



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2017; 6(3): 734-738
Received: 23-03-2017
Accepted: 24-04-2017

Priyanka Verma
Department of Vegetable
Science, Govind Ballabh Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

SK Maurya
Department of Vegetable
Science, Govind Ballabh Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

Ankit Panchbhैया
Department of Vegetable
Science, Govind Ballabh Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

Shivani Dhyani
Department of Vegetable Science
Govind Ballabh Pant University
of Agriculture and Technology,
Pantnagar, Uttarakhand, India

Correspondence
Priyanka Verma
Department of Vegetable
Science, Govind Ballabh Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

Studies on variability, heritability and genetic advance for yield and yield contributing characters in Pointed Gourd (*Trichosanthes dioica* Roxb.)

Priyanka Verma, SK Maurya, Ankit Panchbhैया and Shivani Dhyani

Abstract

In order to determine the magnitude of variability, 35 genotypes of pointed gourd have been evaluated at Vegetable research centre, Pantnagar during rainy season of 2014. Through analysis of variance, a high significant difference was found for almost all characters indicating a greater opportunity of exploit variability. PPG-26 has obtained highest mean for fruit length (10.39) and PPG-2 for fruit diameter (4.35) while PPG-31 genotype was resulted as the earliest among all. High GCV along with high PCV was found for the characters like Number of seeds per fruit (33.22 and 33.45), Fruit yield (q/ha) (31.38 and 33.09), Node number to first female flower (29.39 and 30.26) and Number of fruits per plant (29.29 and 29.70). Whereas, high heritability coupled with greater genetic advance was observed for number of fruit per plant and fruit yield per hectare which indicates that these characters are govern with additive gene effect with minimum environment effect so we can go for direct selection of pointed gourd genotypes for further improvement.

Keywords: Genetic variability, heritability, GCV, PCV, pointed gourd

1. Introduction

The pointed gourd (*Trichosanthes dioica* Roxb.) $2n=2x=22$, also known as king of gourds, is a highly nutritious cucurbitaceous crop with dioecious and perennial growth habit. It is a vine plant of cucurbitaceae family, grown on a trellis system having heart shapes leaves. A wide range of variability is found as per fruit size varies from oval and round to long. Its rich diversity at Assam-Bengal region makes it a primary centre of origin (Singh *et al.*, 1992) [33] and its availability is more during summer and rainy seasons in Indian markets (Barman, 2013) [4]. Hot to moderately warm and humid climate are highly conducive for its bulk production but it is highly susceptible to frost and extreme cold condition. It is a rich source of vitamin A, vitamin C and trace amount of micro nutrient like magnesium, potassium, sulphur and copper, and its fruits have been described to possess anti helminthic, antipyretic, diuretic, expectorant and antirheumatic effects (Sharma and Pant, 1988a) [32] and also used to cure many blood and skin diseases. According to Chandrasekar *et al.* (1988) [9], it has quite medicinal properties as it is rich in protein and vitamin A and it decides its role in circulatory system especially in lowering total cholesterol and blood sugar.

Genetic variability is defined as "The occurrence of a high degree of variation differences among individuals due to differences in their genetic composition and of the environment in which they are raised" (Falconer and Mackay 1996) [15]. The basic requirement for genetic improvement of a crop is to utilize the available or created genetic variability. Yield of pointed gourd fruits is a polygenic character and influenced by a number of biotic and abiotic characters, so it is worthwhile for opting direct selection, as variability of observed characters is the sum total of heritable and environment factors. So, it is desirable to use divider walls between heritable and non heritable components with the help of certain genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (H₂), genetic advance (GA), and genetic advance expressed as percent mean (GAM%). Keeping this current issue in mind, the present investigation was undertaken to estimate genetic variance, heritability and genetic advance of 35 pointed gourd genotypes.

2. Material and methodology:

By taking 35 genotypes of pointed gourd along with two checks (Kashi Alankar and Rajendra Parwal-1) (Table.1), the present investigation was carried out at Vegetable research centre of G.B.P.U.A.T during summer-rainy season of 2014. The one year old vine cuttings (50-60 cm long) were collected from different places of U.P. and Bihar during the month of October and

planted in poly bags for rooting under polyhouse during the winter months. After winter, transplants were transplanted on 18th march 2014. The experiment was laid out in augmented block design with the plot size of 2.5 sq m per germplasm and row to plant distance was maintained at a spacing of 2.5 x 1 m. Twelve yield and its contributing characters were scored on the individual genotypes for the following recorded traits viz, Node number to first female flower, Days to first female flower anthesis, Days to first fruit harvesting, Inter-nodal length (cm), Vine length (m), Fruit length (cm), Fruit diameter (cm), Fruit weight (g), Number of fruits per plant, Fruit yield (q/ha), Number of seeds per fruit and 100 seed weight (g). The analysis of variance for augmented design was done by using the method given by Panse and Sukhatme (1967) [29]. Methods given by Burton and De Vane (1953) [7] were used to determine the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Whereas heritability (broad sense) and genetic advance as per cent of mean were computed as per Allard (1960) [2] and Johnson *et al.* (1955) [20], respectively.

