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Variability and Divergence study in Pointed gourd (*Trichosanthes dioica* Roxb.)

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Abstract
The current research was conducted during the year 2020-21 at Vegetable Research Farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar. The experimental materials included twenty genotypes of pointed gourd, along with a check variety Swarn Rekha. The experiment was carried out in RBD design, with three replications and spacing of 2m × 1m. The findings were recorded on fourteen quantitative traits. The ANOVA indicated existence of highly significant variations among the genotypes for all the characters studied suggesting the existence of abundant extent of variability among the experimented material. The majority of the yield attributing traits including fruit yield exhibited high heritability combined with high GAM, inferring the preponderance of additive gene action which will facilitates in early generation selection on the basis of such traits. The twenty genotypes used for genetic divergence analysis were categorized into six distinct clusters. Highest number of genotypes were entered in Cluster I, because they may be genetically identical with each other The inter-cluster D^2 values of the six clusters depicted that maximum inter-cluster generalized distance (876.82) was between Cluster II and Cluster V, suggesting that to have the superior heterotic recombinants. Materials under investigation in terms of their contribution % to maximal diversity for the attributes of the seed-to-pulp ratio and the node at which the first blossom emerged.

Keywords: Pointed gourd, variability, heritability, GAM, genetic divergence

Introduction
The pointed gourd (*Trichosanthes dioica* Roxb.) is considered as one of the most prominent cucurbit vegetable, having chromosome number 2n=2X=22. It is commonly known as parwal, palwal and patola (Pandit and Hazara, 2008) [27]. It is known as the "King of Gourds" because of its vast diversity and advanced nutritional content than any other cucurbits (Saha *et al.*, 2004; Yadav *et al.*, 2022) [34, 43]. In India it is cultivated in an area about 63,000 ha with production of 7, 52,000 metric tonnes and productivity of 11.94 t ha^{-1} (Ministry of Agriculture and Farmers Welfare, 2021-22).
Fruits of pointed gourds offer pharmaceuticals features that can help in lowering blood sugar and triglycerides levels. The fruits are easy to digest, laxative and diuretic, as well as possessing anti-ulcer effects and a number of other medicinal benefits. Ayurvedic medicine uses the plant's leaves as antipyretic, diuretic, cardio tonic, laxative, antiulcer and other remedies. Leaf is an aperient that is also used as a tonic and febrifuge as well as a diet in instances of enlargement of the liver and spleen (Malek, 2009) [23].
Genetic variability is an important element of every heritable improvement. Assessing the nature and scope of genetic diversity is useful for choosing good genotypes from a germplasm. The wide genetic heterogeneity present in accessible germplasm gives sufficient opportunity for further developments (Singh and Prasad, 1989; Patil *et al.*, 2022) [37, 30]. Heritability is the proportion of phenotypic variation that is passed down by parent to the offspring. More heritable variety means more potential for character fixing through selection techniques. Genetic advance is also significant since it forecasts the level of progress to the following generation through evaluation.

Materials and Methods
The present research work was carried at experimental site of Vegetable Research Farm, Dr. RPCAU Pusa, Samastipur. The experiment was carried out in Randomized Block Design, with three replications and spacing is 2m x 1m (row-to-row and plant to plant). The experimental material for the study comprises 20 genotypes including check (Swarn Rekha) in which 14th

local collection (PGS-1, PGS-2, PGS-3, PGS-4, PGS-5, PGS-6, PGS-7, PGS-8, PGS-9, PGS-10, PGS-11, PGS-12, PGS-13 and PGS-14); three from RCER, Ranchi (Swarn Suruchi, Swarn Alaukik and Swarn Rekha); two from IIVR, Varanasi (Kashi Alankar and Kashi Suphal) and one from BAU, Sabour (Rajendra Parwal-1). The observations were recorded on fourteen quantitative traits *Viz*; number of vines plant^{-1}, vine length (cm), internodal length (cm), node at which first flower appeared, days to 1st flower initiation, number of fruits plant^{-1}, fruit length (cm), breadth of fruit (cm), weight of fruit (g), volume of fruit (ml), number of seeds fruit^{-1}, Seed: Pulp ratio, fruit yield (q ha^{-1}) and TSS (° Brix) in order to quantify correlation coefficient and path coefficient.

The ANOVA was estimated by using strategy of Panse and Sukhatme (1967) [29]. The GCV and PCV were calculated by using the method described by Burton and De Vane (1953) [5]. While GAM and heritability (broad sense) had been calculated according to with Johnson *et al.* (1955) [13] and Lush (1940) [21] methods, respectively. The D^2 statistics calculated by Mahalanobis (1936) [22] method. Statistical analysis was done with the help of R-Studio software.

