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Estimation of genetic variability, heritability and genetic gain in King chilli (*Capsicum chinense* Jacq.)

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Abstract

The present research was carried out at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh with fifteen genotypes of King chilli (*Capsicum chinense* Jacq.) during 2017-18 and 2019-20 to estimate genetic variability, heritability and genetic gain for fruit yield and quality parameters in King chilli genotypes. High GCV and PCV were observed for ascorbic acid content, fruit yield per plant, reducing sugar, chlorophyll content, capsaicin content, number of seeds per fruit and number of primary branches showing that these characters have higher magnitude of variability and thus provide a greater scope for improvement through selection. High heritability coupled with high genetic advance as percent of mean (genetic gain) were also observed for ascorbic acid content, reducing sugar, number of primary branches, chlorophyll content, number of seeds per fruit, total sugar, fruit yield per plant, no. of fruit per plant, non-reducing sugar, capsaicin content, plant height, leaf width, dry weight per fruit, dry weight per 100 fruit, pedicel length of fruit, fruit length and fruit weight, indicating the influence of additive genes. The selection on the basis of characters like ascorbic acid content, fruit yield per plant, reducing sugar, chlorophyll content, capsaicin content, number of primary branches and number of seeds per fruit with high GCV, PCV and high heritability coupled with high genetic advance as percent of mean (genetic gain) would be more effective and reliable for the improvement of this crop.

Keywords: King chilli, heritability, genetic gain, variability, improvement

Introduction

Chillies (*Capsicum* spp.) are considered as one of the most popular vegetable crops which belongs to solanaceae family and grown all over India either in large scale or in backyard of every household which are always a part of dishes prepared every day in Indian kitchen. Chillies are important spice cum vegetable which have great oversea export potential. The genus *Capsicum* has five domesticated species under cultivation namely *Capsicum annuum* L, *C. frutescens* L, *C. chinense* Jacq, *C. pubescens and C. baccatum*. Chillies are used as fresh, canned, pickled, frozen, fermented, dehydrated or processed as chilli powder for consumption. In India, other than sweet items, no dish is complete without chilli. Due to regular requirement of the people, India has emerged few decades back after independent as the foremost producer and exporter of chillies, fulfilling demand of our country and other several countries of the world. Apart from various chilli species cultivating in India, King chilli (*Capsicum chinense* Jacq.) is an important and highly pungent species of chilli grown especially in North East region of India. It is known by various local names in North East region of India such as 'Bhut/Bhot jolokia' or 'Bih jolokia' in Assam, 'Naga King chilli' in Nagaland (Hazarika *et al.* 2013) [8].In the state of Manipur King chilli is commonly known as U-morok. However based on the distinct type of variability in King chilli available in North East India, it can be presented that a wide range of variability is available in King chilli genotypes which provide great scope for improving fruit yield through breeding programs. In the present study, fifteen distinct types of King chillies were collected from different states of North East India to find the differences among them on the basis of fruit colours, size, pungency and fruiting behaviour which differ phenotypically. At the same time, different gene pool may be the source to utilize for improvement of King chilli crop. The probability of receiving superior genotype is high if variability in the population is large due to genetic reason. So, partitioning of observed variability into heritable and non-heritable components are required to be studied. Hence, utilization of this variability needs systematic evaluation through estimation of genetic variability, heritability and genetic advance as percent of mean (genetic gain) of various yield and quality parameters in King chilli genotypes.

Materials and Methods

The present investigation was conducted at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh during year 2017-18 and 2019-20. Fifteen genotypes of King chilli were collected from different region of North East India. The experiment was laid out in Randomized Block Design (RBD) with three replications and spacing of 90 cm x 90 cm. All the agronomical practices were adopted to raise healthy crops. Five randomly selected plants of each genotypes from each replication were taken and the average was worked out for different traits. Observations were recorded on plant height (cm), days to first flowering, days to first fruit set, days to first harvest, number of primary branches, leaf length (cm), leaf width(cm), fruit length (cm), fruit width (cm), pedicel length of fruit (cm), fruit weight (g), no. of fruit per plant, dry weight per fruit (g), dry weight /100 fruit (g), number of seeds per fruit, fruit yield per plant (g), ascorbic acid content (mg/100g), capsaicin content% was taken in fresh green fruit stage, green fruit TSS (°Brix), red fruit TSS (°Brix), total sugar (mg/g), reducing sugar (mg/g), non-reducing (mg/g) and chlorophyll content (mg/g) in leaf was taken. The minimum and maximum values on the basis of individual plant observation were used to indicate the range for a given character. Analysis of variance was calculated according to Gomez & Gomez (1984)[7]. Phenotypic and genotypic coefficients of variation (PCV and GCV, respectively) were calculated as per the formula suggested by Burton and de Vane (1953) [4]. PCV and GCV were classified as recommended by Sivasubramanian and Menon (1973) [21] as low (0-10%), moderate (10-20%) and high (>20%). Heritability in broad sense was calculated as per the methods given by Burton and de Vane (1953) [4]. Heritability percentage was categorised as demonstrated by Robinson *et al*. (1949) [20] as low (0-30%), moderate (30- 60%) and high (> 60%). Genetic advance was calculated as per the methods suggested by Johnson *et al*., (1955) [10]. The genetic advance as percent of mean (genetic gain) was categorised into low, moderate and high as suggested by Johnson *et al*. (1955) [10] i.e. low (0-10), moderate (10-20) and high (>20).

