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## Study on genetic divergence in various genotypes of watermelon [*Citrullus lanatus* (Thunb.) Mansf.].

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### Abstract

The results of the analysis of variance indicated that substantial genetic variability was present for yielding contributing characters. The intra-cluster distance was recorded as the highest for cluster 3 (49.75) which indicates the existence of maximum variability within this cluster. The inter-cluster distance was maximum between clusters 5 and 6 (94.81) which indicates that the genotypes included in these clusters are genetically diverse. So, it is desirable to select accessions from the clusters having high inter-cluster distance in the recombination breeding programs. The minimum inter-cluster distance was observed between cluster 1 and cluster 5 (50.92), indicating the close relationship among the genotypes included in these clusters. Based on yield and yield contributing characters, the genotypes viz., VRW-14, VRW-12, VRW-20 and VRW-17 were found promising for the future improvement programme.

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### Introduction

Watermelon [*Citrullus lanatus* (Thunb.) Mansf.] belongs to the family *Cucurbitaceae* and it is the only cultivated species of this genus (Bisognin 2002; Choudhary et al. 2015). The genus has four diploid species viz. *C. lanatus*, *C. ecirrhosus*, *C. colocynthis*, and *C. rehmii* are widely grown in Africa, Asia and the Mediterranean region (Levi et al. 2001a). *C. lanatus* var. *citroides*, which is most common in central Africa, probably gave rise to domesticated *C. lanatus* var. *lanatus* (Robinson & Decker-Walters 1997). *Citrullus colocynthis* is considered a putative ancestral or progenitor species of watermelon which is

generally found to be grown in India in the north-western plain in fallow lands/fields. It is drought hardy and wide diversity is found in Rajasthan and Gujarat states. Out of the two races of *C. colocynthis*, one is found on the Mediterranean coast and in Israel, the other in the desert region of Negev and Sinai (Mujaju 2010). All *Citrullus* species originated in the Kalahari region of Africa (Maggs-Kolling & Christiansen 2003) with wild species found growing in India and China. Zeven and de Wet (1982) suggested the Hindustani region comprising India and South East Asia as a center for domestication.

In India, watermelon occupied an area of about 99,000 ha with a production of about 2,098,000 MT (NHB 2019). Various marker-assisted diversity studies have reported a narrow genetic base in cultivated watermelon (Levi et al. 2001b; Kwon et al. 2010; Haldhar et al. 2016; Samadia & Haldhar 2020) though species variation exists. Diversity analysis of indigenous watermelon genetic resources from Namibia (Maggs-Kolling & Christiansen 2003), Sudan (Goda 2007), Mozambique (Munisse et al. 2011), Zimbabwe (Mujaju et al. 2010), elucidated the role of landraces play in economy and nutrition of native communities. In India, key watermelon production areas fall in the north-western plains of the Indo-Gangetic region (sub-tropical with mild winters) and coastal states of Tamil Nadu, Karnataka and Orissa (tropical). These regions also harbour maximum watermelon diversity in India (Wehner 2009; Haldhar et al. 2015). The genetic variability study has a paramount role in breeding for wide adaptation. It helps in the selection of desirable parents for an efficient hybridization program. Divergent groupings emerge as a result of hybridization, which is the primary goal of plant breeding programmes. Mahalanobis's (1936)- $D^2$  techniques (based on multivariate analysis) are a powerful tool for accessing genetic divergence and serve to be a good index of genetic diversity. Further, the knowledge of inter-relationships among different characters is helpful because the selection of one trait may directly or indirectly affect the performance of another, which is determining the components of complex characters. Therefore we conducted our research to know the morphological characterization of watermelon genotypes using DUS descriptor traits.

