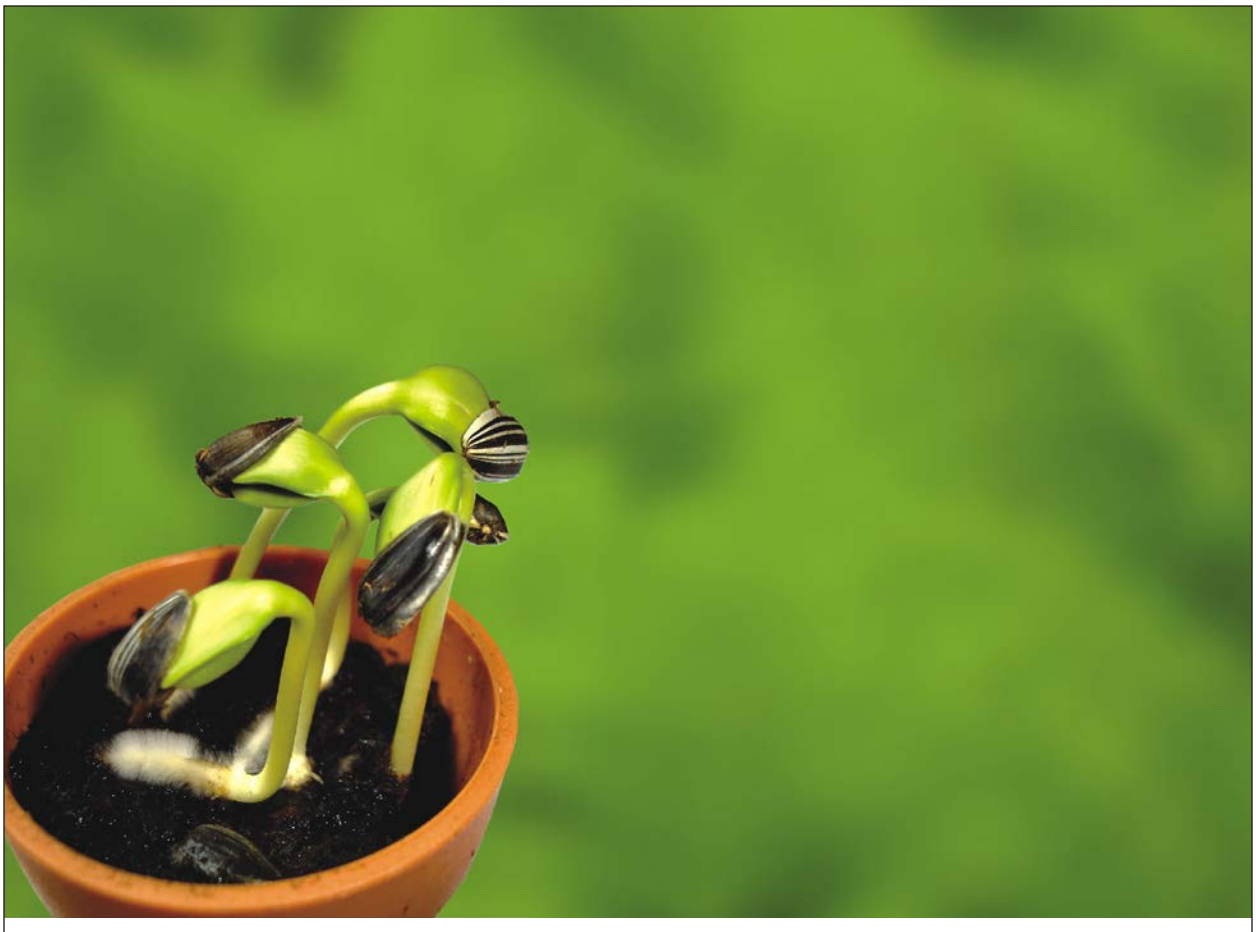

International Journal of Plant Breeding and Genetics

ISSN 1819-3595

Academic Journals Inc.

www.academicjournals.com

International Journal of Plant Breeding and Genetics 6 (4): 238-244, 2012
ISSN 1819-3595 / DOI: 10.3923/ijpbg.2012.238.244

