Genetic diversity in seed purpose watermelon (*Citrullus lanatus*) genotypes under rainfed situations of Thar Desert

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ABSTRACT

An attempt was made to evaluate the available germplasm of watermelon [*Citrullus lanatus* (Thunb.) Matsum & Nakai] for seed yield and related traits during *kharif* 2010 and 2011. Significant differences among the 57 genotypes for eight characters were observed coupled with higher estimates of heritability and genetic advance as percent of mean for seed yield/plant. Seed yield/plant showed direct positive effect as well as significant positive correlation with number of fruits/plant, fruit yield/plant and test weight. All the 57 genotypes were grouped into eight clusters. The maximum intra-cluster distance was observed for cluster VII (10.567) and minimum for cluster IV (0.567) while inter-cluster distance was maximum for cluster III and IV (46.619) followed by cluster I and VII (42.203) and minimum for cluster V and VIII (10.200). On the basis of cluster distance and *per se* performance 10 promising genotypes of watermelon have been identified for seed yield and other component traits for using as parents in breeding programme.

Key words: Diversity, Genetic advance, Heritability, Seed yield, Watermelon

Watermelon [*Citrullus lanatus* (Thunb) Matsum & Nakai] popularly known as *Mateera* or *Kalingada* in the desert region; is an integral component of rainfed agriculture which is being grown along with pearlmillet and clusterbean as a mixed crop. In normal rainfall year, 3-4 q of clusterbean seed or 5-6 q of pearl millet grain yield can be obtained from one hectare along with 50-60 kg of mateera seed yield under rainfed mixed cropping situations. *Mateera* seed price varies from ₹ 5 000–8 000/q (sometimes crossed to ₹ 10 000) in local market which is highest among rainfed *kharif* crops thus supporting the livelihoods of rural people of the arid zone in a big way (Mahla *et al.* 2011). The roasted seeds are taken as a common snack while after removal of seed coat it is mainly used in sweets and pharmaceuticals. Watermelon seeds are supposed to regulate blood sugar levels, increase energy, maintain the nervous system and promote healthy skin. Watermelon seed contains 30–35% oil and 20–25% crude protein (Goyal and Sharma 2009).

Despite its widespread uses and economic importance in arid zone, there is no single genotype of watermelon which is exclusively grown for seed purpose. Therefore, first time an attempt was made to evaluate the available watermelon germplasm under rainfed conditions for seed yield and related traits.

The efficiency of any crop improvement programme mainly depends on the extent of genetic variability present in the germplasm and its utilization through sound breeding programme. To understand the usable variability, grouping of genetic stocks based on suitable scale is quite imperative. Similarly, choice of genetically divergent parents for hybridization under transgressive breeding programme is also dependent upon categorization of breeding materials on the basis of appropriate criteria (Sharma 1999). Genetic parameters such as phenotypic variance, genotypic variance, heritability and genetic advance provide information about the behaviour of the trait and accordingly breeding methods could be devised for improving the trait in question. Further, seed yield is regarded as a complex trait influenced by many component traits both in positive and negative directions. Generally, direct selection for yield may not be sufficiently effective due to low heritability.

Therefore, it is desirable to know the heritability and mutual relationship between various component traits on which selection can be made for improvement in seed yield. In cucurbits the economic part is fruit but in the present study an attempt was made to evaluate the available germplasm for seed yield and related traits keeping in view the immense potential of *mateera* seed to support livelihood of desert dwellers in Thar Desert.