## Material and Methods

The present investigation was carried out on 21 watermelon genotypes during the *summer* season 2020-21 at Research Farm of the Department of Vegetable Science, CCS HAU Hisar (Haryana). The detail of all 21 genotypes as shown in Table 1. The location of the experiment in Hisar was situated at 29.10° N latitude and 75.46° E longitude and an elevation of 215.2 m above mean sea level. Hisar city of Haryana lies on the outer margins of the southwest (SW) monsoon region. It has a tropical monsoonal climate and is characterized as an arid type of climate. The main characteristics of the climate in the Hisar district are its dryness, extreme temperature, and scanty rainfall. The average annual rainfall is around 452 mm. The soil exhibits a mixed pattern of Aeolian and Alluvial deposits. The mean weekly weather condition during the *summer* season 2020-21 is depicted in Figure 1.

The observations for plant growth attributes were recorded on randomly selected five competitive plants per plot in each replication, while for days to emergence of the first staminate flower, days to emergence of the first pistillate flower, blooming periods, and days taken to fruit maturity were recorded on a whole plot basis. Analysis of variance in a Randomized block design for each quantitative character was statistically analysed as described by Panse and Sukhatme (1967). The genetic diversity  $D^2$  analysis was done using the method suggested by Mahalanobis (1936) and elaborated by Murty & Arunachalam (1966). A cluster of genetic traits of Watermelon was made using Tocher's Method (Rao 1952) and the average intra- and inter-cluster average  $D^2$  values were calculated by the formula given by Singh & Chaudhary (1977), Nadarajan & Gunasekaran (2012).

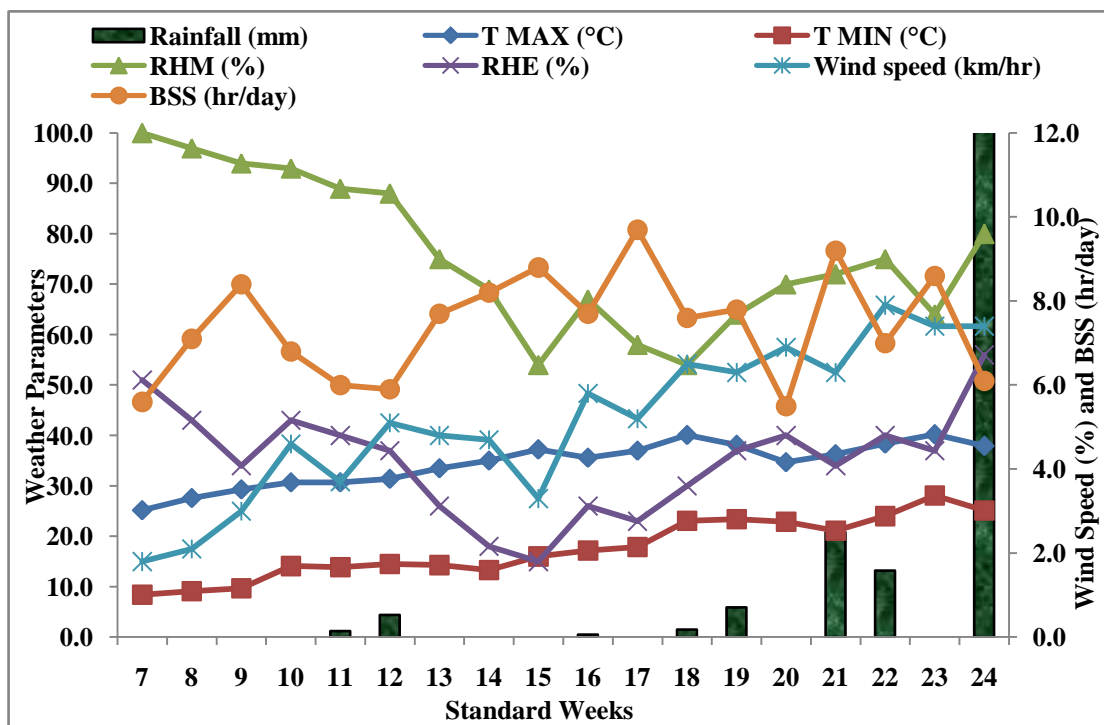


Figure 1. Weather parameters for summer season 2020-21 (Source: Department of Agricultural Meteorology, CCS HAU, Hisar)

