



Genetic diversity in pointed gourd (*Trichosanthes dioica*) genotypes for fruit yield and quality traits under eastern plateau and hill region

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ABSTRACT

The experiment was conducted during summer seasons of 2021–22 and 2022–2023 at ICAR-Research Complex for Eastern Region, Farming System Research Centre for Hill and Plateau Region, Plandu, Ranchi, Jharkhand focused on assessing the genetic diversity for fruit yield and quality parameters among 46 unique pointed gourd (*Trichosanthes dioica* Roxb.) genotypes. The data collected underwent thorough statistical analyses, encompassing genetic variability, analysis of variance (ANOVA), correlation coefficients, path analysis, exploration of genetic divergence and biochemical characterization. The ANOVA results revealed significant variations across the selected genotypes in terms of fruit yield and quality traits. Key attributes, such as the number of fruits/plant, harvest frequency, pulp seed ratio and total phenol content, displayed significant positive correlations with total fruit yield. The noteworthy was the positive direct effect of pulp weight on total fruit yield indicated by a coefficient of 0.99. Further, this study identified total fruit yield as the primary contributor to the observed genetic diversity. Cluster analysis results in to the grouping of 46 genotypes into 12 distinct clusters based on D² values. The study highlighted significant variability among pointed gourd genotypes, suggesting ample opportunities for selection-based improvement. Selection based on characteristics such as the number of fruits per plant, pulp weight and pulp seed ratio is expected to enhance yield potential. Identified genotypes, such as Swarna Alaukik, HAP-79, HAP-70 (for yield-related attributes) and HAP-106 (for quality traits), emerged as promising which hold potential for future breeding initiatives and are recommended for cultivation in the eastern plateau and hill region for augmenting yield potential. Cluster III and cluster XII offer diverse genetics for breeding. Crossing these clusters can create new high-yield cultivars. This strategic cultivation aims to enhance the nutritional well-being of the local population in that area.

Keywords: D² analysis, Fruit quality, Genetic diversity, Pointed gourd, Yield

Pointed gourd (*Trichosanthes dioica* Roxb.), (2n=2x=22) is a perennial and dioecious climber herb belonging to the Cucurbitaceae family. It is native to the Assam-Bengal regions of India (De Candolle 1882) and is characterized by a rich species diversity in the Assam-Bengal region, including Bangladesh, while wild forms can be found in northern India. The plant, colloquially referred to as green potato, is extensively cultivated in tropical and subtropical regions of India, especially in Uttar Pradesh, Bihar, West Bengal and Assam (Bose and Som 1986, Hassan and Miyajima 2019). Being a trailing perennial vegetable, pointed gourd is grown

for its tender fruits and known as the "King of gourds" as it offers high nutritional value, including proteins, vitamin A and minerals, with diuretic and anti-diabetic properties (Pandit and Hazra 2008).

The nutritional value extends to the leaves, shoot tips, and young fruits, used in various culinary applications, including roasting, pickling and desserts (Paris and Maynard 2008, Anonymous 1998). The propagation of this crop relies on vegetative methods due to poor germination and segregation from seed (Bose and Som 1986, Hassan and Miyajima 2019). Dioecious sex expression and pollination problem necessitates in maintaining a ratio of 1 staminate to 10 pistillate plants (Das and Sau 2020). Consumer preference for seedlessness or less seeded varieties is being addressed through breeding programmes aimed in developing tetraploids that are cross compatible across various ploidy levels (Hassan *et al.* 2020). Despite its nutritional and culinary benefits, commercial cultivation is facing various challenges, resulting in low yields for

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farmers, attributed to the absence of region-specific high-yielding varieties. The situation underscores the necessity for comprehensive research on the genetic variability of pointed gourd germplasm in the country. Understanding the nature and extent of variability among genetic stocks is crucial for breeders, especially considering the plant's high cross-pollination and dioecious nature. The analysis of both genotypic and phenotypic factors, along with the study of relationships between yield and contributing attributes, can contribute valuable insights for germplasm improvement, helping identify suitable parents for targeted breeding programmes. Keeping these points in view an experiment was planned to assess the genetic diversity in pointed gourd genotypes for fruit yield and quality traits under eastern plateau and hill region.

