

Estimation of some genetic parameters in abland Cotton (*Gossypium hirsutum* L) under influence of organic material (Humus)

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Abstract

This study was conducted to evaluate the performance of six a new cotton genotypes(*Gossypium hirsutum* L) (Lashata , GA22, Deer ,DUN ,IK229 , and in addition of local variety Ashour), under two Level 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 with three replications. The results were summarized as follows:-

- 1- Significance interaction between genotypes and location ,genotypic ASHOUR gave highest bolls number ,fiber yield ,cotton yield and average bolls weight, in AL suwaira location
- 2- Significance 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 .
- 3- Significance interaction between genotypes ,organic material(humus) and location ,genotypic ASHOUR gave highest bolls co branch fruit num. cotton yield under200 kg/h humus in almusaib location
- 4- The expected genetic advance values were ranged between low in both locations for boll weight, wright of 100seeds, ratio of net ginning and fiber coefficient and medium for plant height and the number of nuts and fiber yield/plant for cotton yield
- 5- The genotypic stability revealed that all the genotypes were stable for all the characters studied in both location .

Introduction

Cotton is a source of fibers used in the textile industry and increasing productivity is important in the unit area by finding suitable varieties for different environmental conditions, so plant breeders paid attention to this aspect when using breeding and improving varieties of cotton, including other crops [1], [2]. 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 so is not considered a genetic coefficient of variation for genetic changes in a real measure permanently. [4]. Others have several definitions of persistence. He explained that genotype is considered to be stable when heterogeneity of the trait from one environment to another is small. [5]. The persistence of quantitative traits in one or several environments falls within the environment overlaps in genetics. Therefore, the susceptibility of genotype is associated with the genotype in showing a particular trait. Quantitative traits, including plant yields significantly affected Environmental factors and their impact is higher than that of qualitative characteristics. Chemical fertilizers adversely affect soil properties through increased salinity. Therefore, there is a need to find alternatives that provide a safer and more productive agriculture using organic fertilization, which improves the physical, chemical and biological properties of the soil, as well as establishing a more stable nutrient recycling system, which increases soil fertility and readiness of major and minor nutrients. The rare need for the plant to meet its nutritional needs [6] [, this study came with the aim of

1. Evaluate the performance of some new cotton genotypes under different levels of organic matter and in two locations to determine their adaptation to environmental conditions and their trade-offs compared to the local variety using the combined analysis of two different sites. To calculate the heritability ratio and the expected genetic improvement for some vegetative traits, yield and its components in cotton and estimate the stability of the varieties in different locations under the organic matter.

Materials and methods

Genotypes and studied traits: -

Six genotypes of upland cotton obtained from Ninewa Cotton Research Station (LASHATA, DEER, GA22, DUN, IK229, ASHOUR) were used in this study. From the Babylon Center (42) km and the second site in a field in the farm Suwayra / Wasit province, which is away from the center of Babylon 100km in the season 2016, and used six genotypes of cotton

upland and two levels of organic matter Humus (0 and 200 kg.h) planted the seeds of six genotypes In both locations, on the fifth of April 2016, in lines, length of 4 meters and a distance of 75 cm. distance between plant 40 cm, three germs of each genotype were planted using the split plate arrangement 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, 160 kg.h urea fertilizer was added 46% N and 160 kg super Phosphate and all soil and crop service operations were carried out according to [7] .The study was carried out on (5) guarded plants taken for each genotype and then according to the average and studied the characteristics of early plants, plant height, the number of open walnuts of the plant, average nut weight, seed coefficient. Percentage of net ginning, fiber yield (gm / plant), cotton yield (g / P) S).

Heritability and Expected genetic advance

The expected genetic improvement is estimated in the manner described [2].

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

whereas :

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

G.A: Represents the expected genetic improvement. : Represents the average characteristic

Inheritance is estimated based on ranges described above [8], less than 40% low, 60-40% medium and more than 60% high.

$$H^2_{B.S} = \frac{\sigma_G^2}{\sigma_P^2}$$

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

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

G: represents the expected genetic improvement

H₂B.S: Inheritance in the broad sense: 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 genotypes were transplanted in three replicates and two environments in two locations in the same year. :

By [10] as follows:

$$\text{homeostasis} = 1 - \frac{S}{X^-}$$

The S: deviation rate of the variety in different environments: the average value of the characteristic 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.

