INNSPUB

International Journal of Agronomy and Agricultural Research (IJAAR)
ISSN: 2223-7054 (Print) 2225-3610 (Online)
http://www.innspub.net
Vol. 6, No. 4, p. 130-137, 2015

RESEARCH PAPER

OPEN ACCESS

Genotypic variation in fruit characters in some genotypes of watermelon cultivated in Morocco

El Madidi Said*, **Hakimi Fatiha**

Laboratory BVRN, Department of Biology Faculty of Sciences, Ibn Zohr University, Agadir, Morocco

Article published on April 14, 2015

Key words: Genotypic variability, Heritability, Genotypic advance, Watermelon.

Abstract

Data from trial of five Moroccan landraces and four commercial watermelons varieties were used to evaluate the phenotypic variability and estimate genotypic parameters. Five characters were used for the estimation of the phenotypic and genotypic variability: fruit weight (FW), fruit length (FL), fruit width (FWd), fruit rind thickness (FRT) and total soluble solids content (TSS).The analysis of variance showed highly significant differences among genotypes in studied characters. The phenotypic coefficient of variation (CV_P) ranged between (17 %) recorded for fruit width and (43%) for fruit weight and a highly and significant correlation was observed between FW and FL and FWd. Moderate to high values of broad-sense heritability were estimates for all characters measured except for_fruit rind thickness. The TSS had the highest value of heritability (62 %). For all the characters, the genotypic correlation coefficient was higher than the corresponding phenotypic correlation coefficient which indicated that the apparent association might be due to genetic reason.

* **Corresponding Author:** El Madidi Said ✉ elmadidi@hotmail.com

Introduction

Citrullus lanatus [(Thunb.) Matsum & Nakai], commonly known as 'watermelon' is an herbaceous plant belonging to the family Cucurbitaceae (Claid *et al.*, 2010) which includes 118 genera and 825 species (Bates *et al.* 1990, Jeffrey ,1990) and is widely cultivated in many countries all over the world. The genus *Citrullus* has four species (C. lanatus, C. ecirrhosus, C. colocynthis, and C.rehmii), which occur mainly in southern Africa with the exception of C. colocynthis, which is distributed from northern Africa to southwest Asia. Cultivated watermelon (C. lanatus) is an annual, mostly monoecious diploid (2n=22) (Shimotsuma, 1963). According to the FAO (2012) (Food and Agriculture Organization), China is the largest producer of watermelon followed by Turkey, Iran and Egypt.

In Morocco, the watermelon is grown in the Souss Massa, Marrakech, Loukous, Sais and some new areas in the south (Zagoura, Ouarzazate, Guelmim…). The global production has reached 567301tons (Agriculture du Maghreb, 2010). Watermelon contains 6% sugar by weight, rest being almost water; the seeds are excellent sources of protein (35%), oil (50%) and dietary fibre (5%).They are also rich in nutrients such as magnesium, calcium, potassium, iron, phosphorous, zinc etc. (Oyewo *et al.*, 2012). Cucurbits are very similar in above ground development, but they have high genetic diversity for fruit shape and other fruit characteristics, resulting in a variety of uses (Bisognin, 2002).

Genetic variation is an essential prerequisite for any crop improvement program.

Breeding for higher levels of a trait requires that there be substantial variation in the plant breeding population and a heritability that is sufficiently high to make ample improvement in the trait. There is now evidence that in many modern cultivars crops, the genetic basis of the modern commercial varieties appeared to be narrow. The genetic diversity in cultivated watermelon has been show to be very low with higher genetic similarity (Levi *et al.*, 2000, 2001; Che *et al.*, 2003 and Solmaz *et al.* 2010). The narrow genetic basis on the commercial improved varieties of crops, has led to a surge of interest in exploring natural biodiversity as a source of novel alleles to improve the productivity, adaptation, quality and nutritional value of crops. Maggs-Kölling *et al.* (2000), reported that, wide variation was found within the local landraces whereas the genetic basis of the commercial type appeared to be narrow.

In watermelon as for other crops, many studies attests, that high variability is present in the local population landraces and this variation is larger than the variation present in the modern cultivars (Frankel *et al.* 1995, Damania *et al.* 1997, Ruiz ***et al***. 2005, El madidi *et al.* 2005, 2006, Rao *et al.* 2006 and Ram *et al.* 2007). Estimates of genotypic variances and derived statistics of pertinent traits are essential for efficient plant breeding programs (Flores *et al.*, 1986). The objective of this research was to estimate the magnitude of the various components of variation, phenotypic variability, genotypic heritability and genotypic advance of fruit characters in watermelon cultivars genotypes with a view to recommending breeding methods for the improvement of these traits.