Result and Discussions

The ANOVA (Table 1) depicted presence of slightly higher significant variation among the genotypes for all the studied parameters. This suggested that existence of a significant level of variability within the genotypes. Similar findings were also reported in pointed gourd by Adhikari *et al.* (2020) [2] in pointed gourd, Tak *et al.* (2020) [38] in Ivy gourd, Abhishek *et al.* (2020) [1] in bottle gourd and Kusmiyati *et al.* (2022) [19] in pointed gourd.

The most promising genotypes, were determined by the mean performance (Table 3) in relation to the check variety (Swarn Rekha). Wide range of variability had been recorded for the trait; number of vines plant^{-1}, node at which first flower appeared, Seed: Pulp ratio as well as fruit yield, indicating that, selection based on these traits will be effective. Based on the mean performance two genotypes *Viz;* PGS-3 and PGS-5 have shown the significant superiority than the check Swarn Rekha for the traits; number of vines plant^{-1}, vine length, number of fruits plant^{-1}, volume of fruits and fruit yield. Suggesting that these genotypes may be beneficial to have the higher yield in pointed gourd.

The phenotypic coefficient variance was greater than that of genotypic coefficient variance reflecting the role of environment with depiction of these traits, as shown in (Table 2). In general, PCV slightly higher than the GCV for all the traits, suggesting that for the expression of the traits major role was played by the genotypes rather to the environment. The GCV value and PCV value for characters that node at which the 1st flower appeared (36.55%, 37.11%), number of vines plant^{-1} (30.89%, 32.67%,), Seed: Pulp ratio (29.69%,30.96%),), number of seeds fruit^{-1} (22.38%, 23.95%) and fruit yield (22.12%, 25.56%) respectively. Characters such as number of vines plant^{-1}, vine length, internodal length, node at which first flower appeared, weight of fruit, volume of fruit, number of seeds fruit^{-1}, Seed: pulp ratio and fruit yield were shown high heritability coupled with high GAM; suggesting that there is a preponderance of additive gene action. Therefore, selection in early generation based on these traits may be rewarding. Other characters including number of fruits plant^{-1}, fruit length and TSSs were found high heritability with moderate GAM; indicating that there is presence of additive as well as non-additive type of gene action, so for the improvement of these traits recurrent selection may be useful. The similar results had been recorded in pointed gourd and other cucurbitatious vegetable by Triveni *et al.,* 2021 [39]; Verma *et al*., 2017 [41]; Kumar and Agrawal 2015 [18]; Jatav and Singh, 2016 [10]; Narayanankutty, 2006 [25]; Rana and Pandit, 2011 [28]; Rajkumar and Karuppaiah, 2007 [32] and Bharathi *et al.,* 2006 [4].

The twenty genotypes used for genetic divergence analysis were categorized into six distinct clusters using the Malalananobis D^2 method. Highest number of genotypes were entered in Cluster I, because they may be genetically identical with each other. Similar findings were reported by Kabir *et al.,* 2009 [14]; Khan *et al.,* 2009 [16]; Tyagi *et al.,* 2017 [40]; Debata *et al.,* 2017 [7]; Mallikarjunarao *et al.,* 2018 [24]; Shilpashree *et al.,* 2022 [35]; Nithinkumar *et al.,* 2021 [26] and Pandit *et al.,* 2011 [28]. The Cluster I had the highest D^2 value (138.10) however, it was observed lowest value in Cluster III, V and VI (0.00), suggesting that the genotypes placed in these clusters are having the wider variability. The inter-cluster D^2 values of the six clusters depicted that maximum inter-cluster generalized distance (876.82) was between Cluster II and Cluster V, suggesting that to have the superior heterotic recombinants. Crossing between the genotypes of "the Cluster II and Cluster V as well as Cluster II and Cluster VI, Cluster I and Cluster VI" may be rewarding. Similar findings were reported by Prasad *et al.*, 1997 [31]; Debata *et al.,* 2017 [7]; Singh *et al.,* 2016 [36]; Verma *et al.,* 2017 [41]; Tyagi *et al.,* 2017 [40]; Shilpashree *et al.,* 2022 [35] and Jatav *et al.,* 2022 [11].

The maximum contribution in manifestation of genetic divergence was exhibited by seed: pulp ratio (32.63), indicating that materials under study have maximum diversity for the traits Seed: Pulp ratio. The contribution of remaining traits such as vine length, number of fruits plant^{-1}, days to 1st flower initiation, breadth of fruit and fruit yield in the manifestation of genetic divergence was zero, suggesting that among the genotypes there is no difference for these traits. Similar outcomes were reported by Khan *et al.,* 2009 [16]; Dalsaniya *et al.,* 2009 [6]; Debata *et al.,* 2017 [7]; Singh *et al.,* 2016 [36]; Nithinkumar *et al.,* 2021; [26] Tyagi *et al.,* 2017 [40]; Jatav *et al.,* 2022 [11] and Shilpashree *et al.,* 2022 [35].