Results and discussion

Table (1) shows the results of the meta-analysis of the two study sites for the studied traits.

Early coefficient

The interaction between sites and genotypes was significant for the genotypes DUN, DEER, GA22 and LASHATA (0.5228) (0.5210) (0.5385) (0.5608) respectively for the first site. At the 5% level, the interaction between HUMUS levels and genotypes was insignificant for all genotypes at both levels of the organic matter and for the two study sites except DEER (52222) at level 0 of HUMUS at 5% probability. Sites and levels of organic matter and compositions LATATA was found at the level of 200KG / h for the first site (0.5393), while it was significant at the level of 200 KGIH for the second site (0.5510). For the first site and

(0.5417) and (0.5397) for the second site, the genotype DUN, DEER and GA22 did not reach the significance at the fertilization levels and the two sites compared to the average mean, while the genotype LASHATA high moral at the second level of organic matter of the first site, which was (0.5947) while Up to the moral at other levels of the site Second p.

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) (148.57) cm sequentially at a 5% level. Between organic matter and genotypes was significant for DUN and DEER, which reached (139.33) (141.47) for the levels of organic matter (148.47) (145.15) cm sequentially, while the rest of the other genotypes did not reach significant, while the overlap between sites and organic matter and genotypes were significant. For ASHOUR genotype at the second level The genetic composition of IK3 was significant at the level of the first and second addition of the organic material and the first site where it reached (143.33) (151.33) cm sequentially and not significant at the levels of organic matter of the second site, while the genotype was DUN Significantly at the second level of organic matter for the first site which reached (149.20) cm and non-significant at the second level which reached (145.80) cm while it did not reach the moral at the second site and at the levels of the first and second organic matter which reached (129.47) (137.17) cm. Sequentially, compared to the average of the adjective, which reached (140.41) The composition of DEER was with At the first organic level of the first site which reached (155.47) cm, the genotype GA22 was significant at the first and second level of the first site which reached (145.73) (151.40) cm sequentially and did not reach the moral in the second site as it reached (126.80). (118.07) cm sequential, and also reached the genotype LASHATA to the moral at the second level of organic matter of the first site as it reached (145.27) while did not reach the moral at the level without the addition of the two sites.

Number of fruit branches

The overlap between sites and genotypes was significant for the genotypes DEER and GA22, which reached (13.53) (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 attribute reached (10.29) branches. As for the rest of the other genotypes, there were no significant differences between them compared to the general mean and the two sites. Overlap between Significance of organic matter and genotypes was significant for the ASHOUR genotype at the level of 200 kglh for the first site which reached (14.40) branch while the genotype of Angeli was significant at the level of the second addition of the first site which reached (11.47) branch and did not reach the moral at the first level which reached (10.27) for the first site and (8.67) (7.77) branch for the second site The genotype DUN was significant at the additive levels of the second site where it reached (14.60) (14.87) branch while did not reach the moral in the second site of the level of the addition, which reached (9.67) (10.93) Compared to the average mean of 12.52 branches, while DEER and GA22 was significant at the two levels of addition to the first site as it reached (13.73) (13.33) (12.67) (13.73) branch in succession and did not reach the moral at the first and second level of the second site which reached (11.87) (8.33) (8.27) (10.53) branch in succession, While the genotype LASHATA was significant at the second level of the first site, which reached (13.27) branches

