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Variability study in watermelon (*Citrullus lanatus)*

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Abstract

Forty four genotypes of water melon (*Citrullus lanatus*) was evaluated for genetic variability, heritability and genetic advance for yield and its contributing characters in watermelon during Summer 2019. Analysis of variance showed significant variation for all the studied characters, indicating presence of sufficient variability in the material. Widest range of variation was observed for fruit girth, fruit length, average fruit weight, fruit yield and fruit diameter. Maximum genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for seed size, average fruit weight and vine length followed by total soluble sugar and first female flowering node. High magnitude of heritability was exhibited in vine length (0.98) and average fruit weight (0.98) followed by seed size (0.97), total soluble sugar (0.91), first female flowering node (0.87), fruit length (0.86) and fruit diameter (0.74). The maximum genetic advance as percent of mean was observed for seed size (85.1), vine length (84.3), average fruit weight (74.9), total soluble sugar (34.8) and first female flowering node (28.4). High heritability coupled with high genetic advanced depicted in characters *viz*., seed size, average fruit weight, total soluble sugar, fruit length, fruit diameter, vine length and first female flowering node indicating that the heritability is most likely due to additive gene effects and thus the chances of fixing by selection.

Keywords: variability, GCV, PCV, heritability and genetic advance

Introduction

Watermelon (*Citrullus lanatus* (Thunb.) is a warm, veining, annual crop and is now grown in all tropical and subtropical areas of the globe. This fruit mostly cultivated for its fresh juice and sweet flesh. The ripe fruit is directly edible and is normally served cool as a dessert. Watermelon seeds are also used in soups and for producing seed oil. Commercial cultivation of watermelon takes place on larger scale in summer season in most of the Asian countries and globe also. China is the largest watermelon producer in the world and Turkey comes second while India ranked at 25 positions. Watermelon belongs to the family of "Cucurbitaceae" and xerophytic genus of "*Citrullus*". The genus *Citrullus* includes several diploid (2*n* = 22) species (Shimotsuma, 1963) [15], including *C. lanatus*, which gave rise to the red-fleshed sweet dessert watermelon, as well as the "egusi" type [also referred to as *Citrullus mucosospermus* (Fursa, 1972) [4], which is cultivated for its large oily seeds. Watermelons are native to the Kalahari Desert of southern Africa (Whitaker and Davis, 1962) [21] and the first recorded watermelon crop was found in Egypt. The fruit size varies from 2 to 15 kg, depending on variety. In Japan, square shaped and love shaped watermelons are popular have great demand.

A new variety as per farmer's demand can be developed from an assembled diverse genetic stock of any crop. Genetic resources are the real sense of building blocks and also fundamental not only to a crop improvement program, but also for the very survival of the species in time and space (Swaminathan, 1983) [18]. An important step in cultivar development is studying the genetic variability found in genetic resources. It is a dynamic process, but requires continuous enrichment and characterization of the materials maintained in germplasm collections (Valls, 2007) [20]. The information on the nature and the magnitude of variability present in the genetic material is of prime importance for a breeder to initiate any effective selection program. Therefore, the present investigation was undertaken with a view to gather information on extent of phenotypic and genotypic coefficient of variation, heritability and genetic gain for yield and yield components in watermelon.

Material and Methods

Experiment material consists of 44 watermelon genotypes which were collected from different agro-climatic zone.. The study was conducted at Ankur Research Farm Neri, Ankur Seed Pvt. Ltd., Nagpur during Summer, 2019. Observations were taken on 5 randomly selected plants from each plot. The data on quantitative parameter of watermelon was recorded on seed size (cm), average fruit weight (kg), total soluble sugar (%), fruit length (cm), fruit diameter (cm), fruit girth (cm), vine length (cm), first female flowering node and fruit yield (t/ha). The analysis of variance was carried out following the procedure of Panse and Sukhatme (1978) [10]. The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in a trait was worked out by the formula given by Burton (1952) [1]. PCV and GCV were categorized as low, moderate and high by following Sivasubramanian and Menon (1973) [16] as (0-10%): Low, (10-20%): Moderate, (Above 20%): High respectively. Heritability in broad sense was estimated as per the procedure presented by Burton and Devane (1953) [2]. The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.* (1949) [13] (0-30%): Low, (30-60%): Moderate and (60% and above): High, respectively. Genetic advance at 5 percent selection intensity was worked out by using the formula given by Johnson *et al*. (1955) [6]. The Genetic advance as percent of mean was categorized as low, moderate and high by following Johnson *et al*. (1955) [6] (0-10%): Low, (10-20%): Moderate and (Above 20%): High, respectively.

