

Performing some inbred lines of squash for earliness and vegetative growth traits in different locations

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ABSTRACT

Significant differences were observed between the two locations for all studied traits except both vine length (VL) and number of leaves per plant (NoLP) traits. The results obtained over seasons, indicated the superiority of Dumat Al-Jandal (L₁) location than Rafha (L₂) location in all studied traits except VL, days to the first male flower (D¹MF) and days to the first female flower (D¹FF) in most inbred lines. It is interesting to note that, some inbred lines behaved constantly at both locations, i.e., inbred line IL₅ with most vegetative growth traits and all inbred lines in both number of leaves/plant and vine length. Inbred line and location interaction were significant in all traits revealing that some inbred lines were superior in all locations, as an average of both season. Furthermore, location had the major effect on the relative genotypic potential of these traits, in which the inbred line × location interaction was highly significant. The best inbred line which ranked the first in the studied traits was inbred line IL₅ for the earliness followed by inbred line IL₆ in D¹MF, in both locations. Slight variations were detected between genotypic (GCV) and phenotypic (PCV) coefficients, indicating the importance of the genetic effects in controlling the inheritance of traits under these environments and referring to highly genotypic variances resulted in high or moderate estimates of broad-sense heritabilities which, in turn, suggesting that phenotypic selection could be efficient.

Key words : Squash, Locations, Inbred lines, Environments

Introduction

Summer squash (*Cucurbita pepo* L.) is one of common necessity necessary from the Cucurbit plants. It was utilized as a food for human, in addition to many medicinal uses. It is a cross pollinated plant and its diploid chromosomal number is (2n=40). Its origin from Northern Mexico (Tropical America)

and is amongst the most ancient cultivated crops in the America (Paris, 1996). Squash is cultivated in all major regions of the world. Squash is once a year plant and widely spread vegetables in many Arab countries, especially during summer and spring seasons. In the recent years many growers used to grow it in the plastic and glasshouse cladding (Al-Mohammed, 1990). The low production of summer

squash in some of production regions due to the deficiency in fruit setting resulted from unfavorable sex expression and bad cross-pollination flowers owing to short blooming period (Abd El-Hadi *et al.*, 2005a; Abdein (2005); El-Adl *et al.*, 2014; Albrifcany, 2015 and Abdein, 2016). Therefore, these restriction needs further studies for some breeding genetic studies environmental factors and cultural practices to increase crop production with desired quality (Mohammed, 1996; Abdein *et al.*, 2017). The genotype selection is also a key management component in any system for production, although high yield potential is a predominant consideration however, earliness and quality characteristics are also major factor to consider. Many authors, *i.e.*, Abdil-All *et al.*, (1975), Metwally (1985), Abd El-Maksoud *et al.*, (2003), Abd El-Hadi *et al.*, 2005b, Al-Araby (2010), Abd El-Hadi *et al.*, 2014a & b, Abdein 2018, Mohamed *et al.*, 2018 and Hikal and Abdein (2018) studied the genetics performance under different conditions. When cultivars are grown in different locations, their performance would vary according to environmental variations of these locations. One cultivar may have the earliest flowering in one location while a second cultivar may excel in another location. Genotypes respond to changes in environmental conditions such as temperature, soil type, moisture and so on (Robertson, 1959). Inconsistent genotypic responses to environmental factors from location to location, is a function of G × E interaction hence resulting in alteration to the ordering of genotypes from one environment to another.

Materials and Method

Two years field trial was performed at two localities, *i.e.*, Dumat Al-Jandal (L₁) and Rafha (L₂), Saudi Arabia. Dumat Al-Jandal (1st location) in Al-Jouf province (near the southern end of Wadi Al-Sirhan) positioned in southwest of Sakaka (43.8 km) and located at 29°48'38.84"N / 39°53'19.56"E, 621m above sea level in Saudi Arabia. It has a dry and hot weather and it is amongst the hottest cities of the province. While, Rafha (2nd location) in the northern borders province, 283.5 km from the capital (Arar) and 482.9 Km Distance from 1st location (Dumat Al-Jandal) and located at 29°38'19.64"N / 43°30'45.4"E, 449.45 m above sea level in Saudi Arabia. Both locations has a desert climate (BWh) according to the Köppen-Geiger climate classification.

