11.23	9	21.50	10	54.59	4	56.74	3	0	10	0	9	21.82	9	44.55	9	106
D4 × D3	12.77	4	24.03	4	53.38	6	48.04	7	1.01	3	0	4	17.17	10	59.6	3	84
D6 × D2	12.30	5	26.58	2	58.51	2	61.29	2	0	6	4.03	1	55.64	3	45.97	8	71
D7 × D2	13.77	1	23.49	5	73.22	1	69.29	1	0	8	0	10	33.99	7	33.99	10	87

D1 = [(LG 174 × BD) × (Ti × CA14)], D2 = [(PC$_1$ × 10B) × (JL × 8B)], D3 = [(UA × PJ) × (PS X 6B)], D4 = [(LG 174 × BD) × (Vang × CA14)], D5 = [(LG 174 × BK) × (Vang × CA14)], D6 = [(GB × BK) × (Vang × CA14)], D7 = [(GB × CA14) × (Vang × LG 181)]

2020). Higher the variance, higher will be the scope for selection of genotypes with desired combination of traits. If the genetic variance and the mean are relatively high, selected progeny is likely to perform to their maximum potential (Bernardo, 2020).

In the present study, BP of 10 MP populations were assessed based on the estimates of trait mean, SR, PCV and TS. When these statistics considered separately, results indicated different choices of MP populations. For instance, based on mean criterion, D4 × D2 with longer fruits (11.34 cm) and higher fruit yield (432.36 g) were adjudged as the one with high BP. Similarly, D4 × D3 and D5 × D2 with higher average fruit weight (5.39 g) and fruit plant^{-1} (109.22), respectively were identified as the populations with high BP (Fig. 1). Higher estimates of trait's mean could be attributed to effect of the genes which intensifies trait's phenotype (Dudley, 1982; Dudley, 1984; Melchinger, 1987; Bernardo, 2020). Unlike mean, SR is a unit independent first degree-based measure of dispersion. MP population, D6 × D2 produced extreme phenotypes for green fruit yield plant^{-1} (4.63). The MP populations namely D4 × D3, D4 × D2 and D7 × D2 produced extreme phenotypes for average fruit length (0.85), average fruit weight (2.35) and fruit plant^{-1} (3.86), respectively as assessed based on SR. Based on second degree statistic criterion namely, PCV, the MP population, D7 × D2 was considered as the one with high BP for average fruit length (13.77 %), fruit plant^{-1} (73.22 %) and green fruit yield plant^{-1} (69.29 %).

Transgressive segregation (TS) has been attributed as major cause for the success of plant breeding and without TS, plant breeding does not work (Mackay et al., 2020). The MP populations namely, D1 × D3, D6 × D2, D2 × D1 and D4 × D2 with greater frequency of TS were considered the ones with high BP for average fruit length, average fruit weight, fruits plant^{-1} and green fruit yield plant^{-1}, respectively (Table 4). Occurrence of TS in segregating populations could be attributed to constellation of complete or incompletely dominant genes that are dispersed among their parents (Chahal & Gosal 2002). Genetic studies conducted by Risenberg et al. (1999) suggest that combination of alleles from multiple parents that have complementary gene effects result in recovery of high frequency of TS with desirable combinations of traits. Thus, it is evident from the results that different MP populations were identified as the ones with high BP

based on different traits and statistical parameter criteria. Hence a rank-sum method which combines both trait and statistical parameters criteria was used to assess the BP of MP populations.

Based on rank-sum method, the MP population, D5 × D2 (with rank-sum 61) was identified as the best one closely followed by D4 × D2 and D6 × D2 (Table 4). Selection from these MP populations is likely to result in identification of elite recombinants with desirable combination of multiple target traits. The differences in the estimates of quantitative trait means, SR and PCV in MP populations could be attributed to differences in the number of genes dispersed between their parents (Kearsey & Pooni, 1996; Bernardo, 2020). The crosses whose parents differ for a larger number of dispersed genes would exhibit higher traits means and variances than those whose parents differ for fewer genes (Kearsey & Pooni, 1996; Bernardo, 2020).

CONCLUSION

BP of multi-parents' crosses involving different combination of parents differed significantly. Three of the ten MP populations exhibited high BP. These MP populations are likely to uncover greater frequency of superior inbred lines for use in developing heterotic hybrids.

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