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Performance, Selection indices for six cotton genotypes to yield and some Components

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Abstract

According to the randomized complete block design, a field experiment was conducted at the Agricultural Research Station in the Daquq Research Station located 40 km south of Kirkuk at the longitude 28 - 44 ° east and latitude 8 - 35 ° north as a factorial experiment with three factors, six genotypes, three doses of potassium fertilizer, and two spacing between lines, the data were analyzed as a factorial experiment using the analysis of variance method, and the trait averages were compared using Duncan's multi-range test at a probability threshold of 5% for all of the traits evaluated. Montana genotype shows the superiority of No. of fruiting branches with an average of (8.15), Coker 310 genotypes No. of balls per plant with an average of (17.81), Montana genotype boll weight with an average of (4.85), and Coker 310 genotypes of Seed cotton yield per plant show an average of (87.26). While for fertilizer, it exceeded (200) Kg h^{-1}, No. of fruiting branches with an average of (8.29), No. of balls per plant of (17.66), boll weight with an average reached (4.86), and Seed cotton yield per plant, with an average of (84.36). As for the distances between the lines, the distance exceeds 60 cm, in Seed cotton yield per plant with an average of 83.99. As for the best selection index, it was (the number of boll per plant and seed cotton yield per plant which amounted to (124.9922), and the expected genetic improvement was I_{1234}, which included (number of fruiting branches, number of boll per plant, boll weight, and seed cotton yield per plant), which amounted to (8.7753), and the highest relative efficiency of the I_2 index, which included (number of bolls per plant) as it reached 3109.95).

Introduction

Cotton breeding efforts sought cultivars with high producing capacity and acceptable lint characteristics. As a result, the success of any breeding effort is directly dependent on the breeder's ability to carry on the segregating population and select progenies genetically better for numerous traits at the same time [1].

The different genotypes in their growth traits yield and its components, as well as their qualitative traits are a tool in the hands of crop breeders and research agencies working in the cotton breeding, whose most important goals are the production of new varieties characterized by their high productivity and good quality traits, and they have a wide adaptation to different environmental regions [2].

Potassium has a major role in the basic functions of plant growth and development, it works on the production of oxidation, reduction, and dehydrogenation enzymes that have a role in controlling the process of closing and opening stomata and through this process plays an important role in drought tolerance by regulating the osmotic pressure of plant cells in addition to that It participates in many physiological functions related to plant health and resistance to biotic and abiotic stress on a large scale, potassium deficiency leads to weak plant growth and a significant decrease in the number and size of leaves, which directly affects the process of carbon metabolism, deficiency and loss in yield and a decrease in fiber quality [3].

The increase in the unit area in addition to selecting the appropriate genotype for the region, which is done by adopting the appropriate plant density, which is one of the most important determinants of the behavior of the genotypes, therefore, following the appropriate density achieves an increase in yield, higher ordinary, and perhaps early ripening of the crop [4].

The study aims to evaluate the performance of six genotypes at three levels of potassium fertilizer and two distances between lines, in addition to construction the selection index for some traits of yield components.

Material and method

A field experiment was conducted at the Agricultural Research Station in the Daquq site as a factorial experiment with three factors, 6 genotypes (lachata, Coker 310, pack coat, Spiro, Montana, and IK259), 3 levels of potassium fertilizer(0, 100 and 200) kg h^{-1}, and 2 spaces between lines(40 and 60) cm. Compound fertilizer (NPK) was added at a rate of 300 Kg. h^{-1} during land preparation before planting and urea fertilizer (N% 46) 160 kg h^{-1} in two batches, the first after germination and the second after a month. Each replicate included (36) experimental units in which the genotypes were distributed twice according to the two planting distances between the genotypes, randomly. Each experimental unit contained three cultivars with a length of 5 m per cultivar. 3-5 cm on the calibration irrigation line in the hole, the distance between them is 0.25 m, at a rate of (4-5) seeds per hole, then thinning was done on one plant per hole, agricultural operations were carried out to serve the crop as needed, the experimental harvested the experience once in a date 10/11/2022. The data were analyzed as a factorial experiment according to the analysis of variance method, according to the randomized complete block design, and based on the SAS program, and the averages of the traits were compared using Duncan's multi-range test at a probability level of 5% for all the studied traits according to [5].