Conclusion

In general, PCV was somewhat greater than GCV, showing that characters had a relatively limited response to their surroundings. 9 characters *Viz*; "the number of vines per plant, the vine length, the internodal length, the node at which the first blossom emerged, the weight of the fruit, the volume of the fruit, the number of seeds per fruit, and the number of seeds per fruit, Seed to pulp ratio and fruit production, especially fruit yield," have demonstrated strong heritability associated with high GAM, showing that additive gene action predominates, implying that early generation selection might be beneficia. Highest number of genotypes were entered in Cluster I, because they may be genetically identical with each other The inter-cluster D^2 values of the six clusters depicted that maximum inter-cluster generalized distance (876.82) was between Cluster II and Cluster V, suggesting that to have the superior heterotic recombinants.

Table 1: Analysis of variance for fourteen characters in Pointed gourd

Sr. No.	Character	Mean sum of square		
		Replication (dof = 2)	Treatment (dof = 19)	Error (dof = 38)
1.	Number of vines plant^{-1}	0.12	16.00 **	0.61
2.	Vine length (cm)	49.38	442.86 **	22.22
3.	Internodal length (cm)	0.20	2.81 **	0.92
4.	Node at which 1st flower appeared	0.15	30.83 **	0.31
5.	Days to 1st flower initiation	18.43	336.99 *	149.45
6.	Number of fruits plant^{-1}	55.95	586.09 **	100.79
7.	Fruit length (cm)	0.10	1.31 **	0.20
8.	Breadth of fruit (cm)	0.01	0.17 *	0.08
9.	Weight of fruit (g)	45.61	66.20 **	11.93
10.	Volume of fruit (ml)	2.75	62.45 **	4.37
11.	Number of seeds fruit^{-1}	0.80	55.98 **	2.59
12.	Seed: Pulp ratio	0.0010	0.007 **	0.0012
13.	TSS (° Brix)	0.03	0.32 **	0.02
14.	Fruit yield (q ha^{-1})	355.23	6145.51 **	617.88

Table 2: Genetic parameters of fourteen characters in Pointed gourd

Sr. No.	Character	σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2 (b.s.) (%)	GA	GA as % Mean
1.	Number of vines plant^{-1}	5.13	5.74	30.89	32.67	89.41	4.41	60.16
2.	Vine length (cm)	140.21	162.43	16.89	18.18	86.32	22.70	32.33
3.	Internodal length (cm)	1.63	1.81	18.75	19.78	89.81	2.50	36.60
4.	Node at 1st flower appeared	10.17	10.49	36.55	37.11	97.01	6.50	74.16
5.	Days to 1st flower initiation	62.51	211.96	5.95	10.96	29.49	8.80	6.67
6.	Number of fruits plant^{-1}	161.76	262.56	9.76	12.43	61.61	20.60	15.78
7.	Fruit length (cm)	0.37	0.57	8.47	10.47	65.47	1.00	14.12
8.	Breadth of fruit (cm)	0.03	0.11	6.03	11.92	25.58	0.20	6.28
9.	Weight of fruit (g)	18.09	30.02	14.44	18.61	60.25	6.80	23.10
10.	Volume of fruit (ml)	11.36	23.73	16.51	18.29	81.57	8.20	30.73
11.	Number of seeds fruit^{-1}	17.80	20.39	22.38	23.95	87.30	8.10	43.08
12.	Seed: Pulp ratio	0.00	0.00	29.69	30.96	92.00	0.09	58.70
13.	TSS (° Brix)	0.10	0.12	9.47	10.39	82.98	0.59	17.77
14.	Fruit yield (q ha^{-1})	1842.54	2460.42	22.12	25.56	74.89	76.50	39.43

Table 3: Mean, range, coefficient of variance and Mean performance of twenty genotypes for fourteen characters in pointed gourd