3. Result and discussion

Analysis of variance for different characters showed a highly significant difference for the traits like days to first female flower, node number of first female flower, fruit yield per hectare, inter-nodal length and number of seed per fruit among check varieties as represented by mean sum of square of checks while days to first fruit harvest, mean fruit weight, vine length, number of fruits per plant and 100 seed weight showed significant value. In support of this Basavarajeshwari *et al.* (2014) [5] reported, the variance due to genotypes was highly significant ($p=0.01$) for vine length (cm), days to first female flower, nodes upto first female flower and number of days to first harvest in cucumber. According to Pathak *et al.* (2014) [27] mean sum of squares due to genotypes and error was found maximum for fruit number followed by fruit weight. The significant difference obtained in current research indicates the presence of huge amount of variability among various traits as presented in Table 2.

Table 1: List of pointed gourd genotypes

Sl. No.	Genotypes	Sl. No.	Genotypes
1.	PPG-1	20.	PPG-21
2.	PPG-2	21.	PPG-22
3.	PPG-3	22.	PPG-23
4.	PPG-4	23.	PPG-24
5.	PPG-5	24.	PPG-25
6.	PPG-6	25.	PPG-26
7.	PPG-7	26.	PPG-27
8.	PPG-8	27.	PPG-28
9.	PPG-9	28.	PPG-29
10.	PPG-10	29.	PPG-30
11.	PPG-12	30.	PPG-31
12.	PPG-13	31.	PPG-32
13.	PPG-14	32.	PPG-33
14.	PPG-15	33.	PPG-34
15.	PPG-16	34.	PPG-35
16.	PPG-17	35.	PPG-36
17.	PPG-18	36.	Kashi Alankar
18.	PPG-19	37.	Rajendra Parwal-1
19.	PPG-20		

Table 2: Analysis of variance (ANOVA) for different characters of pointed gourd genotypes (summer - rainy season, 2014)

Sl. No.	Characters	Mean Sum Of Square			
		Total (9)	Block (4)	Check (1)	Error (4)
1	Days of first female flower anthesis	77.31	1.99	681.28**	1.64
2	Node number to first female flower	3.79	0.38	30.45**	0.54
3	Days of first fruit harvesting	17.62	7.75	105.75*	5.44
4	Fruit length (cm)	0.27	0.08	0.01	0.54
5	Fruit diameter (cm)	0.07	0.04	0.11	0.10
6	Fruit weight (g)	14.06	0.76	98.91*	6.16
7	Inter-nodal length (cm)	0.36	0.35*	1.62**	0.05
8	Vine length (m)	0.31	0.09	1.98*	0.12
9	Number of fruits per plant	28.9	7.36	143.49*	21.93
10	Fruit yield (q/ha)	495.83	38.71	3724.88**	145.69
11	100 seed weight (g)	0.715	0.71	2.81*	0.19
12	Number of seeds per fruit	6.09	3.36	39.08**	0.57

* Significant at 5% level of probability

** Significant at 1% level of probability

Degree of freedom are shown in parenthesis

From the observed mean of different genotypes for different trait a wide range of variation was extracted with maximum range for fruit yield per hectare (38.11-195.19) and fruit per plant (33.36-166.18) whereas minimum range was obtained

for traits like fruit diameter (2.41-4.35), vine length (4.23-9.03), and fruit length (5.41-10.39) as presented in Table.3. For days to first female flower anthesis and first fruit harvest, mean value ranged from 18.74 to 69.74 days and 37.17 to

82.12 days respectively and the genotypes obtaining maximum mean value for both the characters is PPG-31 indicating the earliest one. PPG-26 has obtained highest mean for fruit length (10.39) and PPG-2 for fruit diameter (4.35) but on opposite side PPG-16 has occupied the first position as a heavy yielder (195.19) as it received the maximum number of fruit per plant (166.18). For the traits having high range of variation, represents the broad range of variability for which we can go for direct selection while the traits or genotypes having low range of variation indicated narrow range of variability. The results are in agreement with Malek *et al.* (2007) [24], who has found maximum range for fruit per plant in pointed gourd i.e. 32-159 and for node to first female flower, number of seeds per fruit and weight of yield per plant by (Khan *et al.* 2009) [21]. Similarly, for yield/ha, fruit weight, days to first appearance of female flower by (Yadav *et al.* 2013) [38] in bitter gourd and for number of fruit per plant in Ridge gourd by (Yadav *et al.* 2014) [39].