The same seed lots were used for the two locali-

ties trial. Fourteen inbred lines of summer squash (*Cucurbita pepo*) produced from successive breeding program were evaluated for some vegetative growth and flowering traits during the 2017 and 2018 summer seasons under open field conditions. Inbred lines used in this study are presented in Table a₁. The local meteorological data (average of high and low temperatures) prevailing at (L₁) and (L₂) locations are given in Fig. 1.

Fig. 1: Average of high and low temperatures prevailing at (L₁) and (L₂) locations

Table a₁. Inbred lines code, origin and names of 14 squash lines.

Code	Origin	Name
IL 1	EGYPT	MAbdein 1
IL 2	EGYPT	MAbdein 2
IL 3	EGYPT	MAbdein 3
IL 4	EGYPT	MAbdein 4
IL 5	EGYPT	MAbdein 5
IL 6	EGYPT	MAbdein 6
IL 7	EGYPT	MAbdein 7
IL 8	EGYPT	MAbdein 8
IL 9	EGYPT	MAbdein 9
IL 10	EGYPT	MAbdein 10
IL 11	EGYPT	MAbdein 11
IL 12	EGYPT	MAbdein 12
IL 13	EGYPT	MAbdein 13
IL 14	EGYPT	MAbdein 14

Seeds were directly planted in the open field on the 1st week of February in both locations. Two to four seeds were sown per hill on one side of the ridge in a randomized complete block design with three replicates. The experimental unit was two ridges 5.0 m. long and 1.2 m. wide. Plants were set 50 cm apart in the bed and were subjected to the common agricultural practices. After two weeks of sowing, plants were thinned to one plant per hill. Thus, each plot contained 20 plants occupying 12 m².

Reproductive and vegetative growth data were collected 90 days after sowing, and the following parameters were considered: 1) chlorophyll content (Chl, mg/g fw), 2) number of leaves per plant (NoLP), leaf area (LA, cm²), 3) vine length (VL, cm) 4), 5) days to the first male flower (D¹MF), 6) nodes to the first female flower (No¹FFN) and 7) days to the first female flower (D¹FF).

The data collected were analyzed using ASSISTAT Version 7.7 en , UFCCG-Brazil (Silva and

Azevedo, 2016 a&b) computer program package. The data were first subjected to analysis of variance for each location using the procedure illustrated by Gomez and Gomez (1984) for a complete randomized block design (CRBD) over both years. A combined analysis of variance was computed using the same software (*ASSISTAT*) in order to study the inbred line \times location interaction. Phenotypic (PCV %) and genotypic (GCV %) Coefficients of variability were calculated according to **Singh and Chaudhury (1985)**. Heritability based on **Stanfield (1983)**.

Results

Vegetative growth traits:

The combined analysis of variance over locations and inbred lines are presented in Table 1.

Significant differences were observed between the two locations for all vegetative growth traits except both VL and NoLP traits (Table 1).

Results in Table 2 showed a wide range of variation among the tested inbred lines regarding these traits in both locations.

The Values of traits ranged from 26.2 cm² in (IL₂) to 42.8 cm² in (IL₆) for chlorophyll, 216.3 (IL₂) to 670.3 (IL₇) for leaf area, 39.2 cm (IL₂) to 119.4 cm (IL₁₄) for vine length, 21.4 (IL₂) to 38.3 (IL₇) for number of leaves/plant, 31.0 (IL₅) to 43.1 days (IL₄) for number of days to first male flower, 2.2 (IL₁₂) to 5.8 nodes (IL₄) for number of female flower node and 27.3 (IL₅) to 42.8 days (IL₄) for days to first female flower. The results obtained from each location (over seasons) as shown in Table 2, indicated the superiority of (L₁) than (L₂) location in each of Chlorophyll (Chl), Leaf area LA), Number of leaves per plant (No-LP) and Number of the fruit node (1stNo1FFN) in most inbred lines. It is interested to note that, some inbred lines behaved constantly at both locations, *i.e.*, IL₅ with most vegetative growth traits, IL₇, IL₁₀ and IL₁₁ in leaf area and all inbred lines in both

number of leaves/plant and vine length (Table 3).