Selection index of one trait or more were created, and the expected genetic improvement was evaluated according to them, and the best selective guides whose expected genetic improvement exceeded 100% were selected compared to the selection for the yield unit. Construction selection index were created according to the method of classical selection indices by [6], [7], [8], and [9] where contain the following indicators.

Since:

I = Evidence of selection.

X_1, X_2, X_n = the phenotypic values of the traits included in the selection index.

b_1, b_2, b_n = the relative weights of the attributes included in the index.

The values of (bi) were calculated on the basis that the index gives the total educational values of the breed, as an index was calculated for each genotype, and a comparison was made between the teams according to their evidence. In order to facilitate the mathematical operations, the following symbols were used [8].

b = [p]-1 [G] [a]

Since:

b = vector of the coefficient of partial regressions of the values of traits in the Electoral Index.

[P]-1 = the inverse of the covariance matrix of the phenotypic values of the traits included in the index.

[G] = vector of variance of genetic values between grain yield and traits included in the index.

[a] = vertical vector of economic values.

Thus, the values of (bi) can be estimated by multiplying the inverse of the matrix (p) with the vector (G), then the previously mentioned equation is applied to extract the election evidence. The expected genetic improvement for each selective index was estimated according [10] from the equation:

$$AG = K\sqrt{(b1g1y + b2g2y + bngny)}$$

GA = expected genetic improvement.

K = the intensity of selection, taken at 20%, and its value is (2.06).

The relative efficiency (RE%) was estimated according [10]from the equation

The relative efficiency of any index = (the expected genetic improvement value for any index / the value of expected genetic advance for the index that includes only the trait of the yield) x 100

The relative efficiency of direct selection for the yield is 100%, and if any election evidence is superior to direct selection, it is considered important. The values of the election evidence for each genotype were estimated based on the electoral evidence distinguished in efficiency, analyzes were carried out using the Minitab program, made statistical programs were used to carry out the statistical procedures

Result and Discussion

The first table (1) showed a significant genotypes in the average weight of the boll and the yield of the cotton this result agrees with, [11], [12], [13], and [14].this found significantly different between Genotypes, and non-significant for the other traits, as for the levels of potassium fertilizer, they were significant for the number of fruiting branches, the number of bolls per plant, boll weight, and seed cotton yield per plant, regarding the distance between the lines, they were significant in the seed cotton yield per plant, while the interactions were all non-significant for the studied traits.

Table (1) analysis the variance for studied traits

S.O.V	d.f	MS			
		No. of fruiting branches	No. of balls per plant	boll weight (g)	Seed cotton yield per plant (g)
Replication	2	4.484	0.380	1.739	163.841
Genotypes	5	1.064	*8.010	**1.125	**339.021
level of potassium fertilizer	2	**5.885	**18.325	**5.996	**465.265
distances between lines	1	0.355	7.363	0.579	**717.498
Genotypes× level of potassium fertilizer	10	0.622	3.553	0.079	78.076
Genotypes ×distances between lines	5	0.244	1.338	0.420	87.460
level of potassium×distances between lines	2	0.455	4.450	0.029	46.287
Genotypes× level of potassium fertilizer × distances between lines	10	0.466	1.599	0.350	56.689
Error	70	0.592	2.439	0.294	64.168

(*) (**) significant at 5% and 1% respectively

Table (2) shows the effect of genotype, level of potassium fertilizer, and planting distance between lines on the number of fruiting branches, it shows the superiority of genotype Montana with an average of 8.15, in contrast to the genotype lachata, which took the lowest rate with an average of 7.51, the reason for this is due to the genetic ability of genotypes to exploit the surrounding environmental conditions and use them in the process of photosynthesis, which helped increase the transfer of processed foodstuffs from the source to the downstream and thus led to an increase in the number fruiting per plant.

For fertilizer levels, it exceeded the (200) Kg h^{-1}, with an average of 8.29, the reason for this is attributed to the role of potassium in affecting the process of photosynthesis, which in turn affects the number of fruit in the row, as the number of grains in the row is always variable with the change of growth factors and the change of the environment.

