© 2016 *RELS*
http://rels.comxa.com
rel_sci@yahoo.com

ISSN: 0974-4908
Res. Environ. Life Sci.
9(9) 1069-1071 (2016)

Genetic variability studies in wildmelon (*Cucumis melo* subsp. *agrestis* Naudin)

Shivappa M. Karadi*[1], V.M. Ganiger[1], Vittal Mangi[1], L.B. Basavaraj[2], M. B. Madalageri[1] and Pallavi H.M.[3]
[1]Department of Vegetable Science , [3]Department of Seed Science and Technology,College of Horticulture, Bagalkot -587 103, India
[2]Department of Vegetable Science, Kittur Rani Channamma College of Horticulture, Arabhavi- 591 218, India
***e-mail:** shivukaradi@gmail.com

(Received: October 21, 2015; Revised received: June 10, 2016; Accepted: June 16, 2016)

Abstract: Genetic variability, heritability, genetic advance and its per cent over mean for eighteen characters were assessed by field evaluation of twenty–four wild melon genotypes at College of Horticulture, Bagalkot , Karnataka during 2013-14. High degree of variation was observed for all characters. The difference between phenotypic co–efficient of variation (PCV) and genotypic co–efficient of variation (GCV) are found to be narrow for most of the traits. However, high GCV and PCV was observed for leaf area, number of fruits per vine, average fruit weight, fruit length, fruit breadth, yield per vine, fruit cavity size, number of seeds per fruit, fruit flesh thickness, TSS, vitamin–C and seed to pulp ratio. High heritability coupled with high genetic advance recorded for vine length, leaf area, node at first female flowering, node at first male flowering, number of fruits per vine, average fruit weight, fruit length, fruit breadth, yield per vine, fruit cavity size, fruit flesh thickness and number of seeds per fruit are indicates the predominance of additive gene action. Hence, improvement of these traits through simple selection breeding method for improvement of wild melon would be rewarding.

Key words: Wild melon, Genetic advance, Heritability, Genotypic variance, Phenotypic variance

Introduction

Wild melon (*Cucumis melo* subsp. *agrestis* Naudin) -belongs to family cucurbitaceae with chromosome number 2n= 24. It is commonly called as senat seed, small gourd-, wild musk melon and also called as kachari in Hindi, shinde in Marathi, chibdin in Konkani, gurmi in Assam and mekkekayi in Kannada languages. Wild melon is one of the traditional underutilized vegetable crop that can be exploited in marginal lands in north Karnataka with minimum crop husbandry practice. Even though, it is underexploited cucurbit has attained a status of high value and occupied a pride place in rural traditional cuisine because of its pleasant flavour coupled with rich color diversity namely green, yellow, saffron, red and intermediate colors and nutrient profile. There is no commercial wild melon varieties developed by either public or private sector. Farmers are growing only the local cultivars and landraces. Though, there is a wide range of genetic variability available in India, not much attention has been given to the genetic improvement of this crop. The role of genetic variability in crops is of paramount importance in selecting the best genotypes for making rapid improvement of yield and its related characters as well as to select the most potential parents for successful hybridization programme. With the limited variability, the interested traits cannot possible to incorporate and the breeder will have to enrich the greater variability of genetic resources namely germplasm by hybridization, mutation,polyploidy breeding and also by several other breeding procedure (Kumaran *et al*., 2000).

In spite of many advantages wild melon, there were no research thrusts paid on genetic improvement wild melon. Henceforth, present study trialed to assess the genetic variability of local collections or land races based on morphological and physiological variation.

Material and Methods

The present study carried out at College of Horticulture, Bagalkot, Karnataka during September 2013 with 24 genotypes. The genotypes were assessed in a field experiment under a randomized block design with two replications. 10 plants maintained in each treatment with spacing of 2 m X 1 m between rows and plants, respectively. The data were recorded on five randomly selected plants from each treatment for 19 characters. Observations recorded on vine length (cm), leaf area (cm^2), number of primary branches per vine, days to first male flowering, days to first female flowering, node at first male flowering, node at first female flowering, seeds per fruit (g), number of fruits per plant, average fruit weight (g), fruit length (cm), fruit breadth (cm), fruit yield per vine (kg), fruit flesh thickness (cm), cavity size (cm^2), number of seeds per fruit, vitamin–C (mg/100 g), TSS (^{0}B) and seed to pulp ratio. The variance components and co–efficients of variation (cv) were computed as per Burton (1952). The heritability in broad sense and genetic advance over a mean were determined by using the formula given by Johnson *et al*. (1955).

