



ORIGINAL ARTICLE

## ESTIMATION OF SOME GENETIC PARAMETERS IN ABLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) UNDER INFLUENCE OF ORGANIC MATERIAL (HUMUS)

Jassim Jawad Jader \* , Abdullah Fadhil Sarheed and Rana Rayyis Arrak

Al-Furat Al-Awsat Technical University, Al-Musaib Technical College, Iraq.

E-mail: com.abdf@atu.edu.iq

**Abstract:** This study was conducted to evaluate the performance of six new cotton genotypes (*Gossypium hirsutum* L.) (Lashata , GA22, Deer, DUN, IK229, and in addition of local variety Ashour), under two Levels of organic matter (humus) (0 , 200 kg/h.) in season 2016 for two locations, ALmusaib and ALSuwaira using split plot arrangement in Randomized complete block design (RCBD) with three replications. The results were summarized as follows: significant interaction between genotypes and location ,genotypic Ashour gave highest bolls number, fiber yield, cotton yield and average bollweight, in AL suwaira location, Significant interaction between genotypic and organic material (humus, Ashour genotypic gave highest yield of cotton under 200 kg /h humus level and Deer, GA22 genotypes gave highest fiber yield, significant interaction between genotypes, organic material (humus) and location, genotypic Ashour gave highest branch fruit. Cotton yield under 200 kg/h humus in Almusaiib location. The expected genetic advance values were ranged between low in both locations for boll weight, wright of 100 seeds, ratio of net ginning and fiber coefficient and medium for plant height and the number of bolls and fiber yield/plant for cotton yield. The genotypic stability revealed that all the genotypes were stable for all the traits studied in both location.

**Key words:** Genetic parameters, Abland cotton, *Gossypium hirsutum* L., Humus.

### Cite this article

Jassim Jawad Jader , Abdullah Fadhil Sarheed and Rana Rayyis Arrak (2022). Estimation of some Genetic Parameters in Abland Cotton (*Gossypium hirsutum* L.) under influence of Organic Material (Humus). *International Journal of Agricultural and Statistical Sciences*. DocID: <https://connectjournals.com/03899.2022.18.1913>

### 1. Introduction

Cotton is a source of fibers used in the textile industry and increasing productivity is important by finding suitable varieties for different environmental conditions. Genetic improvement of a trait (quantitative) is the result of dividing the genetic improvement by the arithmetic mean as a percentage. The plant and genetic improvement is expected not directly proportional to the genetic variation coefficient values and so is not considered a genetic coefficient of variation for genetic changes in a real measure permanently. Others have several definitions of persistence [Al-Obaidy 2019)]. They explained that genotype is considered to be stable when heterogeneity of the trait from one environment to another is small [Yan and Kang (2003), Al-Janabi et

al. (2021)]. The persistence of quantitative traits in one or several environments falls within the environment interactions in genetics. Therefore, the susceptibility of genotype is associated with the genotype in showing a particular trait quantitative traits, significantly affected environmental factors and their impact is higher than that of qualitative traits [Ravichandran et al. (2018)] Chemical fertilizers adversely affect soil properties through increased salinity. Therefore, there is a need to find alternatives that provide a safer alternative for higher productivity by improving the physical, chemical and biological properties of the soil, as well as establishing a more stable recycle elements, which increases soil fertility and availability of major and minor bollsrrients. The present study aims to evaluate the

performance of some cotton genotypes under different levels of organic manure application and in two locations to determine their adaptation to environmental conditions and their trade-offs compared to the local cultivars using the combined analysis of two different sites.

## 2. Materials and Methods

Six genotypes of upland cotton obtained from Ninewa Cotton Research Station (LASHATA, DEER, GA22 DUN, IK229, ASHOUR) were used in this study at Babylon Center and Suwayra / Wasit province in the season 2016. The cotton crop was sown on 5 April 2016, in lines, length of 4 meters and a distance of 75 cm distance between plant 40 cm, three germs of each genotype in RCBD design and with three replicates and the levels of organic matter were placed in the main plot and varieties in the secondary plot. The 160 kg. urea/ha was added (46% N) along with 60 kg super Phosphate. The agronomic operations were carried out as per recommendations [Al-Naimi (2014)]. The observations were recorded from 5 plants marked at random in each replication for study of various growth and yield parameter.

The expected genetic improvement is estimated in the manner described in Kempthorne (1969).

$$E.G.A = \frac{G.A}{\bar{X}} \times 100$$

where,

E.G.A: Represents the expected genetic improvement as a percentage of the overall mean trait.

G.A: Represents the expected genetic improvement.

$\bar{X}$  : Represents the average traits.

