



Genetic diversity analysis in ash gourd [*Benincasa hispida* (Thunb.) Cogn.] in Northeast India

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ABSTRACT

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An experiment was conducted in the field to assess the existing variability in ash gourd germplasm based on D^2 statistics for 26 quantitative traits. The whole germplasm was classified into 7 clusters, in which the highest inter cluster distance was recorded between cluster III and cluster VII; Cluster VII shown highest mean value for cotyledon length, cotyledon width, vine length, average fruit weight, seed length, seed width, flesh thickness, vit. C, yield/plant and yield/ha. It has been found that Cluster III shown highest mean value for ovary length and Cluster I shown highest mean value for fruit length and fruit diameter. Principal component analysis revealed total variability of 38.6% among genotypes contributed by PC1 (26.6 %) and PC2 (12%). Hence, simultaneous selection of these traits is advised for genetic improvement in the ash gourd breeding program.

1. Introduction

Ash gourd [*Benincasa hispida* (Thunb.) Cogn.], although being a minor crop among the cucurbits has gained popularity due to its high vitamins, minerals, various nutraceutical properties and good transport qualities. During crisis time of vegetables it comes in the market because of its long storage life. Ashgourd is grown throughout the country. Ash gourd shows variability for various vegetative and qualitative traits *viz.* fruit shape, size, days to flowering, *etc.* North East India has good genetic variability for various traits in ash gourd and no exploration has been taken to tap the diversity till now. The concept of the magnitude and nature of variability or genetic diversity among the germplasm of ash gourd is very important for the breeder to tackle the production or yield related problems. The genetic variability studies and the degree of association along with genetic divergence among the yield contributing traits are helpful for designing a successful breeding programme for any crop. For quantification of genetic divergence, various biometrical protocols have been developed which can be used in isolating genetically different parents to carry out an effective hybridization plan (Uddin *et al.*, 2014). Hence, assessment of genetic diversity is of ultimate important to identify the genetic resources which are to be engaged in the hybridization programme (Amin *et al.*, 2014). The huge genetic diversity in the genetic material provides better opportunity of getting diverse traits in the segregating

generations which helps in improvement of any crop. The selection of parents based on genetic divergence is more significant for an efficient hybridization program (Kumar and Gurumurthi, 2000). Yield, being a complex character, are controlled by a many number of contributing characters and interactions among them. A correlation study between different characters of quantitative nature gives an idea of association that could be effectively tapped to design selection plan for yield components improvement.

In any effective breeding programme, considering the relative magnitude of association of different characters with yield are more desirable. The path analysis technique of Wright (1921), estimates direct and indirect effect of various components in construction the total correlation towards yield. It is an important tool for the better understanding of the crop inheritance in respect of yield.

Hence, the present experiment was conducted to compute the genetic diversity present among the selected ash gourd genotypes and to select suitable parents to use in future hybridization programs.

2. Materials and Methods

The trial was conducted at horticulture farm at School of Agricultural Sciences and Rural Development, Medziphema, Nagaland University during March to September for both years 2018 and 2019. Thirty seven genotypes of ash gourd from different places of India have

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been collected to conduct the experiment as shown in Table 1. The treatments were designed in a Randomized Block Design in 3 replications consisting of 8 plants for each genotype. The plantation was done at a distance of 4m x 0.6 m. The standard packages of practices for better growth of plants in the field were followed.

Traits including cotyledon length (cm) and cotyledon width (cm) were recorded at unfolded leaf stage. Length of internodes (cm), leaf length (cm), leaf width (cm), number of lobes and petiole length (cm) were recorded at 50 % flowering stage (first pistillate flower appears in 50% plant). Days to first female flower appears, nodes at which first female flower appears, ovary length (cm) were recorded at initial flowering stage. Peduncle length (cm), fruit length

(cm), fruit diameter (cm), flesh thickness (cm), number of primary branches, vine length (m), crop duration (days), number of fruits per plant, average fruits weight(g), TSS (⁰B), vitamin C (mg/100g), yield/plant(kg) and yield/ha(q) were recorded at marketable maturity of fruit. Seediness, seed length (cm), seed width (cm) and 100 seed weight (g) were recorded at full maturity (seed harvest maturity).