Variability, Heritability and Genetic Advance in Egyptian Sweet Melon (*Cucumis melo* var. *aegyptiacus* L.) Under Water Stress Conditions

E.A. Ibrahim
Department of Cross Pollinated Vegetable Crops Research, Horticulture Research Institute, 9 Cairo University St., Orman, Giza, Egypt

ABSTRACT

The objective of the study was to generate genetic information, which can help in breeding sweet melon cultivars with improved drought tolerance. Thirteen sweet melon genotypes collected from different places in Egypt were evaluated for variability, heritability and genetic advance. The experimental material was sown in a randomized complete blocks design with three replicates under irrigation as well as drought stress conditions. Significant differences were observed among genotypes for all the studied traits under normal irrigation and water stress. The irrigation×genotypes interactions were found to be significant for all the studied traits except fruit length. The estimates of phenotypic coefficient of variation were higher than the estimates of genotypic coefficient of variation for all the characters, which suggested that the apparent variation is not only due to the genotypes but also due to the influence of environment. High heritability coupled with high genetic advance was noted for fruit weight and yield per plant. This provided that these parameters were under the control of additive genetic effects. This indicates that selection should lead to fast genetic improvement of the material. Moreover, magnitude of mean performance for all the traits decreased in water stress environment. Fruit length was very less affected by water stress, but yield per plant was very high affected by water stress.

Key words: *Cucumis melo*, sweet melon, variability, heritability, genetic advance, water stress

INTRODUCTION

Sweet melon (*Cucumis melo* var. *aegyptiacus* L.) is a staple and refreshing fruit in Egypt. Fruits are consumed in the summer period and are popular because the pulp of the fruit is very refreshing, high nutritional and sweet with a pleasant aroma (Melo *et al*., 2000). A large number of local sweet melon genotypes are cultivated in Egypt but no serious attempts have been made to upgrade the productivity and acceptability of this crop within the country. The presence of genetic variation in the breeding material at hand determines the success or failure of any breeding or bio-engineering program. Therefore, the measurement of genetic variation and understanding of mode of inheritance of quantitative traits are essential steps in any crop improvement program.

The most of cultivation of sweet melon is based on local open pollinated varieties which are maintained by farmers, produced for self-consumption and sold on local markets. The commercially important improved cultivars of sweet melon are Kahera-6, Ananas El-Dokki and Shahd El-Dokki. So, developing local sweet melon, based on local genotypes, may result in very promising outputs, especially because the germplasm of sweet melon available in Egypt is having high genetic variability (El-Shimi and Ghoneim, 2006).

Egypt is expected to be seriously affected by the adverse impacts of climate change on water sources and availability and severe water stress conditions will affect crop productivity, particularly that of vegetables (McCarthy and IPCC, 2001; Boutraa, 2010; Xoconostle-Cazares *et al*., 2010; Ruzana Adibah and Ainuddin, 2011). So, the main goal of sweet melon breeding is improvement of stress tolerance that represents a major goal for the plant breeders and for the agriculture in the future. Agriculture researchers are trying to develop crops that use water more efficiently, i.e., with higher water use efficiency and can perform better for yield even in water limited conditions (Manickavelu *et al*., 2006; Kusvuran *et al*., 2010). There is dire need to make and select sweet melon genotypes that have no or only little effect of water stress.

The present study provides information on nature of genetic variability for yield and yield components under normal and drought condition in sweet melon genotypes. The information derived from the study will help in breeding sweet melon for drought tolerance.

MATERIALS AND METHODS

Thirteen sweet melon genotypes (10 local open-pollinated cultivars and 3 commercial cultivars) were used as genetic material for this study (Table 1). Local open-pollinated cultivars were collected from different places in Egypt and single plants from each cultivar were selfed for one generation during the growing season of 2008. The soil texture at the experimental site is clay-loam.