Results and Discussion

The analysis of variance revealed significant differences among genotypes for all the characters, which indicated the presence of variability among the lines evaluated and which indicated existence of ample scope for genetic improvement of wild melon by selection breeding methods. Estimates of genetic parameters and components of variance are presented in (Table 1). In general, the PCV values were higher than GCV values, indicating that the variation among the genotypes is due to the influence of environment. Both GCV and PCV were high for number of fruits per vine (48.33% and 49.46%), average fruit weight (56.57% and 57.72%), fruit length (38.40% and 38.73%), fruit breadth (20.71% and 21.30%), yield per vine (40.48% and 42.01%), number of seeds per fruit (21.18% and 23.73%) and fruit flesh thickness (34.53% and 35.04%). The present findings are in agreement with Gopalakrishnan *et al*. (1988) pumpkin Singh *et al.* (1988) pumpkin, Kumaran *et al*. (2000) pumpkin -indicating greater genetic variability among the accessions and responsiveness of the attributes for making further improvement by selection.

The co–efficient of variation does not offer full scope to estimate the heritable variation. The relative heritable variation is assessed with the help of heritability; its estimates in broad sense are helpful in identifying the appropriate character for selection and enable breeders to select superior genotypes in genetic advancement of wild melon. High estimates of heritability in broad sense were observed for all the traits, which indicated that selection based on phenotypic performance would be rewarding. Burton (1952) suggested that high GCV along with heritability estimates high values of GCV and heritability estimates supplemented with greater genetic gain are also indicative of additive gene effect control the inheritance of the traits (Narayan *et al*., 1996). Therefore, such

Table-1: Analysis of variance for growth, earliness, yield and quality parameters in wild melon (*Cucumis melo* subsp. agrestis Naudin)

Source of variation/character	Replication	Treatment	Error	CD(1%)	CD(5%)
Degrees of freedom	1	23	56		
Growth parameters					
Vine length (m)	328.39	805.71**	62.13	22.12	16.30
Leaf area (cm^2)	11.76	790.25**	17.35	8.61	11.69
Number of primary branches	0.22	1.046**	0.38	1.74	1.82
Earliness parameters					
Days to first male flowering	14.52	1.04**	0.38	1.74	1.28
Days to first female flowering	86.08	23.29**	7.77	7.89	5.76
Nodes to first male flowering	0.02	0.60**	0.06	0.69	0.51
Nodes to first female flowering	0.00	3.34**	0.47	1.92	1.41
Yield parameters					
Number fruits per vine	1.84	312.27**	14.13	10.55	7.77
Average fruit weight (g)	121.44	4229.60**	166.83	36.26	26.71
Fruit length (cm)	0.37	13.04**	0.22	1.31	0.97
Fruit breadth (cm)	0.03	1.58**	0.08	0.826	0.60
Yield per vine (kg)	0.17	0.77**	0.05	0.659	0.48
Quality parameters					
Fruit cavity size (cm^2)	0.504	100.39**	1.01	2.82	2.08
Number of seeds per fruit	2106.75	14664.56**	2983.57	153.34	112.99
Fruit flesh thickness (cm)	0.005	0.162**	0.00	0.19	0.14
TSS (° brix)	0.381	2.451**	0.42	1.95	1.43
Vitamin C (mg/100g)	1.60	23.45**	2.71	4.62	3.40
Seed to pulp ratio	0.00	0.028**	0.00	0.08	0.06

**** Significant at 1% level**

Table-2: Estimates of mean, range, components of variance, heritability and genetic advance for growth, earliness, yield and quality parameters in wild melon (*Cucumis melo* subsp. *agrestis*)