Table 1. List of genotypes and their source

S. No.	Genotype	Crop	Variety	Source	Origin
1.	VRW-1, VRW-2, VRW-3, VRW-6, VRW-7, VRW-9, VRW-12, VRW-14, VRW-16, VRW-17, VRW-18, VRW-19, VRW-20, VRW-21, VRW-23, VRW-24, VRW-26	<i>Citrullus lanatus</i> var. <i>lanatus</i>	Germplasm	IIVR, Varanasi	India
2.	NSC-747 P, Misthi	<i>Citrullus lanatus</i> var. <i>lanatus</i>	F <sub>1</sub> Hybrid	NSC, N. Delhi	India
3.	Durgapura Lal	<i>Citrullus lanatus</i> var. <i>lanatus</i>	Variety	RRS, Durgapura	India

### Results and Discussion

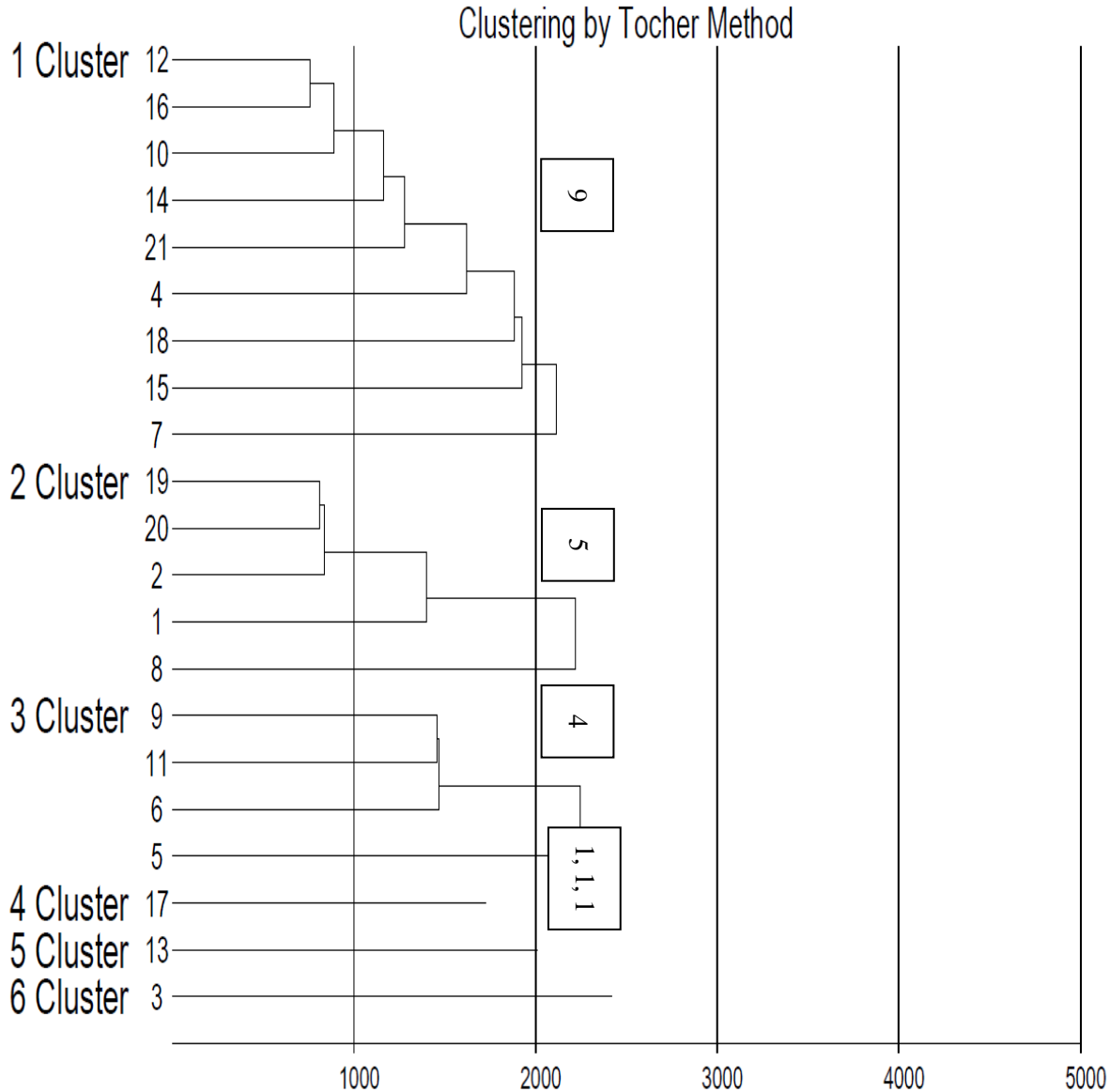
The results of the analysis of variance revealed that there was sufficient variability present in 21 genotypes for the 23 characters under investigation, but it did not explain the extent of variability. To find the extent of variability among the genotypes, Mahalanobis D<sup>2</sup> statistics (1936) as described by Rao

