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Deciphering genetic variability in melon (*Cucumis melo* L.) using morphological characters

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Abstract

Genetic variability, heritability and genetic advance were investigated in 96 melon (*Cucumis melo* L.) genotypes from 4 horticultural or 6 varietal groups using 10 quantitative traits. The results of the analysis of variance showed that there was enough variation among the genotypes for all the attributes. The highest phenotypic and genotypic coefficients of variations (PCV and GCV) were observed for node to first male flower (40.98 and 31.3%), average fruit weight (36.23 and 30.8%) and total soluble solids (28.01 and 26.67%), while days to first male flower anthesis (10.49 and 8.85%) and days to first female flower anthesis (8.86 and 7.4%) had the least coefficients of variations. The high difference between PCV and GCV estimates exhibited that environmental factors had more influence on trait expression. High heritability coupled with high-moderate GAM was observed for TSS and flesh thickness, indicating that additive genes govern these traits and that these traits could be effectively breed through selective improvement. Nine promising genotypes were identified for further breeding for earliness and lateness in order to extend melon supply in the market.

Keywords: Melon (*Cucumis melo* L.), Genetic variability, Heritability, Genetic advance.

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Introduction

Melon (*Cucumis melo* L., 2n=24), commonly known as *Kharbooja* in India, is an important vegetable crop belonging to the Cucurbitaceae family, grown in the world's warm tropical and subtropical areas. After China and Turkey, India is the 3rd largest producer of melon in the world, accounting for 1.478 million tons from an area of 0.075 million ha (Anonymous 2021). India's major melon-producing states are Uttar Pradesh, Andhra Pradesh, Madhya Pradesh, Punjab and Haryana. Most commercial varieties of melon have medium crop duration with high productive potential, nutritive quality and capacity to produce well in off-season cultivation. Consequently, farmers are increasingly growing muskmelon during off-seasons called *diara* land cultivation in order to capture early markets and fetch higher profits (Singh 2012). Melon was traditionally believed to have originated in Africa, but a recent study has revealed that it actually hails from Asia, with abundant genetic resources of native melon in China and India (Endl *et al.* 2018). It is regarded as one of the most polymorphic, diversified and outcross species in the Gourd family, leading to progressively evolving horticultural classifications by incorporating the theories of numerous researchers. In such recent classification, Pitrat (2017) reported 19 intra-specific horticultural melon groupings that included cultivated, wild, and feral melons. Most of these infraspecific groupings of melons are inter-crossable with each other.

Further, the widespread adoption of improved varieties, including exotic cultivars in the country for commercial viability, has led to the bottling down of genetic variability and the domestication of several intermediate forms. Any crop improvement effort must have a solid understanding of the genetic variability present in a crop species for the traits being advanced. Heritability gives information on the degree of trait inheritance from parent to offspring, whereas genetic advance will aid in determining the projected gain under selection. When heritability is combined with high genetic advance, the resultant information would be more reliable in selecting the best genotypes (Pandey *et al.* 2009). Though there are quite a lot of genetic variability studies in melon throughout the country (Bhimappa *et al.* 2019, Silpa *et al.* 2020, Anusha *et al.* 2021, Patel *et al.* 2021), however, attempt to identify potential genotypes from various horticultural groups were limited. Therefore, this study was conducted to assess genetic variability parameters, heritability and genetic advance in 96 melon genotypes from 4 horticultural or 6 varietal groups to facilitate selection of superior genotypes for future melon breeding.