Result and Discussion

Analysis of variance showed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability in the genotypes.

The estimate of genetic parameter namely, mean, range, phenotypic and genotypic coefficient of variation along with heritability in broad sense, genetic advance and genetic advance as percentage of mean for different characters are given in (Table 1). In the perusal of data presented in (Table 1) revealed that, the range of mean values revealed sufficient variation for all the characters under study. The range of variation was recorded maximum for ascorbic acid content (114.07 to 309.00 mg/100g) and minimum for dry weight per fruit (0.60 to 0.99g) indicates the presence of variability showing potential for further improvement. Wide range of variation in the characters provide abundant scope for selecting desired types for further breeding programme.

In the present study, high phenotypic coefficient of variation (PCV) and genotypic coefficient of variations (GCV) were observed for ascorbic acid content (30.48% and 30.22%), reducing sugar (27.58 and 27.35), fruit yield per plant (25.26% and 22.43%), number of primary branches (24.95 and 24.34%), number of seeds per fruit (24.29% and 23.16%), chlorophyll content (23.63% and 23.23%) and capsaicin content (23.21% and 22.27%) respectively. The characters with high PCV and GCV shows that these characters indicates higher magnitude of variability and thus, offers a good scope for selection. Manju and Sreelathakumary (2002) [16] also observed high PCV and GCV for characters yield per plant and seeds per fruit. Jyothi *et al*. (2011)[11] also reported high PCV and GCV for character like number of seeds per fruit. Hazarika *et al*. (2013) [8] also reported higher PCV and GCV for number of seeds per fruit. In another study Amit *et al*. (2014) [2] also reported high PCV and GCV for number of branches per plant. Chakrabarty and Islam (2017)[5] also reported high GCV and PCV fruit yield per plant at green stage. High GCV and PCV of fruits yield per plant was also reported by Krishna *et al*. (2021) [14]. High PCV and GCV for capsaicin, ascorbic acid, chlorophyll and fruit yield per plant were observed by Kumar *et al*. (2020) [15]. Bhoomika *et al*. (2021) [3] also reported high GCV and PCV for number of primary branches per plant, fruit yield per plant and number of seeds per fruit. Low PCV and GCV were recorded for leaf length (8.47% and 7.03%), green fruit TSS (7.89% and 7.04%), days to first flowering (6.03% and 4.14%) and days to first fruit set (5.41% and 3.83%) respectively. The lowest estimates of PCV and GCV were recorded in case of days to first harvest (4.54% and 3.30%). These low PCV and GCV indicates limited variability for these characters. Manju and Sreelathakumary (2002) [16] also observed low PCV and GCV for days to first flowering. Low PCV and GCV in characters days to 50% flowering was also recorded by Amit *et al*. 2014 [2]. As per the data presented (Table 1) PCV was found slightly higher than the corresponding GCV for all the characters, indicating low environmental influence on the expression of these characters. Estimation of heritability indicated that the heritability for the attributes taken under investigation, ranged from 47.05 to 98.31 percent, showed medium to high. As the result explained in the investigation, high heritability was recorded for most of the characters ranged from 68.08 percent to 98.31 percent for characters like plant height (86.38%), number of primary branches (95.21%), leaf length (68.96%), leaf width (83.02%), fruit length (76.46%), pedicel length of fruit (84.15%), fruit weight (68.08%), no. of fruit per plant (81.60%), dry weight per fruit (77.78%), dry weight per 100 fruit (76.40%), number of seeds per fruit (90.90%), fruit yield per plant (78.82%), ascorbic acid content (98.31%), capsaicin content (92.27%), green fruit TSS (79.81%), total sugar (92.61%), reducing sugar (98.26%), non-reducing sugar (92.51%) and chlorophyll content (96.72%). Whereas, days to first flowering (47.05%), days to first fruit set (50.25%), days to first harvest (52.82%), fruit width (53.33%) and red fruit TSS (48.97%) observed moderate heritability (Table 1). Manju and Sreelathakumary (2002) [16] also reported similar findings with high heritability for plant height, fruits per plant, fruit length, pedicel length, fruit weight, seeds per fruit, yield per plant, capsaicin and ascorbic acid. Chattopadhyay *et al*. (2011) [6] registered high heritability for green fruit yield per plant, ascorbic acid content and number of fruits per plant. Hazarika *et al*. (2013)[8] also noticed high heritability for characters like plant height, number of primary branches, leaf length, leaf width, fruit length, fruit weight, no. of fruits per plant and number of seeds per fruit. Yatung *et al*. (2014) [24] reported high heritability range between 68.47% and 98.44% for all the characters. Meena *et al.* (2016) [17] also reported similar findings for high heritability for no. of fruits per plant, pedicel length, fruit length and plant height. Singh *et al.* (2017) [22] also reported high heritability for average fruit weight and number of fruit per plant. (Abrham, 2019) [1] also reported similar findings for high heritability for fruit length, plant height and no. of seeds per fruit. Krishna *et al.* (2021) [14] observed high heritability for characters plant height, no. of fruits per plant, fruit length, fruit weight, number of seeds per fruit, total soluble solids and fruits yield per plant. The characters with high heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and were less influenced by environmental condition and it indicates, the possibility and extend to which improvement in these characters is possible through selection.