Phenotypic coefficient of variation is the sum total of genotypic and environmental coefficient of variation which mean that morphological characters of any cultivars are under the influence of environment condition and its genetic characters. Any character showing high PCV is not effective for selection in breeding program. So, it is important that selection should be performed on the basis of its calculated genetic values. In the present study a narrow range of genetic differences between the PCV and GCV indicates that the traits are mostly governed by genetic factors with minimum environmental influence on the phenotypic expression of these traits. Maximum PCV were observed for number of seed per fruit (33.25) followed by fruit yield per hectare (33.09), node number to first female flower (30.26) and number of fruit per plant (29.70). However the lowest PCV were observed for days to first fruit harvesting (12.51). This indicates that these traits are least influence by the environment and are under the control of genotypes itself. Thus, selection of these traits on the basis of their phenotypic values becomes effective. The GCV ranged from 8.11 for fruit diameter to 33.22 for number of seeds per fruit. The GCV was maximum for number of seeds per fruit (33.22) followed by

fruit yield per hectare (33.18), node number to first female flower (29.49) and number of fruit per plant (29.29). The high GCV indicates the presence of exploitable genetic variability for these traits which help in proper selection process. Similar to this study high GCV was reported for fruit yield and number of fruit per plant by (Malek *et al.* 2007) [24], (Dubey *et al.* 2013) [14], for number of seed per fruit by (Kumar *et al.* 2013) [23], for number of fruits per plant, average fruit weight, fruit length by (Pathak *et al.* 2014) [27], (Devi and Mariappan, 2014) [12].

High GCV along with high PCV was found for the characters like Number of seeds per fruit, Fruit yield (q/ha), Node number to first female flower, 100 seed weight, fruit weight, vine length and Number of fruits per plant. Similar results were also reported by Arunkumar, *et al.* (2011) [3] in cucumber and Pandey *et al.* (2009) [28] in snap melon for yield per plant. Basavarajeshwari *et al.* (2014) [8] in cucumber found high GCV and PCV for vine length i.e. 26.14% and 26.84% respectively. According to Jatav *et al.* (2016) [18], high magnitude (>25%) of PCV along with GCV were observed for number of fruits per plant (45.74% and 43.61%), fruit yield per plant (42.46% and 40.33%), fruit yield per hectare (42.46% and 40.33%), average fruit weight (26.20% and 25.27%) and fruit length (26.04% and 23.40%), whereas days to first male flower (13.82% and 11.82%), fruit diameter (13.07% and 9.03%) and days to first harvest (11.79% and 9.975) showed low estimates of PCV and GCV.

According to Singh, (2001) [34] "Heritable variation present among genotypes is most important for permanent genetic improvement in any crop". Heritability in its predictive role along with GCV helps to indicate the reliability of the phenotypic value as a guide to breeding value (Dabholkar, 1992 and Falconer and Mackay, 1996) [10, 15]. It provides the most unswerving estimates of the amount of genetic advance to be expected through phenotypic selection Burton, (1952) [6]. Range of heritability in broad sense varied from 41.54% to 98.63% (Table.3). Maximum heritability was observed for average inter-nodal length (98.63%) followed by days to first female anthesis (98.61%), number of seed per fruit (98.60%), number of fruits per plant (97.30%), 100 seed weight.