Recipe number of walnuts

The overlap between sites and genotypes was significant for the genotypes ASHOUR and GA22 for the second site (55.82) (54.50) walnuts sequentially and not significant for the first site (46.12) (41.25) walnuts respectively, while the genotype DUN was significant for the two sites (64.58) (70.32) walnut sequentially, while the rest of the other genotypes did not reach the significant, while the interaction between organic matter and genotypes was significant for the genotype ASHOUR at the level of 200KGIH organic substance, which amounted to (56.15) walnuts and not significant at the level of 0 organic matter. The genetic DEER was significantly (66.58) (68.37) Nut Palt Continued while the rest of the other genotypes did not reach the moral, but the overlap between sites and organic matter and genotypes was significant for the genotype Ashour at the level of 200 KGIH for the second site which reached (60.43) nut while the genotype IK3 to the moral when adding 200 KGIH

to the first site DER was not significant for the two sites, while the DEER and LASHATA genotype were significant at the second level of the second site, which reached (72.53) (48.20) nut respectively and not significant for the first level and for the two sites (65.07) (64.20). (68.10) (40.53) (40.83) (43.33) Walnut for the first and second level of the The birth of the first organic site first and second location sequentially

Average nut weight g

The overlap between sites and organic matter was not significant for all genotypes except ASHOUR and DUN genotypes for the second site, whereas the overlap between organic matter and genotypes was not significant and the levels of addition of organic matter to all genotypes, while the overlap between sites, material and genotypes was not significant for all genotypes. Genetic at the levels of organic matter for the two sites except the genotype IK229 and DEER at the second level of the addition of the first site and at the level of 5%. The characteristic weight of 100 seeds note that the overlap between sites and genetic structures However, the interaction between organic matter and genotypes was also not significant for all genotypes of the added levels except the genotype IK3 of the second addition level of organic matter, whereas the overlap 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.

Fiber quotient cloud

It is noticed from the results of the synthesis analysis of fiber yield that the overlap between sites and genotypes was significant for ASHOUR and GA22 for the second site as their rates were (42.58) (43.88) gm sequentially and the interaction was significant for the DEER genotypes of the two sites (46.03) (52.42) gm respectively. Non-significant for the genotype IK3 which was (22.90) (26.12) g for the two sites sequentially and the genotype LASHATA which reached (35.70) (36.93) g sequentially, while it was significant for the genotype DUN for the first site which amounted to (36.40) g, while the overlap between the organic matter and the structures It was not significant for all genotypes except Walter DEER, which reached (47.70) (50.75) g for the levels of organic

matter sequentially and the genotype of the second additive level (41.45 g), while the overlap between sites and organic matter and genotypes was significant for the ASHOUR genotype at the second additive level of the second site organic matter which reached (46.83) gm and non-significant for the rest of the levels of the two sites that amounted to (31.03) (34.60) g for the first site (38.33) g for the second site and the interaction was significant for the genotype IK229 for the second addition level for the first and second site, which was (27.07) (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) (37.03) gm sequentially

Net ginning ratio

It is noticed from the results of the aggregate analysis of the ratio of net scoop that the overlap 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. The interaction between organic matter and genotypes was not significant for the genotypes ASHOUR (23.908) (24.657) or IK3 (22.550) (22.690) for the two levels of sequential addition. The organic matter reached (26.345) and was not significant at the level of addition While the genotype GA22 was significant at the second additive level (26.040) and was not significant at the first level without addition and reached (25.498), but the overlap between sites and organic matter and genetic structures was significant for all genotypes at the additive levels. The first and second sites of the first genome were ASHOUR (29.377) (30.090), IK3 (28.250) (28.593), DUN (29.767) (30.157), 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

Staple coefficient

Interaction between sites and genotypes was insignificant 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%.

Cast cotton quotient

The results of the meta-analysis showed that there were significant differences between the sites and genotypes. 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) while it was not significant in The second site was (114.72), while the genetic composition of DEER was significant for the two sites as they reached (131.03) (148.23) g respectively. The genotype GA22 was significant in the second site where it reached (127.42) gm and not significant at the first which reached (96.37) gm. The genotype LASHATA did not reach the significance of the two sites which reached (95.00) (107.85) g The interaction between the organic matter and the genotypes was significant and the levels added to the genotypes ASHOUR and DEER (105.37) (116.90) and (136.40) (142.87) g respectively. In addition, the genetic composition of GA22 was significant at the level of the second addition of organic matter which reached (121.57) gm and not significant at the first level of addition (102.22) gm. Organic and genotypes were significant for ASHOUR genotypes (123.40 g) At the second addition level of the second site and not significant for the rest of the levels which reached (95.13) (110.40) in the first site (115.60) g for the second site while the genotype IK3 was significant at the second level to add to the second site which was (75.00) and non-significant for the rest of the levels which The site was (57.53) (52.40) for the first site (54.80) gm for the second site The genetic structure DUN was significant at the level of addition 200KG / H organic material for the second site, which reached (121.67) 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, but the genetic structure DEER was