Materials and Methods

The experimental germplasm consisted of 96 melon genotypes belonging to 4 horticultural or 6 varietal groups, per Robinson and Decker-Walters (1997) and Pitrat (2017). The panels included *reticulatus* (49), *inodorous* (9), *cantalupensis* (7), *momordica* (19), *callosus* (2) and *conomon* (2), including derived intercrossed progenies (8) available and maintain at Division of Vegetable Science, ICAR- IARI, New Delhi, India were selected for the study (Table 1). The panels also included five commercial *reticulatus* varieties

Table 1: List of melon genotypes used in the study as per Robinson and Decker- Walters (1997) and Pitrat (2017)

S. No.	*Genotypes*	*Horticultural groups/ Pedigree*	*S. No.*	*Genotypes*	*Horticultural groups/ Pedigree*	*S. No.*	*Genotypes*	*Horticultural groups/ Pedigree*
1	Kashi Madhu	*reticulatus*	33	DMM 224	*reticulatus*	65	DMM 255	*reticulatus*
2	Hara Madhu	*reticulatus*	34	DMM 225	*reticulatus*	66	DMM 256	*reticulatus*
3	Pusa Madhurima	*reticulatus*	35	DMM 226	*reticulatus*	67	DMM 257	*reticulatus*
4	Pusa Madhuras	*reticulatus*	36	DMM 227	*reticulatus*	68	DMM 258	*reticulatus*
5	Charentais	*cantalupensis*	37	DMM 228	*reticulatus*	69	DMM 259	*reticulatus*
6	DMM 201	*reticulatus* × *momordica*	38	DMM 229	*reticulatus*	70	DMM 260	*reticulatus*
7	Pusa Sarda	*inodorous*	39	DMM 230	*reticulatus*	71	DMM 261	*reticulatus*
8	DMM 202	*inodorous*	40	DMM 231	inodorous	72	DMM 262	*reticulatus*
9	DMM 203	*inodorous*	41	DMM 232	inodorous	73	DMM 263	*momordica*
10	DMM 204	*reticulatus* × *momordica*	42	Pusa Sunehari	inodorous	74	DMM 264	*momordica*
11	CM17187	*momordica*	43	DMM 233	*cantalupensis*	75	DMM 265	*reticulatus*
12	DSM 11	*momordica*	44	DMM 234	inodorous	76	DMM 266	*reticulatus*
13	DMM 205	*conomon*	45	DMM 235	inodorous	77	DMM 267	*reticulatus*
14	DMM 206	*momordica*	46	DMM 236	*cantalupensis*	78	DMM 268	*reticulatus*
15	DSM 132	*callosus*	47	DMM 237	*reticulatus*	79	DMM 269	*reticulatus*
16	DMM 207	*momordica*	48	DMM 238	*reticulatus* × *momordica*	80	DMM 270	*cantalupensis*
17	DMM 208	*momordica*	49	DMM 239	inodorous	81	DMM 271	*reticulatus*
18	DMM 209	*callosus*	50	DMM 240	*inodorus* × *cantalupensis*	82	DMM 272	*momordica*
19	DMM 210	*reticulatus* × *momordica*	51	DMM 241	*inodorus* × *cantalupensis*	83	DMM 273	*reticulatus* × *momordica*
20	DMM 211	*momordica*	52	DMM 242	*cantalupensis*	84	DMM 274	*reticulatus*
21	DMM 212	*momordica*	53	DMM 243	*cantalupensis*	85	DMM 275	*reticulatus*
22	DMM 213	*reticulatus*	54	DMM 244	*reticulatus*	86	Pusa Shandar	*momordica*
23	DMM 214	*reticulatus*	55	DMM 245	*reticulatus*	87	DMM 276	*momordica*
24	DMM 215	*momordica*	56	DMM 246	*reticulatus*	88	DMM 277	*momordica*
25	DMM 216	*reticulatus*	57	DMM 247	*reticulatus*	89	DMM 278	*momordica*
26	DMM 217	*momordica*	58	DMM 248	*reticulatus*	90	DMM 279	*conomon*
27	DMM 218	*momordica*	59	DMM 249	*reticulatus*	91	DMM 280	*reticulatus*
28	DMM 219	*momordica*	60	DMM 250	*reticulatus*	92	DMM 281	*reticulatus*
29	DMM 220	*momordica*	61	DMM 251	*reticulatus*	93	Pusa Kazri	*reticulatus*
30	DMM 221	*reticulatus*	62	DMM 252	*reticulatus*	94	DMM 282	*reticulatus*
31	DMM 222	*reticulatus*	63	DMM 253	*reticulatus* × *momordica*	95	DMM 283	*reticulatus*
32	DMM 223	*cantalupensis*	64	DMM 254	*reticulatus*	96	DMM 284	*reticulatus*