Some inbred lines fluctuated from one location to another with certain traits, *i.e.*, mean of days to 1st male flower (Table 4) for G₁₃ was 33.7 (34 days) in 1st location while it was 32.2 (32 days) in the 2nd one. Also, leaf area (Table 3) in the same inbred line was 409.7 cm² in the 1st region and 392.2 cm² in the second and most of inbred lines fluctuated in both Number of the fruit node (1stNo¹FFN) and mean of days to 1st female flower (D¹FF) from one location to another (Table 4).

The interaction between location and inbred line were significant for all vegetative growth traits. The best inbred line which ranked the first in most vegetative traits was inbred line IL₁₂ and IL₆ in both locations in No¹FFN and chlorophyll, respectively; IL₅ in the earliness of both male and female flower traits; IL₇ for both leaf area and number of leaves/plant as well as IL₁₄ for vine length in both regions followed by IL₁₄ in locality 2 for chlorophyll and both locations for number of leaves/plant, IL₁₀ in locality 1 for chlorophyll, each of IL₉, IL₇ and IL₂ for leaf area, vine length and number of 1st node of female flower (No¹FFN), respectively in both locations and IL₆ and IL₁₃ for the earliness of both male and female flower traits, respectively in both locations.

The pertinent of variance components in addition to genotypic (GCV) and phenotypic (PCV) coefficients of variability for vegetative growth traits are presented in Table 5. Genetic variation (σ^2g) were large in magnitude compared to error one (σ^2e) and $\sigma^2g \times l$ in all studied traits. Estimates of the genotypic and phenotypic coefficients of variation (Table 5) were determined with slight differences between them for leaf area (LA), vine length (VL) and days to 1st female flowering (D¹FF) in 1st region and for all vegetative growth traits in the 2nd one.

Discussion

The interaction between inbred line and location

Table 1. Mean squares of combined analysis of variance over two locations for vegetative growth traits

VS	df	Chl	LA (cm ²)	VL (cm)	No-LP	D ¹ MF	No ¹ FFN	D ¹ FF
Location (L)	1	14.45*	2471.44*	47.701	6.630	30.6**	28.78*	37.14*
Error-a	2	0.5786	132.878	3.5371	0.9633	0.082	0.7206	1.9497
Inbred line (I)	13	133.92**	124861.36**	2753.66**	110.64**	63.34**	6.79**	135.41**
I \times L	13	1.56*	72.94*	2.32*	3.27*	3.02**	0.692*	0.93*
Error-b	52	0.796	38.443	1.157	1.546	0.727	0.327	0.442

*,** Significant and highly significant at 0.05 and 0.01% probability levels, respectively

Table 2. The combined means of vegetative growth traits as affected by locations (L) and inbred lines (IL) of squash.

Treatment	Chl	LAc ^m ²	VLcm	NoLP	D ¹ MF	No ¹ FFN	D ¹ FF
Location							
L ₁	37.5	475.1	81.7	29.3	35.8	4.2	33.1
L ₂	36.7	464.4	83.2	28.7	34.6	3.0	32.0
LSD	0.7	10.0	NS	NS	0.3	0.8	1.0
Inbred lines							
IL ₁	31.1	408.8	65.0	26.9	39.1	4.8	40.1
IL ₂	26.2	216.3	39.2	21.4	38.8	5.1	37.1
IL ₃	35.0	284.6	55.6	25.3	37.1	3.8	35.1
IL ₄	32.6	558.4	77.5	29.8	43.1	5.8	42.8
IL ₅	41.2	442.5	100.2	33.8	31.	3.3	27.3
IL ₆	42.8	413.3	88.8	28.6	31.9	2.5	29.3
IL ₇	37.4	670.3	112.4	38.3	34.9	4.5	33.0
IL ₈	36.1	332.3	81.2	26.9	33.5	3.0	27.9
IL ₉	39.7	654.1	90.6	29.8	33.9	3.0	31.9
IL ₁₀	40.6	614.7	93.6	31.4	34.5	3.0	30.5
IL ₁₁	36.6	571.3	73.5	26.9	33.7	2.8	28.8
IL ₁₂	41.0	393.1	86.2	27.3	33.8	2.2	30.8
IL ₁₃	40.1	400.9	70.8	26.1	32.9	3.0	27.8
IL ₁₄	41.7	616.3	119.4	34.3	35.0	4.0	33.8
LSD	2.03	12.7	2.7	3.4	1.7	1.3	1.3
Mean	37.3	469.8	82.4	29.0	35.2	3.6	32.6
Minimum	26.2	216.3	39.2	21.4	31.0	2.2	27.3
Maximum	42.8	670.3	119.4	38.3	43.1	5.8	42.8