As for the distance between the lines, no differences were shown between the two distances. As for the interaction between the genotypes with potassium fertilizer, the combination of the genotype of lachata with the (200) Kg h^{-1} fertilizer level was 8.38, in contrast to the treatment of the genotype of lachata with the (0) Kg h^{-1} fertilizer level, with an average of 6.91. Interaction between the fertilizer levels with the distance between the lines, the treatment was superior to the (200) Kg h^{-1} fertilizer level and a distance of 60 cm, which had the highest average of 8.48, in contrast to the treatment of the (0) Kg h^{-1} fertilizer level with a distance of 60, had the lowest average of 7.47. As for the interaction between the genotype and the distance between the lines, there were no significant differences.

The interaction between the genotype, the fertilizer level, and the distance between the line, the treatment of the genotype of lk259 and Coker 310 with the (100) Kg h-1 level and the distance of 60 cm were superior, taking the highest mean of 8.80 in contrast to the treatment of the genotype of lachata and the (0) Kg h-1 fertilizer level and the distance of 40 cm. This is for human not for things took the lowest average of 6.70, that the number of fruiting branches is one of the important traits that affect the good performance of the genotype, if their number is greater, then the number of flowers increases, and then the number of bolls formed increases, which leads to an increase in the yield of cotton. This is a trait that directly affects the number of plant bolls, which is one of the main components of the yield of cotton blossom in cotton. The reason may be because each genotype has an optimal plant density that gives the best number of fruiting branches and that the number of fruiting branches is mainly affected by the genotypes as well as environmental conditions.

Table (2) effect of genotype, potassium fertilizer level, and distance between line to No. of fruiting branches

Genotypes	level of potassium fertilizer Kg h^{-1}			Mean of Genotypes
	0	100	200	
Lachata	6.91 c	7.23 bc	8.38 a	7.51 b
Cocker 310	6.96 c	7.93 a-c	8.36 a	7.75 ab
pack coat	7.46 a-c	8.15 ab	8.21 ab	7.94ab
Spiro	7.73 a-c	7.83 a-c	8.35 a	7.97 ab
Montana	8.10 ab	8.13 ab	8.23 ab	8.15 a
IK259	7.78 a-c	8.36 a	8.23 ab	8.12 a

level of potassium fertilizer Kg h^{-1}	distances between lines (cm)		the mean level of potassium fertilizer
	40	60	
0	7.51 b	7.47 b	7.49 b
100	7.93 ab	7.95 ab	7.94 a
200	8.11 a	8.48 a	8.29a

distances between lines (cm)	Genotypes						The mean distances between lines
	Lachata	Cocker 310	pack coat	Spiro	Montana	IK259	
40	7.52 a	8.34 a	7.94 a	8.05 a	7.97 a	7.91 a	7.85 a
60	7.50 a	7.80 a	7.94 a	7.88 a	8.33 a	8.34 a	7.96 a

Genotypes	0		100		200	
	40	60	40	60	40	60
Lachata	6.70 e	7.13 b-e	7.53 a-e	6.93 c-e	8.33 a-e	8.43 a-c
Cocker 310	7.13 b-e	6.80 de	8.06 a-e	7.80 a-e	7.93 a-e	8.80 a
pack coat	7.66 a-e	7.26 a-e	7.80 a-e	8.50 ab	8.36 a-c	8.06 a-e
Spiro	8.00 a-e	7.46 a-e	8.13 a-e	7.53 a-e	8.03 a-e	8.66 ab
Montana	7.93 a-e	8.26 a-d	8.13 a-e	8.13 a-e	7.86 a-e	8.66 ab
IK259	7.66 a-e	7.90 a-e	7.93 a-e	8.80 a	8.13 a-e	8.33 a-d

The different letters within the levels of the factor or the interaction indicate that significant differences 0.05 between the treatments.

Table (3) showed the effect of the genotype, the level of potassium fertilizer, and the distance between the lines on the number of plant bolls, the superiority of the genotypes of Coker 310 with an average of 17.81, and the opposite of the genotype of Lachata, which had the lowest rate with an average of 15.94, perhaps is due to genotypes' genetic ability to exploit surrounding environmental conditions and use them in the process of photosynthesis, which aided in the transfer of processed foodstuffs from the source to the downstream, increasing the number of boll per plant.

