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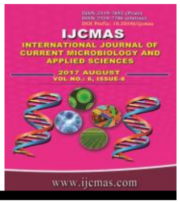

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Genetic Diversity Assessment for Growth and Yield Traits in Cauliflower

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ABSTRACT

An investigation entitled "Genetic diversity assessment for growth and yield traits in Cauliflower (*Brassica oleracea var. botrytis*L.)" was conducted at Horticulture Complex, Department of Horticulture, College of Agriculture JNKVV, Jabalpur (M.P.) during the year 2015-16. The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for total plant weight (572.27-1220.87), curd weight (238.58-508.83), net curd weight (169.80-392.97), marketable curd yield (76.86-169.13), curd yield per hectare (79.21-172.45), curd circumference (9.17-40.40), days to 50% curd formation (25.00-47.33), days to harvest (40.67-59.33) and curd length (3.40-14.88). The phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however the differences was narrow which implied their relative resistance to environmental variation. The phenotypic coefficient of variations was highest for characters viz., curd length, curd circumference, core length, curd width, net curd weight, curd yield per hectare, marketable curd yield, curd yield per plot, total plant weight and curd weight. However, low PCV was exhibited by traits viz., for stalk length at 45 DAT, days to harvest, stalk length at 30 DAT and days to 50% curd formation. High genotypic coefficient of variation was noted for curd length, curd circumference, core length, curd width, net curd weight, curd yield per hectare, marketable curd yield, curd yield per plot, curd weight and total plant weight. While it was observed low in the characters i.e. stalk length at 45 DAT, stalk length at 30 DAT, days to harvest, number of leaves per plant at 15 DAT. The value of heritability (broad sense) was recorded very high for curd length, days to harvest, days to curd initiation, curd circumference, days to 50% curd formation, number of leaves per plant at 45 DAT, curd yield per hectare, marketable curd yield, curd yield per plot. Core length, curd weight, total plant weight, number of leaves per plant at 30 DAT, curd width and net curd weight. Genetic advance as percentage of mean ranged between 13.84% for stalk length at 45 DAT to 103.65% for curd length. The highest estimate of genetic advance as percentage of mean was recorded for curd length, curd circumference, core length, curd width, curd yield per hectare, curd yield per plot, marketable curd yield, net curd weight, curd weight and total plant weight. Stalk length at 45 DAT showed significant and negative correlation with days to curd initiation, days to 50% curd formation and number of leaves per plant at 45 DAT. Number of leaves per plant at 45 DAT showed significant and positive correlation with curd circumference, curd width, days to curd initiation, total plant weight, curd weight, curd length, days to 50% curd formation, core length and days to harvest. Net curd weight showed significant and positive correlation with curd weight.

Keywords

Genetic variability, Correlation analysis, Heritability, Genetic advances.