Table 3. The combined means of chlorophyll, leaf area, number of leaves/plant and vine length as affected by the interaction of locations and inbred lines of squash.

Item	Chl		LAc ^m ²		VLcm		NoLP	
	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂
IL ₁	31.6	30.5	413.7	403.8	63.8	66.1	27.7	26.2
IL ₂	26.7	25.6	222.3	210.2	37.4	41.1	21.7	21.2
IL ₃	35.5	34.4	290.7	278.5	54.9	56.2	25.7	24.8
IL ₄	33.2	32.0	566.3	550.5	76.8	78.2	29.7	28.8
IL ₅	40.9	41.4	441.7	443.3	98.9	101.5	33.7	33.8
IL ₆	43.3	42.3	421.7	404.8	87.9	89.7	29.3	27.8
IL ₇	38.0	36.7	675.7	664.8	110.7	114.1	36.3	40.3
IL ₈	36.7	35.6	339.3	325.2	80.9	81.6	27.3	26.5
IL ₉	37.2	36.2	659.7	648.5	90.5	90.7	30.3	29.2
IL ₁₀	39.5	41.8	611.3	618.0	92.9	94.2	31.7	31.2
IL ₁₁	37.3	35.9	575.3	567.2	73.1	73.8	27.7	26.2
IL ₁₂	41.8	40.3	399.7	386.5	86.4	85.9	27.3	27.2
IL ₁₃	40.8	39.4	409.7	392.2	70.6	71.0	27.3	24.8
IL ₁₄	42.2	41.2	624.7	607.8	118.5	120.3	34.3	34.2
LSD	2.87	11.42	1.61	3.70				
Mean	37.5	36.7	475.1	464.4	81.7	83.2	29.3	28.7
Minimum	26.7	25.6	222.3	210.2	37.4	41.1	21.7	21.2
Maximum	43.3	42.3	675.667	664.8	118.5	120.3	36.3	40.3

were significant for all traits revealing that some inbred lines were superior in all locations, as an average of both season. Furthermore, location had the major effect on the relative genotypic potential of these traits, in which the inbred line \times location interaction was highly significant, these results indicate the importance of testing inbred lines in more than one environment, *i.e.*, year, location, with great emphasis on location testing to select the best inbred line suitable for particular environment. These results are in accordance with those described by Kumar and Wehner (2011); Valdés-Restrepo *et al.*, (2013); Rani (2014); Abdein *et al.*, (2017). They reached similar results, and reported significant differences for all studied characters among the differ-

ent inbred lines, while the inbred line \times environment interaction was present for most traits.

These results also indicate that the differences detected due to the diverse inbred lines were more pronounced compared to the locations, which confirm the relatively higher stability of the diverse inbred lines over locations. These results suggest that it is necessary for evaluation squash inbred lines in large diverse environments in general breeding program to select the best inbred line suitable for particular environment (Rani, 2014).

Genetic variation (σ^2g) were large in magnitude compared to error one (σ^2e) in all studied traits, reflecting the genetic differences among inbred lines. On the other hand, small differences were observed

Table 4. The combined means of days to 1st male and female flowers as well as the number of first female flowering node as affected by the interaction of locations and inbred lines of squash.