(1952) were used. For any plant breeding programme, the information regarding the genetic diversity present within as well as among the groups of genotypes is of prime importance as it is helpful in the selection of diverse and better parents for any crossing programme, which leads to better heterotic progenies.

**Group constellation**

Grouping of genotypes into different clusters was done by the method suggested by the Tocher and described by Rao 1952. The 21 genotypes were grouped into 6 clusters using Tocher’s Method, as shown in Table 2. The

maximum number of genotypes were found in cluster number 1 (9), followed by cluster number 2 (5), cluster number 3 (4) and cluster number 4, 5 and 6, which consisted of a single genotype each. The dendrogram was depicted in Figure 2.



**Figure 2.** Dendrogram showing the clustering pattern of 21 genotypes of watermelon

**Table 2.** Grouping of genotypes into different clusters using Tocher’s method

Cluster	Number of Genotypes	Name of Genotypes
Cluster 1	9	VRW-18, VRW-23, VRW-16, VRW-20, DURGAPURA LAL, VRW-6, VRW-26, VRW-21, VRW-12

Cluster 2	5	NSC-747P, Misty, VRW-1, VRW-2, VRW-14
Cluster 3	4	VRW-15, VRW-17, VRW-9, VRW-7
Cluster 4	1	VRW-24
Cluster 5	1	VRW-19
Cluster 6	1	VRW-3

The pattern of clustering of genotypes revealed that there was substantial diversity presented among the genotypes for the characters under investigation. The knowledge of a sufficient amount of diversity will be helpful in the selection of diverse and better parents for any hybridization programme for isolating the better segregates. These results were also reported in the literature information of Krishna Prasad et al. (2002), Hakimi and El-Madidi (2015), Rahman et al. (2016), Lima et al. (2017) and Singh et al. (2018). The results of group constellation also indicated that the genotypes from the different sources were also present together in the same cluster and hence; geographical diversity, though important, is not a necessary parameter of group constellation. Therefore, selections of parents merely based on geographical diversity do not reward performance for any hybridization programme. So, in the selection of parents for any hybridization programme, it is desirable to select the diverse parents on the basis of genetic diversity rather than geographical diversity. This finding of lack of

parallelism between genetic and geographical diversity was in consonance with the finding of Souza et al. (2005) and Singh et al. (2018) in watermelon; Prasad and Singh (1997) in parwal; Masud et al. (2002) and Kumar et al. (2006) in pumpkin; and Ara et al. (2014) in bottle gourd. The reason for the lack of parallelism between genetic and geographical diversity may be genetic drift.