MATERIALS AND METHODS

The experiment was conducted during summer seasons of 2021–22 and 2022–2023 at ICAR-Research Complex for Eastern Region, Farming System Research Centre for Hill and Plateau Region, Plandur, Ranchi (altitude of 625 m amsl), Jharkhand. During the first year, diligent care was provided during the establishment stage, particularly since it was propagated vegetatively. Subsequently, after the winter period and the conclusion of dormancy, the plant commenced the production of flowers and the setting of fruit. The research farm is located within the tropical to sub-tropical climatic zone. The annual rainfall at the site averages between 1400–1450 mm, with the majority occurring during the south-east monsoon period from June-August. The average temperature ranged from 7.5°C in December to 37.7°C in May. Relative humidity varied from 55% during winter to 88% in the rainy season. The research field has been identified as having laterite soil with a sandy loam texture on the surface, and the soil pH ranges from 4.5–5.5. In February 2021, plants prepared from vine cuttings were transplanted into the field with 3 replications in a 4 m × 2 m plot size using a randomized block design (RBD) at intervals of 2 m × 1 m, with 12 plants/treatment. The recommended cultivation practices were followed to ensure a healthy and successful pointed gourd crop. Experimental material consisted of 46 unique pointed gourd genotypes including 3 varieties, viz. Swarna Rekha, Swarna Suruchi and Swarna Alaukik developed by the centre; 2 hybrids HAPH-1, HAPH-2; and the remaining 41 genotypes (HAP) were the clonal selection of germplasm collected from eastern plateau and hill region. Data were collected from 46 pointed gourd genotypes across various agro-morphological characteristics during distinct fruit developmental stages. Observations were made on 18 traits, including total fruit yield (t/ha), number of fruits/plant, fruit weight (g), fruit length (cm), fruit diameter (cm), fruit volume (ml), number of seeds/fruit, seed weight (g), pulp weight (g), days to first harvest, frequency of harvest, moisture percentage, total carbohydrate by Anthrone reagent method (%), total protein (%) by Kjeldhal plus method, Total soluble solid (TSS) by Refractometer (°Brix), total phenol

by Folin-Ciocalteu Reagent method (mg GAE/100 g), total antioxidant by Ferric reducing antioxidant potential (FRAP) reagent method (mg AEAC/100 g of fruit) and ascorbic acid by using volumetric method (2,6 Dichlorophenolindophenol dye method) (mg/100 g fruit).

Statistical analyses: INDOSTAT software was utilized to conduct statistical analyses, including ANOVA, genotypic and phenotypic correlation, and path analysis, to explore the connections between yield and its contributing factors.

RESULTS AND DISCUSSION

The analysis of variance demonstrated highly significant mean sum of squares attributed to the genotypes for all the traits. All 46 pointed gourd genotypes showed significant variations (at a significance level of $P \leq 0.01$) for all the recorded parameters. These results closely aligned with the findings of Sarnaik *et al.* (1999) in the context of ivy gourd. Comparable outcomes were also observed in the studies conducted by Bharathi and Vishalnath (2010) on pointed gourd.

Genotypic correlation coefficients were higher than phenotypic ones for all traits, indicating a robust inherent association (Table 1, Fig. 1). Additionally, the results highlighted the minimal disparity between genotypic and phenotypic correlation values across all traits, implying that the impact of the environment on trait relationships is limited. Both at the phenotypic and genotypic levels, attributes such as the number of fruits/plant (0.891**P, 0.890**G), harvest frequency, pulp seed ratio, and total phenol content exhibited positive and notably significant ($P=0.01$) correlations with total fruit yield. This implies that opting for traits closely tied to total fruit yield could offer benefits in developing high-yield pointed gourd genotypes. The total fruit yield showed a strong and statistically significant negative correlation with days to first harvest (-0.308 and -0.308) and ascorbic acid (-0.330 and -0.329) at both the phenotypic and genotypic levels respectively. Total fruit yield exhibits a negative correlation with yield traits such as seed weight and quality traits such as total phenol and antioxidant activity. The findings suggest that concentrating on improving specific traits like the number of fruits/plant, harvest frequency, and pulp seed ratio has the potential to enhance pointed gourd fruit yield. These results align with the findings of Sarkar *et al.* (1999), Dora *et al.* (2002) and Khan *et al.* (2009) in pointed gourd.