Table 2: Analysis of variance for different traits in melon genotypes

S. No.	Characters	Mean sum of squares				
		Replication (3)	Genotypes (96)	Error (96)	CD (1%)	CV (1%)
1	Days to first male flower anthesis	10.53	40.65***	4.84	4.63	5.63
2	Days to first female flower anthesis	7.191	39.60***	4.998	4.7	4.87
3	Node to first male flower	4.420	6.86***	1.318	2.42	26.45
4	Node to first female flower	16.542	15.64***	4.254	4.33	25.65
5	Average fruit weight (g)	59902.2	150044.9***	17007.3	274.3	19.07
6	Fruit length (cm)	2.445	22.17***	1.757	2.79	12.56
7	Fruit width (cm)	2.057	8.55***	0.828	1.91	8.8
8	Flesh thickness (cm)	0.188	0.91***	0.068	0.55	11
9	Cavity width (cm)	0.226	2.77***	0.564	1.58	13.38
10	TSS (° **Brix)**	0.838	16.65***	0.556	1.57	8.59

*** Significance at 0.1 % level values in parenthesis indicating degrees of freedom

(Kashi Madhu, Hara Madhu, Pusa Madhurima, Pusa Madhuras and Pusa Kazri); two exotic *inodorous* varieties adapted and bred in India (Pusa Sarda and Pusa Sunehari), three genetic stocks- CM17187 and DSM 11 for fusarium wilt resistance and DSM 132 for ToLCNDV resistance and one exotic reference genotype (Charentais). The present study was conducted in a randomized block design with three replications during the spring–summer season of 2019. The plants were spaced 0.6 m apart and rows were 2.0 m apart, accommodating 20 plants per genotype in each replication block. All of the prescribed standard agronomical and plant protection practices were followed during the experiment. Data was obtained for 10 quantitative attributes on 5 randomly tagged plants per replication i.e., days to first male flower anthesis, days to first female flower anthesis, node to first male flower, node to first female flower, average fruit weight (g), fruit length (cm), fruit width (cm), flesh thickness (cm), cavity width (cm) and total soluble solids (°Brix). The mean values of the data were subjected for analysis of variance as per Panse and Sukhatme (1967); genetic variability parameters (Burton, 1952); heritability and genetic advance (Johnson *et al.* 1955) were analyzed using statistical package SPAR version 2.0.

Results and Discussion

Analysis of variance

The analysis of variance revealed significant variation for each attribute, proving that the 96 genotypes under consideration have sufficient variability (Table 2). These results corroborate the previous findings of Mehta *et al.* (2009) and Bhimappa and Choudhary (2017) in muskmelon. Sufficient variability in crop genetic resources is essential for successful selection to enhance quantitative traits.

Mean performance of horticultural characters

Variability can be easily measured using range. A wider range of mean values observed in our investigation indicated the presence of abundant variability for the characters examined (mean data not shown). Amongst the flowering characters i.e., days to first male flower anthesis (32 days in DSM 11 to 50 days in DMM 264), days to first female flower anthesis (37 days in DSM 11 to 55.33 days in DMM 272), node to first male flower (1.67 in DSM 132 to 10 in DMM 272) and node to first female flower (3.33 in DSM 132 to 13.33 in DMM 233). Similarly, significant variations were observed for fruit characters *i.e.*, average fruit weight (191.67 gin DMM 206 to 1403.33 g in DMM 279), fruit length (4.57 cm in DMM 206 to 22.3 cm DMM 279), fruit width (6.43 cm in DMM 267 to 14.3 cm Kashi Madhu), cavity width (3.53 cm in DMM 206 to 7.43 cm in DMM 225, DMM 262 and DMM 283), flesh thickness (1.2 cm in DMM 206 to 3.53 cm in Kashi Madhu and total soluble solids (3.97 °Brix in DMM 263 to 12.03 °Brix in DMM 203). Bhimappa and Choudhary (2017) and Indraja *et al.* (2021) also described a wide range of variability in melon for different traits. The market class sweet groups belonging to subspecies *melo* showed the upper range for desirable fruit qualities (average fruit weight, flesh thickness, and TSS), whereas the wild *agrestis* group showed the lower range for most of the traits studied.