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Introduction

Cauliflower (*Brassica oleracea var. botrytis* L.) commonly known as "phoolgobhi" is the most popular vegetable introduced in India in 1822 by Dr. Jemson, who was the In-charge of Botanical Garden, Saharanpur, Uttar Pradesh (Nath *et al.*, 1994). The original introduction were Cornish type which originated in England, followed by temperate types, originated in Germany and Netherland in 18th Century (Swarup and Chatterjee, 1972). It is grown in all parts of the country from 11ºN to 35ºN latitude (Nath *et al.*, 1994). India is the second largest producer of cauliflower in the world**.** Area under cauliflower in India is 433.9 thousand hectare with production of 8573.3 thousand metric tonnes and productivity is 19.8 tonnes/ha. Cauliflower occupies 4.12% area out of a total land under vegetable. It is grown in 25.1 thousand hectare area in Madhya Pradesh with a total annual production of 703.8 thousand metric tonnes and with productivity 28.1 metric tonnes/hectare (National Horticulture Board, 2014). The important cauliflower growing states are West Bengal, Bihar, Haryana, Gujarat, Assam, Uttar Pradesh, Rajasthan, Karnataka and Tamil Nadu. It is also commonly grown in Northern Himalayas, Nilgiri hills, hills of Uttarakhand and J&K. The edible part of cauliflower botanically known as prefloral fleshy apical meristem or flowering primordial or immature inflorescence and is also called as curd (Sidki, 1962). Cauliflower contains vitamins to the tune of 70 IU vitamin A, 50 mg/100 g vitamin B and 75 mg/100 g vitamin C and among minerals, 0.73 per cent Ca, 0.38 per cent P, 2.71 per cent K, 205 ppm Iron and 15 ppm Cu. Besides vitamins and minerals, cauliflower also contains 2.47 per cent protein, 4.8 per cent total carbohydrate, 0.2 per cent fat and 91.7 per cent water (Brown and Hutchison, 1989).According to Boswell (1949) cauliflower is originated in the Iceland of Cyprus from where it moved to other areas like Syria, Turkey, Egypt, Spain and North Western Europe. In cultivation for a little more than 2500 years back it appeared in about 15 centuries later than cabbage Boswell (1949). According to Allard (1960) cabbage, cauliflower, broccoli, Brussels sprout and other varieties of oleracea have been reported morphologically on the basis of few gene differences. The varieties of *B. oleracea* have same chromosome number (n=9). *Brassica oleracea* is a triple tetrasomic with the genomic formula ABBCCDEEF with 6 basic genomes and showing some secondary pairing (Gerhard, 1960).

Studies on genetic variability with the help of suitable biometrical tools such as coefficient of variability, heritability, and genetic advance become indispensable in breeding programmes for tangible results of desired values. To give a better insight of ancillary characters under selection, correlation and path coefficient analysis are the tools, which are being effectively used for determining the rate of various yield components in different crops, leading to the selection of superior genotypes.

Materials and Methods

The present investigation on **"**Genetic diversity assessment for growth and yield traits in Cauliflower" was conducted at Horticulture complex, Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during the year 2016-17. The experimental material includes 30 genotypes with two checks of the cauliflower collected from different states of India. The experiment was laid out in Randomized Complete Block Design with three replications and each replication consisted of thirty two genotypes. All the genotypes were randomized separately in each replication.

Estimation of mean, components of variance, phenotypic, genotypic and environmental coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean:

The mean of different characters were calculated by conventional method:-

$$\text{Mean} = \frac{\Sigma x_i}{n}$$

Where,

Σx_i = The sum of all the observation for ith character.
n = Number of observations.

Range was recorded by observing the lowest and the highest mean values for each character.

$\sigma^2 g_i = M_I - E_i$
$\sigma^2 e_i = E_i$
$\sigma^2 p_i = \sigma^2 g_i + \sigma^2 e_i$

Where,

$\sigma^2 g_i$ = Genotypic variance for i^{th} character.
$\sigma^2 e_i$ = Environmental variance for i^{th} character.
$\sigma^2 p_i$ = Phenotypic variance for i^{th} character.

Phenotypic and genotypic coefficient of variation (expressed in %) were calculated by using the formula given by Burton (1952).

Genotypic coefficient of variation (GCV) was calculated as below:

$$\text{GCV\%} = \frac{\sqrt{\sigma^2 g_i}}{\overline{X}_i} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV\%} = \frac{\sqrt{\sigma^2 p_i}}{\overline{X}_i} \times 100$$

Where,

X_i = General mean of the i^{th} character under consideration.

$\sigma^2 g_i$ and $\sigma^2 p_i$ = Genotypic and phenotypic standard deviation of the i^{th} character respectively.