#### Intra- and inter-cluster $D^2$ value

The results of Intra and inter-cluster average  $D^2$  value were depicted in Table 3, where the diagonal values represented the intra-cluster and below diagonal values represented the inter-cluster average  $D^2$  values. The maximum intra-cluster  $D^2$  value was recorded for cluster number 3 (49.75), which suggested that this cluster had maximum genetic heterogeneity among the genotypes presented in the cluster, whereas, minimum/zero intra-cluster  $D^2$  value was recorded for clusters number 4, 5 and 6 (0.00), suggested that the cluster number 4, 5 and 6 had minimum genetic heterogeneity among the genotypes presented in this cluster.

**Table 3.** Intra (diagonal) and inter-cluster (below diagonal) average  $D^2$  values

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	44.67					
Cluster 2	55.15	44.74				
Cluster 3	59.98	63.49	49.75			
Cluster 4	55.20	70.45	73.25	0.00		
Cluster 5	50.92	62.37	78.88	62.93	0.00	
Cluster 6	77.15	62.20	64.77	93.01	94.81	0.00



The maximum inter-cluster  $D^2$  value was recorded for cluster number 5 and cluster number 6 (94.81) which indicated that the genotypes present in these two clusters had the highest genetic diversity. The selection of parents from these clusters for the hybridization programme will be fruitful, as the genotypes are genetically diverse. Selection of parents from the clusters having maximum inter-cluster distance for hybridization had also been proposed by Krishna Prasad et al. (2002), Hakimi and El-Madidi (2015), Lima et al. (2017) and Singh et al. (2018). The minimum inter-cluster  $D^2$  value was recorded for cluster number 1 and cluster number 5 (94.81), which suggested the

close relationship among the genotypes of these clusters.

#### Cluster means

The results of the cluster mean were presented in Table 4. From the above discussion, it was observed that the cluster number 5 had maximum cluster value of cotyledon size (59.72), vine length (4.7), days to emergence of 1st staminate flower (50.33), days to emergence of 1st pistillate flower (60.33), days taken to fruit maturity (90), fruit length (27.81), fruit weight (5.57), seed length (8.1) and seed width (4.3). The above finding was in consonance with the finding of Krishna Prasad et al. (2002), Souza et al. (2005), Lima et al. (2017) and Singh et al. (2018).

**Table 4.** Mean value of different clusters for 32 characters

S. No.	Character	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
1.	Germination percentage (%)	68.78	75.56	73.95	88.72	59.72	78.94
2.	Cotyledon size (cm)	2.72	2.59	2.59	2.65	2.83	2.67
3.	Leaf blade length (cm)	12.86	12.24	14.23	13.30	14.10	15.50
4.	Leaf blade width (cm)	1.68	1.77	1.66	1.68	1.48	1.92
5.	Leaf blade ratio	1.68	1.77	1.66	1.68	1.48	1.92
6.	Petiole length (cm)	7.14	7.13	7.66	6.51	7.51	7.75
7.	Internode length (cm)	9.97	9.05	10.86	10.77	10.14	14.62
8.	Vine length (m)	4.16	3.37	4.04	3.72	4.70	3.97
9.	Number of primary branches	6.60	4.53	6.86	5.79	4.66	4.69
10.	Number of sr branches	16.51	11.33	17.17	14.48	11.65	13.58
11.	Days to emergence of 1 <sup>st</sup> staminate flower	43.19	40.67	45.67	39.67	50.33	46.33
12.	Days to emergence of 1 <sup>st</sup> pistillate flower	52.81	50.73	55.58	48.67	60.33	57.00
13.	Days taken to fruit maturity	84.22	79.73	85.50	67.67	99.00	81.33
14.	Blooming period	102.56	99.93	100.83	107.33	94.67	98.67
15.	Fruit length (cm)	24.12	19.06	19.96	27.11	27.81	16.38
16.	Fruit diameter (cm)	20.83	16.12	16.26	18.32	18.54	15.71
17.	Fruit weight (kg)	4.53	2.99	3.16	3.74	5.57	2.05
18.	Number of fruits per vine	3.33	2.68	3.85	3.02	2.51	4.31
19.	Pericarp thickness (mm)	15.15	10.90	11.93	21.57	11.59	14.86
20.	TSS ( $^{\circ}$ Brix)	12.44	10.58	11.79	9.26	12.36	10.66
21.	Seediness	493.47	374.23	724.80	743.57	423.43	262.38
22.	Seed length (cm)	7.78	7.64	7.42	7.60	8.10	7.70
23.	Seed width (cm)	3.88	3.94	3.53	3.90	4.30	3.90