Results and Discussion

The range in the values reflect the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype × environmental interaction components and does not reveal as to which character is showing higher degree of variability. Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable) and epistasis (no allelic interaction). Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates the extent of variability existing for various traits.

The analysis of variance indicating the genotypic differences were highly significant for all the characters indicating considerable amount of genetic variability among the genotypes tested (Table 1). Similar results were reported by Damor *et al*. (2016) [3] and Sultan *et al*. (2018) [17].Wide range of variation observed from 19.6 to 28.8 tonn/ha with mean value 21.0 tonn/ha, for seed size mean value was 1.04 cm and range varied from 0.3 to 1.8 cm, for average fruit weight mean varied from 1.5 to 12.1 kg with mean 9.63 kg, total soluble sugar mean value was 9.76 (brix) and varied from 7.2 to13.5 brix, fruit length was varied 29.8 to 45.8 cm with mean value was 37.5 cm, for fruit girth mean value was 56.9 cm and range varied from 49.9 to 68.0 cm, for fruit diameter mean value was 16.79 cm and range varied from 11.8 to 19.7 cm, for vine length range varied from 14.4 to 19.8 cm and mean value was 19.03 cm, average value for first female flowering node was 9.79 node and range varied between 7.9 to 14.3 node. This indicates that presence of sufficient variability among the genotypes for respective triats.

The estimates of variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variance (GCV), heritability (broad sense) and genetic advance as percent mean are presented in Table 2. The wide range of genotypic and phenotypic variation was observed for vine length (cm) (61.9 and 63.3) followed by fruit length (12.8 and 14.9), fruit girth (6.8 and 15.3), average fruit weight (5.5 and 5.7) indicating that presence of sufficient variability among the genotypes these are used for selecting desirable characters. But total sugar soluble (3.1 and 3.4), fruit diameter (2.7 and 3.6), first female flowering node (2.01 and 2.4), seed size (0.193 and 0.199) and fruit yield (0.429 and 0.796) as recorded minimum variation and less scope for selection of this character from the present collection.

In general the phenotypic and genotypic coefficients of variation were almost similar with slight higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation. This was in agreement with the study of Husna *et al.* (2011) [5], Sultan *et al*. (2018) [17] and Rashid *et al.* (2020) [12]. Higher estimate of phenotypic and genotypic coefficient variance was recorded for seed size (cm), average fruit weight (g) and vine length indicating that genotypes had broad genetic base for these characters. Moderate estimate of GCV and PCV in total soluble sugar and first female flowering node. These results are in accordance with those of Tomar *et al*. (2008) [19], Joydip *et al*. (2015) [7] and Sultan *et al*. (2018) [17]. Characters which possessed moderate to high coefficients of variation suggested that there is better potential for improvement through selection. A wide range of variability along with high estimates of phenotypic and genotypic coefficients of variation further indicate that these attributes would respond to selection. Lower to moderate estimates of GCV and PCV was estimated in attributes is fruit yield, fruit length, fruit girth and fruit diameter. Those characters which showed low phenotypic and genotypic coefficients of variation were less amenable for improvement through selection. This was in conformity with findings Pandit *et al*. (2009) [9] and Husna *et al.* (2011) [5]. A perusal of the estimates of environmental component of variance in relation to their genotypic counterpart revealed that the estimates of genotypic coefficient of variance were higher than genotypic coefficient of variance for most of the characters. The higher magnitude of genotypic variance suggested little influence of environments in the expression of genetic variability.

Even phenotypic and genotypic coefficients of variation do not give a true picture about the extent of inheritance of the character. Therefore, the heritability of a character can be relied upon, as it enables the breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a character provided it is considered in conjunction with the predicated genetic advance as suggested by Panse and Sukhatme (1957) [11] and Johnson *et al.* (1955) [6] as heritability is influenced by bio-metrical method, generation of hybrid, sample size of experimental material and environment. Furthermore the progress in selection is also directly proportional to the amount of genetic advance. Therefore, the effect of selection is realized more quickly in those characters which have high heritability as well as high genetic advance. The relative amount of heritable portion of variation was, therefore, estimated with the help of heritability estimates and genetic advance.