Materials and methods

Experimental site

This study was carried out at “Agricultural Training Center of Sidi Bibi”. near Agadir in the Chtouka ait Baha province. The site lies at latitude 30° 11' 18.3" N, longitude 9° 32' 17.6" W and 74.460 m above the sea. The area receives an annual rainfall of 250 mm; the soil is sandy/silty with pH 7.7.

Plant materials

The material for this study comprised 5 landraces and 4 commercial watermelons varieties: Cerrato, Venizia, Daytona and Farao. The samples of landraces were collected in two different localities of south Morocco (Table 1 lists the local landraces and their origins). The samples of local landraces were selfed and multiplied previously in order to make each local cultivar homogenous.

Field experimental setup

The experimental design was a randomized complete block with three replications. Data were recorded on 15 randomly selected fruit for each plot. A total of 45 fruits were scored for each cultivar No fertilizer or insecticide spraying was applied at any time for the duration of the trial. Other agronomic practices including irrigation and weeding were conducted as required uniformly in all the plots.

Characters studied

The trial was regularly monitored throughout the growing season and characters scored according to a descriptor list designed for this study. Characters that were measured include: fruit weight (FW), fruit length (FL), fruit width (FWd), fruit rind thickness (FRT) and total soluble solids content (TSS).

The phenotypic variability

Data on five quantitative characters were used for the estimation of phenotypic and genotypic variability. 45 fruits per genotype were measured in where, mean, minimum, maximum, standard deviation, phenotypic coefficient of variation were calculated and correlation analyses were performed for four characters.

The genotypic variability and genotypic parameters

Difference among genotypes was tested by analysis of variance. Genotypic variance ($\hat{\sigma}^2_G$) were calculated by: $\boxed{\frac{GMS - EMS}{n}}$, where, GMS = genotypic mean square, EMS = error mean square and n = replication.

The error mean square was considered as error variance ($\hat{\sigma}^2_E$).

Broad-sense heritability was estimated:

$$\boxed{\hat{H}^2 = \frac{\hat{\sigma}^2_G}{\hat{\sigma}^2_G + \hat{\sigma}^2_E}}$$

Broad-sense heritability on mean basis was estimated: $\boxed{H^2_m = \frac{\hat{\sigma}^2_G}{(\hat{\sigma}^2_E / n) + \hat{\sigma}^2_G}}$

The expected genotypic advance (genotypic gain) was estimated by:

$\Delta G = i\, H^2 \hat{\sigma}_P$ and $\Delta G_m = i\, H^2_m \hat{\sigma}_P$

i= selection differential, the value is 1.40 at 20 % selection intensity.

Statistical analysis

The data were analyzed for ANOVA and subsequent comparison of means was performed using the Duncan's Test. Correlation analyses were conducted using Pearson correlation coefficient to determine the relationship among all the traits. Phenotypic and genotypic correlation coefficients were computed from the variance and covariance components. Statistic analysis was carried out using computer software SAS version 9.3 (SAS Institute Inc. 2010)

Results

Phenotypic variation

Analysis of variance (ANOVA) indicated statistically significant differences among the 9 varieties for all the characters analyzed (Table 3). The commercial variety "Farao" had the highest average fruit weight (8.3 kg) and the longest and largest fruit with 31.7 and 23.2 cm respectively. It recorded also the thickest fruit rind with 17.7 mm and the highest TSS (9.1°Brix). The minimum fruit weight was noted for the landrace Rm2 with 4.4 kg which had also the shortest and the tiniest fruit with 24.3 and 18.4 cm respectively. It recorded, as well, the lowest TSS (7.7 °Brix). The thinnest fruit rind was noticed in the commercial variety Venizia with 14.7 mm. Table 2 shows that extent of variation in fruit weight was more as compared to the fruit length, fruit width, rind thickness and TSS. The phenotypic coefficient of variation (CV_P) ranged between (17 %) recorded for fruit width and (43%) for fruit weight. The ranking order of the 9 genotypes was different except for the commercial variety "Farao ; the ranking order of Farao was the first (1st) of the all the characters analyzed (Table 3). The ranking order of Daytona was the 3th and the 5th for the fruit weight and TSS respectively. The ranking order of the landrace ZG1 was the 5th in fruit weight and the 8th for the TSS.A highly and significant correlation was observed between FW and FL and FWd (r = 0,87*** and r = 0,78***, respectively). Moderate values of phenotypic correlation were observed between TSS and FW and FL (r = 0,46** and r = 0,38**, respectively).