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MATERIALS AND METHODS

The germplasm for the present study was procured from different sources, viz 30 from NBPGR, Regional Station, Jodhpur; 21 from Agricultural Research Station, SKRAU, Mandore; 71 (52 *egusi* type and 19 *citroides* type) from Southern Regional PI Station, USDA, ARS, Plant Genetic Resources Conservation Unit, Experiment Street, Giffin, Georgia (USA) through National Bureau of Plant Genetic Resources, New Delhi. These 122 germplasm accessions along with 20 local landraces collected from farmer's field during 2009 were evaluated at CAZRI, Regional Research Station, Jaisalmer during *kharif* 2010 under rainfed conditions. During the season (July to October) 267 mm rainfall was received in 15 rain events. On the basis of per se performance 35 lines were selected from 122 accessions initially evaluated. These 35 lines along with 22 advance breeding lines shared by Agricultural Research Station, SKRAU, Mandore, were evaluated in a randomized block design replicated thrice under rainfed conditions during *kharif* 2011 (265.8 mm rainfall in 15 rain events). All the 57 lines were sown in two row plots of 4 m length spaced 3.0 m apart keeping plant to plant distance of 1.0 m. Hence, there were 8 plants in each accession per replication. Observations for fruit weight, rind weight, fruit diameter, number of seeds per fruit were recorded on 5 randomly selected fruits while fruit yield/plant, number of fruits/plant, seed yield/plant and test weight were based on the mean value of all the eight plants. The analysis of variance was done following the standard statistical methods. Genetic parameters were worked out using the formulae of Johnson *et al.* (1955) while correlations and path analysis was done as per the procedure outlined by Dewey and Lu (1959). The diversity analysis was done as per the Ward's (1963) minimum variance method.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the 57 genotypes for all the eight characters studied though, different traits showed differential magnitude of variability. A close association between genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) for fruit weight, rind weight, fruit diameter, number of seeds/fruit and test weight were observed indicating that these traits were not much affected by the environment. But number of fruits/plant, fruit yield/plant and seed yield/plant showed considerable difference between GCV and PCV values showing significant role of environment in expression of these traits compared to other traits (Table 1). In the present study higher estimates of heritability was observed for all the traits coupled with moderate to high genetic advance. This might be due to diverse germplasm exhibiting wide variability for seed yield and related traits. Samadhia (2011) also observed higher estimates of heritability along with higher genetic advance for fruit yield and contributing traits in ridge gourd. Considerable variability for various

Table 1   Variability for various quantitative traits in seed purpose watermelon

Character	Range	Mean ± SEm	GCV	PCV	h^2	Genetic advance (GA)	GA (as % of mean)
No. of fruits/plant	3.02 – 20.3	11.94 ± 1.11	31.37	35.29	0.79	6.859	57.45
Fruit yield/plant (kg)	3.88 – 15.28	8.45 ±0.57	26.25	28.74	0.83	4.175	49.39
Fruit weight (g)	755.0 – 2457.0	1298.6 ± 54.8	31.56	32.39	0.95	822.412	63.33
Fruit diameter (cm)	34.4 – 50.0	41.8 ± 0.57	7.34	7.72	0.91	6.011	14.39
Rind weight (g)	471.7 – 1719.7	885.1 ± 42.8	31.72	32.81	0.93	559.251	63.19
No. of seeds/fruit	243.8 – 1070.0	583.8 ±28.28	25.43	26.78	0.90	290.466	49.75
Seed yield/plant (g)	48.8 – 431.4	215.5 ±17.25	43.57	45.73	0.91	184.307	85.54
Test weight (g)	33.4 – 82.7	62.9 ±1.87	17.45	18.19	0.92	21.677	34.48

Table 2   Direct and indirect effect of various quantitative traits on seed yield of watermelon

Characters	Number of fruits/plant	Fruit yield/ (kg)	Fruit weight (g)	Fruit diameter (cm)	Rind weight (g)	Number of seeds/plant	Test weight (g)	Correlation with seed yield/ plant (g)
Number of fruits/plant	0.1494	0.0312	–0.0205	–0.0086	–0.0223	–0.0061	0.0061	0.358*
Fruit yield/plant (kg)	0.1832	*0.2899*	–0.0218	0.0124	–0.0251	0.0452	0.0680	0.384*
Fruit weight (g)	0.0636	0.0115	–0.1534	–0.1138	–0.1508	–0.0707	–0.0133	–0.297
Fruit diameter (cm)	0.0350	–0.0086	–0.1491	–0.2010	–0.1413	–0.0722	–0.0422	–0.278
Rind weight (g)	–0.0228	–0.0044	0.0497	0.0356	0.0506	0.0195	0.0058	–0.232
Number of seeds/fruit	0.0079	–0.0100	–0.0294	–0.0229	–0.0247	–0.0638	–0.0136	–0.081
Test weight (g)	0.0392	0.0739	0.0273	0.0661	0.0361	0.0672	0.3153	0.326*
Seed yield/plant (g)	0.3556	0.3837	–0.2973	–0.2323	–0.2774	–0.0810	0.3262	1.000