Heritability and genetic advance

Heritability (broad sence) which is ratio of genotypic variance to the total phenotypic variance is symbolized as h2 (BS) and expressed in percentage. Estimation of heritability was done as per the formula given by Hanson *et al.*, (1956).

$$h^2(BS) = \frac{\sigma^2 g_i}{\sigma^2 p_i} \times 100$$

OR

$$= \frac{\text{Genotypic variance of the ith character}}{\text{Phenotypic variance of the ith character}}$$

Genetic advance

The estimation of genotypic and phenotypic variance and heritability were used to determine the expected genetic advance as suggested by Johnson *et al.*, (1955) and expressed as –

Genetic advance (GA) = $k \times \sigma^2 p \times h^2$

Where,

k = constant, 2.06 at 5% selection intensity
$\sigma^2 p$ = phenotypic standard deviation
h^2 = heritability in broad sense

Genetic advance as a percentage of mean was calculated as per formula given below:

$$\text{GA as percentage of mean} = \frac{\text{GA}}{\bar{x}} \times 100$$

Where,

GA = Genetic advance

$\bar{x}$ = mean

Correlation coefficients

Correlation coefficients were calculated in all possible combinations taking all the characters into consideration at genotypic, phenotypic and environmental levels by using the formula as proposed by Miller *et al.,* (1958).

$$r = \frac{\Sigma xy - \frac{\Sigma x \times \Sigma y}{n}}{\sqrt{\left(\Sigma x^2 - \frac{(\Sigma x)^2}{n}\right)\left(\Sigma y^2 - \frac{(\Sigma y)^2}{n}\right)}}$$

Where,

r = Correlation coefficient
n = Number of treatments
X and Y = Character under study

Results and Discussion

Genetic variability

The mean performance of the genotypes (Table 2) revealed a wide range of variability for all the traits. The variation was highest for total plant weight (572.27-1220.87), curd weight (238.58-508.83), net curd weight (169.80-392.97), marketable curd yield (76.86-169.13), curd yield per hectare (79.21-172.45), curd circumference (9.17-40.40), days to 50% curd formation (25.00-47.33), days to harvest (40.67-59.33) and curd length (3.40-14.88). The findings were similar to as reported by Singh *et al.,* (2006) found the wide range of variability for curd weight and net curd weight, Kumar *et al.,* (2010) reported the highest variation for days to 50%curd formation and net curd weight, Kumar *et al.,* (2011) found the wide range of variability for days to 50% curd formation, net curd weight, marketable curd yield. Chittora and Singh (2015) reported highest variation for total plant weight and net curd weight. Kumari *et al.,* (2016) reported highest variation for total plant weight and marketable curd yield.

Coefficient of variation

In the present findings phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however the differences was narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The findings of Singh *et al.,* (2006) and Kumar *et al.,* (2011) were similar to that of the present findings.

Phenotypic coefficient of variations

The phenotypic coefficient of variation ranged from 11.32% for stalk length at 45 DAT to 51.42% for curd length. The phenotypic coefficient of variations was highest for characters viz., curd length, curd circumference, core length, curd width, net curd weight, curd yield per hectare, marketable curd yield, curd yield per plot, total plant weight and curd weight. The findings are in close harmony with the result of Thakur and Thakur (2002) and Sharma *et al.,* (2003) for head yield per plot, Singh *et al.,* (2006) for curd length, Singh *et al.,* (2011) for total plant weight, Singh *et al.,* (2013) for curd weight.

However, low PCV was exhibited by traits viz., for stalk length at 45 DAT, days to harvest, stalk length at 30 DAT and days to 50% curd formation. The findings of Kumar *et al.*, (2010) and Singh *et al.*, (2011) for days to 50% curd formation were similar to that of the present findings. Stalk length at 15 DAT, days to curd initiation, number of leaves per plant at 45 DAT, number of leaves at 30 DAT, number of leaves at 15 DAT exhibited moderate phenotypic coefficient of variation. The findings of Singh *et al.*, (2011) for total plant weight and number of non-wrapper leaves, Singh *et al.*, (2013) for days to curd initiation were similar to that of the present findings.