In crop improvement, only the genetic component of variation is important since only that component is transmitted to the next generation. Heritability indicated the effectiveness with which selection of genotypes would be based on phenotypic performance. In present investigation, characters *viz*., seed size, average fruit weight, total soluble sugar, fruit length, fruit diameter, vine length and first female flowering node recorded high heritability. These indicating that the characters are less influenced by environmental effects and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a character and thus selection based on phenotypic expression could be relied upon. Similar results were also reported by Sharma *et al.* (2010) [14] and Rashid *et al.* (2020) [12]. While characters namely fruit yield, fruit girth are grouped into moderate level of heritability. These indicate phenotypic expression is little bit influence by environment factors. High heritability characters are suggesting the important role of genetic constitution in the expression of the characters and these traits are considered to be dependent from breeding point of view.

Shift in gene frequency towards superior side under selection pressure is termed as genetic advanced and is generally expressed as percentage of mean (genetic gain). Johnson *et al*. (1955) [6] found it more useful to estimate heritability values together with genetic advanced in predicting the ultimate choice of the best genotypes by selection. However, high genetic gain along with high heritability showed most effective conditions for selection. High heritability coupled with high genetic advanced was observed in seed size, average fruit weight, total soluble sugar, vine length and first female flower node. This indicated that these characters are governed by additive gene action and real progress in improvement through selection. Similar results were reported by Singh and Kumar (2002) [8]. High heritability coupled with moderate genetic advanced in fruit length and fruit diameter. High heritability is being exhibited due to preponderance of non additive gene action and favorable influence of environment rather than genotype. Moderate to low heritability association with low genetic advanced was noticed in fruit yield and fruit girth. This indicated that the character is highly influenced by environment effects and selection would be ineffective for traits.

It is clear from the above discussion that tremendous potential exists for converging the elite allelic resources present in these watermelon genotypes through a systematic breeding and selection approach so as to recover high yielding recombinants, with good quality characteristics. Analysis of variance revealed that significant variation existed among various characters under study. seed size (cm), average fruit weight (g) and vine length recorded high phenotypic and genotypic coefficients of variation, indicating that the genotypes had broad genetic base for these characters. High heritability coupled with high genetic advance (as percent of mean) was observed for seed size, average fruit weight, total soluble sugar, vine length and first female flower node.

Table 1: Analysis of variance with respect to MSS for various characters in watermelon

Source of variation	d.f.	Mean sum of squares								
		Seed size (cm)	Average Fruit weight (kg)	Total Soluble Sugar (%)	Fruit Length (cm)	Fruit Girth (cm)	Fruit Diameter (cm)	Vine Length (cm)	First female flowering node	Fruit yield (t/ha)
Replication	2	0.001	0.07	1.14	0.56	4.40	3.15	9.44	0.15	2.3
Genotypes	43	0.6**	17.1**	10.0**	44.7**	45.9*	10.7**	189.8**	7.2**	13.7*
Error	86	0.017	0.38	0.94	6.43	19.46	2.74	3.98	0.93	3.07
C.V. (%)		12.7	6.4	9.9	6.8	8.8	9.9	10.5	9.9	9.1
Mean		1.04	9.63	9.76	37.54	56.93	16.79	19.03	9.79	21.0
Min		0.3	1.5	7.2	29.8	49.9	11.8	14.4	7.9	19.6
Max		1.8	12.1	13.5	45.8	68.0	19.7	19.8	14.3	28.8

**,* Significant at 1and 5 per cent probability levels, respectively

Table 2: Estimates of genotypic and phenotypic variance and other genetic parameters for fruit yield and yield-attributing traits in Watermelon

	Seed size (cm)	Average Fruit weight (kg)	Total Soluble Sugar (%)	Fruit Length (cm)	Fruit Girth (cm)	Fruit Diameter (cm)	Vine Length (cm)	First female flowering node	Fruit yield (t/ha)
Environment var. (EV)	0.006	0.13	0.31	2.14	8.49	0.92	1.33	0.31	1.23
Environment Coefficient var. (ECV)	12.664	9.63	9.76	6.76	8.86	9.87	10.49	9.86	1.12
Genotypic var.(GV)	0.193	5.58	3.09	12.76	6.81	2.65	61.93	2.09	0.43
Genotypic Coefficient var. (GCV)	41.947	36.78	17.71	9.52	4.58	9.70	41.35	14.77	3.12
Phenotypic var. (PV)	0.199	5.70	340	14.90	15.30	3.577	63.26	2.40	0.80
Phenotypic Coefficient var. (PCV)	42.579	37.20	18.59	10.28	6.87	11.25	41.79	15.83	4.25
Broad Sense Heritability (%)	0.97	0.98	0.91	0.86	0.45	0.74	0.98	0.87	0.54
Genetic advancement (as % of mean)	85.13	74.92	34.77	18.14	6.30	17.24	84.285	28.40	4.72

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