significant at the levels of addition of organic matter for the site The second, which amounted to (144.73) (151.73) and g sequentially insignificant in the first site, which amounted to (128.07) (134.00) g sequentially. 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, while the genotype LASHATA was significant at the second addition level of the second site which reached (112.90) and not significant for the rest of the levels which reached (92.20) (97.80) in the first site (102.80) g in the second site

Table (1) Performance of Genotypes under the Effect of Organic Matter Using Aggregate Analysis of Experimental Locations

Studied qualities		Genotype	ASHOUR	IK229	DUN	DEER	GA22	lashata	Means
Early coefficient	Loc. VRE	Loc. 1	0.5107	0.4465	0.5228	0.5210	0.5385	0.5608	0.5167
		Loc. 2	0.5377	0.5407	0.5370	0.5098	0.4962	0.4428	0.5107
	Hum .VRE	hum 1	0.5032	0.4492	0.5085	0.5222	0.5037	0.4838	0.4951
		hum 2	0.5452	0.5380	0.5513	0.5087	0.5310	0.5198	0.5323
	Loc. hum. VRE	L1	0.4820	0.3567	0.4833	0.5183	0.5327	0.5270	
		hum1	0.5393	0.5363	0.5623	0.5237	0.5443	0.5947	
		IRE2 L2	0.5243	0.5417	0.5337	0.5260	0.4747	0.4407	
		Ihum1	0.5510	0.5397	0.5403	0.4937	0.5177	0.4450	
		hum2							
		Means	0.5242	0.4936	0.5299	0.5154	0.5173	0.5018	
Plant height	Location. VRE	Location 1	135.88	147.33	133.32	151.93	148.57	139.80	142.81
		Location 2	117.23	120.12	147.50	141.68	122.43	134.90	130.64
	Location. hum. VRE	L1	128.40	143.33	129.47	155.47	145.73	134.33	
		hum.1	143.37	151.33	137.17	148.40	151.40	145.27	
		Hum.2	116.73	114.67	149.20	141.47	126.80	133.60	
	hum.1 L2	117.73	125.57	145.80	141.90	118.07	136.20		
	hum.2								
	Means	126.56	133.72	140.41	146.81	135.50	137.35		
Number of fruit branches	Location. VRE	Location 1	12.57	10.87	10.30	13.53	13.20	11.67	12.02
		Location 2	9.23	8.22	14.73	10.10	9.40	10.03	10.29
	Location. Ihum.VRE	Hum.1	10.73	10.27	9.67	13.73	12.67	10.07	
		L1	14.40	11.47	10.93	13.33	13.73	13.27	
		hum2	8.67	8.67	14.60	11.87	8.27	9.27	
		L2	9.80	7.77	14.87	8.33	10.53	10.80	
		hum.1							
hum.2									
	Means	10.90	9.54	12.52	11.82	11.30	10.85		