The fertilizer levels, surpassed (200) Kg h^{-1} level with an average of 17.66, perhaps the reason for this is attributed to the role of the appropriate distance in obtaining the plant to obtain high photosynthesis and its outputs to be transported to the cotton crop as for the planting distances, there were no differences between the two planting distances.

As for the interaction between genotypes and potassium fertilizer, the treatment of the genotypes of Coker 310 with the average level of the second fertilizer was 18.866, in contrast to the treatment of the genotype of Lachata with the level of the (0) Kg h^{-1} fertilizer, which was lower with an average of 14.150, as for the interaction between the fertilizer levels with the distances between the lines, the treatment was superior to the (200) Kg h^{-1} fertilizer level and a distance of 60 cm, which took the highest mean of 18.31, in contrast to the treatment of the (0) Kg h^{-1} fertilizer level with a distance of 60 cm, which took the lowest average of 16.37, as for the interaction between the genotype and the distance, the treatment of the genotype Coker 310 was superior with a distance of 60 cm, which took the highest mean of 18.24.

For the interaction between genotype, fertilizer level, and the two distances between lines, the treatment of the Coker 310 genotype

with the (100) Kg h^{-1} fertilizer level and the distance of 60 cm were superior, taking the highest mean of 19.20, in contrast to the treatment of the genotype of Lachata with the (0) Kg h^{-1} fertilizer level and the distance of 40 cm, which took the lowest, the average amounted to 13.20. The importance of the total number of bolls per plant comes from its direct contribution to the yield of cotton, as the total number of bolls increases, it is expected that the yield will increase, the importance of this statistic is the number of open bolls from it is the most important in contributing to the yield, these results are consistent with [15] is found significantly different between genotypes in this trait.

Table (3) effect of genotype, potassium fertilizer level, and distance between line to No. of bolls per plant

Genotypes	level of potassium fertilizer Kg h^{-1}			Mean of Genotypes
	0	100	200	
Lachata	14.15 d	16.36 bc	17.16 a-c	15.94 b
Cocker 310	17.46 a-c	18.86 a	17.100 a-c	17.81 a
pack coat	16.150 c	17.416 a-c	18.400 ab	17.32 a
Spiro	16.55 bc	17.63 a-c	17.20 a-c	17.12 a
Montana	17.46 a-c	17.40 a-c	17.75 a-c	17.53a
IK259	16.60 bc	17.93 a-c	18.20 a-c	17.57 a

level of potassium fertilizer Kg h^{-1}	distances between lines (cm)		the mean level of potassium fertilizer
	40	60	
0	16.41 c	16.37 c	16.39b
100	17.45abc	17.75ab	17.602a
200	17.005bc	a18.31	17.66a

distances between lines (cm)	Genotypes						mean of distances between lines
	Lachata	Cocker 310	pack coat	Spiro	Montana	IK259	
40	15.62 c	17.37 ab	17.47 ab	16.51 bc	17.25 ab	17.51 ab	16.95 a
60	16.26 bc	Genotypes	0	17.74 ab	17.82 ab	17.64 ab	17.48 a

	0		100		200	
	40	60	40	60	40	60
Lachata	13.20 c	15.10 bc	16.66 ab	16.06 ab	17.00 ab	17.63 ab
Cocker 310	17.33 ab	17.60 ab	18.53 a	19.20 a	16.26 ab	17.93 ab
pack coat	17.30 ab	15.00 bc	17.06 ab	17.76 ab	18.06 ab	17.76 ab
Spiro	16.33 ab	16.76 ab	17.13 ab	18.13 ab	16.06 ab	18.33 a
Montana	17.86 ab	17.06 ab	17.00 ab	17.80 ab	16.90 ab	18.60 a
IK259	16.46 ab	16.73 ab	18.33 a	17.53 ab	17.73 ab	18.66 a

The different letters within the levels of the factor or the interaction indicate that significant differences 0.05 between the treatments.

Table (4) showed the effect of genotype, potassium fertilizer level, and the distance between lines on the boll weight, it shows the superiority of the Montana genotype, with an average of 4.85, in contrast to the Cocker 310 genotype, which took the lowest rate, with an average of 4.14, the reason for this may be due to the genetic variation between the genotypes and to the increase in the number of seeds in the boll, which in turn leads to an increase in the weight of the boll.