Sr. No.	Character →	1	2	3	4	5	6	7	8	9	10	11	12	13	14
	Genotype ↓	Number of vines plant-1	Vine length (cm)	Internodal length (cm)	Node at which first flower appeared	Days to 1st flower initiation	Number of fruits plant-1	Fruit length (cm)	Breadth of fruit (cm)	Weight of fruit (g)	Volume of fruit (ml)	Number of seeds fruit-1	Seed: Pulp ratio	TSS (° Brix)	Fruit yield (q ha-1)
1.	PGS-1	5.67	65.53	7.19	14.67	139.17	121.67	7.04	2.70	26.94	23.80	16.00	0.084	3.23	174.49
2.	PGS-2	6.67	66.60	6.94	10.20	136.27	127.33	7.14	2.74	28.75	26.00	24.00	0.208	3.93*	185.22
3.	PGS-3	14.33 *	99.40 *	5.07*	13.00	108.62 *	159.00 *	8.20	3.20	39.35 *	36.80 *	22.00	0.111	3.53	312.58 *
4.	PGS-4	6.33	66.57	7.01	4.67 *	138.09	123.33	7.12	2.73	28.71	25.60	20.33	0.210	3.13	182.24
5.	PGS-5	11.33 *	88.00 *	5.36	6.33 *	118.37	156.33 *	8.08	3.17	37.12	34.20 *	29.00	0.127	3.20	289.61 *
6.	PGS-6	5.33	57.87	8.44	6.33 *	146.72	113.67	6.64	2.51	23.12	21.60	22.33	0.148	3.37	152.87
7.	PGS-7	7.00	68.40	6.55	5.67 *	133.66	129.00	7.30	2.82	29.70	26.80	23.00	0.125	3.27	188.75
8.	PGS-8	5.00	46.47	9.35	7.67	147.37	108.00	5.32	2.29	19.59	17.40	21.00	0.155	3.27	123.45
9.	PGS-9	5.67	66.20	7.05	7.33 *	138.42	123.00	7.10	2.72	28.43	24.80	19.00	0.122	3.37	177.64
10.	PGS-10	5.00	54.47	9.23	7.00 *	147.25	110.33	6.44	2.45	22.60	19.80	19.33	0.124	3.63 *	134.89
11.	PGS-11	7.67	84.07*	5.49	10.00	118.78	142.33	7.80	3.08	32.91	30.40	22.00	0.256	3.17	222.20
12.	PGS-12	9.33 *	82.27	5.63	10.00	120.42	141.00	7.71	3.06	32.72	30.00	15.00	0.212	2.77	221.95
13.	PGS-13	5.67	61.33	8.25	6.33 *	141.81	119.00	6.44	2.65	26.27	23.77	16.00	0.226	3.73 *	166.39
14.	PGS-14	5.33	61.07	8.32	14.00	142.66	117.33	6.66	2.61	25.95	23.60	17.00	0.199	2.97	153.60
15.	Rajendra Parwal-1	7.00	68.40	6.64	15.33	134.69	127.67	7.28	2.77	29.32	26.00	16.00	0.149	3.70 *	187.99
16.	Kashi Alankar	7.67	74.00	5.92	6.33 *	128.67	137.67	7.46	2.87	31.63	28.00	14.00	0.199	3.13	202.28
17.	Kashi Suphal	7.33	69.13	6.09	7.33 *	130.33	134.67	7.44	2.85	30.31	27.20	14.00	0.199	3.80 *	191.06
18.	Swarn Suruchi	9.00	78.20	5.74	8.00	129.04	136.00	7.44	3.04	30.65	27.87	18.00	0.128	3.27	192.22
19.	Swarn Alaukik	7.33	69.27	5.94	6.00 *	127.67	140.67	7.66	2.87	32.67	29.80	19.00	0.151	2.70	211.90
20.	Swarn Rekha (C)	8.00	74.87	5.86	8.33	133.53	139.00	7.56	2.90	32.16	29.40	10.00	0.096	3.30	210.02
CD (5%)		1.294	7.821	0.713	0.930	20.210	16.659	0.734	0.478	5.732	3.470	2.670	0.024	0.236	41.245
CV (%)		7.33	6.72	6.31	6.42	9.20	7.70	6.15	10.28	11.73	7.85	8.54	8.980	4.28	12.80
Mean		7.33	70.11	6.80	8.73	132.83	130.35	7.19	2.80	29.45	26.64	18.85	0.161	0.16	194.07
Minimum		5.00	46.47	5.07	4.67	108.62	108.00	5.32	2.29	19.59	14.40	10.00	0.08	2.70	123.45
Maximum		14.33	99.40	9.35	15.33	147.37	159.00	8.20	3.20	39.35	36.80	29.00	0.26	3.93	312.58

Table 4: Clustering pattern of twenty genotypes of pointed gourd on the basis of D^2 statistic

Cluster No.	No. of Genotypes with in cluster	Genotypes in cluster
Cluster I	12	PGS-6, PGS-10, PGS-9, PGS-8, PGS-4, PGS-13, PGS-7, PGS-2, Kashi Suphal, Kashi Alankar, Swarn Alaukik and Swarn Suruchi
Cluster II	3	PGS-1, Rajendra Parwal-1 and PGS-14
Cluster III	1	Swarn Rekha
Cluster IV	2	PGS-12 and PGS-11
Cluster V	1	PGS-5
Cluster VI	1	PGS-3

Table 5: Mean intra and inter cluster distance (D^2) among six clusters in pointed gourd