Genotypic coefficient of variation (GCV)

The genotypic coefficient of variation varied from 8.72% for stalk length at 45 DAT to 50.84% for curd length. High genotypic coefficient of variation was noted for curd length, curd circumference, core length, curd width, net curd weight, curd yield per hectare, marketable curd yield, curd yield per plot, curd weight and total plant weight. The findings are in close harmony with Kumar and korla (2001), Sharma *et al.*, (2003), Singh *et al.*, (2013), Kumari *et al.*, (2016) were similar to that of the present findings.

While it was observed low in the characters i.e. stalk length at 45 DAT, stalk length at 30 DAT, days to harvest, number of leaves per plant at 15 DAT. The findings of Meena *et al.*, (2010) for days to harvest, Singh *et al.*, (2011) and Singh *et al.*, (2013) for leaves per plant were similar to that of the present findings which indicated that there is limited scope for improvement. Rest of the characters viz., days to curd initiation, stalk length at 15 DAT, number of leaves per plant at 45 DAT, number of leaves at 30 DAT, days to 50% curd formation, were showed moderate genotypic coefficient of variation. The findings of Singh *et al.*, (2013) for days to curd initiation, Kumari *et al.*, (2016) were similar to that of the present findings.

Heritability (Broad sense)

The heritability (BS) was computed for each of the characters by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors. The estimates of heritability (BS) for all the characters have been discussed in table 2. It was partitioned as very high (above 90%), high (70 to 90%), medium (50-70%) and low (less than 50%).The value of heritability (broad sense) was recorded very high for curd length, days to harvest, days to curd initiation, curd circumference, days to 50% curd formation, number of leaves per plant at 45 DAT, curd yield per hectare, marketable curd yield, curd yield per plot. core length, curd weight, total plant weight, number of leaves per plant at 30 DAT, curd width and net curd weight. The results were in close proximate to that of the Kumar and Korla (2001) for number of non-wrapping leaves per plant, Sharma *et al.*, (2003), Meena *et al.*, (2010) and Meena *et al.*, (2011) for yield and head width, Soni *et al.*, (2013) for days to harvest, core length, head weight and curd yield per hectare. It reflected that the phenotypes were the true representative of their genotype and selection based on phenotypic performance would be reliable. However, it was recorded to be high for stalk length at 15 DAT, number of leaves per plant at 15 DAT. Moderate heritability was recorded for stalk length at 30 DAT and stalk length at 45 DAT. The findings of Singh *et al.*, (2006), Soni *et al.*, (2013) for stalk length for 45 DAT were similar to that of the present findings.

Genetic advance (as % of mean)

Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations.

Therefore, to attain relative comparison of the characters in relation to environment genetic advance as percentage of mean was calculated to predict the genetic gain. The estimated values of genetic advance as percent of mean were classified as high (more than 45%), moderate (30-45%) and low (less than 30%).

Genetic advance as percentage of mean ranged between 13.84% for stalk length at 45 DAT to 103.65% for curd length. The highest estimate of genetic advance as percentage of mean was recorded for curd length, curd circumference, core length, curd width, curd yield per hectare, curd yield per plot, marketable curd yield, net curd weight, curd weight and total plant weight. The findings of Singh *et al.*, (2006) for curd width, Singh *et al.*, (2011) for core length, net curd weight, total plant weight, Singh *et al.*, (2013) for curd weight, curd yield per hectare, marketable curd yield, Soni *et al.*, (2013) for core length, curd yield per hectare, curd weight, Chura *et al.*, (2016) for curd yield per plot, net curd weight were similar to that of the present findings.

Days to curd initiation, number of leaves at 45 DAT, number of leaves at 30 DAT, stalk length at 15 DAT and days to 50% curd formation showed moderate value of genetic advance as percentage of mean. The findings of Kumar *et al.*, (2010) for days to 50% curd formation, Singh *et al.*, (2013) for days to curd initiation, Soni *et al.*, (2013) for stalk length, Chittora and Singh (2015) for days to curd initiation, Chura *et al.*, (2016) for number of leaves at 45 DAT and stalk length were similar to that of the present findings. Whereas, low estimates were observed for number of leaves at 15 DAT, days to harvest, stalk length at 30 DAT and stalk length at 45 DAT. The findings of Singh *et al.*, (2011), Singh *et al.*, (2013), Chittora and Singh (2015) for days to harvest and stalk length at 45 DAT were similar to that of the present findings.