As for fertilizer levels, they exceeded (200) Kg h^{-1} level with an average reached 4.86, as for the planting distances between the lines, no differences significant appeared between the two distances.

Table (4) effect of genotype, potassium fertilizer level, and distance between lines to the boll weight

Genotypes	level of potassium fertilizer Kg h^{-1}			Mean of Genotypes
	0	100	200	
Lachata	3.92 c-e	4.21 b-e	4.86 ab	4.33 bc
Cocker 310	3.60 e	4.11 b-e	4.69 ab	4.14 c
pack coat	3.87 de	4.35 b-d	4.65 a-c	4.29 bc
Spiro	4.25 b-e	4.52 c-e	4.86 ab	4.54 ab
Montana	4.38 c-e	4.85 ab	5.32 a	4.85 a
IK259	4.24 b-e	4.54 b-d	4.796 ab	4.52 abc

level of potassium fertilizer Kg h^{-1}	distances between lines (cm)		The mean level of potassium fertilizer
	40	60	
0	3.94 d	4.15 dc	4.04 c
100	4.38 c	4.48 bc	4.43 b
200	4.80 ab	4.93 a	4.86 a

distances between lines (cm)	Genotypes						mean of distances between lines
	Lachata	Cocker 310	pack coat	Spiro	Montana	IK259	
40	4.20 bc	4.21 bc	4.05 c	4.30 bc	4.96 a	4.51 a-c	4.37 a
60	4.46 a-c	4.06 c	4.53 a-c	4.78 ab	4.74 ab	4.54 a-c	4.52 a

Genotypes	0		100		200	
	40	60	40	60	40	60
Lachata	3.67 gh	4.18 b-h	4.27 b-h	4.16 b-h	4.67 a-h	5.05 a-d
Cocker 310	3.65gh	3.56 h	4.49 a-h	3.37 f-h	4.49 a-h	4.89 a-d
pack coat	3.77 g-f	3.97 d-h	3.89 f-h	4.81 a-h	4.49 a-h	4.81 a-f
Spiro	4.06 c-h	4.44 b-h	4.33 b-h	4.71 a-h	4.53 a-h	5.20 ab
Montana	4.24 b-h	4.53 a-h	5.10 a-c	4.60 a-h	5.54 a	5.10 a-c
IK259	4.26 b-h	4.22 b-h	4.21 b-h	4.87 a-e	5.07 a-d	4.52 a-h

The different letters within the levels of the factor or the interaction indicate that significant differences 0.05 between the treatments.

The interaction between genotypes with potassium fertilizer, the treatment outperformed the Montana genotypes with the (200) Kg h^{-1} level, an average of 5.32, in contrast to the treatment of the Cocker 310 genotype with the (0) Kg h^{-1} fertilizer level, which took the lowest average of 3.60. The treatment outperformed the (200) Kg h^{-1} fertilizer level with a distance of 60 cm was taken at an average of 4.39, in contrast to the treatment, the (0) Kg h^{-1} fertilizer level with a distance of 40 cm, which took the lowest mean of 3.94.

For the interaction between the genotype and the distance between the lines only, the treatment of the Montana genotype with the distance of 40 cm, which took the highest average, was 4.96, in contrast to the treatment of the genotype of pack coat, with the distance of 40 cm, which took the lowest average of 4.05.

As for the interaction between the genotype, fertilizer level, and the distance between the lines, the treatment of the genotype was superior to Montana with the (200) Kg h^{-1} fertilizer level and the distance of 40 cm, taking the highest mean of 5.54, in contrast to the treatment of the genotype Coker 310, the (0) Kg h^{-1} fertilizer level, and the distance of 60 cm, which took the lowest, average of 3.56, these results are consistent with [15] and [16]found significant differences between genotypes in this trait.

Table (5) showed the effect of the genotype and level of potassium fertilizer and the two planting distances between the lines on the Seed cotton yield per plant, the genotypes of Coker 310 show an average of 87.26, in

contrast to the genotype of Lachata, which took the lowest rate with an average of 74.46, The reason may be due to the superiority of these genotypes in most components of the yield, which was reflected in the yield of cotton.