Item	D ¹ MF		No ¹ FFN		D ¹ FF	
	L ₁	L ₂	L ₁	L ₂	L ₁	L ₂
IL ₁	39.7	38.5	5.3	4.2	40.7	39.5
IL ₂	39.3	38.2	5.7	4.5	37.7	36.5
IL ₃	37.7	36.5	4.3	3.2	35.7	34.5
IL ₄	43.7	42.5	6.3	5.2	43.3	42.2
IL ₅	31.6	30.4	3.9	2.8	27.9	26.8
IL ₆	32.4	31.3	3.1	1.9	29.9	28.8
IL ₇	35.4	34.3	5.1	3.9	33.6	32.4
IL ₈	34.1	32.9	3.6	2.4	28.4	27.3
IL ₉	34.4	33.3	3.6	2.4	32.4	31.3
IL ₁₀	35.1	33.9	3.6	2.4	31.1	29.9
IL ₁₁	34.3	33.0	3.3	2.3	29.3	28.3
IL ₁₂	34.3	33.3	2.7	1.7	31.3	30.3
IL ₁₃	33.7	32.2	3.7	2.4	28.3	27.3
IL ₁₄	35.7	34.4	4.7	3.4	34.3	33.3
LSD	1.35	1.10	1.14			
Mean	35.8	34.6	4.2	3.0	33.1	32.0
Minimum	31.6	30.4	2.7	1.7	27.9	26.8
Maximum	43.7	42.5	6.3	5.2	43.3	42.2

Table 5. Pertinent of variance components from combined analysis over two locations, genotypic (gcv) and phenotypic (pcv) coefficients of variation and heritabilities (h²) in both locations for vegetative growth traits.

Parameter	Chl	LAcM	VLcm	NoLP	D ¹ MF	No ¹ FFN	D ¹ FF	
σ^2g	22.06	20798	458.6	17.9	10.05	1.02	22.41	
σ^2e	0.082	0.278	0.179	1.877	1.483	0.148	0.244	
σ^2l	0.307	57.11	1.081	0.080	0.656	0.669	0.862	
$\sigma^2g \times l$	0.254	11.49	0.387	0.575	0.763	0.122	0.163	
L ₁	PCV%	19.5	1447.3	188.6	19.2	10.3	10.9	23.0
	GCV%	18.36	1442.9	187.51	14.63	9.46	8.23	22.68
	h ² %	0.97	0.99	0.99	0.90	0.97	0.90	0.99
L ₂	PCV%	18.96	1488.7	186.94	19.48	9.97	8.96	22.59
	GCV%	18.84	1487.8	186.72	18.82	9.88	8.79	22.57
	h ² %	0.99	0.99	0.99	0.98	0.99	0.99	0.99

between p.c.v.% and g.c.v.%, indicating the importance of the genetic effects in controlling the inheritance of traits under these environments and referring to highly genotypic variances resulted in high or moderate estimates of broad-sense heritabilities which, in turn, suggesting that phenotypic selection could be efficient. The high heritability for most studied characters indicates there is a less influence of environment. It reveals that these characters were governed by additive genes and selection for improvement under these environments would be beneficial. The results are in accordance with those described by Abd El-Hadi and El-Gendy (2004) and El-Khatib (2013). On the other hand, Abdein (2016) stated that a major part of the total genotypic variance is non-additive in nature for all earliness traits except of number of first female flowering node trait, which are governed by additive genetic effect. This further suggested that a major part of the total phenotypic variance for these traits was due to dominance genetic variance and environmental effects. In cucumber Mishra *et al.*, (2007) reported maximum heritability for number of nodes per vine and vine length. They reported that minimum value of heritability was detected for days to flowering of first female flower. These finding led to the conclusion that the selection for such traits must be done in the late generation. The results are in general covenant with that reported by Abd El-Hadi and El-Gendy (2004); Waleed and Al-Hamdany (2011); El-Khatib (2013) and Abdein *et al.*, 2017.

Conclusion

The study presented a high variations for earliness and vegetative growth traits in terms of different inbred lines. The 14 squash inbred lines evaluated in this study showed a high significant variability in both location for earliness and vegetative growth traits. The high genetic diversity found could be used in breeding programs to obtain new inbred lines and provide relevant information for the genetic diversity.

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