All genotypes were sown and evaluated under irrigated and drought conditions at Qaha vegetable research station, Qalubia governorate on 6 April of 2009 season. Each of two experiments was designed in a randomized complete blocks with three replicates. Each experimental unit area was consisted of four ridges each of 5 m length and 1.5 m in width and one plant per hill with 50 cm apart. The culture practices were done according to the general program of sweet melon cultivation. Drought conditions were started after first irrigation and created by reducing the frequency of irrigation watering by one half to that of irrigated crop, i.e., missing alternate irrigation.

At the harvesting time, a random sample of 12 plants was taken from each experimental unit and data were recorded for number of fruits per plant, fruit weight (g), total yield per plant (g), fruit length (cm), fruit width (cm) and flesh fruit thickness (cm).

Table 1: The names and sources of sweet melon genotypes used in the study

Cultivars or lines	Collection place/area	Pedigree
Shahd El-Dokki	Agricultural Research Center	Commercial variety
Ananas El-Dokki	Agricultural Research Center	Commercial variety
Kahera-6 improved	Agricultural Research Center	Commercial variety
Ismaelawi	Ismaelia	Local variety
Shahd Edfina	Al-Behira	Local variety
Kouz El-Asal	Al-Behira	Local variety
Albasosi	Qulybiya	Local variety
Al-Gezawi	Bush-Beni Sueif	Local variety
FBS	Al-Fashn-Beni Sueif	Local variety
AEF	Abo-Elsoud-Fayoum	Local variety
BMM	Bani Mazar-Al-Minia	Local variety
NGS	Nag El-Gawahra-Sohag	Local variety
AQ	Armant-Qena	Local variety

Estimates of broad sense heritability for different traits were computed using the variance components method based on the combined analyses over both water conditions according to Snedecor and Cochran (1980). The components of variance were computed using the observed mean square values as outlined by Johnson *et al.* (1955) by using following formulae:

$$\sigma^2 g = \frac{(MS_g - MS_{gw})}{rw},\ \sigma^2_{gw} = \frac{(MS_{gw} - MS_e)}{r},\ \sigma^2 e = MS_e \text{ and } \sigma^2 ph = \frac{\sigma^2_g + \sigma^2_{gw}}{r} + \frac{\sigma^2_e}{rw}$$

where, $\sigma^2 g$, $\sigma^2 gw$, $\sigma^2 e$ and $\sigma^2 ph$ are the variances due to genotypes, genotypes×water levels (G×W) interaction, experimental error and phenotypes, respectively, MS_g, MS_{gw} and MS_e are the mean squares of genotypes, genotypes×water levels (G×W) interaction and pooled error, respectively and w denotes the number of environments (i.e., water levels) and r the number of replicates.

Phenotypic (PCV) and genotypic (GCV) coefficient of variation were evaluated according to the methods of Johnson *et al.* (1955) and Hanson *et al.* (1956) as follows:

$$PCV = \frac{\sqrt{\sigma^2 ph}}{X} \times 100$$

$$GCV = \frac{\sqrt{\sigma^2 g}}{X} \times 100$$

where, $\sigma^2 ph$, $\sigma^2 g$ and X are the phenotypic variances, genotypic variances and grand mean for each trait, respectively.

Broad sense heritability ($h^2 B$) was calculated according to Allard (1999) as the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 ph$).

Expected genetic advance after one generation of selection (GA) and GA as percentage of the mean assuming selection of the superior 5% of the genotypes were estimated according to the formulae given by Johnson *et al.* (1955) as follows:

$$GA = K \cdot h^2 B \cdot \sqrt{\sigma^2 ph};\ GA\ (\text{as \% of the mean}) = \left(\frac{GA}{X}\right) \times 100$$

where, K is the selection differential (2.06 for selecting 5% of the genotypes).