High genetic variability coupled with high genetic advance as percentage of mean for traits like curd length, curd circumference, curd width, total plant weight, curd weight, net curd weight, curd yield per plot, marketable curd yield, curd yield per hectare and core length suggested that the preponderance of additive genes. It also indicated higher response for selection to high yields as these characters are governed by additive gene actions. The results were in consonance with Singh *et al.*, (2011).High heritability supplemented with moderate genetic advances as percentage of mean were manifested by days to curd initiation, days to 50% curd formation, number of leaves per plant at 45 DAT and 30 DAT and stalk length at 15 DAT which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about.

The results were in consonance with Chittora and Singh (2015).High heritability coupled with low genetic advance as percentage of mean was observed for days to harvest, number of leaves per plant at 15 DAT, stalk length at 30 DAT and 45 DAT. These findings were in agreement with Singh *et al.*, (2011). This revealed the predominance of non-additive gene action in the expression of these characters; hence direct selection would not be effective.

Correlation coefficient analysis

Correlation coefficient was worked out at phenotypic, genotypic and environmental levels for all possible combination of twelve yield and its attributing characters (Table 3). Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component characters on which selection can be made for genetic improvement of yield. Investigation regarding the presence of component and nature of association among themselves is essential and pre-requisite for improvement in yield. The results of phenotypic correlation coefficients have been discussed only as the genotypic and environmental correlation were mostly influenced by the environmental conditions, hence phenotypic correlation will give the correct idea about the association between two variables. The magnitude of genotypic correlation was higher than the phenotypic correlation for all the traits that indicated inherent association between various characters. The findings were in agreement to Rai *et al.*, (2003), Rai and Asati (2004), Meena *et al.*, (2012).

The component of variance was calculated as follows

S. No.	**Source**	**M.S.S.**	**Expected M.S.S.**
1.	Replications	-	-
2.	Genotypes	M i	$\sigma^2 ei + r.\sigma^2 gi$
3.	Error	E i	$\sigma^2 ei$

Table.1 Details of genotypes and checks used in the study

S. No.	**Treatment**	**Symbol**	**Source**	**S. No.**	**Treatment**	**Symbol**	**Source**
1.	JBOB-1	T1	IIVR,VARANASI	17.	JBOB-17	T17	IIVR,VARANASI
2.	JBOB-2	T2	IIVR,VARANASI	18.	JBOB-18	T18	IIVR,VARANASI
3.	JBOB-3	T3	IIVR,VARANASI	19.	JBOB-19	T19	IIVR,VARANASI
4.	JBOB-4	T4	IIVR,VARANASI	20.	JBOB-20	T20	IIVR,VARANASI
5.	JBOB-5	T5	IIVR,VARANASI	21.	JBOB-21	T21	IIVR,VARANASI
6.	JBOB-6	T6	IIVR,VARANASI	22.	JBOB-22	T22	IIVR,VARANASI
7.	JBOB-7	T7	IIVR,VARANASI	23.	JBOB-23	T23	IIVR,VARANASI
8.	JBOB-8	T8	IIVR,VARANASI	24.	JBOB-24	T24	IIVR,VARANASI
9.	JBOB-9	T9	IIVR,VARANASI	25.	JBOB- 25	T25	IIVR,VARANASI
10.	JBOB-10	T10	IIVR,VARANASI	26.	JBOB-26	T26	IIVR,VARANASI
11.	JBOB-11	T11	IIVR,VARANASI	27.	JBOB-27	T27	IIVR,VARANASI
12.	JBOB-12	T12	IIVR,VARANASI	28.	JBOB-28	T28	IIVR,VARANASI
13.	JBOB-13	T13	IIVR,VARANASI	29.	JBOB-29	T29	IIVR,VARANASI
14.	JBOB-14	T14	IIVR,VARANASI	30.	JBOB-30	T30	IIVR,VARANASI
15.	JBOB-15	T15	IIVR,VARANASI	31.	Pusa sharad (C)	T31	IIVR,VARANASI
16.	JBOB-16	T16	IIVR,VARANASI	32.	PH-2 (C)	T32	IIVR,VARANASI