Consumers often prefer medium to large fruits (800-1200 gm) with thick flesh, musky aroma and high TSS (>10°Brix). Since earliness (days to first female flower anthesis at 37-42 days after sowing) along with desirable fruit traits (800-1200 g average fruit weight and >10°Brix TSS) are essential for early flowering and fruiting in order to catch early market and fetch higher price when melon supply is limited (Table 3). We have identified DMM 236 (*cantalupensis*), DMM 241 (*inodorous* × *cantalupensis*), DMM 242 (*cantalupensis*), DMM 258 (*reticulatus*) and DMM 275 (*reticulatus*) for further refinement to develop early cultivar/ hybrid. Similarly, medium-late blooming genotypes (44-53 days after sowing), such as DMM 229 (*reticulatus*), DMM 238 (*reticulatus* × *momordica*), DMM 253 (*reticulatus* × *momordica*) and DMM 269 (*reticulatus*), were identified in order to extend melon

Table 3: List of nine promising genotypes for earliness and lateness identified during the investigation

S. No.	*Genotypes*	*Horticultural groups/ Pedigree*	*DTMF*	*DTFF*	*NTMF*	*NTFF*	*AFW (g)*	*FL (cm)*	*FWD (cm)*	*FLT (cm)*	*CW (cm)*	*TSS (°Brix)*
	Earliness											
1	DMM 236	*cantalupensis*	36.33	40.33	2.67	8	1050	12.73	12.67	3.3	5.47	11.5
2	DMM 241	*I X C*	32.33	40.33	2	6.33	733.33	9.77	9.9	2.9	3.93	10.87
3	DMM 242	*cantalupensis*	37.33	40.67	3.67	6.33	950	9.73	11.43	3.27	4.67	11.63
4	DMM 258	*reticulatus*	32	40.33	2.33	6	1250	11.5	11.93	3.03	5.87	10.77
5	DMM 275	*reticulatus*	36	42.33	5.67	11	808.33	11.47	10.9	3.03	5.5	11.37
	Medium-lateness											
6	DMM 229	*reticulatus*	47.33	53.33	4.33	9.33	941.67	10.77	13.23	2.87	7.43	10.4
7	DMM 238	*reticulatus* x *momordica*	40.33	47.33	3.33	6	866.67	10.27	11.5	3.33	4.9	11.57
8	DMM 253	*reticulatus* x *momordica*	36	44.67	4.67	6.33	800	10.53	11.83	3.03	6.27	10.1
9	DMM 269	*reticulatus*	41.33	45.33	6	11.67	800	10.17	11.83	2.57	6.87	11.6

DTMF- Days to first male flower anthesis, DTFF- Days to first female flower anthesis, NTMF- Node to first male flower, NFFF- Node to first female flower, AFW- Average fruit weight, FL- Fruit length, FWD- Fruit width, FLT- Flesh thickness, CW- Cavity width, TSS- Total Soluble Solids

Table 4: Variability, heritability and genetic advance estimates for 10 quantitative traits in 96 melon genotypes

S. No.	*Characters*	*Range*	*Grand mean*	*PCV (%)*	*GCV (%)*	*H^2 (%)*	*Genetic advance*	*GA as %age of mean*
1	Days to first male flower anthesis	32.0-50.0	39.09	10.49	8.85	71.15	5.37	59.08
2	Days to first female flower anthesis	37.0-55.33	45.90	8.86	7.4	69.77	5.08	11.07
3	Node to first male flower	1.67-10.0	4.34	40.98	31.3	58.33	1.8	41.47
4	Node to first female flower	3.33-13.33	8.04	35.28	24.23	47.16	2.21	27.49
5	Average fruit weight (g)	191.7-1403.3	684.55	36.23	30.8	72.28	331.94	48.49
6	Fruit length (cm)	4.57-22.3	10.56	27.31	24.72	79.49	4.44	42.05
7	Fruit width (cm)	6.43-14.3	10.34	17.83	15.51	75.66	2.63	25.44
8	Flesh thickness (cm)	1.2-3.53	2.38	24.9	22.33	80.4	0.91	38.24
9	Cavity width (cm)	3.53-7.43	5.61	20.32	15.29	56.61	1.13	19.93
10	TSS (° **Brix)**	3.97-12.03	8.69	28.01	26.67	90.61	4.42	50.86