The data were analyzed using Mahalanobis (1936) D² statistics and Tocher's method according to Rao (1952) for estimating group constellation. Average inter-cluster was estimated according to Singh and Choudhary (1977). Principal component analysis was done using the statistical package R with the help of agricolae package (De Mendiburu, 2014).

Table 1. Details of the genotypes with their source of collection.

Sl. No.	Name of the institutes	Name of the varieties	Source of Collection
1.	Indian Institute of Vegetable Research (IIVR), Varanasi.	KashiSurbhi KashiUjjwal KashiDhawal	Institute
2.	Indian Agriculture Research Institute (IARI), New Delhi.	PusaUjjwal PusaSabjiPetha	Institute
3.	Kerala Agricultural University (KAU), Thrissur.	Indu KAU-Local	Institute
4.	Dr. Y S R Horticultural University, A.P.	Shakti	Institute
5.	KVK, Buxer	Bux-1	Institute
6.	ICAR Research Complex, NER, Tripura	TAG-1 TAG -2 TAG -3 TAG -4 TAG -5 TAG -6 TAG -7 TAG -8 TAG -9	Institute
7.	Uttar BangaKrishiVishwavidyalaya (UBKV), Coochbihar	Pundibari Local-1 Pundibari Local-2 Basirhat Bhagyalaxmi	Institute
8.	ICAR, Goa	Panaji Local	Institute
9.	TNAU, Coimbatore	CO-2	Institute
10.	CSAUAT, Kanpur	KAG-1	Institute
11.	PAU, Ludhiana	PAG-3	Institute
12.	G.B. Pant University of Agriculture and Technology, Pantnagar	Pant Petha-1	Institute
13.	Manipur	Manipur-1 Manipur-2 Manipur-3	Imphal, Local Market
14.	Meghalaya	Meghalaya-1 Meghalaya-2 Meghalaya-3	Shillong, Local Market
15.	Assam	AS-1	Majuli,

		AS-2	Local Market
16.	Nagaland	Nagaland local-1 Nagaland local-2	Dimapur, Local Market

3. Results and Discussion

The data on the mean performance of 37 genotypes for 26 quantitative traits are given in the table 2. The 37 genotypes were grouped into 7 clusters based on Tocher's method (Table 2; Figure 1). The highest number of genotypes were found in cluster VII (9 genotypes), while cluster II was solitary cluster with single genotype (Figure 1). The mean of inter-cluster D^2 – values varied from 543.91 to 3568.03, where maximum inter-cluster distance (3568.03) was noticed in between cluster III and cluster VII, shows the selection of the divergent parents from these clusters will yield good segregation for the traits of interest (Chippy *et al.*, 2021). However, the minimum inter-cluster distance (543.91) was noticed in between cluster I and clusters III (Table 3; Figure 2).

Table 2: Inter cluster distances values in ash gourd.

Cluster number	Number of genotypes included	Name of genotypes
I	7	KashiDhawal, TAG-4, TAG-5, PusaUjjwal, KAU Local, KashiUjjwal, KAG-1
II	1	PAG-3
III	7	KashiSurbhi, Indu, CO-2, Shakti, Bhagyalaxmi, PusasabjiPetha, Pant Petha-1
IV	4	TAG-1, TAG-3, TAG-2, TAG-6
V	7	TAG-7, TAG-8, TAG-9, Pundibari Local-1, Pundibari Local-2, Panji Local, Bashirhat
VI	2	Bux-1, AS-1
VII	9	Manipur-1, Manipur-2, Manipur-3, Nagaland Local-1, Nagaland Local-2, AS-2, Meghalaya-1, Meghalaya-2, Meghalaya-3.