Inheritance is estimated based on ranges described above [Ali (1999)], less than 40% low, 60-40% medium and more than 60% high.

$$H^2_{B.S} = \frac{G^2}{\sigma_p^2}$$

Inheritance represents in a broad sense the genetic variation of the trait, the phenotypic variation of the trait.

$$G.A = K.H^2_{B.S} \cdot \sigma_p$$

where, G: Represents the expected genetic

improvement.

$H^2_{B.S}$  : Inheritance in the broad sense

$\sigma_p$  : The standard deviation of the appearance variation.

K: Selection intensity is equal to 2.06 when 5% of plants are elected.

### Genetic Stability Analysis

The cultivars were cultivated in three replicates and two locations in the same year:

By Al-Naimi (2014), we have

$$\text{Homeostasis} = 1 - \frac{S}{\bar{X}}$$

where, S is the deviation rate of the variety in different environments and  $\bar{X}$  is the average value of the traitistic of the variety in all environments.

On this basis, the stability of less than 85% is considered low and that the variety is not fixed and rejects agriculture in that region.

## 3. Results and Discussion

### 3.1 Plant height (cm)

The interaction between the sites and genotypes of the first site was significant for the genotypes IK229, DEER and GA22, which reached (147.33), (151.93) and (148.57) cm sequentially. And non-significant at the second level which reached (145.80) cm. The genotype GA22 was significant at the first and second level of the first site which reached (145.73) and (151.40) cm sequentially and did not reach the significant in the second site as it reached (126.80) and (118.07) cm sequentially, and also reached the genotype LASHATA to the significant at the second level of organic matter of the first site as it reached (145.27) while did not reach the significant at the level without the addition of the two sites (Tables 1, 2, 3, 4).

### 3.2 Number of fruit branches

The interaction between the genotypes DEER and GA22, which reached (13.53) and (13.20) branches, respectively for the first site compared to the average mean of (12.02) branches and DUN (14.73) branches for the second site compared to the average for the traits reached (10.29) branches. As for the rest genotypes, there were no significant differences between them compared to the general mean and the

**Table 1:** Heritability ratio of some traits of cotton.

Studied qualities		Number of bolls	Average weight of bolls	Weight of 100 seeds(g)	Fiber yield (g)	Net ginning percentage	Cotton yield
AL-Musaib . location	0 kg.h	99.45	5.00	20.15	98.73	66.76	99.27
	200 kg .h	99.48	94.17	44.76	96.02	89.20	99.45
AL-Suwaira. location	0 kg.h	90.15	34.05	48.07	96.82	57.38	98.80
	200 kg.h	99.55	85.74	27.98	98.45	86.30	99.32

two sites. Interaction between organic matter while the genotype LASHATA was significant at the second level of the first site, which reached (13.27) branches.

### 3.3 Recipe number of bolls

The interaction between the genotypes ASHOUR and GA22 for the second site reached (55.82) and (54.50) bolls sequentially and not significant for the first site (46.12), (41.25) bolls respectively, while the ( IK229) genotype was significant when adding 200 Kg.ha<sup>-1</sup> to the first location and DEER genotype was not significant for the two location, while the DEER and LASHATA genotype were significant at the second level of the second site, which reached (72.53), (48.20) bolls respectively and not significant for the first level and for the two sites.

### 3.4 Average bolls weight (g)

The interaction between sites and organic matter was not significant for all genotypes except ASHOUR and DUN genotypes for the second site, whereas the interaction between organic matter and genotypes was not significant and the levels of addition of organic matter to all genotypes, whereas the interaction between sites and organic matter and genotypes was not significant. Significant for all genotypes at the additive levels and for the sites at 5% level.

### 3.5 Fiber quotient cloud

It is noticed from the results of the synthesis analysis of fiber yield that the interaction between sites and genotypes was significant for ASHOUR and the interaction was significant for the genotype IK229 for the second addition level for the first and second site,

which was (27.07) and (27.90) g, respectively and the level of the first addition of the two sites, which reached (18.73), (24.33) gm sequentially, while the interaction was significant for the genotype GA22 at the additive levels of the second site as it reached (41.90), (45.87) gm sequentially and not significant at the first site which was (28.20) and (37.03) gm sequentially.

### 3.6 Net ginning ratio

It is noticed from the results of the aggregate analysis of the ratio of net scoop that the interaction between sites and genotypes is not significant for all genotypes of the first site, while it was significant for the second site of the genotype DUN, DEER, GA22 and LASHATA which amounted to (23.535), (22.135), (21.040), (23.107) sequentially and not significant to the genotype ASHOUR. DEER, (30.470) (29.843), GA22 (30.390) (30.607), and LASHATA (30.460). (30.407) for the first and second addition levels respectively and not significant for the second site.