RESULTS AND DISCUSSION

Analysis of variance: Combined analysis of variance for the studied traits is presented in Table 2. Water levels mean squares were significant for all the studied traits except fruit length. The mean squares for genotypes were highly significant for all the studied traits. This indicates the

Table 2: Mean squares from the combined analysis of variance for the studied traits of 13 sweet melon genotypes over two tested water conditions

Source of variation	df	Fruit weight (g)	No. of fruits/plant	Total yield/plant (g)	Fruit length (cm)	Fruit width (cm)	Flesh fruit thickness (cm)
Irrigation	1	2427756*	1.579*	42927743*	82.3	54.7*	3.563*
Error	2	1160152	0.659	1732635	70.0	15.4	1.908
Genotypes	12	92168169**	7.997**	355195857**	1638.7**	440.1**	22.126**
Irri × Geno	12	588946**	0.417**	9543489**	7.2	9.6**	0.205
Error	48	210270	0.169	734349	23.7	3.6	0.427

***Significant at 0.05 and 0.01 probability, respectively, df: Degrees of freedom

Table 3: Estimates of components of variance, phenotypic coefficient of variation (PCV) and genetic coefficient of variation (GCV), broad sense heritability (h^2) and genetic advance (GA) for the studied traits of 13 Egyptian sweet melon genotypes tested in two environments

	Estimates of components of variation*						
Characters	σ^2ph	σ^2g	σ^2	PCV (%)	GCV (%)	h^2 (%)	GA (%) of mean
Fruit weight (g)	1280113	1271934	14899	44.06	43.92	99.36	90.19
No. fruits plant^{-1}	0.11	0.11	0.01	14.24	13.86	94.79	27.81
Total yield plant^{-1} (g)	4933276	4800727	259997	38.48	37.96	97.31	77.15
Fruit length (cm)	22.76	22.66	0.035	21.73	21.68	99.56	44.57
Fruit width (cm)	6.11	5.98	0.242	15.26	15.10	97.82	30.76
Flesh fruit thickness (cm)	0.31	0.30	0.01	16.21	16.14	99.07	33.09

*σ^2ph, σ^2g and σ^2 are phenotypic, genotypic and error variances of genotype means, respectively

existence of a high degree of genetic variability in the material to be exploited in breeding program and that also reflected the broad ranges observed for each trait. The water levels×genotypes interactions were found to be significant for all the studied traits except fruit length. These results have partial agreement with Kohpayegani and Behbahani (2008) and Naroui Rad *et al.* (2010).

Genetic variation: The values of genotypic, phenotypic and error variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance are presented in Table 3. For all the studied traits, the genotypic and phenotypic estimated variance appeared large, in comparison with the estimated values of error variance, such a result seemed to indicate that the number of replicates used in the evaluation experiment of these genotypes were adequate to give a better estimation for the error variance.

High coefficients of phenotypic (PCV) and genotypic (GCV) variation were observed for several characters, the highest being for fruit weight followed by yield per plant and fruit length. The estimates of Phenotypic Coefficient of Variation (PCV) in general, were higher than the estimates of Genotypic Coefficient of Variation (GCV) for all the characters, which suggested that the apparent variation is not only due to the genotypes but also due to the influence of environment. The characters with high phenotypic coefficient of variation indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection program because the environmental variations are unpredictable in nature and may mislead the results. Similar, findings were reported by Rahman *et al.* (2002) on snake gourd, Rakhi and Rajamony (2005), Taha *et al.* (2007) and Naroui Rad *et al.* (2010) on melon, Torkadi *et al.* (2007) and Tomar *et al.* (2008) on muskmelon, Pandit *et al.* (2009) on bottle gourd and Yadav *et al.* (2009) on cucumber, Dar and Sharma (2011) on tomato, Abd El-Kareem and El-Saidy(2011) on wheat and Degewione *et al.* (2011) on shallot.

Broad sense heritability estimates among all the traits studied are very high (>90%). High heritability estimates indicate the presence of large number of fixable additive factors and hence these traits may be improved by selection. However, selection should be made very carefully as heritability is measured in broad sense, which may be influent. High heritability does not mean a high genetic advance for a particular quantitative character. Johnson *et al.* (1955) reported that effectiveness of selection depends not only on heritability but also on genetic advance. Therefore, genetic advance was also computed as percentage of mean. In the present investigation, high heritability associated with high genetic advance was found in the characters like fruit weight and yield per plant. This indicated that these two characters were mostly governed by additive gene

Table 4: Ranges, means, percentage decrease under water stress (D%), standard deviation (SD) and coefficient of variation (CV) for 6 characters for 13 sweet melon genotypes at the two tests water conditions