**Table 5.** Superior genotypes selected from the different clusters

Clusters	Genotypes	Superior Characters
Cluster 1	VRW-26	Fruit diameter, TSS, Cotyledon size, Vine length, Number of primary branches, Number of secondary branches, Blooming period, Fruit weight, Pericarp thickness, Seed length
Cluster 2	VRW-2	Leaf blade width, Leaf blade ratio, Seed width
Cluster 3	VRW-7	Number of primary branches, Number of secondary branches, Leaf blade length, Petiole length, Internode length, Days taken to fruit maturity, Number of fruits per vine, Seediness
Cluster 4	VRW-24	Germination percentage, Blooming period, Pericarp thickness, Seediness, Fruit length
Cluster 5	VRW-19	Cotyledon size, Vine length, Days to emergence of 1st staminate flower, Days to emergence of 1st pistillate flower, Days taken to fruit maturity, Fruit length, Fruit weight, Seed length, Seed width, Fruit diameter, TSS
Cluster 6	VRW-3	Leaf blade length, Leaf blade width, Leaf blade ratio, Petiole length, Internode length, Number of fruits per vine, Germination percentage, Days to emergence of 1st staminate flower, Days to emergence of 1st pistillate flower

Superior genotypes selected from the different clusters on the basis of their performances for various characters are depicted in Table 5 below.

**Contribution of individual character towards genetic divergence**

The results of the contribution of individual characters towards genetic divergence were depicted in Table 6. The per cent contribution of seed yield and its attributing characteristics in genetic divergence was reported maximum for the number of fruits per vine (20.48%), seediness

(13.33%), seed width (12.38%), pericarp thickness (11.90%), fruit weight (8.10%), fruit diameter (7.62%), fruit length (6.19%), TSS (5.71%), days to emergence of 1<sup>st</sup> pistillate flower (5.45%), days to emergence of 1<sup>st</sup> staminate flower (3.19%), number of secondary branches (1.37%), germination percentage (0.95%), petiole length (0.95%), vine length (0.95%), days taken to fruit maturity (0.95%) and number of primary branches (0.48%). The rest of the characters had a minute (less than zero) per cent contribution to genetic divergence.

**Table 6.** Contribution of individual characters towards genetic divergence

S. No.	Source	Contribution %
1.	Germination percentage	0.95
2.	Cotyledon size	0.00
3.	Leaf blade length	0.00
4.	Leaf blade width	0.00
5.	Leaf blade ratio	0.00
6.	Petiole length	0.95
7.	Internode length	0.00
8.	Vine length	0.95
9.	Number of primary branches	0.48
10.	Number of secondary branches	1.37



11.	Days to emergence of 1 <sup>st</sup> staminate flower	3.19
12.	Days to emergence of 1 <sup>st</sup> pistillate flower	5.45
13.	Days taken to fruit maturity	0.95
14.	Blooming period	0.00
15.	Fruit length	6.19
16.	Fruit diameter	7.62
17.	Fruit weight	8.10
18.	Number of fruits per vine	20.48
19.	Pericarp thickness	11.90
20.	TSS	5.71
21.	Seediness	13.33
22.	Seed length	0.00
23.	Seed width	12.38

### Conclusion

The 21 genotypes were grouped into 6 clusters using Tocher's Method. The pattern of clustering of genotypes revealed that there was substantial diversity presented among the genotypes for the characters under investigation. The maximum intra-cluster  $D^2$  value was recorded for cluster number 3, which suggested that the cluster number 3 had maximum genetic heterogeneity among the genotypes present in this cluster, whereas, the maximum inter-cluster  $D^2$  value was recorded between cluster number 5 and cluster number 6 which indicated that the genotypes present in these two clusters had highest genetic diversity. The selection of parents from these clusters for the hybridization programme will be fruitful, as the genotypes are genetically diverse. There is a greater possibility of improvement of all attributes found in this vegetable crop. Further, to incorporate parent in hybridization programme.