Path coefficient analysis is a statistical approach based on multiple regression that aims to explore causal relationships between a dependent variable and two or more independent variables. Based on the path matrix data from the current experiment, it was observed that pulp weight had the highest positive direct impact on total fruit yield with a value of 0.9995 (Table 2). Following this, the number of fruits/plant (0.8487), seed weight (0.2125), pulp seed ratio (0.2073), frequency of harvest (0.1510), number of seeds/fruit (0.1043), total antioxidant content (0.0871), fruit volume (0.0682), fruit diameter (0.0556), total phenol (0.0530), moisture content (0.0503) and days to

Table 1 Phenotypic and genotypic correlation between different pairs of character in pointed gourd

Character	NFP	FW	FL	FD	FV	NSF	SW	PW	PSR	DFH	FH	M	TC	TP	TPh	TA	AA	TFY
NFP	1	-0.170*	-0.017	-0.177*	-0.214*	-0.098	-0.239**	-0.138	0.094	-0.348**	0.641**	-0.083	0.208*	0.068	0.282**	-0.254**	-0.254**	0.891**
FW	1	-0.170*	-0.017	-0.178*	-0.214*	-0.098	-0.239*	-0.137	0.094	-0.347**	0.638**	-0.083	0.208*	0.069	0.283**	-0.254*	-0.023*	0.890**
FL	1.000	0.734**	0.456**	0.806**	0.806**	0.481**	0.734**	0.984**	0.189*	0.096	-0.096	0.201*	-0.253**	-0.160	-0.020	0.119	-0.075	0.071
FD	1.000	0.735**	0.457**	0.806**	0.806**	0.481**	0.735**	0.984**	0.190*	0.098	-0.099	0.204*	-0.251*	-0.157	-0.019	0.119	-0.076	0.069
FV	1.000	0.167	0.790**	0.219**	0.407**	0.219**	0.407**	0.756**	0.315**	-0.028	0.029	0.090	-0.277**	-0.052	0.020	0.051	-0.069	0.132
NSF	1.000	0.171*	0.790**	0.219*	0.408**	0.219*	0.408**	0.757**	0.315**	-0.025	0.024	0.094	-0.275*	-0.049	0.021	0.051	-0.070	0.130
SW	1.000	0.371**	0.368**	0.471**	0.413**	0.368**	0.471**	0.414**	-0.050	0.051	-0.042	0.151	-0.071	-0.135	-0.234**	-0.077	-0.145	0.011
PW	1.000	0.373**	0.368**	0.472**	0.472**	0.368**	0.472**	0.414**	-0.049	0.052	-0.054	0.157	-0.070	-0.133	-0.233*	-0.076	-0.148	0.008
PSR	1.000	0.222*	0.368**	0.488**	0.488**	0.222*	0.488**	0.821**	0.310**	0.108	-0.091	0.065	-0.313**	-0.111	0.094	0.310**	0.020	0.014
DFH	1.000	0.222*	0.368**	0.488**	0.488**	0.222*	0.488**	0.821**	0.310**	0.109	-0.094	0.068	-0.312*	-0.110	0.094	0.310**	0.019	0.013
FH	1.000	0.832**	0.347**	0.347**	0.347**	0.832**	0.347**	0.347**	-0.583**	0.117	-0.175*	0.167*	0.119	-0.189*	-0.372**	-0.219**	-0.036	0.005
M	1.000	0.832**	0.347**	0.347**	0.347**	0.832**	0.347**	0.347**	-0.583**	0.117	-0.176*	0.168*	0.119	-0.189*	-0.372**	-0.219*	-0.036	0.004
TC	1.000	0.601**	0.347**	0.347**	0.347**	0.601**	0.347**	0.347**	-0.503**	0.223**	-0.157	0.268**	0.053	-0.212*	-0.291**	-0.079	0.054	-0.072
TP	1.000	0.601**	0.347**	0.347**	0.347**	0.601**	0.347**	0.347**	-0.502**	0.224*	-0.159	0.270*	0.053	-0.210*	-0.290**	-0.079	0.053	-0.073
TPh	1.000	0.356**	0.054	0.054	0.054	0.356**	0.054	0.054	0.356**	0.056	-0.075	0.166	-0.312**	-0.132	0.053	0.161	-0.102	0.103
TA	1.000	0.356**	0.056	0.056	0.056	0.356**	0.056	0.056	0.356**	0.081	0.086	0.169*	-0.310*	-0.130	0.054	0.161	-0.103	0.101
AA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.077	-0.219**	0.081	-0.399**	0.143	0.350**	0.248**	-0.132	0.168*
TFY	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.076	0.076	0.083	-0.398**	0.143	0.350**	0.248*	-0.133	0.167*
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.219**	-0.217*	0.083	0.086	0.007	-0.173*	0.208*	0.299**	-0.308**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.087	-0.217*	0.083	0.087	0.010	-0.171*	0.208*	0.298**	-0.308**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.154	1.000	-0.085	0.154	-0.013	0.245**	-0.138	-0.143	0.655**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.153	1.000	-0.090	0.153	-0.013	0.244*	-0.137	0.137	0.654**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.057	1.000	1.000	-0.057	-0.548**	-0.140	-0.229**	-0.172*	0.011
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.056	1.000	1.000	-0.056	-0.544**	-0.139	-0.228*	-0.173*	0.009
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.077	-0.126	-0.175*	0.078	0.070
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.078	-0.125	-0.175*	0.078	0.070
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.152	0.084	0.238**	-0.050
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.154	0.083	0.237*	-0.050
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.491**	0.102	0.319**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.490**	0.103	0.318**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.229**	-0.137
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.228*	-0.137
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.330**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.329**
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