Table 3: Inter cluster distances values in ash gourd.

Cluster number	I	II	III	IV	V	VI
I						
II	2426.08					
III	543.91	2730.91				
IV	694.27	1831.38	907.62			
V	1126.77	1543.82	1604.03	932.90		
VI	1839.66	1123.44	2306.11	1519.26	737.55	
VII	3249.87	837.85	3568.03	2668.36	2293.16	1717.00

The mean of cluster shows the average performance of all the genotypes which is grouped in a single cluster (Table 4). Cluster VII shown highest mean value for cotyledon length (3.55), cotyledon width (2.00), vine length (6.72), average fruit weight (5701.08), seed length (1.28), seed width (0.70), flesh thickness (4.50), vit. C (42.57), yield/plant (21.70) and yield/ha (904.16); cluster VI shown highest mean value for number of primary branches (3.52), leaf length (16.80), leaf width (22.70), number of lobes(6.97), seediness (1478.23) and seed weight (5.62); Cluster V shown highest mean value for internodal length (15.21), petiole length (14.52), peduncle length (7.45) and crop duration (133.20); Cluster IV shown highest mean value for days for 1st female flower (76.46), nodes for 1st female flower (20.99), no. of fruit/plant (5.42) and TSS (2.29); Cluster III shown highest mean value for ovary length (3.13) only and Cluster I shown highest mean value for fruit length (27.98) and fruit diameter (20.32). Hence, cross breeding programme among these genotypes would end up in getting transgressive segregants (Chippy *et al.*, 2021).

The Principal component analysis was calculated to dispense the combined variance into the principle components for selecting the better germplasm which is based on the average amount of different traits. The principal factors PC are a powerful tool that provides lenience for getting suitable parental genotypes to design useful breeding

programs (Naziret *et al.*, 2013). The 1st principle component (PC1) contributed maximum towards total variability (26.6%). Cotyledon length, cotyledon width, length of internodes, number of primary branches, vine length, leaf width, number of lobes, petiole length, peduncle length, fruit length, fruit diameter, flesh thickness, Seediness, seed length, seed width, crop duration, average fruits weight, 100 seed wt., vitamin C and yield/plant were positively loaded while days to first female flower appears, nodes at which first female flower appears, ovary length, number of fruits per plant and TSS were negatively loaded (Figure 3). The second principal component (PC2) contributed 12% towards total variability. The traits including cotyledon width, length of internodes, number of primary branches, leaf length, leaf width, number of lobes, petiole length, ovary length, peduncle length, flesh thickness, seediness, 100 seed wt., TSS and vitamin C were positively loaded while cotyledon length, vine length, days to first female flower appears, nodes at which first female flower appears, fruit length, fruit diameter, seed length, seed width, crop duration, number of fruits per plant and average fruits weight was negatively loaded. The PC bi-plot shows the genotypes distributed and variables and the gap within characters concerning PC1 and PC2 exhibited the contribution of these traits in creating variation among the germplasm (Figure 3).

Figure 1. Dendrogram showing the clustering pattern of thirty seven genotypes of ash gourd. (Clustering by Tocher Method)