supply in the market. Therefore, using these identified potential genotypes in future breeding programme will aid strategically in the long-term marketing of melon cultivars.

Phenotypic and genotypic coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were assessed to determine the degree of variability and the intensity of environmental effect on trait expression (Table 4). The traits like node to first male flower, average fruit weight, total soluble solids (TSS), fruit length, node to first female flower and flesh thickness all had high PCV and GCV (>20%) values. Similar findings were also reported for most of the characters, i.e., for average fruit weight in snapmelon (Pasha *et al.* 2019); in oriental melon (Lakshmi *et al.* 2017) and in muskmelon (Reddy *et al.* 2013; Reddy and Shanthi, 2013; Bhimappa and Choudhary, 2017; Indraja *et al.* 2021); for flesh thickness in muskmelon (Indraja *et al.* 2021) and in oriental melon (Lakshmi *et al.* 2017); and for TSS in muskmelon (Reddy and Shanthi, 2013, Indraja *et al.* 2021). On the other hand, low estimates for PCV and GCV (<10%) were recorded for days to first male flower anthesis and days to first female flower anthesis. Our results agreed with Reddy *et al.* (2013) and Bhimappa and Choudhary (2017) for days to first male flower anthesis in muskmelon; Mishra *et al.* (2017) and Pasha *et al.* (2019) and Indraja *et al.* (2021) for days to first female flower anthesis in snap melon and muskmelon, respectively. For all of the traits investigated, PCV was much higher than those of GCV, indicating that the variation was mainly attributed due to genotypic and environment interaction, with higher degree of environmental factors on the expression of these traits. This finding is consistent with prior studies in snapmelon by Pandey *et al.* (2009) and Pasha *et al.* (2019). On the other hand, previous studies in by muskmelon by Bhimappa and Choudhary (2017) and Indraja *et al.* (2021) and in culinary melon by Rakhi and Rajamony (2006) have reported only modest differences between PCV and GCV, demonstrating that environment has little impact on traits expression. The attributes with high PCV and GCV (>20%) estimates suggest that there is lot of genetic variability in the germplasm. Therefore, it offers larger scope

for improving these traits through crop selection. However, the current study found that environment has played a greater role in the expression of these traits; as a result, selective improvement solely based on phenotype should be avoided. The attributes with low PCV and GCV (<10%) estimates indicate little genetic variability. Therefore, these attributes can be enhanced via heterosis breeding rather than crop selection, which would be unsuccessful.

Heritability and Genetic advance

The heritability estimate is a useful indicator to the breeders in choosing the best accession for predicting the desirable trait enhancement through phenotypic selection and is presented in Table 4. High estimates of heritability (>80%) were recorded for TSS and flesh thickness; moderate heritability (70–80%) in fruit length, fruit width, average fruit weight and days to first male flower anthesis and low heritability (<70%) in days to first female flower anthesis, node to first male flower, cavity width and node to first female flower. High heritability estimates were also reported for TSS in muskmelon (Mehta *et al.* 2009; Reddy and Shanthi, 2013; Priyanka, 2019; Indraja *et al.* 2021), in culinary melon (Rakhi and Rajamony, 2006) and for flesh thickness in muskmelon (Bhimappa and Choudhary, 2017; Indraja *et al.* 2021). Low heritability was also reported in muskmelon for node to first female flower (Priyanka, 2019). Nevertheless, Bhimappa and Choudhary (2017) reported high heritability for fruit length and moderate heritability by Priyanka (2019) for days to first female flower opening in musk melon.