NFP, Number of fruits/plant; FW, Fruit weight; FL, Fruit length; FD, Fruit diameter; FV, Fruit volume; NSF, Number of seed/fruit; SW, Seed weight; PSR, Pulp weight; PW, Pulp weight; TP, Total phenol; TA, Total antioxidant; AA, Ascorbic acid; TFY, Total fruit yield.

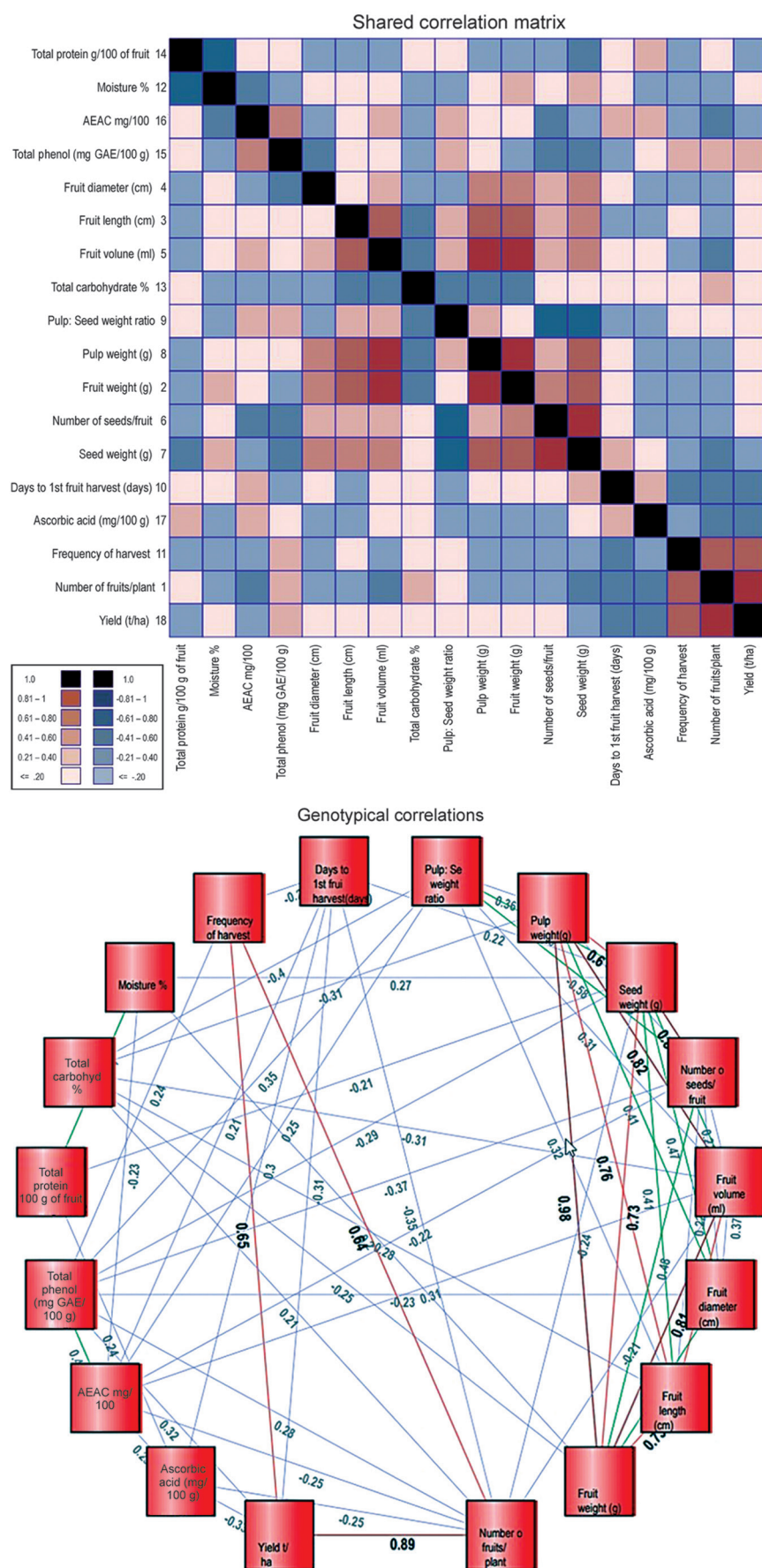


Fig. 1 Standard genotypic correlation matrix graph of pointed gourd genotypes for various traits.

first harvesting (0.0202) also exhibited positive direct effects on fruit yield. On the other hand, certain factors showed negative direct effects on fruit yield. These included average fruit weight (-0.5393), ascorbic acid content (-0.0852), total carbohydrate content (-0.0525), fruit length (-0.0451), and total protein content (-0.0411). The highest indirect effect on fruit yield per plant was expressed by pulp weight via days to first harvest (0.9912). Considering the residual factor effect (0.3312) on total fruit yield, it is evident that diversity has been explained to a maximum extent by characters selected for study. The comprehensive path analysis of the data revealed that total fruit yield showed a significant positive direct effect with average pulp weight, number of fruits/plant, seed weight, pulp seed ratio, frequency of harvest number of seeds/fruit, total antioxidant content, fruit volume, fruit diameter, total phenol, moisture percentage and days to first fruit harvest. The observed outcomes are likely a result of the combined influence of various genes affecting these traits. This aligns with the findings of Khan *et al.* (2009), who emphasized the direct and positive impact of the average number of fruits/plant on yield. Similar findings were drawn by Sarkar *et al.* (1999) in pointed gourd.

In 1936, Mahalanobis introduced D^2 statistics to measure genetic distance between populations. Ram *et al.* (2001) applied this concept to pointed gourd genotypes, calculating D^2 values and using Non-Hierarchical Euclidean method. In the current study, 46 genotypes under study classified into 12 clusters based on fruit yield and related components (Fig. 2). Bharathi and Vishalnath (2010) exploited D^2 statistics values to classify 22 pointed gourd genotypes into 5 clusters. Similarly, Debata (2016) and Verma *et al.* (2017) carried out separate studies on the genetic divergence of genotypes of pointed gourd and identified 7 clusters, which align with the findings of the current work. Significant differences were observed in the average cluster means of 18 pointed gourd traits. The highest total