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	138.10	384.33	289.13	209.36	370.83	529.31
Cluster II		104.82	443.29	297.71	876.82	538.95
Cluster III			0.00	373.09	385.85	225.85
Cluster IV				99.60	383.26	396.49
Cluster V					0.00	315.23
Cluster VI						0.00

Table 6: Cluster mean for fourteen characters in pointed gourd

Character → Cluster ↓	Number of vines plant^{-1}	Vine length (cm)	Internodal length (cm)	Node at which 1st flower appeared	Days to 1st flower initiation	Number of fruits plant^{-1}	Fruit length (cm)	Breadth of fruit (cm)	Weight of fruit (g)	Volume of fruit (ml)	Number of seeds fruit^{-1}	Seed: Pulp ratio	TSS (°Brix)	Fruit yield (q ha^{-1})
Cluster I	6.50	64.88	7.21	6.91	137.11	125.22	6.96	2.71	27.70	24.89	19.17	0.17	3.38	175.74
Cluster II	6.00	65.00	7.38	14.67	138.84	122.22	6.99	2.70	27.40	24.47	16.33	0.14	3.30	172.03
Cluster III	8.00	74.87	5.86	8.33	133.53	139.00	7.56	2.90	32.16	29.40	10.00	0.10	3.30	210.02
Cluster IV	8.50	83.17	5.56	10.00	119.60	141.67	7.75	3.07	32.82	30.20	18.50	0.23	2.97	222.07
Cluster V	11.33	88.00	5.36	6.33	118.37	156.33	8.08	3.17	37.12	34.20	29.00	0.13	3.20	289.61
Cluster VI	14.33	99.40	5.07	13.00	108.62	159.00	8.20	3.20	39.35	36.80	22.00	0.11	3.53	312.58