Table 1. Geographical locations of the two local landraces.

Landrace Code	Origin	Latitude	Longitude	Altitude
Rm1	Rasmouka	29°48'08.0"N	9°32'46.9"W	134.327 m
Rm2				
Rm3				
Zg1	Zagoura	30°19'48.5"N	5°50'16.2"W	736.338 m
Zg2				

Table 2. Variation in some fruit characters.

	N	Mean	Min	Max	SD	CV$_P$
FW(kg)	405	5.69	1.07	15.72	2.44	43 %
FL(cm)	405	27.37	12	46	5.55	20 %
FWd(cm)	405	19.81	12	32	3.34	17 %
FRT(mm)	405	16.41	6.43	36.01	4.23	26 %
TSS(°Brix)	405	8.42	2.4	12.8	1.74	21 %

The genotypic variation and genotypic parameters

The broad-sense heritability on the individual basis values for fruit TSS (62%), fruit length (45%), fruit width (43%) and fruit weight (41%) were observed to be moderate to high (Table 4) as compared to low value obtained for the rind thickness (13%). The values of the estimate of the broad-sense heritability on the mean basis (H_m^2) were higher than those of the estimated broad-sense heritability on the individual basis for all the traits analyzed. The values varied from (30%) observed for the rind thickness and (81%) for TSS. The mean-based heritability is more often used than the individual plant based heritability in plant breeding in order to selection among cultivars. (Nyquist, 1991). The high value of heritability in case of TSS, fruit length, fruit width, and fruit weight indicates that they are under genetic control (Table 4). Traits with high heritability values can be improved with rapidity and with less intensive evaluation than traits with low heritability (Nyquist, 1991).

Table 3. Means values and ranking order for different characters of the 9 genotypes.

Var	FW	R	FL	R	FWd	R	FRT	R	TSS	R
FARAO	8.27 a	1	31.65 a	1	23.16 a	1	17.63 a	1	9.13 a	1
CERRATO	6.50 b	2	29.09 b	3	20.44 b	2	17.4 a	2	8.62 ab	3
DAYTONA	5.92 bc	3	27.96 bc	5	20.08 bc	5	16.02 ab	7	8.54 ab	5
VENIZIA	5.57 bcd	6	26.97 bcd	6	20.3 b	3	14.72 b	9	9.02 a	2
ZG 1	5.71 bc	5	28.69 b	4	18.72 bc	8	17.23 a	3	7.86 b	8
ZG 2	5.74 bc	4	29.26 b	2	19.17 bc	6	16.44 ab	5	8.58 ab	4
RM 1	4.91 cd	8	25.11 d	8	19.01 bc	7	16.28 ab	6	8.34 ab	6
RM 2	4.44 d	9	24.32 d	9	18.44 c	9	15.64 ab	8	7.7 b	9
RM 3	5.26	7	25.54 cd	7	20.26 b	4	17.02 ab	4	8.18 ab	7

Means followed by the same letter (s) are not significantly different at 5 % level of probability.

In all the studied characters, the highest value of the individual genotypic advance (ΔG_i) was recorded for fruit length (3.5%), followed by fruit width (2.01%), fruit TSS (1.51%), and fruit weight (1.40%). The minimum genotypic advance value (0.77%) was recorded for fruit rind thickness. For the genotypic advance on the mean basis (ΔG_m), the highest value was recorded for FL (5,52) and the lowest value was observed for FRT (1,78). For all the characters, the values of (ΔG_m) were higher than those estimated for (ΔG_i). The genotypic correlation co-efficient are presented in Table 5. For all the characters, the values of the genotypic correlation were higher than those recorded for phenotypic correlation. Fruit weight showed very strong significant positive genotypic correlation with fruit length and fruit width (0.92 and 0.83 respectively). Significant genotypic correlation was observed between TSS and FW, FL and FWd (0.57, 0.44 and 0.41 respectively), however, there was no genotypic and phenotypic correlation between fruit rind thickness (FRT) and the other characters.

Table 4. The genotypic parameters and genotypic gain.