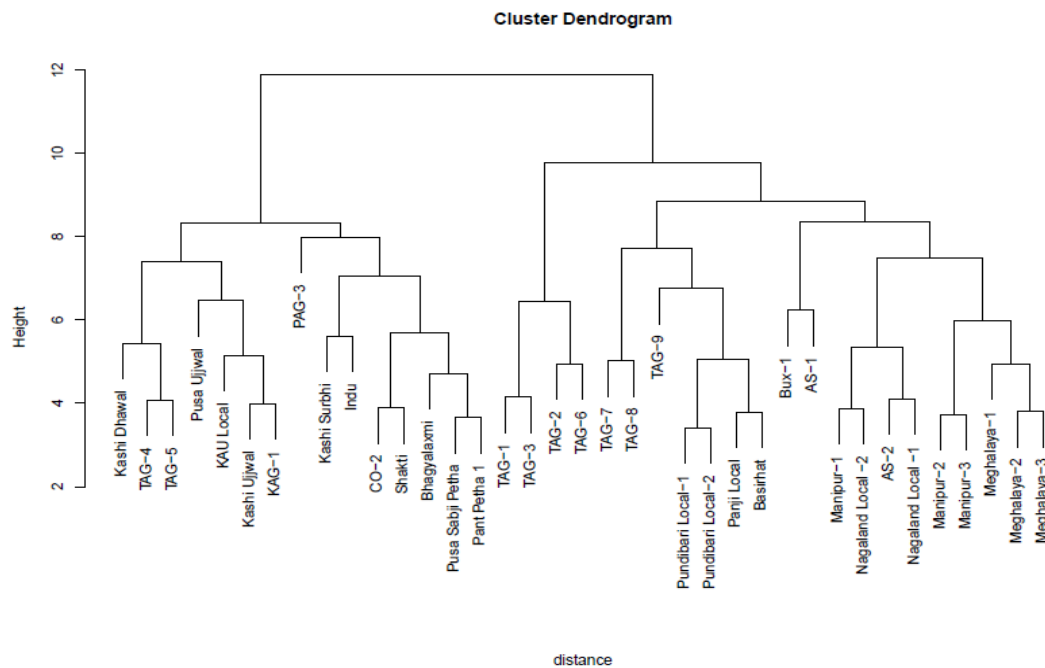


Figure 2. Inter-cluster distance among seven groups of ash gourd genotypes.

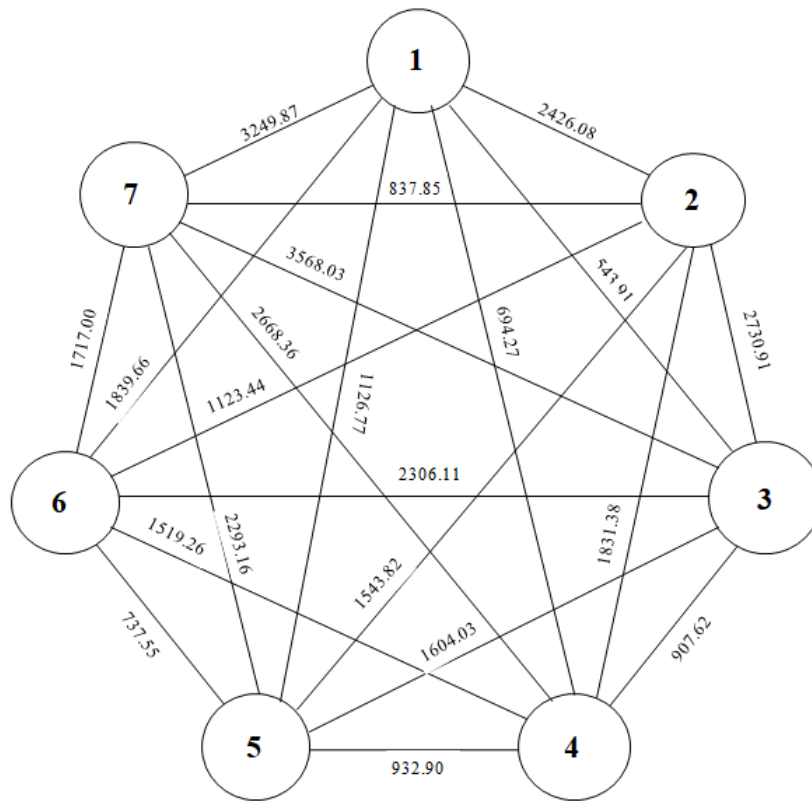


Table 4. Mean Performance of germplasm in each cluster for yield and its components in ash gourd.