### References

Anonymous. 2019. Area & Production of Horticulture Crops: All India. National Horticulture Board. [http://nhb.gov.in/statistics/State\\_Level/2018-19%20\(3rd%20Adv.Est.\)%20-%20Website.pdf](http://nhb.gov.in/statistics/State_Level/2018-19%20(3rd%20Adv.Est.)%20-%20Website.pdf).

Ara ZG, Zakaria M, Uddin MZ, Rahman MM, Rasul MG & Kabir AFMR. 2014.

Genetic divergence in bottle gourd. *International Journal of Natural & Social Sciences*, 1:20-25.

Bisognin DA. 2002. Origin and Evolution of Cultivated Cucurbits. *Ciencia Rural*, 32 (5): 715-723.

Choudhary BR, Haldhar SM, Maheshwari SK, Bhargava R & Sharma SK. 2015. Phytochemicals and antioxidants in watermelon (*Citrullus lanatus*) genotypes under hot arid region. *Indian Journal of Agricultural Sciences*, 85 (3): 414-417.

Goda M. 2007. Diversity of local genetic resources of watermelon (*Citrullus lanatus* (Thunb.) Matsum and Nakai) in Sudan. M. Sc. thesis, *Swedish Biodiversity Centre*, Uppsala, Sweden.

Hakimi F & El-Madidi S. 2015. Variability of agro-morphological traits in some Moroccan watermelon landraces [*Citrullus lanatus* (Thunb.) Matsum and Nakai]. *International Journal of Current Sciences*, 17: 90-96.

Haldhar SM, Choudhary BR & Bhargava R. 2016. Susceptibility of watermelon genotypes to fruit fly *Bactrocera cucurbitae* (coquillett). *Indian Journal of Entomology*, 78(2): 170-173.