Number of walnuts	Location. VRE	Location 1	46.12	31.55	42.45	64.63	41.25	40.68	44.45
		Location 2	55.82	29.37	43.93	70.32	54.50	45.77	49.95
	hum. VRE	Hum. 1	45.78	27.78	41.15	66.58	45.12	41.93	44.73
		hum. 2	56.15	33.13	45.23	68.37	50.63	44.52	49.67
	Location. IREE. VRE	L1	40.37	28.27	41.37	65.07	37.30	40.53	
		hum.1	51.87	34.83	43.53	64.20	45.20	40.83	
		Hum.2	51.20	27.30	40.93	68.10	52.93	43.33	
		L2	60.43	31.43	46.93	72.53	56.07	48.20	
		hum.1							
		hum.2							
	Means	50.97	30.46	43.19	67.47	47.88	43.23		
Average nut weight	Location. VRE	Location 1	4.312	4.650	4.472	4.827	4.567	4.932	4.626
		Location 2	4.880	3.550	4.950	4.183	4.717	4.765	4.507
	hum. VRE	Hum. 1	4.497	3.868	4.628	4.337	4.633	4.755	4.453
		Hum. 2	4.695	4.332	4.793	4.673	4.650	4.942	4.681
	Location. hum. VRE	L1	4.093	4.470	4.323	4.707	4.467	4.813	
		hum.1	4.530	4.830	4.620	4.947	4.667	5.050	
		Hum.2	4.900	3.267	4.933	3.967	4.800	4.697	
		L2	4.860	3.833	4.967	4.400	4.633	4.833	
		hum.1							
		Ihum.2							
	Means	4.596	4.100	4.711	4.505	4.642	4.848		
Weight 100 Seed	Location. VRE	Location 1	8.973	9.175	9.083	9.025	8.692	8.567	8.919
		Location 2	8.553	9.335	8.440	8.828	8.505	8.082	8.624
	hum. VRE	Hum. 1	8.777	8.940	8.972	8.930	8.520	8.362	8.750
		Hum. 2	8.750	9.570	8.552	8.923	8.677	8.287	8.793
	Location. hum. VRE	L1	9.080	8.817	9.650	8.833	8.650	8.917	
		hum.1	8.867	9.533	8.517	9.217	8.733	8.217	
		Hum.2	8.473	9.063	8.293	9.027	8.390	7.807	
		L2	8.633	9.607	8.587	8.630	8.620	8.357	
		hum.1							
		Ihum.2							
	Means	8.763	9.255	8.762	8.927	8.598	8.324		
Fiber quotient	Location. VRE	Location 1	32.82	22.90	36.40	46.03	32.62	35.70	34.41
		Location 2	42.58	26.12	38.23	52.42	43.88	36.93	40.03
	hum. VRE	hum 1	34.68	21.53	35.02	47.70	35.05	35.52	34.92
		hum 2	40.72	27.48	39.62	50.75	41.45	37.12	39.52
	Location. hum VRE	L1	31.03	18.73	35.40	44.37	28.20	36.17	
		hum1	34.60	27.07	37.40	47.70	37.03	35.23	
		Hum2	38.33	24.33	34.63	51.03	41.90	34.87	
		hum1 L2	46.83	27.90	41.83	53.80	45.87	39.00	
		hum2							
		Means	37.70	24.51	37.32	49.23	38.25	36.32	
Net ginning ratio	Location. VRE	Location 1	29.733	28.422	29.962	30.157	30.498	30.433	29.868
		Location 2	18.832	16.818	23.535	22.135	21.040	23.107	20.911
	hum. VRE	hum 1	23.908	22.550	26.468	26.345	25.498	26.668	25.240
		hum 2	24.657	22.690	27.028	25.947	26.040	26.872	25.539

		Means	24.283	22.620	26.748	26.146	25.769	26.770		
Staple coefficient	Location. VRE	Location 1	2.500	1.933	1.983	2.550	2.592	2.367	2.321	
		Location 2	1.933	1.867	2.650	2.500	2.383	2.333	2.278	
	hum. VRE	hum 1	2.083	1.833	2.233	2.683	2.392	2.350	2.262	
		hum 2	2.350	1.967	2.400	2.367	2.583	2.350	2.336	
	Location. hum. VRE	L1	2.333	1.800	1.867	2.767	2.450	2.267		
		hum1	2.667	2.067	2.100	2.333	2.733	2.467		
		Hum2 Ihum1 L2 hum2		1.833	1.867	2.600	2.600	2.333	2.433	
				2.033	1.867	2.700	2.400	2.433	2.233	
		Means	2.217	1.900	2.317	2.525	2.487	2.350		
	Cast cotton yield	Location. VRE	Location 1	102.77	54.97	106.20	131.03	96.37	95.00	97.72
Location 2			119.50	64.90	114.72	148.23	127.42	107.85	113.77	
hum. VRE		Hum1 1	105.37	56.17	106.05	136.40	102.22	97.50	100.62	
		hum 2	116.90	63.70	114.87	142.87	121.57	105.35	110.88	
Location. hum. VRE		L1	95.13	57.53	104.33	128.07	84.40	92.20		
		hum1	110.40	52.40	108.07	134.00	108.33	97.80		
		hum2 hum1 L2 hum2		115.60	54.80	107.77	144.73	120.03	102.80	
				123.40	75.00	121.67	151.73	134.80	112.90	
	Means	111.13	59.93	110.46	139.63	111.89	101.42			