Character	Range	Mean	GV	PV	GCV(%)	PCV(%)	h^2(%)	GA	GAM(%)
Growth parameters									
Vine length (cm)	114.70-200.60	156.78	371.78	402.85	12.30	12.80	92.29	38.15	24.34
Leaf area (cm^2)	55.12-156.62	92.74	386.45	395.12	21.19	21.43	97.00	40.04	43.18
No.of primary branches/vine	4.10-6.40	5.12	0.33	0.52	11.22	14.11	63.27	0.94	18.39
Earliness parameters									
Days to first male flowering	31.80-46.75	38.86	14.54	17.46	9.81	10.75	83.00	7.17	18.49
Days to first female flowering	32.17-43.99	39.53	7.75	11.64	7.04	8.63	66.62	4.68	11.84
Node to first male flowering	2.20-4.45	2.89	0.27	0.30	18.05	19.03	89.96	1.02	35.27
Node to first female flowering	4.30-9.05	6.26	1.43	1.67	19.15	20.66	85.95	2.29	36.59
Yield parameters									
Number of fruits per vine	13.50-54.25	25.26	149.07	156.13	48.33	49.46	95.47	24.57	97.28
Average fruit weight (g)	19.08-182.75	79.66	2030	2114.80	56.57	57.72	96.06	90.99	114.21
Fruit length (cm)	4.17-15.00	6.59	6.41	6.52	38.40	38.73	98.31	5.17	78.43
Fruit breadth (cm)	2.91-5.62	4.18	0.74	0.79	20.71	21.30	95.54	1.73	41.48
Yield per vine (kg)	0.56-3.64	1.47	0.35	0.38	40.48	42.01	92.84	1.18	80.36
Quality parameters									
Fruit cavity size (cm^2)	6.59-31.51	15.26	49.69	50.19	46.16	46.40	98.89	14.44	94.62
Number of seeds per fruit	262.50-571	360.70	5840.49	7332.28	21.18	23.73	79.65	140.50	38.95
Fruit thickness (cm)	0.37-1.37	0.81	0.07	0.08	34.53	35.04	97.14	0.570	70.11
Total soluble solids- (°B)	2.95-6.18	4.46	0.984	1.22	22.19	24.77	80.31	1.83	40.97
Vitamin C (mg/100g)	6.97-19.16	11.23	10.37	11.72	28.67	30.49	88.43	6.23	55.55
Seed to pulp ratio	0.08-0.50	0.22	0.01	0.01	51.30	52.44	96.83	0.23	104.61

characteristics reflect greater selective value and offer ample scope for efficient selection. High value of heritability associated with moderate to high GCV and genetic gain -manifestation would provide better picture, amount of advance expected by phenotypic selection. Heritability estimates in conjunction with genetic gains are more effective and dependable in predicting the improvement through selection (Johnson *et al*., 1955). Since, the units of measurements influence the magnitude of genetic advance (GA), the GA as per cent mean is considered as an essential selection parameter. If, heritability is due to additive gene action, genetic gain would be high and if it is due to non-additive gene action, then the genetic gain would be low (Panse, 1957). Simultaneous consideration of the three genetic parameters provides the best picture of the response to selection. High values of GCV and heritability estimates supplemented with greater genetic gain are also indicative of additive gene action controlling the inheritance of the traits (Naryan *et al*., 1996). Therefore, such characteristics reflect greater selective value and offer ample scope for efficient selection. High value of heritability associated with moderate to high GCV and genetic gain were manifested by vine length, leaf area, number of fruits per vine, average fruit weight and number of seeds per fruit, which might be ascribed to additive gene action governing the expression of these traits and phenotypic selection for their improvement.

Reference

Burton, G.W. and Devane, R.W.: Estimating heritability in tall foscuue (*Festuca arundinaces)* from replicated clonal material. *Agron. J.,* **45**: 478-481 (1953).

Gopalakrishnan, T.R., Gopalakrishnan, K.G. and Peter, K.V.: Variability, heritability and correlation among some polygenic characters in pumpkin. *Indian J. Agric. Sci*., **50**: 925-930 (1980).

Johnson, H.W., Robinson, H.F. and Comstock, R.S.: Estimation of genetic and environmental variability in soyabean. *Agron. J.*, **41**: 314-318 (1955).

Kumaran, S.S., Natarajan S. and Thamburaj S.: Genetic variability in pumpkin (*Cucurbita moschata* Duch. Ex. Poir.). *South Indian Hort*., **45**: 10-12 (2000a).

Narayan, R., Singh, S.P., Sharma, D.K. and Rastogi, K.B.: Genetic variability and co-relation parameter in bottle gourd. *Ind. J. Hort*., **53**: 53-58 (1996).

Panse, U.G.: Genetics of quantitative characters in relation to plant breeding. *Ind. J. Genet.,* **17**: 318-328 (1957).

Singh, J.K., Kumar, J.C. and Sharma, J.R.: Genetic variability and heritability of some economic traits in pumpkin in different seasons. *The Punjab Horticultural Journal*, **28**: 238-242 (1988).