Table 2 Path coefficient analysis for different characters in pointed gourd

Characters	NFP	FW	FL	FD	FV	NSF	SW	PW	PSR	DFH	FH	M	TC	TP	TPh	TA	AA	TFY
NFP	0.8487	-0.1444	-0.0148	-0.1507	-0.1816	-0.0832	-0.2028	-0.1165	0.0798	-0.2943	0.5417	-0.0708	0.1765	0.0582	0.2400	-0.2156	-0.2147	0.8904**
FW	0.6408	-0.5393	-0.9356	-0.578	-0.4232	-0.0696	-0.9462	-0.5275	-0.8621	-0.1464	0.1973	-0.7707	0.6978	0.8282	0.174	-0.4537	0.7350	0.0694
FL	0.0008	-0.0331	-0.0451	-0.0077	-0.0356	-0.0099	-0.0184	-0.0342	-0.0142	0.0011	-0.0011	-0.0043	0.0124	0.0022	-0.001	-0.0023	0.0032	0.1295
FD	-0.0099	0.0254	0.0095	0.0556	0.0207	0.0205	0.0262	0.0230	-0.0027	0.0029	-0.0030	0.0087	-0.0039	-0.0074	-0.013	-0.0042	-0.0082	0.0078
FV	-0.0146	0.0550	0.0538	0.0254	0.0682	0.0151	0.0333	0.0559	0.0211	0.0075	-0.0064	0.0046	-0.0212	-0.0075	0.0064	0.0211	0.0013	0.0127
NSF	-0.0102	0.0502	0.0228	0.0384	0.0232	0.1043	0.0868	0.0362	-0.0608	0.0122	-0.0184	0.0175	0.0124	-0.0197	-0.0388	-0.0228	-0.0038	0.0044
SW	-0.3958	0.4416	0.8044	0.7007	0.9395	0.8219	0.2125	0.5453	-0.1304	0.1869	-0.2569	0.8359	0.7596	-0.9873	-0.1148	-0.1182	0.7526	-0.0733
PW	-0.2748	0.1420	0.1333	0.9308	0.4947	0.3759	0.866	0.9995	0.8627	0.9912	-0.9626	0.9676	-0.4192	-0.8678	0.8791	0.5363	-0.4699	0.1011
PSR	0.0195	0.0393	0.0653	-0.0101	0.0642	-0.1208	-0.1040	0.0738	0.2073	-0.0392	0.0157	-0.0311	-0.0825	0.0297	0.0726	0.0515	-0.0275	0.1673*
DFH	-0.0070	0.0020	-0.0005	0.0010	0.0022	0.0024	0.0045	0.0011	-0.0038	0.0202	-0.0044	0.0017	0.0018	0.0002	-0.0035	0.0042	0.0060	-0.3080**
FH	0.0964	-0.0150	0.0036	-0.0082	-0.0142	-0.0266	-0.0240	-0.0113	0.0114	-0.0328	0.1510	-0.0137	0.0231	-0.0019	0.0369	-0.0207	-0.0208	0.6535**
M	-0.0042	0.0103	0.0047	0.0079	0.0034	0.0084	0.0136	0.0085	-0.0075	0.0042	-0.0045	0.0503	-0.0028	-0.0274	-0.0070	-0.0115	-0.0087	0.0087
TC	-0.0109	0.0132	0.0145	0.0037	0.0164	-0.0062	-0.0028	0.0163	0.0209	-0.0046	-0.0080	0.0029	-0.0525	-0.0041	0.0066	0.0092	-0.0041	0.0698
TP	-0.0028	0.0065	0.0020	0.0055	0.0045	0.0078	0.0086	0.0053	-0.0059	-0.0004	0.0005	0.0224	-0.0032	-0.0411	-0.0063	-0.0034	-0.0097	-0.0504
TPh	0.0150	-0.0010	0.0011	-0.0123	0.0050	-0.0197	-0.0153	0.0029	0.0186	-0.0091	0.0129	-0.0073	-0.0066	0.0081	0.0530	0.0260	0.0054	0.3182**
TA	-0.0221	0.0104	0.0044	-0.0067	0.0270	-0.019	-0.0069	0.014	0.0216	0.0181	-0.0119	-0.0199	-0.0152	0.0073	0.0427	0.0871	0.0199	-0.1366
AA	0.0215	0.0065	0.006	0.0126	-0.0016	0.0031	-0.0045	0.0088	0.0113	-0.0254	0.0117	0.0148	-0.0066	-0.0202	-0.0087	-0.0194	-0.0852	-0.3291**

Residual effect = 0.3312. NFP, Number of fruits/plant; FW, Fruit weight; FL, Fruit length; FD, Fruit diameter; FV, Fruit volume; NSF, Number of seed/fruit; SW, Seed weight; PW, Pulp weight; PSR, Pulp: Seed ratio; TP, Total phenol; TA, Total antioxidant; AA, Ascorbic acid and TFY, Total fruit yield.