Table.2 Estimates of genetic parameters of variations for various characters

Characters		**Grand Mean**	**Range**		**Coefficient of variations**		**Heritability % (BS)**	**Genetic Advance**	**GA as % of mean**
			Min.	**Max.**	**Phenotypic**	**Genotypic**			
Stalk length (cm) at	**15 DAT**	0.81	0.53	1.33	22.40	19.64	76.91	0.29	35.69
	30 DAT	1.23	0.97	1.60	12.18	10.09	68.61	0.21	17.35
	45 DAT	1.38	1.10	1.77	11.32	8.72	59.25	0.19	13.84
Number of leaves per plant at	**15 DAT**	12.08	8.27	16.33	17.44	15.15	75.49	3.28	27.12
	30 DAT	16.24	10.80	21.47	19.04	18.32	92.55	5.90	36.32
	45 DAT	17.30	11.87	22.47	19.08	18.64	95.42	6.49	37.50
Days to curd initiation		27.64	19.33	37.33	20.44	20.13	97.02	11.29	40.86
Days to 50% curd formation		37.73	25.00	47.33	15.58	15.23	95.53	11.57	30.66
Days to harvest		47.18	40.67	59.33	12.09	11.95	97.72	11.48	24.33
Curd length (cm)		8.20	3.40	14.88	51.42	50.84	97.76	8.50	103.65
Curd circumference (cm)		24.68	9.17	40.40	41.09	40.39	96.64	20.19	81.81
Curd width (cm)		10.35	5.23	16.30	28.69	27.51	91.94	5.62	54.34
Core length (cm)		7.18	4.03	11.40	34.80	33.85	94.63	4.87	67.88
Total plant weight (kg)		915.35	572.27	1220.87	24.77	24.00	93.92	438.66	47.92
Curd weight (g)		381.39	238.58	508.83	24.75	24.01	94.13	183.05	47.99
Net curd weight (g)		280.00	169.80	392.97	26.25	24.95	90.32	136.77	48.85
Curd yield per plot (kg)		7.63	4.752	10.345	24.95	24.35	95.25	3.74	49.01
Marketable curd yield (q/ha)		124.17	79.21	172.45	24.95	24.35	95.25	62.34	48.96
Curd Yield per hectare (q/ha)		127.32	76.86	169.13	24.99	24.39	95.26	60.88	49.03

Table.3 Estimates of genotypic and phenotypic correlation coefficients among curd yield and its attributing traits