In the present study the traits such as days to first flowering, days to first fruit set, days to first harvest, fruit width and red fruit TSS observed moderate heritability. Kole and Saha (2013) [12] suggested that such characters with moderate heritability were influenced moderately by environment. Krishnamurthy *et al.* (2013) [13] also registered moderate heritability for fruit width in earlier research. Pandiyaraj *et al.* (2017) [19] also reported moderate heritability for days to first flowering. Kumar *et al.* (2020) [15] also observed moderate heritability for days to first flowering which were similar with present findings.

In the present study the characters like ascorbic acid content, reducing sugar, number of primary branches, chlorophyll content, number of seeds per fruit, total sugar, fruit yield per plant, no. of fruit per plant, non-reducing sugar, capsaicin content, plant height, leaf width, dry weight per fruit, dry weight per 100 fruit, pedicel length of fruit, fruit length and fruit weight recorded high heritability coupled with high genetic advance as percent of mean (genetic gain). These characters with high estimate of genetic advance as percent of mean accompanied with high heritability are most likely due to predominance of additive gene effect and this shows that selection would be effective to improve these characters. In support of above findings, Manju and Sreelathakumary (2002) [16] reported high heritability coupled with high genetic advance as percent of mean for yield per plant, fruit weight, and fruit length. Chattopadhyay *et al.* (2011) [6] also observed high broad-sense heritability and genetic advance as percent of mean for green fruit yield per plant, ascorbic acid content and number of fruits per plant. Amit *et al.* (2014) [2] reported number of the fruits per plant, green fruit yield per plant, number of seeds per fruits and plant height exhibited high genetic advance as percent of mean along with high heritability. Yatung *et al.* (2014)[24] also reported high heritability with high genetic advance as percent of mean for plant height, number of seed per fruit, number of fruit per plant, ascorbic acid and green fruit yield per plant. Janaki *et al.* (2017)[9] also reported similar findings in earlier for high heritability along with high genetic advance as percent of mean for characters such as no. of fruits per plant, fruit length and no. of seeds per fruit. Nagaraju *et al.* (2018)[18] also observed high heritability coupled with high genetic advance as percent of mean for plant height, number of primary branches per plant, number of fruits per plant, fruit length, fruit weight, number of seeds per fruit, capsaicin content and ascorbic acid content. Vaishnavi *et al.* (2018) [23] also found similar findings where high heritability along with high genetic advance as percent of mean were observed for characters such fruit length, dry weight of 100 fruits, number of seeds per fruit and capsaicin content.

In the present study the characters like ascorbic acid content, fruit yield per plant, reducing sugar, chlorophyll content, capsaicin content, number of primary branches and number of seeds per fruit observed high GCV, PCV and high heritability coupled with high genetic advance as percent of mean suggesting the existence of higher magnitude of variability, less environmental influence and predominance of additive gene action of these characters and selection on the basis of these characters would be more fruitful for further improvement of this crop. Nagaraju *et al.* (2018) [18] also reported high GCV, PCV and high heritability coupled with high genetic advance as percent of mean were observed for characters like number of seeds per fruit, capsaicin content and ascorbic acid content.

Table 1: Estimates of mean, range and genetic parameters for yield and quality parameters in King chilli genotypes.