	$\hat{H}^2$	$\hat{H}^2_m$	ΔG_i	$R\Delta G_i$	ΔG_m	$R\Delta G_m$
FW	0.41	0.67	1.40	24.68%	2.29	40.33%
FL	0.45	0.71	3.50	12.60%	5.52	19.88%
FWd	0.43	0.70	2.01	10.23%	3.27	16.66%
FRT	0.13	0.30	0.77	4.73%	1.78	10.92%
TSS	0.62	0.81	1.51	18.23%	1.97	23.81%

Discussion

The objectives of this study were to evaluate the genotypic variation in fruit characteristics and analysis the relationship between these traits in some Moroccan genotypes of Watermelon. Estimates of genotypic variance and derived statistics parameters of pertinent traits are essential for efficient plant breeding programs. In crop improvement, it is imperative to determine the extent of genetic variation for a trait to be improved (Flores *et al.*, 1986; Milligan *et al.*,1990). A high genotypic advance, indicated considerable improvement potential. The broad-sense heritability is the proportion of phenotypic variation that is due to total (additive and non-additive) genotypic effects. Heritability, like genetic advance, is a property not only of a character, but also of the population, of the environmental conditions to wich the individuals are submitted (Nyquist 1991, Falconer and Mackay 1996).The individual heritability and genotypic advance estimates for fruit weight, fruit length and fruit width ranged from 0.41 to 0.45, indicates large environmental effect. Gusmini and Wehner (2007), reported that narrow- and broad-sense heritability estimates for fruit weight were low to intermediate (mean, 0.59 and 0.41, respectively) and a high number of effective factors (mean, 5.4) was found to influence fruit this character in watermelon. They authors suggested that Watermelon breeders should use quantitative methods such as recurrent selection for population improvement to change fruit weight in the development of new cultivars. For total soluble solids content (TTS), high individual heritability is observed in this study. Similar results was also reported in watermelon (Kumar 2009, Lou 2009, Choudhary *et al*, 2012, Kumar and Wehner, 2013,) suggesting that genotypic components may play an important role in the improvement of this trait in watermelon and genetic advance could be effectively used in selection on the basis of phenotypic performance.

The genotypic correlation measures the degree to which different traits are controlled by the same genes or genes that are closely linked and used to predict how selection on one trait influences response in another trait. The genotypic correlation between traits is strong and highly significant for fruit weight, fruit length and fruit width suggesting that similar magnitude of genotypic effects are involved in the control of both traits. This result indicates a high genotypic influence on relationships and selection for one trait will change the level of the other trait in the same direction. However, because the genotypic correlation between fruit weight and TTS is no strong (0.56) indicate the rate of change in the same direction will be moderate and simultaneous selection is more difficult.

Table 5. Genotypic (G) and phenotypic (P) correlation coefficients among different characters (N=438).

		FL (cm)	FWd (cm)	FRT(mm)	TSS(°Brix)
FW	G	0.92 (***)	0.83 (***)	0.07 (ns)	0.57 (**)
	P	0.87 (***)	0.78 (***)	0.14 (ns)	0.46 (**)
FL	G		0.74 (***)	0.13 (ns)	0.44 (*)
	P	-	0.68 (***)	0.08 (ns)	0.38 (**)
FWd	G			0.05 (ns)	0.41 (*)
	P		-	0.10 (ns)	0.33 (*)
FRT	G				-0.06 (ns)
	P			-	-0.15 (ns)

*, **, *** Significant at 0.05, 0.01 and 0.001 levels, respectively.

The estimates of genotypic parameters presented here do to provide important information on the magnitude of genotypic effects and demonstrate the potential of using quantitative traits variation to identify promising selection criteria in watermelon. Estimates of narrow-sense heritability and additive genetic correlation are needed. This because, that additive genetic effects can be effectively exploited through selection (Falconer and Mackay, 1996)

References

Bates DM, Robinson RW, Jeffrey C. 1990. Biology and utilization of the Cucurbitaceae. Cornell University Press.

Bisognin DA. 2002. Origin and evolution of cultivated cucurbits. Ciencia Rural **32,** 715-723.

Che K, Liang C, Wang Y, Jin D, Wang B, Xu Y, Kang G, Zhang H. 2003. Genetic assessment of watermelon germplasm using the AFLP technique. HortScience **38(1),** 81-84

Choudhary BR, Sudhakar Pandey, Singh PK. 2012. Morphological diversity analysis among watermelon (Citrullus lanatus(Thunb) Matsum) genotypes. Progessive Horticulture **44(2),** 321-326

Claid M, Sehic J, Werlemark G, Garkava-gustavsson L, Fatih M, Nybom H. 2010. Genetic iversity in watermelon (Citrullus lanatus) landraces from Zimbabwe reveled by RAPD and SSR markers. Hereditas **147,** 142–153.

Damania AB, Pecetti L, Qualset CO, Humeid B O. 1997. Diversity and geographic distribution of stem solidness and environmental stress tolerance in a collection of durum wheat landraces from Turkey. Genetic Resources and Crop Evolution 44(2), 101-108.