For highly heritable traits, selection can be done based on phenotypic performance. When heritability is researched alongwith genetic advance, it is possible to find out heritable variation with a higher degree of accuracy. Our study recorded high estimates for genetic advance as per cent of mean (>50%) for days to first male flower anthesis and TSS. High heritability (>80%) coupled with high genetic advance as percent of mean (>50%) was recorded for TSS. This outcome was previously supported by Reddy *et al.* (2013), Reddy and Shanthi (2013) and Harsh and Pal (2022) in muskmelon for TSS. This suggests that additive genetic activity played a dominant role in the manifestation of this trait. Since the estimations of PCV and GCV are similar and parallel, and phenotypic variability being a strong indicator of genotypic variability, there is greater room for improvement of this trait via selection. High heritability (>80%) and moderate genetic advance as a percent of mean (35–50%) was observed for flesh thickness, was in conformity with the earlier reports in muskmelon (Bhimappa and Choudhary, 2017) and in culinary melon (Rakhi and Rajamony, 2006). This showed that in situations when direct selection pressure on these qualities would leave little potential for improvement, high heritability was more likely to be attributed to favorable environmental influences than to genotypes. Therefore, it would be best to use particular specific pairings followed by random mating of lines to increase this feature.

Low to moderate heritability (<75%) and low to moderate genetic advance as a percent of mean (<45%), were recorded for fruit width, days to first female flower anthesis, node to first male flower, node to first female flower and cavity width. All the attributes with low-moderate heritability and low-moderate genetic advance as percent of the mean, revealed that non-additive gene actions govern these attributes and are highly influenced by the environment, thus, restricting the improvement of these traits through direct selection. The findings of this study will help breeders plan a targeted breeding programme to improve muskmelon yield traits and also plan a long-term marketing strategy by utilizing identified potential genotypes from various horticultural groups.

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सारांश

खरबूजा के कुल 96 जननद्रव्यों की 4 औद्यानिक अथवा 6 किस्म समूहों बनाकर 10 मात्रात्मक घटकों का उपयोग कर अनुवांशिक विविधता, वंशागति और अनुवांशिक उन्नयन का अध्ययन किया गया। विचरण विश्लेषण के परिणामों से स्पष्ट हुआ कि सभी गुणों के लिए जीन प्रारूप में पर्याप्त भिन्नता पायी गयी। उच्चतम बाह्यस्वरूप एवं अनुवांशिक गुणांक की विविधता प्रथम नर पुष्प के पार्श्व गांठ (40.98 प्रतिशत, 31.3 प्रतिशत), औसत फल भार (36.23 प्रतिशत, 30.8 प्रतिशत) और कुल विलेयक ठोस (28.01, 26.67 प्रतिशत) पाया गया जबकि प्रथम नर फूल पुष्पन के दिन (10.49 प्रतिशत, 8.85 प्रतिशत) और प्रथम मादा पुष्पन (8.86, 7.4 प्रतिशत) विविधता गुणांक सबसे कम पाया गया। सबसे अधिक विभिन्नता बाह्य स्वरूप गुणांक और अनुवांशिक प्रारूप गुणांक अनुमानों के बीच प्रदर्शित हुआ जो पर्यावरणीय घटकों ने लक्षण के अभिव्यक्ति पर अधिक प्रभाव डाला। कुल विलेय ठोस और छिलके की मोटाई के लिए उच्च-मध्यम जी.ए.एम. के साथ उच्च अनुवांशिकता देखी पायी गई जो यह दर्शाता है कि ये सभी गुण योज्य जीन द्वारा नियंत्रित होते हैं और इन गुणों को चयनात्मक सुधार के माध्यम से प्रभावी ढंग से प्रजनन के लिए उपयोग में लाया जा सकता है। बाजार में खरबूजा की आपूर्ति बढ़ाने के लिए अति अगेतीपन और विलंबता बुआई हेतु आगे प्रजनन के लिए नौ आशाजनक बीज प्रारूपों की पहचान की गई।