Table 3   Intra (Diagonal) and inter cluster (Below diagonal) distance among watermelon germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII
I	9.127							
II	16.201	6.694						
III	21.530	17.292	10.128					
IV	26.430	26.378	46.619	0.567				
V	23.365	13.662	27.170	15.084	7.341			
VI	38.912	26.469	41.392	20.275	10.386	4.817		
VII	42.203	29.723	33.937	28.014	17.029	13.089	10.567	
VIII	26.011	14.225	19.494	28.595	10.200	10.832	12.361	4.037

Table 4   Clustering pattern of 57 genotypes of watermelon evaluated during *kharif* 2011

Cluster	Number of genotypes	Germplasm accession(s)
I	3	DRB 661, MGPK 10-3 and SPS 2
II	5	DRB 664, SPS 5, SKGPK 35, MGPK 10-1 and DRB 653
III	3	SKNK 711, MGPK 10-4 and SKNK 679
IV	3	DRB 663, MGPK 10-5 and DRB 671
V	21	DRB 677, CZJK 10-1, MK 45-3, DRB 662, SKNK 112, SKGPK 21, SPS 4, SKGPK 32, SKGPK 23, SKNK 653, MGPK 10-2, SKNK 1003, SKNK 0902, SKGPK 22, SKGPK 30, SKNK 806, SPS 3, SKNK 807, SKNK 1004, SKNK 901 and MK 81-1
VI	11	DRB 675, SKNK 138, SKNK 683, SPS 8, SKGPK 24, SKNK 0903, SKGPK 29, SKGPK 30, GK 1, SKNK 1001 and MGPK 1
VII	5	SKNK 136, SPS 7, SPS 1, SKNK 665, DRB 654
VIII	6	SKGPK 25, SKGPK 34, SKGPK 27, SKGPK 28, SKGPK 31 and SKGPK 33

quantitative traits and higher estimates of heritability and genetic advance were also reported in cucumber (Yadav *et al.* 2009). Further, Sanwal *et al.* (2008) also recorded high values of GCV along with high heritability and genetic advance for number of fruits/plant and fruit yield/plant in chow-chow.

It is well established fact that seed yield is a complex trait and depends on other component traits directly or indirectly. In the present study also number of fruits/plant, fruit yield/plant and test weight had shown direct effect as well as significant positive correlation with seed yield (Table 2). Seed yield in watermelon could be increased through number of fruits/plant, fruit yield/plant and test weight. Therefore, genotypes found promising for these three traits may be rewarding parents for hybridization for obtaining transgressive segregants. Narayanankutty *et al.* (2006) noticed high positive direct effects for fruit weight, fruit number, days to first harvest, seeds/fruit and 100 seed weight in snake guard. Significant positive correlation of fruit yield with fruit weight, fruit girth, pulp thickness and fruits/plant was also recorded in muskmelon (Mehta *et al.* 2009).