SL. No.	Characters	Mean±SE(m)	Range		Coefficient of variability (%)		Heritability %	Genetic advance	Genetic advance as % of mean (Genetic gain)
			Lowest	Highest	PCV	GCV			
1	Plant height(cm)	65.11±1.48	46.37	84.79	15.06	14.00	86.38	17.45	26.80
2	Days to first flowering	81.71±1.46	76.38	87.44	6.03	4.14	47.05	4.78	5.85
3	Days to first fruit set	89.36±1.39	83.72	95.94	5.41	3.83	50.25	5.00	5.60
4	Days to first harvest	117.20±1.49	111.66	125.22	4.54	3.30	52.82	5.79	4.94
5	Number of Primary branches	4.45±0.10	3.36	7.41	24.95	24.34	95.21	2.18	48.90
6	Leaf Length(cm)	10.85±0.21	9.52	12.05	8.47	7.03	68.96	1.31	12.03
7	Leaf width(cm)	6.02±0.15	4.83	7.60	15.30	13.94	83.02	1.58	26.18
8	Fruit length(cm)	6.42±0.18	5.35	8.45	14.26	12.46	76.46	1.44	22.44
9	Fruit width(cm)	2.85±0.11	2.41	3.69	13.59	9.93	53.33	0.43	14.94
10	Pedicel Length of fruit(cm)	2.87±0.07	2.37	3.59	14.90	13.66	84.15	0.74	25.81
11	Fruit weight (g)	6.18±0.22	5.353	8.115	15.73	12.98	68.08	1.36	22.06
12	No. of fruit /plant	36.28±1.30	27.38	53.28	20.40	18.43	81.60	12.44	34.30
13	Dry Weight / fruit(g)	0.79±0.03	0.60	0.99	16.94	14.83	77.78	0.21	26.72
14	Dry Weight /100fruit(g)	78.66±2.64	60.10	98.94	16.94	14.81	76.40	20.98	26.67
15	Number of seeds per fruit	37.72±1.13	26.22	59.89	24.29	23.16	90.90	17.16	45.48
16	Fruit Yield per plant(g)	224.95±10.68	163.64	300.36	25.26	22.43	78.82	92.27	41.02
17	Ascorbic Acid content (mg/100g)	181.74±2.94	114.07	309.00	30.48	30.22	98.31	112.18	61.72
18	Capsaicin content%	1.96±0.05	1.29	2.72	23.21	22.27	92.27	0.86	44.01
19	Green fruit TSS (°Brix)	4.09±0.06	3.61	4.56	7.89	7.04	79.81	0.53	12.94
20	Red fruit TSS (°Brix)	6.93±0.11	6.55	7.50	5.50	3.83	48.97	0.38	5.50
21	Total sugar (mg/g)	12.60±0.28	8.19	15.63	19.85	19.10	92.61	4.77	37.86
22	Reducing sugar (mg/g)	4.43±0.07	2.55	6.56	27.58	27.35	98.26	2.48	55.85

23	Non- reducing (mg/g)	7.76±0.15	5.34	9.21	17.18	16.52	92.51	2.54	32.74
24	Chlorophyll content (mg/g)	1.81±0.03	1.21	2.52	23.63	23.23	96.72	0.85	47.05

Conclusion

The present study can be concluded that significant differences were observed among the genotypes for all the characters indicating the presence of sufficient genetic variability in the genotypes. The estimate of PCV were higher than the corresponding GCV for all the characters, although range of difference was narrow between PCV and GCV indicating low environmental influence on the expression of these characters. High GCV and PCV were observed for ascorbic acid content, fruit yield per plant, reducing sugar, chlorophyll content, capsaicin content, number of seeds per fruit and number of primary branches indicating a higher magnitude of variability in these characters and thus provide a better scope for improvement through selection. High heritability coupled with high genetic advance as percent of mean (genetic gain) were observed for ascorbic acid content, reducing sugar, number of primary branches, chlorophyll content, number of seeds per fruit, total sugar, fruit yield per plant, no. of fruit per plant, non-reducing sugar, capsaicin content, plant height, leaf width, dry weight per fruit, dry weight per 100 fruit, pedicel length of fruit, fruit length and fruit weight indicating predominance of additive gene action for these characters and this shows that selection would be effective to improve these characters. The selection on the basis of characters like ascorbic acid content, fruit yield per plant, reducing sugar, chlorophyll content, capsaicin content, number of primary branches and number of seeds per fruit with high PCV, GCV and high heritability coupled with high genetic advance as percent of mean (genetic gain) would be more effective and reliable for the improvement of this crop.

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