Table 3: Estimation of coefficient of variation and other genetic parameter in pointed gourd (summer-rainy season 2014)

Sl. No.	Characters	General mean	Range	Coefficient of variation			Heritability (%)	Genetic advance	G.A. as % mean
				ECV%	GCV%	PCV%			
1	Days of first female flower anthesis	44.24	18.74-69.74	2.34	19.70	19.84	98.61	22.03	40.299
2	Node number to first female flower	10.69	3.29-18.09	6.79	29.49	30.26	94.96	6.44	59.21
3	Days of first fruit harvesting	59.63	37.14 -82.12	3.59	11.98	12.51	91.76	15.36	23.65
4	Fruit length (cm)	7.9	5.41-10.39	9.08	10.98	14.25	59.39	1.41	17.44
5	Fruit diameter (cm)	3.38	2.41-4.35	9.62	8.11	12.58	41.54	0.36	10.76
6	Fruit weight (g)	32.24	16.03-48.45	8.03	24.71	25.98	90.44	14.95	48.40
7	Average inter-nodal length (cm)	8.47	2.80-14.15	2.20	18.73	18.86	98.63	4.10	38.33
8	Vine length (m)	6.63	4.23-9.03	5.52	20.40	20.17	92.50	2.41	38.44
9	Number of fruits per plant	104.77	33.36-166.18	4.87	29.29	29.70	97.30	57.15	59.53
10	Fruit yield (q/ha)	121.65	38.11-195.19	10.48	31.38	33.09	89.95	70.56	61.31
11	100 seed weight (g)	8.37	2.49-14.26	4.44	20.95	21.42	95.69	4.13	42.22
12	Number of seeds per fruit	24.47	7.05-41.89	3.95	33.22	33.45	98.60	13.03	67.96

(95.69%), node number to first female flower (94.96%), vine length (92.50%), days to first fruit harvesting (91.76), mean fruit weight (90.44%), fruit yield per hectare (89.95%) whereas lowest for fruit length (59.39%) and fruit diameter (41.54%). These findings, in general with conformity with earlier reports of Malek *et al.* (2007) [24] for fruit yield and fruit number per plant, (Dubey *et al.* 2013) [14] for yield per plant, number of seed per fruit, average fruit weight, (Kumar *et al.* 2013) [23] for number of fruits per plant, average fruit

weight, fruit length. The genetic advance was found maximum for fruit yield per hectare (70.56) followed by number of fruits per plant (57.15), days to first female anthesis (22.03), days to first fruit harvesting (15.36), mean fruit weight (14.95) and number of seed per fruit (13.03). High genetic advance as percent of mean was recorded maximum for number of seed per fruit (67.96) followed by fruit yield per hectare (61.31), number of fruits per plant (59.23), node number to first female flower (59.21), mean

fruit weight (48.40), 100 seed weight (42.22), days to first female anthesis (40.29), vine length (38.44), average inter nodal length (38.33), days to first fruit harvesting (23.65), fruit length (17.44) and fruit diameter (10.76). Similar result was also obtained by Jat *et al.* (2014)^[19] in cucumber where maximum genetic gain in per cent was observed for total yield per vine (47.49). Similarly, Jatav *et al.* (2016)^[18] in bitter gourd found maximum genetic advance for fruit yield per plant (978.14) and fruit yield per hectare (81.51) and high genetic advance as percent of mean for number of fruit per plant (85.71%), weight of seed per fruit (82.01%) and fruit yield per plant (78.94%).

According to Panse (1957)^[30] “if heritability is chiefly due to additive gene effects, a high genetic advance may be expected”. In the present investigation high heritability coupled with greater genetic advance was observed for number of fruit per plant and fruit yield per hectare which indicates that these characters are governed with additive gene effect with minimum environment effect so we can go for direct selection for crop improvement. Similar results were also obtained by Dey *et al.* (2009)^[13], Islam *et al.* (2009)^[17], Sundaram *et al.* (2011)^[37], Naik *et al.* (2012)^[26], Chakraborty *et al.* (2013)^[8], Husna *et al.* (2013)^[16] and Singh *et al.* (2014)^[35] for yield per plant. Similarly by Khule *et al.* (2011)^[22], Devi and Mariappan (2013)^[12], Akter *et al.* (2013)^[1] and Pathak *et al.* (2014)^[27] for number of fruits per plant and Kumar *et al.* (2013)^[23] for average fruit weight. In the present research high heritability with low genetic advance was obtained for vine length, average inter nodal length, 100 seed weight and low heritability coupled with low genetic advance was observed for fruit length and fruit diameter which indicates that these characters have less response to selection as it is influenced by non additive gene effect and in case for further improvement, heterosis breeding is the only solution. This result is supported by Sanwal *et al.* (2007)^[31] for fruit length in sweet gourd, Sundaram *et al.* (2010)^[36] in water melon for fruit diameter, Munawar *et al.* (2015)^[25] for fruit length and fruit diameter in bitter gourd and Jatav *et al.* (2016)^[18] for 100 seed weight (94.6 and 6.71), inter nodal length (47.99 and 0.88) and fruit diameter (47.70 and 0.46),

4. Conclusion

From the above result, it is concluded that there is a wide range of variability present among the germplasm for almost all characters indicating that a wide scope for genetic improvement of crop. The narrow difference was retained between genotypic correlation coefficient and phenotypic correlation coefficient indicating a little effect of environment in the expression of characters. So, selection of these traits on the basis of their phenotypic values becomes effective. High heritability coupled with greater genetic advance was observed for number of fruit per plant and fruit yield per hectare which indicates that these characters are governed with additive gene effect with minimum environment effect so we can go for direct selection for crop improvement.