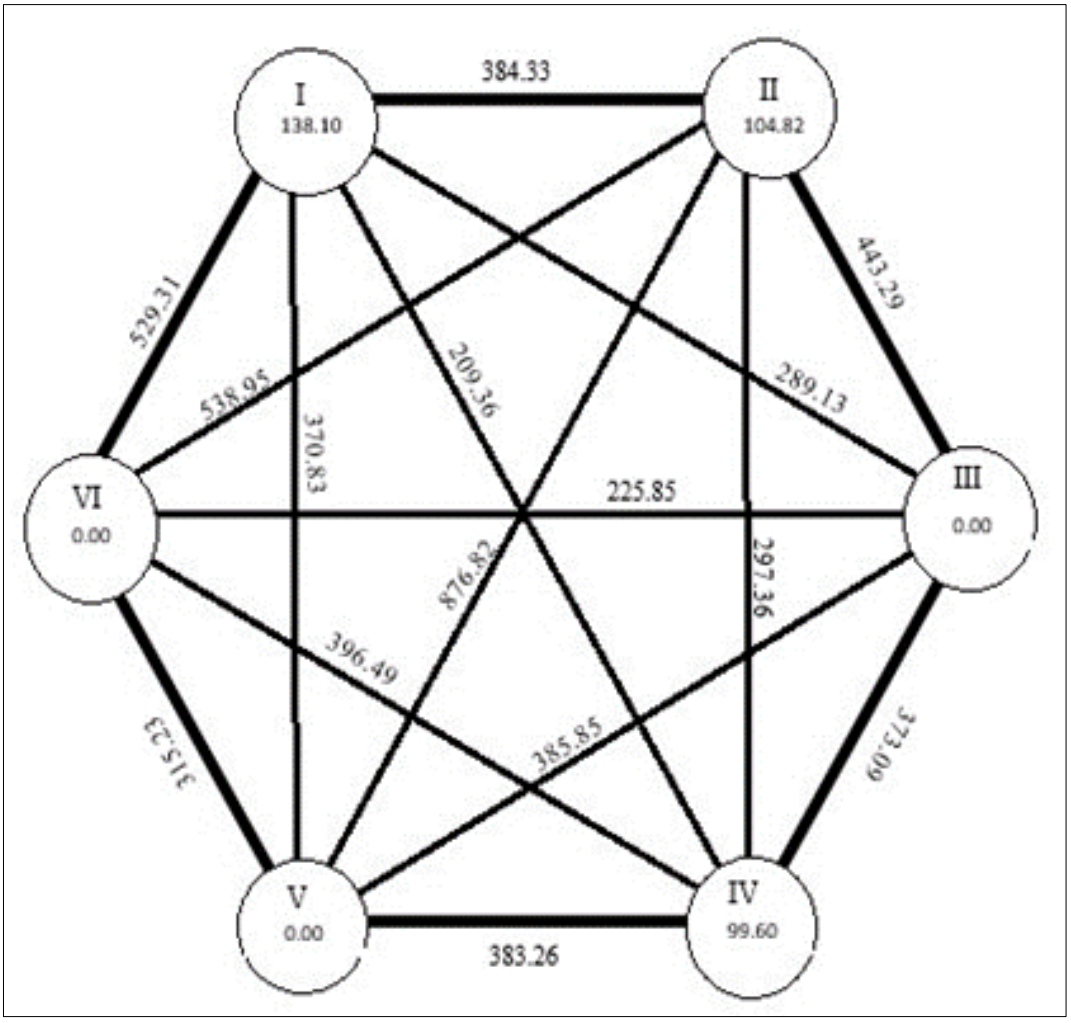

Fig 1: Diagrammatic representation of divergence by Tocher's method

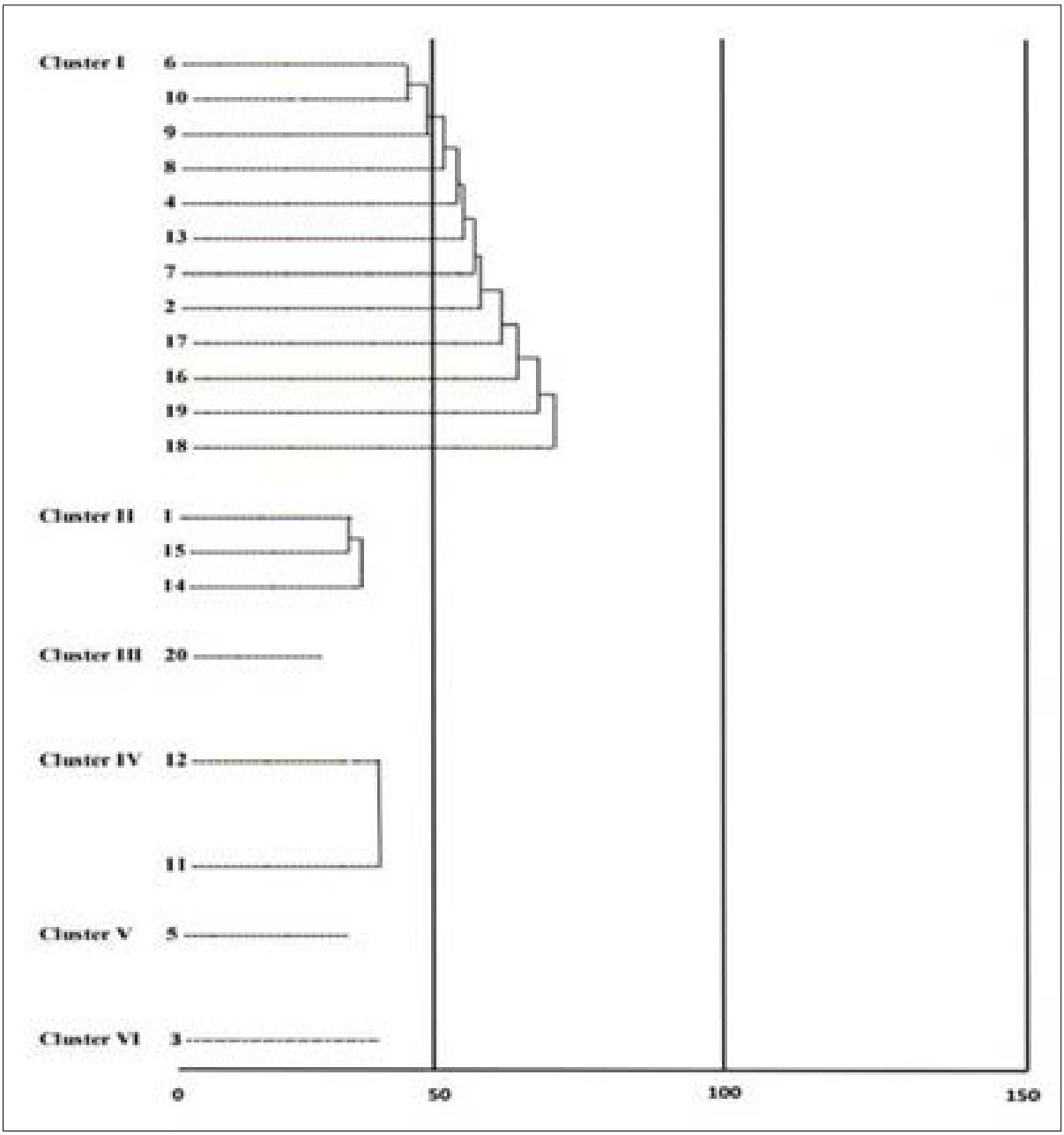

Fig 2: Clustering pattern of twenty genotypes based on D2 statistics by Tocher's methods

Table 7: Contributing percentage of fourteen characters towards genetic divergence