Haldhar SM, Choudhary BR, Bhargava R & Meena SR. 2015. Antixenotic and

- allelochemical resistance traits of watermelon against *Bactrocera cucurbitae* in a hot arid region of India. *Florida Entomologist*, 98 (3): 827-834.
- Krishna PVS, Pitchaimuthu M & Dutta OP. 2002. Adaptive responses and diversity pattern in watermelon. *Indian Journal of Horticulture*, 59 (3): 298-306.
- Kumar J, Singh DK & Ram HH. 2006. Genetic diversity in indigenous germplasm of pumpkin. *Indian Journal of Horticulture*, 63 (1): 101-102.
- Kwon YS, Oh YH, Yi SI, Kim HY, An JM, Yang SG & Shin JS. 2010. Informative SSR markers for commercial variety discrimination in watermelon (*Citrullus lanatus*). *Genes & Genomics*, 32(2), 115-122.
- Levi A, Thomas CE, Keinath AP & Wehner TC. 2001a. Genetic diversity among watermelon (*Citrullus lanatus* and *Citrullus colocynthis*) accessions. *Genetic Resources and Crop Evolution*, 48(6): 559-566.
- Levi A, Thomas CE, Wehner TC & Zhang XP. 2001b. Low genetic diversity indicates the need to broaden the genetic base of cultivated watermelon. *Horticulture Science*, 36(6): 1096-1101.
- Lima MNR, de Queiroz MA, da Silva Oliveira AE, da Silva Lima Neto I & de Oliveira RS. 2017. Integration of quantitative and qualitative descriptors for genetic diversity studies of watermelon accessions. *Australian Journal of Crop Science*, 11(8): 1005-1015.
- Maggs-Kölling GL & Christiansen JL. 2003. Variability in Namibian landraces of watermelon (*Citrullus lanatus*). *Euphytica*, 132(3): 251-258.
- Maggs-Kölling GL, Madsen S & Christiansen JL. 2000. A phonetic analysis of morphological variation in *Citrullus lanatus* in Namibia. *Genetic Resources and Crop Evolution*, 47(4): 385-393.
- Mahalanobis PC. 1936. On the generalized distance in statistics. *Proceedings of the National Institute of Science of India*, 2 (1): 49-55.
- Masud MAT, Habib AKM, Ahmed SU & Hossain SMM. 2002. Genetic diversity in sponge gourd (*Luffa cylindrica* Roem.). *Bangladesh Journal of Plant Breeding and Genetics*, 14: 37-41.
- Mujaju C, Sehic J, Werlemark G, Garkava-Gustavsson L, Fatih M & Nybom H. 2010. Genetic diversity in watermelon (*Citrullus lanatus*) landraces from Zimbabwe revealed by RAPD and SSR markers. *Hereditas*, 147(4): 142-153.
- Munisse P, Bode S, & Jensen BD. 2011. Diversity of landraces, agricultural practices and traditional uses of watermelon (*Citrullus lanatus*) in Mozambique. *African Journal of Plant Science*, 5(2), 75-86.
- Murty BR & Arunachalam V. 1966. The nature of divergence in relation to breeding system in some crop plant. *Indian Journal of Genetics and Plant Breeding*, 26(A):188-198.
- Nadarajan N & Gunasekaran M. 2012. Quantitative genetics and biometrical techniques in plant breeding. *Kalyani publishers, New Delhi* 182-193.
- Panase VG. 1957. Genetics of quantitative characters in relation to Plant Breeding. *Indian Journal of Genetics and Plant Breeding*, 17: 318-328.
- Prasad VSR & Singh DP. 1997. Genetic divergence in parwel (*Trichosanthes dioica* Roxb.). *Indian Journal of Plant Genetic Resources*, 10(1): 91-96.
- Ramanujam S & Thirumalachar DK. 1967. Genetic variability of certain characters in red pepper (*Capsicum annum*).



- Mysore Journal of Agricultural Sciences*, 1: 30-36.
- Rao CR. 1952. Advanced statistical methods in biometric research. *A Division of Macmillan Publishing Co, Inc New York; Collier-Macmillan Publishers; London*.
- Robinson RW & Decker-Walters DS. 1997. Cucurbits. CAB International, Wallingford, UK. 22610-1557.
- Samadia DK & Haldhar SM. 2020. Mateera, watermelon (*Citrullus lanatus*) germplasm utilization for improving fruit quality and marketable harvest under hot arid climate of India: approaches and out-put. *Journal of Agriculture and Ecology*, 10: 01-21.
- Singh D, Singh R, Saini JS & Singh PK. 2018. Morpho-biochemical characterization and D<sup>2</sup> analysis of watermelon (*Citrullus lanatus*) landraces from India and exotic germplasm. *Indian Journal of Agricultural Sciences*, 88(10): 1633-1639.
- Singh RK & Chaudhary BD. 1977. Biometrical methods in quantitative genetic analysis. *Biometrical Methods in Quantitative Genetic Analysis*.
- Souza FDF, Queiroz MAD & Dias RDCS. 2005. Genetic divergence in watermelon lines. *Horticultura Brasileira*, 23(2): 179-183.
- Wehner TC. 2009. Watermelon. In: Prohens J, Nuez F, (eds.). *Vegetables I. Asteraceae, Brassicaceae, Chenopodiaceae and Cucurbitaceae*. New Delhi, India: Springer, pp. 381-418.
- Zeven AC & De Wet JM. 1982. *Dictionary of cultivated plants and their regions of diversity: excluding most ornamentals, forest trees and lower plant*