Characters		**No. of leaves / plant at 45 DAT**	**Days to curd initiation**	**Days to 50% curd formation**	**Days to harvest**	**Curd length (cm)**	**Curd circumference (cm)**	**Curd width (cm)**	**Core length (cm)**	**Total plant weight (kg)**	**Net curd weight (g)**	**Curd weight (g)**
Stalk length (cm) 45 DAT	G	-0.460	-0.327	-0.333	-0.024	-0.108	-0.157	-0.105	-0.124	-0.168	-0.082	-0.167
	P	-0.349**	-0.226*	-0.255*	-0.025	-0.101	-0.116	-0.057	-0.104	-0.106	-0.040	-0.108
No. of leaves / plant at 45 DAT	G		0.705	0.655	0.484	0.688	0.795	0.733	0.639	0.708	0.042	0.708
	P		0.676**	0.631**	0.469**	0.666**	0.770**	0.691**	0.613**	0.670**	0.037	0.670**
Days to curd initiation	G			0.916	0.764	0.835	0.857	0.767	0.883	0.902	0.385	0.903
	P			0.876**	0.747**	0.814**	0.830**	0.733**	0.847**	0.872**	0.372**	0.872**
Days to 50% curd formation	G				0.853	0.825	0.864	0.741	0.842	0.846	0.340	0.846
	P				0.825**	0.795**	0.830**	0.695**	0.797**	0.793**	0.306**	0.794**
Days to harvest	G					0.743	0.814	0.692	0.722	0.757	0.239	0.757
	P					0.725**	0.793**	0.664**	0.702**	0.727**	0.226*	0.726**
Curd length (cm)	G						0.745	0.644	0.894	0.835	0.379	0.835
	P						0.730**	0.599**	0.858**	0.794**	0.348**	0.795**
Curd circumference (cm)	G							0.921	0.778	0.864	0.133	0.863
	P							0.878**	0.746**	0.822**	0.123	0.822**
Curd width (cm)	G								0.738	0.788	0.133	0.787
	P								0.694**	0.746**	0.137	0.745**
Core length (cm)	G									0.911	0.489	0.912
	P									0.866**	0.459**	0.866**
Total plant weight (kg)	G										0.410	0.978
	P										0.454**	0.999**
Net curd weight (g)	G											0.411
	P											0.454**

Significant at 5% level = *; Significant at 1% level = **

Stalk length at 45 DAT

Stalk length at 45 DAT showed significant and negative correlation with days to curd initiation, days to 50% curd formation and number of leaves per plant at 45 DAT. These results are in agreement with the finding of Rai *et al.*, (2003).

Number of leaves per plant at 45 DAT

Number of leaves per plant at 45 DAT showed significant and positive correlation with curd circumference, curd width, days to curd initiation, total plant weight, curd weight, curd length, days to 50% curd formation, core length and days to harvest. These results are in agreement with the finding of Rai *et al.*, (2003).

Days to curd initiation

Days to curd initiation expressed significant and positive correlation with days to 50% curd formation, total plant weight, curd weight, core length, curd circumference, curd length, days to harvest, curd width and net curd weight.

Days to 50% curd formation

Days to 50% curd formation expressed significant and positive correlation with curd circumference, days to harvest, core length, curd length, curd weight, total plant weight, curd width and net curd weight. These results are in close harmony with the finding of Sheemar *et al.*, (2012) for curd circumference and net curd weight.

Days to harvest

Days to harvest showed significant and positive correlation with curd circumference, total plant weight, curd weight, curd length, core length, curd width and net curd weight.

Curd length

Association of Curd length was exhibited significant and positive with core length, curd weight, total plant weight, curd circumference, curd width and net curd weight.

These findings corroborated the earlier findings of Antonova (2009), Adzic *et al.*, (2012) for head weight.

Curd circumference

The correlation coefficient of curd circumference was found to be positive and significant with curd width, total plant weight, curd weight and core length.

These results are in agreement with the findings of Antonova (2009) for head weight, Kibar *et al.*, (2014).

Curd width

Curd width showed significant and positive correlation with total plant weight, curd weight and core length.

These results are in close harmony with the findings of Antonova (2009), Adzic *et al.*, (2012) for head weight, Kibar *et al.*, (2014) for total plant weight and curd weight.

Core length

Correlation coefficient of core length was found to be positive and significant with total plant weight, curd weight and net curd weight.

Total plant weight

Total plant weight expressed significant and positive correlation with curd weight and net curd weight. The results corroborated the findings of Rai and Asati (2004), Meena *et al.*, (2010) for curd weight and net curd weight.

Net curd weight

Net curd weight showed significant and positive correlation with curd weight. These results are in similar with the findings of Kumar *et al.*, (2005), Singh *et al.*, (2006), Singh *et al.*, (2013) for curd weight.

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