El Madidi S, Diani Z, Bani-Aameur F. 2005. Variation of agromorphological characters in Moroccan barley landraces under near optimal and drought conditions. Genetic Resources and Crop

Evolution **52(7),** 831-838.

El Madidi S, El Baroudi B, Bani-Aameur F. 2006**.** Genotypic Variation for salt tolerance in Moroccan Barley landraces at seed germination. Plant Breeding and Seed Science **53,** 63-70.

Falconer DS, Mackay TFC. 1996. Introduction to quantitative genetics. 4th Edn., Benjamin Cummings, England, ISBN-10 : 0582243025.

FAO, Food and AgricultureOrganization. 2012. http://faostat.fao.org.

Flores CI, Ross WM, Maranville JW. 1986. Quantitative genetics of agronomic and nutritional traits in related grain sorghum random-mating population as affected by selection. Crop Science **26 (1),** 9-18.

Frankel OH, Brown AHD, Burdon JJ. 1995. The Conservation of Plant Biodiversity, Cambridge University Press, Cambridge, UK, 299 p.

Jeffrey C. 1990. Systematics of the Cucurbitaceae: an overview. *Biology and utilization of the Cucurbitaceae*, Cornell University Press, Ithaca, New York, 3-9 P.

Gusmini G, Wehner TC. 2007. Heritability and genetic variance estimates for fruit weight in watermelon. HortScience **42(6),** 1332-1336.

Kumar R. 2009. Inheritance of fruit yield and other horticul-turally important traits in watermelon [Citrulluslanatus(Thunb.) Matsum. & Nakai. Ph.D Thesis, North CarolinaState Univ, Raleigh.

Kumar R, Wehner TC. 2013. Quantitative Analysis of Generations for Inheritance of Fruit Yield in Watermelon. HortScience **48(7),** 844-847.

Levi A, Thomas CE, Wehner TC, Zhang X. 2001. Low genetic diversity indicates the need to broaden the genetic base of cultivated watermelon. HortScience **36(6),** 1096-1101.

Levi A, Thomas CE, Keinath AP, Wehner TC. 2000. Estimation of genetic diversity among *Citrullus* accessions using RAPD markers. Acta Horticulturae **510,** 385-390.

Maggs-Kolling G, Madsen S,Christiansen JL. 2000. A phenetic analysis of morphological variation in Citrullus lanatus in Namibia. Genetic Resources and Crop Evolution **47,** 385–393.

Milligan SB, Gravois KA, Bischoff KP, Martin FA. 1990 Crop Effects on Broad-Sense Heritabilities and Genetic Variances of Sugarcane Yield Components**.** Crop Science **30(2),** 344-349.

Nyquist WE. 1991. Estimation of heritability and prediction of selection response in plant population. Crit Rev Plant Sci. **10,** 235-322.

Oyewo OO, Onyije FM, Akintunde OW, Ashamu EA. 2012. Effects of Aqueous Extract of *Citrullus lanatus* on the Histology of the Kidney of Adult Wistar Rats. World Applied Sciences Journal **17 (9),** 1178-1181.

Querol D. 1987. Genetic Resources-A Practical Guide to their Conservation. Zed Books Ltd, London and New Jersey **52,** 55-57.

Ram SG, Thiruvengadam V, Vinod K K. 2007. Genetic diversity among cultivars, landraces and wild relatives of rice as revealed by microsatellite markers. Journal of applied genetics **48(4),** 337-345.

Rao R, Corrado G, Bianchi M, Di Mauro A. 2006. (GATA)4 DNA fingerprinting identifies morphologically characterized ‘San Marzano’ tomato plants. Plant Breeding **125,** 173-176.

Ruiz JJ, Alonso A, Garcia-Martinez S, Valero M, Blasco P, Ruiz-Bevia F. 2005. Quantitative analysis of flavour volatiles detects differences among closely related traditional cultivars of tomato. Journal of the Science of Food and Agriculture **85,** 54-60.

SAS Institute. 2010. Statistical analysis Software version 9.3 user's manual., Cary, NC: SAS Institute Inc. USA.

Shimotsuma M. 1963. Cytogenetical studies in the genus Citrullus. VII. Inheritance of several characters in watermelons. Jpn. J. Genet. **13,** 235-240.

Solmaz I, Sari N, Aka-Kacar Y,Yesim Yalcin-Mendi N. 2010; The genetic characterization of Turkish watermelon (Citrullus lanatus) accessions using RAPD markers. Genetic Resources and Crop Evolution **57(5),** 763 – 771.