	I	II	III	IV	V	VI	VII
CL	2.71	3.27	2.82	2.82	2.77	2.88	3.55
CW	1.38	2.00	1.52	1.47	1.63	1.67	2.00
LOI	12.95	14.98	13.62	12.64	15.21	14.29	14.12
NPB	3.10	3.50	3.17	3.44	3.28	3.52	3.48
VL	5.88	5.77	5.00	6.36	6.28	6.60	6.72
LL	11.87	14.53	12.20	13.13	15.50	16.80	13.72
LW	15.55	20.81	16.91	18.06	20.91	22.70	19.52
NOL	5.84	6.31	6.16	5.21	6.06	6.97	5.98
PL	9.32	15.40	11.16	11.24	14.52	14.46	12.92
DFFF	72.22	72.85	73.17	76.46	70.44	75.49	73.48
NFFF	18.21	15.79	19.04	20.99	19.28	13.30	19.77
OL	3.00	2.97	3.13	2.88	2.86	3.00	2.58
PEDL	5.94	6.23	7.08	5.97	7.70	7.10	7.45
FL	27.98	26.90	20.23	23.54	23.86	25.23	27.24
FD	20.32	18.82	15.16	19.78	18.01	18.53	18.58
FT	3.86	4.20	3.85	3.57	4.31	3.93	4.50
SEE	965.44	543.21	545.76	557.87	1320.09	1478.23	574.38
SL	0.99	1.20	0.94	1.06	1.14	1.20	1.28
SW	0.52	0.69	0.47	0.57	0.66	0.66	0.70
CD	119.56	120.85	117.44	119.74	133.20	130.50	128.66
NFP	5.34	4.04	5.16	5.42	3.66	4.33	3.80
AFW	2493.54	4868.38	2160.38	3042.38	3562.81	4247.85	5701.08

SEW	4.35	5.21	4.29	4.14	4.87	5.62	4.87
TSS	2.24	2.24	1.92	2.29	2.06	1.33	2.24
VC	39.39	39.12	40.45	38.58	40.64	34.13	42.57
YIP	13.38	19.62	11.15	16.28	13.04	18.38	21.70
YIH	557.47	817.41	464.74	678.31	543.36	765.93	904.16

CL-Cotyledon length, CW: Cotyledon width, LOI: Internodal length, NPB: number of primary branches, VL: Vine length, LL: Leaf length, LW: Leaf width, NOL Number of Lobes, PL: Petiole length , DFFF: Days to first female flower, NFFF: Nodes of first female flower, OL: Ovary length, PEDL: Peduncle length, FL: Fruit length, FD: Fruit diameter, FT: Flesh thickness, SEE: Seediness, SL: Seed length, SW: Seed width, CD: Crop duration, NFP: Number of fruit per plant, AFW: Average fruit weight, SEW: 100 seed weight, TSS: TSS, VC: Ascorbic acid content.

4. Conclusion

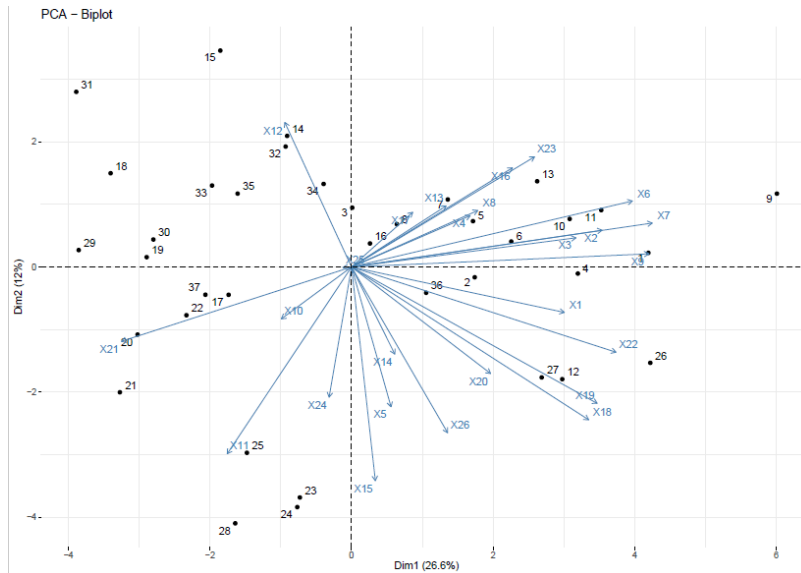
Thus, it can be concluded that when planning for hybridization programme or the development of heterotic hybrids and better transgressive segregants are done then one should select genotypes from cluster VII for cotyledon length, cotyledon width, vine length, flesh thickness, seed length, seed width, average fruit weight, vitamin C and more yield. Similarly, for crop duration or earliness, genotypes from cluster V should be selected and for fruit length and diameter, genotypes from cluster I should be selected. For more number of fruits per plant and TSS, genotypes from cluster IV should be selected and for more number of seeds, genotypes from cluster VI should be selected for breeding programme.