Characters	Water conditions	Min.	Max.	Mean	D (%)	SD (+)	CV
Fruit weight (g)	Normal	868	4522	2744	12.9	1184	1.79
	Stress	760	3982	2391		1037	3.40
No. fruits plant^{-1}	Normal	1.8	3.2	2.5	12.0	0.36	2.11
	Stress	1.7	3	2.2		0.33	2.99
Total yield plant^{-1} (g)	Normal	2768	10030	6513	22.8	2436	0.83
	Stress	2280	7846	5030		1932	3.31
Fruit length (cm)	Normal	13.4	31.7	23	8.7	5	2.13
	Stress	12.6	30.1	21		5	4.14
Fruit width (cm)	Normal	13.8	22.1	17.0	9.4	2.5	1.38
	Stress	12.1	20.7	15.4		2.4	1.98
Flesh fruit thickness (cm)	Normal	2.4	5	3.6	11.1	2.53	2.53
	Stress	2.2	4.4	3.2		2.95	2.95

action. Breeding methods based on progeny testing and mass selection could be useful in improving these traits (Panse, 1957). High heritability accompanied by low genetic advance for number of fruits per plant is indicative of non-additive gene actions' predominance which could be exploited through heterosis breeding. These results were in harmony with those obtained by Rahman *et al.* (2002) on snake gourd, Rakhi and Rajamony (2005) and Taha *et al.* (2007) on melon, Torkadi *et al.* (2007) and Tomar *et al.* (2008) on muskmelon, Pandit *et al.* (2009) on bottle gourd, Yadav *et al.* (2009) on cucumber and Shiri *et al.* (2010) on maize.

Ranges, means, standard deviation and coefficient of variation among sweet melon genotypes revealed the presence of genetic variation for all studied traits in this experiment at both studied water conditions (Table 4). Moreover, magnitude of mean performance for all the traits decreased in water stress environment. Mean value of fruit weight, number of fruits per plant, total yield per plant, fruit length, fruit width and flesh fruit thickness decreases 12.9, 12, 22.8, 8.7, 9.4 and 11.1%, respectively. Fruit length was very less affected by water stress, but fruit weight was very high affected by water stress. Possible reason for decrease of mean value of traits can be deficiency of water that slowed the physiological processes. Similar observations were made by Cabello *et al.* (2009) on melon, who reported that under severe deficit irrigation, the yield was reduced by 22% mainly due to decrease fruit weight.

CONCLUSION

The data in this study showed the possibility of improving Egyptian sweet melon by selection for fruit weight and yield per plant under water stress conditions in Egypt. Based on the high heritability and high genetic advance shown by these characters, it could conclude that the determinant genetic effects of the phenotypic expression of these characters are fundamentally of the additive type. For this reason, a high response should be achievable after several selection cycles.

REFERENCES

Abd El-Kareem, T.H.A. and A.E.A. El-Saidy, 2011. Evaluation of yield and grain quality of some bread wheat genotypes under normal irrigation and drought stress conditions in calcareous soils. J. Biol. Sci., 11: 156-164.

Allard, R.W., 1999. Principles of Plant Breeding. 2nd Edn., John Wiley and Son, New York, USA.

Boutraa, T., 2010. Improvement of water use efficiency in irrigated agriculture: A review. J. Agron., 9: 1-8.

Cabello, M.J., M.T. Castellanos, F. Romojaro, C. Martinez-Madrid and F. Ribas, 2009. Yield and quality of melon grown under different irrigation and nitrogen rates. Agric. Water Manag., 96: 866-874.

Dar, R.A. and J.P. Sharma, 2011. Genetic variability studies of yield and quality traits in tomato (*Solanum lycopersicum* L.). Int. J. Plant Breed. Genet., 5: 168-174.

Degewione, A., S. Alamerew and G. Tabor, 2011. Genetic variability and association of bulb yield and related traits in shallot (*Allium cepa* var. *Aggregatum DON.*) in Ethiopia. Int. J. Agric. Res., 6: 517-536.