5. References

- Akter S, Rasul MG, Islam AKM, Hossain MM. Genetic variability, correlation and path coefficient analysis of yield and quality traits in pumpkin (*Cucurbita moschata* Duch ex Poir.). Bangladesh Journal of Plant Breeding and Genetics. 2013; 26(1):25-33.
- Allard RW. Principles of Plant Breeding. New York, John Wiley and Sons Inc, 1960, 485.
- Arunkumar KH, Ramanjinapa V, Ravishankar M. Path coefficient analysis in F2 population of cucumber (*Cucumis sativus* L.). Plant Archives. 2011(b); 11:471-474.
- Barman A. Instant Vegetable Science. 2nd ed. New Delhi, Shara Publications and Distributers. 2013, 63.
- Basavarajeshwari MR, Nagaraja KS, Sikanth LG, Mahamadtoofee H, Shivaningapp K. Genetic Variability, Heritability and Genetic Advance for Growth and Earliness Parameters in Cucumber (*Cucumis sativus* L.). Trends in Biosciences. 2014; 7(15):1968-1970.
- Burton GW. Quantitative inheritance in grasses. In: Proceedings of the 6th International Grassland Congress. State College, PA, USA: Pennsylvania State College. 1952, 277-283.
- Burton GW, Devane EW. Estimating heritability in fall fescue (*Festuca arundinacea*) form replicated clonal material. Agron. J. 1953; (4):78-81.
- Chakraborty L, Acharyya P, Raychaudhuri S. Diversity analysis of *Momordica charantia* L. accessions from eastern and north eastern India based on morphological, yield related traits and molecular marker. Proceedings of FVHH, Thailand. 2013.
- Chandrasekar B, Mukherjee B, Mukherjee SK. Blood sugar lowering effect of (*Trichosanthes dioca* Roxb.) in experimental rat models. International journal of crude drug research. 1988; 26:102-106.
- Dabholkar AR. Elements of Biometrical Genetics. New Delhi, India: Concept Publishing Company. 1992.
- Devi ND, Mariappan S. Genetic variability, heritability and genetic advance for yield and its components snake gourd (*Trichosanthes anguina* L.). African Journal of Agricultural Research. 2013; 8(28):3857-3859.
- Devi ND, Mariappan S. Studies on genetic diversity in snake gourd (*Trichosanthes anguina* L.). Universal journal of agricultural research. 2014; (1):1-5.
- Dey SS, Behera TK, Munshi AD, Bhatia R. Genetic variability, genetic advance and heritability in bittergourd (*Momordica charantia* L.). Indian Agriculturist. 2009; 53(1/2):7-12.
- Dubey RK, Singh V, Upadhyay G. Genetic variability and interrelationship among some ridge gourd (*Luffa acutangula* L.) accessions under foot hills of Arunachal Pradesh. Progressive Horticulture. 2013; 45(1):191-197.
- Falconer DS, Mackay TFC. Introduction to Quantitative Genetics. 4th ed. London, UK: Benjamin Cummings. 1996, 122-125.
- Husna A, Mahamud F, Islam MR, Mahamud MAA, Ratna M. Genetic Variability, Correlation and Path Coefficient Analysis in Bottle Gourd (*Lagenaria siceraria* L.). Advance in Biological Research. 2013; 5(6):323-327.
- Islam MR, Hossain MS, Bhuiyan MSR, Husna A, Syed MA. Genetic Variability and Path-Coefficient Analysis of bitter gourd (*Momordica charantia* L.). Int. J. Sust. Agri. 2009; 1:53.
- Jatav V, Singh DK. Genetic Variability, Heritability and Genetic advance for yield and related traits in bitter gourd (*Momordica Charantia* L.). J. Env. Bio-Sci. 2016; 30(2):421-426.
- Jat RK, Ameta KD, Choudhary RC. Genetic variability, heritability and genetic advance for yield and yield attributing traits in Valan kakri (*Cucumis sativus* var. *utilissimus* L.). Proceeding of National Conference on Harmony with Nature in Context of Environmental Issues and Challenges of the 21st Century, Udaipur, India. 2014.