S. N.	Source	Times Ranked 1st	Contribution (%)
1..	Number of vines plant^{-1}	7	3.68
2.	Vine length (cm)	0	0.00
3.	Internodal length (cm)	15	7.89
4.	Node at which first flower appeared	57	30.00
5.	Days to 1st flower initiation	0	0.00
6.	Number of fruits plant^{-1}	0	0.00
7.	Fruit length (cm)	1	0.53
8.	Breadth of fruit (cm)	0	0.00
9.	Weight of fruit (g)	3	1.58
10.	Volume of fruit (ml)	4	2.11
11.	Number of seeds fruit^{-1}	26	13.68
12.	Seed: Pulp ratio	62	32.63
13.	TSS (º Brix)	15	7.89
14.	Fruit yield (q ha^{-1})	0	0.00

References

1. Abhishek VR, Kumar J, Tomar S. Study of genetic variability, heritability and genetic advance among the characters of Bottle gourd. Plant Archives. 2020;20:506-

509.
2. Adhikari S, Biswas A, Saha S, Biswas A, Ghosh P. SPAR methods reveal high genetic diversity within populations and moderate gene flow of Pointed gourd (*Trichosanthes dioica* Roxb.) germplasm. Biocatalysis and Agricultural Biotechnology. 2020;29:101760.
3. Anonymous. IndiaStat Database. Ministry of Agriculture and Farmers Welfare. 2021.
4. Bharathi LK, Naik G, Dora DK. Studies on genetic variability in Spine gourd. Indian journal of horticulture. 2006;63(1):96-97.
5. Burton GW, Devane DE. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material 1. Agronomy journal. 1953;45(10):478-481.
6. Dalsaniya SB, Poshiya VK, Savaliya JJ, Pansuriya AG, Davada BK. Genetic divergence in Cowpea [Vigna unguiculata (l.) Walp.]. Legume Research. 2009;32(4):250-254.
7. Debata J, Maurya SK, Yadav H, Bhat L. Study on genetic diversity of Pointed gourd using morphological traits. International Journal of Current Microbiology Applied Sciences. 2017;6(12):1511-1519.
8. Fisher RA, Yates F. Statistical tables for biological, agricultural and medical research. 1938.
9. Galton H. How the czech language lost its correlation of palatalization. Case Study of Languages in. 1988.
10. Jatav V, Singh DK. Genetic Variability, Heritability and Genetic advance for yield and related traits in Bitter gourd (*Momordica Charantia* l.). Journal of Environment Bio-Science. 2016;30(2):421-426.
11. Jatav V, Singh D, Singh N, Panchbhaiya A. Principal component analysis in Bitter gourd (*Momordica Charantia* L.). Bangladesh Journal of Botany. 2022;51(1):1-7.
12. Jena AK, Suseela T, Patro TSKKK, Sujatha RV. Studies on genetic variability, heritability and genetic advance in Pointed gourd (*Trichosanthes dioica* Roxb.). International Journal of Current Microbiology and Applied Sciences. 2017;6(8):1857-1863.
13. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in Soybeans 1. Agronomy journal. 1955;47(7):314-318.
14. Kabir MY, Khan ASMMR, Hassain MS. Genetic divergence in Pointed gourd. Journal of Agriculture & Rural Development. 2009;7(1-2):87-92.
15. Kannan A, Rajamanickam C, Krishnamoorthy V, Arunachalam P. Genetic variability, correlation and path analysis in f4 generation of Ridge gourd [*Luffa acutangul* (Roxb) L.]. International journal of chemical studies. 2019;7(3):208-213.
16. Khan ASMMR, Kabir MY, Alam MM. Variability, correlation path analysis of yield and yield components of Pointed gourd. Journal of Agriculture & Rural Development. 2009;7(1-2):93-98.
17. Koppad SB, Chavan M, Hallur R. Character association studies and path coefficient analysis for yield and yield attributing traits in Ridge gourd [*Luffa acutangul* (L.) Roxb.]. Electronic Journal of Plant Breeding. 2016;7(2):275-281.
18. Kumar J, Agrawal V. Cure of Diabetes mellitus by some medicinally important dioecious plants. International Journal of Research in Biosciences. 2015;4(3):1-7.
19. Kusmiyati F, Anwar S, Herwibawa B. Study on genetic variability and heritability in f5 segregating generation for yield and its components in Yard long bean. In International Conference on Tropical Agri food, Feed and Fuel (ICTAFF 2021). Atlantis Press. 2022, 44-48.
20. Kutty MS, Dharmatti PR. Correlation and path coefficient studies in Bitter gourd (*Momordica Charantia* L.). Karnataka Journal of Horticulture. 2004b;1(3):7-11.
21. Lush JL. Heritability of quantitative characters in farm animals. 1949.
22. Mahalanobis PC. On the generalized distance in statistics. National Institute of Science of India. 1936.
23. Malek MA. *In vitro* propagation of Pointed gourd (*Trichosanthes dioica* Roxb.) through encapsulated shoot tips. Bangladesh Journal of Agricultural Research. 2009;34(4):555-563.
24. Mallikarjunarao K, Das AK, Nandi A, Baisakh B, Tripathy P, Sahu GS. Heterosis and combining ability of quality and yield of Bitter gourd (*Momordica Charantia* L.). Journal of pharmacognosy and phytochemistry. 2018;7(3):05-09.
25. Narayanankutty C, Sunanda CK, Jaikumaran U. Genetic variability and character association analysis in Snake gourd. Indian Journal of Horticulture. 2006;63(4):402-406.
26. Nithinkumar KR, Varalakshmi B, Mushrif SK. Genetic divergence study in Bitter gourd (*Momordica Charantia* L.). Journal of Horticultural Sciences. 2021;16(2):193-198.
27. Pandit MK, Hazra P. Pointed gourd. Scientific cultivation of vegetables. New Delhi, Kalyani Publication. 2008, 218-228.
28. Pandit MK, Saha AK, Bhattacharya S. Multivariate analysis for genetic divergence in Snake gourd (*Trichosanthes anguina* L.) genotypes. In I International Symposium on Sustainable Vegetable Production in Southeast Asia. 2011;958:157-161.
29. Panse VG, Sukhatme PV. Statistical methods for agricultural workers ICAR New Delhi. 1967;2:381.
30. Patil SJ, Khandare VS, Gurve VR, Baghele RD. Assessment of genetic variability and character association in yield and yield-attributing traits in Spine gourd (Momordica dioica Roxb.). Biological Forum – An International Journal. 2022;14(1):115-120.
31. Prasad VSR, Singh DP. Genetic divergence in parwal (*Trichosanthes dioica* Roxb.). Indian Journal of Plant Genetic Resources. 1997;10(1):91-96.
32. Rajkumar M, Karuppaiah P. Variability studies in Snake gourd (*Trichosanthes anguina* L.). Plant Archives. 2007;7(2):699-701.
33. Rana NP, Pandit MK. Studies on genetic variability, character association and path analysis in Snake gourd (*Trichosanthes anguina* L.) genotypes. Journal of Crop and Weed. 2011;7(2):91-96.
34. Saha G, Das SN, Khatua DC. Fruit and vine rot of Pointed gourd-etiology, epidemiology and management. Journal of Mycopathological Research. 2004;42(1):73-81.
35. Shilpashree N, Anjanappa M, Fakrudin B, Pitchaimuthu M, Ramachandra RK, Shankarappa KS, *et al*. Genetic diversity studies in Ridge gourd [*Luffa acutangul* (L.) Roxb.] Genotypes. The Pharma Innovation Journal. 2022;11(3):101-105.
36. Singh P, Kurrey VK, Minz RR, Moharana DP.