### 3.7 Staple coefficient

Interaction between sites and genotypes was in significant for all genotypes and for the two sites except GA22 in the first and DUN genotypes in the second site. The interaction between fertilization and genotypes was not significant for all genotypes except DEER at a level without the addition of the material to the organic. Sites, organic matter and genotypes are not significant for all genotypes except ASHOUR at the second addition level of organic material for the first site and DUN at the level 0 for the second site End abstract level 5%.

**Table 2:** Expected Genetic Improvement of Some Traits of Cotton in Organic Levels at two location.

Studied qualities		Number of bolls	Average weight of bolls	Weight of 100 seeds(g)	Fiber yield (g)	Net ginning percentage	Cast Cotton yield
AL-Musaib . location	0 kg.h	23.50	2.24	2.39	17.07	3.36	42.58
	200 kg .h	25.94	2.34	2.68	17.00	6.36	53.72
AL-Suwaira. location	0 kg.h	18.71	2.37	2.70	13.49	3.05	49.70
	200 kg.h	26.37	2.87	3.51	17.21	6.44	46.11

**Table 3:** Genetic result and genetic stability in six genotypes in cotton.

Studied qualities		Genotype						Mean
		IK229	ASHOUR	GA22	DEER	DUN	LASHATA	
Number of bolls (bolls/plant)	Average trait	50.97	30.45	30.45	67.19	67.19	43.23	47.2
	Homeostasis	0.86	0.88	0.88	0.98	0.98	0.96	0.92
	G.R	0.92	0.56	0.56	0.99	0.99	0.88	0.85
Average weight of bolls	Average trait	4.60	4.1	4.1	4.51	4.51	4.85	4.57
	Homeostasis	0.97	0.92	0.92	0.95	0.95	0.97	0.96
	G.R	0.97	0.82	0.82	0.93	0.93	0.97	0.93
Weight of 100 seeds	Average trait	8.76	9.25	9.25	8.88	8.88	8.33	8.76
	Homeostasis	0.99	0.95	0.95	0.99	0.99	0.99	0.98
	G.R	0.99	0.99	0.99	0.99	0.99	0.94	0.97

**Table 4:** Genetic result and genetic stability in six genotypes in cotton.

Studied qualities		Genotype						Mean
		IK229	ASHOUR	GA22	DEER	DUN	LASHATA	
Fiber yield	Average trait	37.79	24.51	24.51	49.23	49.23	36.32	37.24
	Homeostasis	0.89	0.83	0.83	0.96	0.96	0.97	0.90
	G.R	0.90	0.55	0.55	0.96	0.96	0.94	0.85
Net ginning percentage	Average trait	24.28	22.28	22.28	26.15	26.15	26.77	24.93
	Homeostasis	0.98	0.99	0.99	0.99	0.99	0.99	0.97
	G.R	0.95	0.89	0.89	0.99	0.99	0.99	0.94
Seed cotton yield	Average trait	111.14	59.94	59.94	139.63	139.63	101.43	105.77
	Homeostasis	0.93	0.91	0.91	0.93	0.93	0.95	0.92
	G.R	0.97	0.51	0.51	1.2	1.2	0.90	0.91

### 3.8 Cast cotton yield

There were significant differences between the two genotypes (ASHOUR) and 102.77 (119.60) gm respectively. DUN found no significant difference at the first site (106.20). The genotype GA22 was significant in the second site where it reached (127.42) gm and not significant for the rest of the levels, which reached (104.33), (108.07) for the first site (107.77) gm for the second site. The GA22 genotype was significant at the second site level (120.03), (134.80) gm sequentially and not significant at the first site which reached (84.40), (108.33) gm sequentially.

### 3.9 Heritability and expected genetic improvement for both sites

The heritability ranged between 3 bolls and 99% for most traits, where the highest inheritance rate was the cast cotton yield and the number of bolls and fiber yield for both sites. It is noted that the inheritance rate was very high for the number of bolls and for the two levels respectively, reaching 99.45 and 99.48%, respectively. Very low level was without adding 0 as it dropped to less than 40% while it was high level of

organic matter. As for the weight of 100 seeds heritability rate was low without the adding 20.15%. These results agree with Killi Fatih and Mustafayev Sffe (2005) and Kahan *et al.* (2010) and others who found varied inheritance values from one trait to another. The expected genetic improvement values as a percentage to the general average of the recipe were low. The average nut weight was 2.37, 2.87 and 100 seed weight 2.70, 2.50 and net ginning percentage was 3.07 and 6.44 respectively, while the number of recipes for medium nut 18.71 and 26.37 and holds fiber 13.49 and 17.21 sequentially, and genetic improvement was highly expected to cast a recipe holds cotton as 48.70 and 46.11 were sequentially. This is consistent with what Al-Bayati (2005) and Allard and Bradshaw (1964) found that most genetic traits have low genetic improvement values.

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