For any crop improvement programme genetic diversity among the germplasm material and further its assessment through well laid field experiment and data analysis with proper statistical procedure are prerequisite. The D^2 values

determining the genetic distances among the genotypes were calculated and 57 genotypes were grouped into eight clusters (Table 3). Cluster V has the maximum number of genotypes (21) followed by cluster VI (11) while minimum (3) genotypes were represented in cluster I, III and IV (Table 4). The maximum intra-cluster distance was observed for cluster VII (10.567) and minimum for cluster IV (0.567) while inter-cluster distance was maximum for cluster III and IV (46.619) followed by cluster I and VII (42.203) and minimum for cluster V and VIII (10.200). Perusal of cluster mean values (Table 5) for different traits across the clusters showed that cluster III had maximum mean values for fruit weight (2207.8 g), fruit diameter (46.46 cm), rind weight (1532.2 g) and number of seeds/plant (965.42) while cluster VII for number of fruits/plant (18.75) and fruit yield/plant (12.47 kg). The maximum mean values for seed yield/plant was observed in cluster VI (309.42 g) while for test weight in cluster II (75.99 g). Sanwal *et al.* (2008) also grouped 38 genotypes of chow-chow of NEH region into seven clusters for diversity analysis. Clusters I, IV, V and VIII did not show higher mean values for any of the trait, these 4 clusters had 33 genotypes (57 per cent of the total germplasm evaluated) and genotypes represented in these clusters may not be rewarding for hybridization programme.

The success in obtaining highly heterotic hybrids and

Table 5   Cluster mean values of various quantitative traits in watermelon genotypes

Clusters	Number of fruits/plant	Fruit yield/ (kg)	Fruit weight (g)	Fruit diameter (cm)	Rind weight (g)	Number of seeds/fruit	Seed yield/ plant (g)	Test weight (g)
I	6.14	6.72	2166.3	45.53	1413.8	516.08	132.02	50.86
II	7.23	6.30	1630.5	44.49	1122.4	693.75	119.81	75.99
III	11.77	9.44	2207.8	46.46	1532.2	965.42	200.17	66.74
IV	10.83	5.07	1058.5	41.01	677.1	457.24	58.42	34.50
V	10.31	7.72	1223.7	40.74	839.0	586.34	215.95	62.03
VI	14.89	9.09	915.6	39.54	633.8	451.23	309.42	62.97
VII	18.75	12.47	1103.5	40.84	748.0	615.82	180.72	62.34
VIII	13.82	10.35	1380.1	44.12	939.3	606.36	278.19	73.32
Mean	11.92	8.45	1298.5	41.77	885.1	583.84	215.47	62.86

Table 6   Promising genotypes identified for seed yield and related traits

Genotype	Cluster	Seed yield/ plant (g)	Number of fruits/plant	Fruit yield/ plant (kg)	Fruit weight (g)	Fruit diameter (cm)	Rind weight (g)	Number of seeds/fruit	Test weight (g)
SKGPK 24	VI	431.4	16.4	8.84	963	40.8	633	556.4	68.8
SKNK 138	VI	400.0	16.6	9.69	755	38.0	551	480.6	65.6
SKGPK 31	VIII	355.6	13.8	10.35	1221	43.0	773	658.8	69.7
SKNK 665	VII	355.0	20.2	15.28	1481	45.0	1008	635.0	65.9
DRB 675	VI	341.9	14.9	11.11	757	36.4	547	400.6	62.9
SPS 8	VI	339.4	15.5	9.16	830	37.6	556	598.6	62.0
SKGPK 33	VIII	338.6	13.8	10.82	1207	42.4	834	514.6	67.2
SKNK 0903	VI	317.5	14.7	8.39	875	41.4	606	539.0	69.9
SKGPK 29	VI	311.0	16.1	9.08	1037	41.2	758.0	365.0	58.9
SKNK 679	III	310.0	12.3	12.63	2195	43.2	1371	1070.0	65.9

creating variability for efficient selection of useful recombinants in breeding programme depends on the degree of divergence among the parents selected. The more diverse the parents more chances of pronounced heterotic effects and increased spectrum of variability in segregating generations. On the basis of cluster mean and distance, 10 promising genotypes were identified (Table 6) that will be used in hybridization programme for improving seed yield in watermelon. Cluster VI comprised 6 genotypes having higher seed yield coupled with maximum number of fruits/plant while rest of the 4 genotypes represented in 4 different clusters showing higher mean values for one or more traits and hence can be used as a parent in breeding programme.

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