Heritability and expected genetic improvement for both sites

The values of heritability ranged in the wide sense between 3% very low for the average weight of walnuts and very high as it reached 99% for most traits, where the highest inheritance rate was the cast cotton recipe and the number of walnuts and fiber yield for both sites. Table (2) shows the inheritance in the broad sense of the traits studied under the influence of organic matter at the Musyyib site. It is noted that the inheritance rate in the broad sense was very high for the number of walnuts and for the two levels respectively, reaching 99.45 and 99.48%, respectively. Very low level 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, it was noted that the heritability rate was low without the addition of 20.15%, while the mean level of addition was 200 kg.h as it reached 44.76%, while the heritability rate was high for the fiber yield and for the addition levels 98.73 and 96.02% respectively. While the inheritance rate in the broad sense was high for the ratio of net scoop ratio of 66.76 and 89.10% for the two levels respectively, while the inheritance ratio in the broad sense of the characteristic of cotton cotton yield 99.27 and 99.45% and for the

levels of addition 0 and 200 respectively, and this is consistent with both [11] And [12], [13] and [7] who indicated that higher values of some traits facilitate the opportunity to improve these traits through Direct election. In alsuwaira, the inheritance rate of walnuts increased by 90.15% and 99.55% respectively. As for the average weight of the nut, it is noted that the heritability rate in the broad sense is reduced to less than 40% for the level without the addition of organic matter (34.05%). In addition, the level of heritability was 200 kg / h, while in the broad sense, the mean weight of 100 medium seed without addition was 48.07%, while it was low for the level of 200kg / h, and the level of heritability was 27.98%. 96.82% and 98.45% for the two levels respectively, respectively Note that the inheritance rate was medium to the level without the addition of 57.38%, while it was high for the level of 200kg / h reached 86.30%, while the quality of the cotton yield is noticeable that the rate of inheritance in the broad sense was very high and the levels of the addition, which reached 98.80% and 99.32% respectively, these results agree With [14] and others [15] and others who found varied inheritance values from one trait to another. Table (3) shows the expected genetic improvement values as a percentage to the average of the trait as it was low at Mussayab site for the average nut weight attributes of 2.24 and 2.34 nut / plant, 100 seed weight 2.39 and 2.68 g and net scoop ratio 3.36 and 5.25 for the two levels respectively. Nutrients were 23.50 nuts / plant, 25.94 and fiber yield 17.07 and 17 g / plant respectively. The expected genetic improvement was high for the cast cotton yield (42.58 and 53.72 respectively). In alsuwaira, 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 n Pric net ginning 3.07 and 6.44 sequentially, 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 [17] [18] found that most genetic traits have low genetic improvement values

Table (2) Heritability Ratio of Some Characteristics of Cotton to Organic Levels at two location

Studied qualities		Number of walnuts	Average weight of walnut	Weight of 100 seeds	Fiber yield	Net ginning ratio	Cast cotton yield
ALMusaib loc.	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
ALSuwaira loc.	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

Table (3) Expected Genetic Improvement of Some Characteristics of Cotton in Organic Levels at two location

Studied qualities		Number of walnuts	Average weight of walnut	Weight of 100 seeds	Fiber yield	Net ginning ratio	Cast cotton yield
ALMusaib loc.	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
ALSuwaira loc.	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

Genetic outcome and genetic stability of genotypes and for all studied traits

Stability of genotypes is beneficial and desirable for wide use in agriculture. Genotypes with good performance are characterized under varying environmental conditions. [19] and others.