5. Acknowledgement.

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6. Conflicts of Interest. None

Figure 3. Biplot of thirty seven genotypes of ash gourd using PCA analysis.



X₁: Cotyledon length (cm), X₂: Cotyledon width (cm), X₃: Length of internodes (cm), X₄: Number of primary branches, X₅: Vine length (m), X₆: Leaf length (cm), X₇: Leaf width (cm), X₈: Number of lobes, X₉: Petiole length (cm), X₁₀: Days to first female flower appears, X₁₁: Nodes at which first female flower appears, X₁₂: Ovary length (cm), X₁₃: Peduncle length (cm), X₁₄: Fruit length (cm), X₁₅: Fruit diameter (cm), X₁₆: Flesh thickness (cm), X₁₇: Seediness, X₁₈: Seed length (cm), X₁₉: Seed width (cm), X₂₀: Crop Duration (days), X₂₁: Number of fruits per plant, X₂₂: Average fruits weight(g), X₂₃: 100 seed wt. (g), X₂₄: TSS, X₂₅: Vitamin C (mg/100gm), X₂₆: Yield/Plant(kg).

Figure 4. Map view of place of collections of genotypes.



7. References

- Amin, M. F., Hasan, M., Barma, N. C. D., Rasul, M. G. and Rahman, M. M., Genetic diversity analysis in spring wheat (*Triticum aestivum* L.) *Bangladesh J. Agril. Res.*, 2014, 39(2): 189-196.
- Chippy, A. K., Pillai, M. A. and Shoba, D., Genetic diversity analysis in black gram [*Vignamungo* (L.)Hepper].*Electronic J. Plant Breeding*, 2021, 12(1): 37-45.
- De Mendiburu, F., *Agricolae: Statistical procedures for agricultural research. R package version*, 2014, 1(1).
- Kumar, A. and Gurumurthi, K., Genetic divergence studies on clonal performance of *Casuarina equisetifolia*. *Silvae Genetica*, 2000, 49(2): 57-59.
- Mahalanobis, P. C., On the generalized distance in Statistics.*Proc. Nat. Sci.*, 1936, 2: 49-55.
- Nazir, A., Farooq, J., Mahmood, A., Shahid, M. and Riaz, M., Estimation of genetic diversity for CLCuV, earliness and fiber quality traits using various statistical procedures in different crosses of *Gossypiumhirsutum* L. *VestnikOrelgau*, 2013, 9(43): 2-9.
- Rao, C. R., *Advanced Statistical Method in Biometric Research*, John Wiley and Sons, New York, 1952, pp. 351-64.
- Singh, P. K. and Choudhary, R. D., *Biometrical methods. In: Quantitative Genetic Analysis*, Kalyani Publishers, New Delhi, 1977, pp. 178-185.
- Uddin, M. S., Rahman, M. M. Hossain, M. M. and Mian, M. A. K., Genetic diversity in eggplant genotypes for heat tolerance.*SAARC J. of Agri.*, 2014, 12(2): 25-39.
- Wright, S., *Correlation and causation. J. Agric. Res.*,1921, 20: 557-585.