20. Johnson HW, Robinson HF. Comstock. Estimates of genetic and environmental variability in soybean. *J. Agric.* 1955; 45:478-481.
21. Khan ASMMR, Kabir MY, Alam MM. Variability, correlation path analysis of yield and yield components of pointed gourd. *Journal of agriculture and rural development.* 2009; 7(1/2):93-98.
22. Khule AA, Tikka SBS, Jadhav DJ, Kajale DB. Genetic variability and heritability studies in local collections of sponge gourd (*Luffa cylindrica* (Linn.) M. Roem.). *Asian Journal of Biological Science.* 2011; 6(1):119-120.
23. Kumar KH, Dubey RB, Pareek S. Genetic variability, correlation and path analysis in sponge gourd (*Luffa cylindrica* Roem.). *African Journal of Biotechnology.* 2013; 12(6):539-543.
24. Malek MA, Milan MAB, Islam MO, Hoque AMMM, Gomes R. Genetics, variability, heritability and genetics advance in pointed gourd (*Trichosanthes dioica* Roxb.). *Bangladesh journal of plant breeding and genetics.* 2007; 20(1):47-52.
25. Munawar M, Hammad G, Nadeema K. Assessment of genetic diversity in Tinda gourd through Multivariate Analysis. *International Journal of Vegetable Science.* 2015; 21:157-166.
26. Naik A, Akhtar S, Thapa U, Hazra P. Genetic variability, heritability and genetic advance in teasle gourd (*Momordica subangulata* Blume. Subsp. renigera). *Envi. Ecol.* 2012(b); 30(3):865-867.
27. Pathak M, Kaur M, Pahwa K. Genetic variability, correlation and path coefficient analysis in bittergourd (*Momordica charantia* L.). *International Journal of Advance Research.* 2014; 2(8):179-184.
28. Pandey S, Kashya SK, Jha A, Choudhary BR, Kumar S, Singhal DK *et al.* Inter-trait association and genetic variability assessment in Snap melon (*Cucumis melo* var. momordica). *Indian Journal of Plant Genetic Resources.* 2009; 22(2):113-116.
29. Panse VG, Shukhatme PV. *Statistical Methods for Agricultural Workers.* 2nd Edn. ICAR Publications Krishi Anusandhan Bhavan, Pusa, New Delhi-11001.1967.
30. Panse VG. Genetics of quantitative. *Indian Journal of Genetics.* 1957; 17:318-328.
31. Sanwal SK, Yadav RK, Rai N, Yadav DS, Singh PK. Genetic diversity and interrelation analysis in sweet gourd (*Momordica cochinchinensis*) genotypes of northeast India. *Vegetable Science.* 2007; 34(1):64-66.
32. Sharma G, Pant MC. Effect of feeding *Trichosanthes dioica* on blood sugar, serum triglycerides, phospholipid, cholesterol and high-density lipoprotein cholesterol levels in the normal albino rabbits. *Current science.* 1988(a); 57:1085-1087.
33. Singh AK, Singh RD, Singh K. Genetic variability, heritability and genetic advance for some traits in pointed gourd (*Trichosanthes dioica* Roxb.). *Haryana J. Hort. Sci.* 1992; 21(3-4):236-240.
34. Singh BD. *Plant Breeding: Principles and methods.* Kalyani publishers, New Delhi. 2001, 896.
35. Singh MK, Bhardwaj DR, Upadhyay DK. Genetic architecture and association analysis in bitter gourd (*Momordica charantia* L.) landraces. *The bioscan.* 2014; 9:707.
36. Sundaram V. Studies on character association in bitter gourd (*Momordica charantia* L.) under salt stress. *The Asian Journal of Horticulture.* 2010; 5(1):99-102.
37. Sundaram MS, Kanthaswamy V, Kumar GA. *Pro. Hort.* 2011; 43:20.
38. Yadav M, Pandey TK, Singh DB, Singh GK. Genetic variability, correlation coefficient and path analysis in bitter gourd. *Indian J. Hort.* 2013; 70:144.
39. Yadav H. Genetic divergence revealed by morphological and biochemical markers in ridge gourd. Thesis, M. Sc. (Ag.) Horticulture, Vegetable Science, G.B.P.U.A&T, Pantnagar. 2014, 65.