The results of Table (4) indicate that there is a variation between the values of genetic yield and values of genetic stability of the studied traits, where the values of the genetic outcome were different for the number of walnuts and for all genotypes where they were low and below the recommended range of the genotype (ASHOUR) and (GA22) and reached (0.56 (0.84)%, the rest of the genotypes (IK229) (DEER) (LASHATA) ((DUN) amounted to (0.92) (0.99) (0.88) (0.92)% sequentially, the genetic stability varied all the values of the genotypes and followed the same behavior and achieved Percentages exceeded the recommended limit, exceeding 85% where the values of other genotypes (IK229) (Coker) (GA22) (DEER) (DUN) (LASHATA) were (0.86) (0.88) (0.93) (0.98) (0.92) The average nut weight was high for genotypes (IK229) (GA22) (DEER) (DUN) (LASHATA) which reached (0.97) (0.98) (0.93). (0.99) (0.97)% sequentially and exceeded the recommended range except the genotype (ASHOUR) which scored less than the recommended limit was (0.82%), the genetic stability was high and for all genotypes of this trait and exceeded the recommended limit (IK22 ((ASHOUR) (GA22) (DEER) (DUN) (LASHATA) of (0.97) (0.92) (0.95) (0.98) (0.99) (0.97)% sequentially, indicating that genotypes followed the same genetic behavior In this capacity, the values of the total were Genetic stability and stability of the weight of 100 different seeds of this trait and was high and exceeded the recommended range as the values of the genetic yield of the genotypes (IK229) (ASHOUR) (GA22) (DEER) (DUN) (LASHATA), which reached (0.99) (0.99) (0.97) (0.99) (0.98) (0.94)% sequentially, while the genetic stability values of the genotypes (IK229) (ASHOUR) (GA22) (DEER) (DUN) (LASHATA) were (0.99) (0.95) (0.97)). (0.99) (0.99)% sequentially suggesting that all these genotypes of this trait exhibited the same genetic behavior. The quality of the fiber yield varied the genetic yield values of all genotypes (IK229) (GA22) (DEER) (DUN) (LASHATA) which reached (0.90) (0.91) (0.96) (0.89) (0.94)% sequentially as it was high and exceeded the limit Recommended except for the genotype (ASHOUR) which scored (0.55%) which is lower than the recommended, while the values of genetic stability was also high and exceeded the recommended range except the genotype (ASHOUR) which was (0.83%) which is lower than the recommended The rest of the genotypes (IK229) (GA22) (DEER) (DUN) (LASHATA) amounted to (0.89) (0.91) (0.96) (0.88) (0.97)%

sequentially. While the values of genetic yield and genetic stability varied for all genotypes of the net scoop ratio and scores exceeded the recommended range except the genotype of the genotype (GA22, which gave a lower percentage than the recommended range of 0.84%) and the genotype values of the genotypes (IK229) ((ASHOUR) (DEER) (DUN) (LASHATA) by (0.95) (0.89) (0.99) (0.99) (0.99)% sequentially while the values of genetic stability (Angeli) (Coker) (S29) (S118) (GA22) Cotton yield varied between genotypes and values of genotypes (IK229) (ASHOUR) (GA22) (DEER)) (SP886) (0.98) (0.99) (0.88) (0.99) (0.99) (0.99)%. DUN) (LASHATA) (0.97) (0.51) (0.97) (1.2) (0.92) The sequence of ASHOUR genotypes is observed to decrease by giving it the lowest stability, the genetic stability of the genotypes (IK229) (ASHOUR) (GA22) (DEER) (DUN) (LASHATA) reached (0.93) (0.91) (0.94) (0.93). (0.88) (0.95)% sequentially as it is noticed that it is high and exceeded the recommended limit, which indicates that the behavior of the stability of these genotypes was similar in this characteristic and that the behavior of most genotypes of all traits were similar and stable in different environments. This is consistent with what he found [1]

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

Genotype		IK229	ASHOUR	GA22	DEER	DUN	LASHATA	Mean
Studied qualities								
Number of walnuts	Average character	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 walnut	Average character	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 character	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
Fiber yield	Average character	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 ratio	Average character	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
Cast cotton yield	Average character	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

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