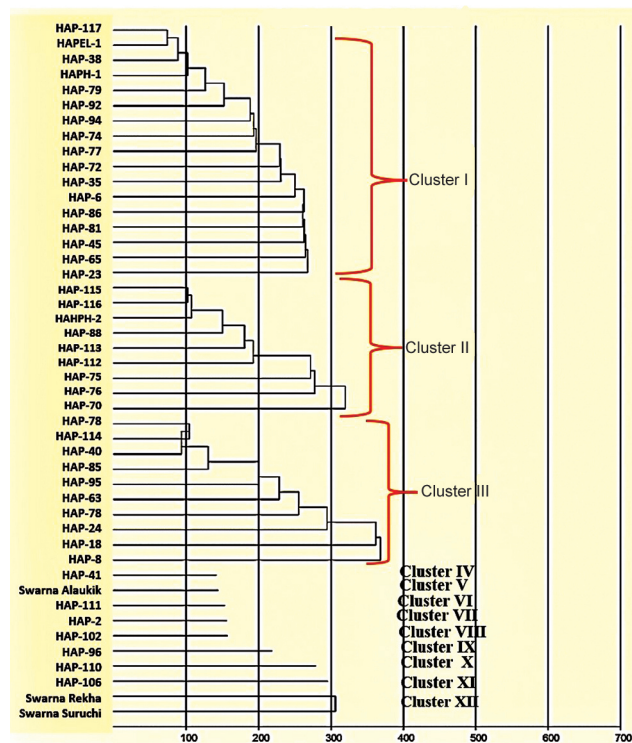


Fig. 2 Cluster analysis for divergence of pointed gourd genotypes by Tocher method.

fruit yield was in cluster V (23.73), followed by clusters XII (21.10) and IV (13.61). The lowest yield was in cluster IX (6.23). HAP-79 in cluster I had the highest total fruit yield. Cluster V exhibited the highest mean for the number of fruits per plant (151.00), with the lowest in cluster IX (16.67). HAP-79 in cluster I had the maximum number of fruits per plant. The wider range of cluster means suggested genetic variation among studied genotypes. Hybridization between divergent clusters, especially those with high yields, is recommended for incorporating desirable traits. The highest yielding variety, Swarna Alaukik, was in cluster V. Utilizing genotypes from clusters I and II in breeding programmes can provide diversity and improve economic characteristics.

In this study, intracluster distances ranged from 0 to 17.87. Maximum intracluster distance was within cluster III (17.87), followed by clusters XII (17.49), II (16.74), and I (15.95), while minimum intracluster distance (0) was observed in clusters IV, V, VI, VII, VIII, IX, X, and XI. The highest intercluster distance was between clusters III and XII (40.82), followed by clusters IV and XII (40.11), with the lowest intercluster distance between clusters VI and VIII (12.53). Higher intercluster distance indicates higher genetic disparity within clusters, while lower values suggest shared genetic diversity. For higher heterosis potential in yield and quality, crosses between genotypes from cluster III and XII may exhibit greater diversity. Therefore, special attention should be given to genotypes from these clusters during inbred line selection after crossing. Overall, the analysis indicates higher inter-cluster distances, highlighting the genetic diversity among genotypes and their distinct

characteristics.

The study identified significant genetic variability in the available pointed gourd germplasm in terms of fruit yield and quality traits. Traits like number of fruits per plant, harvest frequency, pulp-to-seed ratio and phenol content correlated strongly with total fruit yield. Emphasizing traits such as number of fruits per plant and pulp weight can enhance overall yield. Varieties like Swarna Alaukik and HAP-79 exhibited high yields, suggesting their potential as breeding parents. The cluster III (HAP-78, HAP-114, HAP-40, HAP-85, HAP-95, HAP-63, HAP-78, HAP-24, HAP-18, HAP-8) and cluster XII (Swarna Rekha and Swarna Suruchi), with maximum intercluster distance, offer ideal genetic diversity for breeding programmes. Intercrossing diverse clusters can generate novel cultivars with high yield potential.

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