El-Shimi, I.Z.A. and M.I. Ghoneim, 2006. Evaluation of morphological and pathological performance for some local melon *landraces*. Mansoura Univ. J. Agric. Sci., 28: 6879-6896.

Hanson, C.H., H.F. Robinson and R.E. Comstock, 1956. Biometrical studies of yield in segregating populations of Korean Lespedeza. Agron. J., 48: 268-272.

Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.

Kohpayegani, J.A. and M. Behbahani, 2008. Genetic diversity of some populations of Iranian melon using SSR markers. Biotechnology, 7: 19-26.

Kusvuran, S., H.Y. Dasgan, S. Kucukkomurcu and K. Abak, 2010. Relationship between drought tolerance and stomata density in melon. Acta Hort. (ISHS), 871: 291-300.

Manickavelu, A., R.P. Gnanamalar, N. Nadarajan and S.K. Ganesh, 2006. Genetic variability studies on different genetic populations of rice under drought condition. J. Plant Sci., 1: 332-339.

McCarthy, J.J. and IPCC, 2001. Climate Change 2001: Impacts, Adaptation and Vulnerability: Contribution of Working Group II to the Third Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press, UK., ISBN-13: 9780521015004, Pages: 1032.

Melo, M.L.S., N. Narain and P.S. Bora, 2000. Characterisation of some nutritional constituents of melon (*Cucumis melo* hybrid AF-522) seeds. Food Chem., 68: 411-414.

Naroui Rad, M.R., M. Allahdoo and H.R. Fanaei, 2010. Study of some yield traits relationship in melon (*Cucumis melo* L.) germplasm gene bank of Iran by correlation and factor analysis. Trakia J. Sci., 8: 27-32.

Pandit, M.K., B. Mahato and A. Sarkar, 2009. Genetic variability, heritability and genetic advance for some fruit characters and yield in bottle gourd (*Lagenaria siceraria* Molina. Standl.) genotypes. Acta Hort. (ISHS), 809: 221-226.

Panse, V.G., 1957. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet. Plant Breed., 17: 318-328.

Rahman, M.A., M.D. Hossain, M.S. Islam, D.K. Biswas and M. Ahiduzzaman, 2002. Genetic variability, heritability and path analysis in snake gourd (*Trichosanthes anguina* L.). Pak. J. Biol. Sci., 5: 284-286.

Rakhi, R. and L. Rajamony, 2005. Variability, heritability and genetic advance in landraces of culinary melon (*Cucumis melo* L.). J. Trop. Agric., 43: 79-82.

Ruzana Adibah, M.S. and A.N. Ainuddin, 2011. Epiphytic plants responses to light and water stress. Asian J. Plant Sci., 10: 97-107.

Shiri, M., R.T. Aliyev and R. Choukan, 2010. Water stress effects on combining ability and gene action of yield and genetic properties of drought tolerance indices in maize. Res. J. Environ. Sci., 4: 75-84.

Snedecor, G.W. and W.G. Cochran, 1980. Statistical Methods. 7th Edn., Iowa State University Press, Ames, IA., USA., ISBN-13: 9780813815602, Pages: 507.

Taha, M., A.E. Eljack and S. Omara, 2007. Estimation of genetic variability and broad sense heritability of some traits in melon (*Cucumis melo* L.). Sudan J. Agric. Res., 8: 51-57.

Tomar, R.S., G.U. Kulkarni, D.K. Kakade, A.D. Patel and R.R. Acharya, 2008. Genetic variability, correlation and path analysis in muskmelon (*Cucumis melo* L.). Asian J. Hortic., 3: 158-161.

Torkadi, S.S., A.M. Musmade and K.K. Mangave, 2007. Genetic variability studies in muskmelon (*Cucumis melo*). J. Soils Crop, 17: 308-311.

Xoconostle-Cazares, B., F.A. Ramirez-Ortega, L. Flores-Elenes and R. Ruiz-Medrano, 2010. Drought tolerance in crop plants Am. J. Plant Physiol., 5: 241-256.

Yadav, Y.C., B.B. Sanjay Kumar and S.K. Dixit, 2009. Genetic variability, heretability and genetic advance for some traits in cucumber. Indian J. Hortic., 66: 488-491.