Correlation coefficient analysis between fruit yield and qualitative traits of Pointed gourd (*Trichosanthes dioica* Roxb.) in Chhattisgarh region. International Quarterly Journal of Environmental Sciences. 2016;9:33-38.
37. Singh DP, Prasad VSR. Variability and correlation studies in Pointed gourd (*Trichosanthes dioica* Roxb.). Indian Journal of Horticulture. 1989;46(2):204-209.
38. Tak JK, Pilania S, Kaushik RA, Lakhawat SS, Meena MK, Rajawat KS, *et al*. Genetic variability analysis in local germplasm of Ivy gourd (*Coccinia grandis* L.) in Southern Rajasthan conditions. 2020;39(15):104-111.
39. Triveni D, Uma Jyothi K Dorajee Rao AVD, Mamatha K, Uma Krishna K, Saloomi Suneetha DR. Correlation and path analysis for yield and yield contributing traits in Bitter gourd (*Momordica Charantia* L.). Vegetos. 2021;34(4):944-950.
40. Tyagi N, Singh VB, Tripathi V. Studies on genetic divergence in Bitter gourd (*Momordica Charantia* L.). Indian Journal of Ecology. 2017;44(5):607-609.
41. Verma P, Maurya SK, Panchbhaiya A, Dhyani S. Studies on variability, heritability and genetic advance for yield and yield contributing characters in Pointed gourd (*Trichosanthes dioica* Roxb.). Journal of Pharmacognosy and Phytochemistry. 2017;6:734-738.
42. Wray N, Visscher P. Estimating trait heritability. Nature Education. 2008;1(1):29.
43. Yadav N, Singh AK, Emran TB, Chaudhary RG, Sharma R, Sharma S, *et al*. Salicylic acid treatment reduces lipid peroxidation and chlorophyll degradation and preserves quality attributes of Pointed gourd fruit. Journal of Food Quality. 2022, 20-22.