The fertilizer levels, exceeded (200) Kg h^{-1} level, with an average of 84.36, as for the distances between the lines, the distance exceeds 60 cm, with an average of 83.99.

As for the interaction between the genotype with the potassium fertilizer, the treatment of

the genotypes of Coker 310 with the (200) Kg h^{-1} fertilizer level averaged 90.600 in contrast to the treatment of the genotype of Lachata with the (200) Kg h^{-1} fertilizer level was taken lower with an average of 69.773, the treatment of the (200) Kg h^{-1} fertilizer level, a distance of 60 cm, which took the highest average of 88.24, in contrast to the treatment of the (0) Kg h^{-1} fertilizer level, with a distance of 40 cm, which took the lowest average of 75.40.

Table (5) effect of genotype, potassium fertilizer level, and distance between lines to the Seed cotton yield per plant

Genotypes	level of potassium fertilizer Kg h^{-1}			Mean of Genotypes
	0	100	200	
Lachata	75.09 def	78.52 b-f	69.77 f	74.46 c
Cocker 310	82.10 a-e	89.097 ab	90.60 a	87.26 a
pack coat	74.25 of	82.79 a-e	83.400 a-e	80.14 b
Spiro	78.57 b-f	83.85 a-e	87.03 abc	83.15 ab
Montana	75.83 def	78.06 c-f	85.80 a-d	79.90 b
IK259	78.61 b-f	82.535 a-e	89.57 a	83.57 ab

level of potassium fertilizer Kg h^{-1}	distances between lines (cm)		The mean level of potassium fertilizer
	40	60	
0	75.40 c	79.41 bc	77.41 b
100	80.63 bc	84.32 ab	82.47 a
200	80.48 bc	88.24 a	84.36 a

distances between lines (cm)	Genotypes						The mean distances between lines
	Lachata	Cocker 310	pack coat	Spiro	Montana	IK259	
40	75.18 de	83.71 a-d	75.70 cde	78.57 b-e	76.72 b-e	83.13 a-d	78.84b
60	73.74 e	90.81 a	84.59 ab	87.73 a	83.07 a-d	84.00 abc	83.99 a

Genotypes	0		100		200	
	40	60	40	60	40	60
Lachata	71.89 efg	78.28 b-g	79.61 a-f	77.43 c-g	74.04 d-g	65.50 g
Cocker 310	80.63 a-g	83.58 a-f	84.68 a-e	93.50 ab	85.84 a-e	95.36 a
pack coat	67.85 gf	80.65 a-g	82.28 a-f	83.29 a-f	76.97 c-g	89.83 a-d
Spiro	76.21 c-g	80.93 a-g	80.26 a-g	87.44 a-e	79.23 a-g	94.83 a
Montana	73.66 de	78.00 b-g	76.62 c-g	79.50 a-g	79.88 a-g	91.72 abc
IK259	82.18 a-f	75.03 d-g	80.32 a-g	84.74 a-e	86.90 a-e	92.24 abc

The different letters within the levels of the factor or the interaction indicate that significant differences 0.05 between the treatments.

For the interaction between the genotype and the distance between the lines only, the treatment of the genotype Coker 310 with a distance of 60 cm, which took the highest average, was 90.81, in contrast to the treatment

of the genotype of Lachata with the distance of 60 cm, which took the lowest average, which reached 73.74. As for the interaction between the genotype and the fertilizer level and the two distances between the lines were superior to the

treatment of the genotype of Coker 310 with the (200) Kg h^{-1} fertilizer level and the distance of 60 cm, which took the highest mean of 95.36, in contrast to the treatment of the genotype of Lachata and the level of (200) Kg h^{-1} fertilizer and the distance of 60 cm, which took the lowest mean of 65.50, these results are consistent with [15] and [16] found a significantly different between genotypes in this trait.

Selection index

Due yield trait is one of the quantitative traits that represent the main objective of any breeding program, so the selection index is a technique used in crop breeding and improvement programmers, as Table (6) shows the selection index for the cotton yield and some of its components (the number of fruiting branches, the number of bolls per plant, boll weight, and Seed cotton yield per plant) respectively, in which it is noted that the highest selection index is I_{124} for the number of fruiting branches, the number of bolls per plant, and Seed cotton yield per plant, which amounted to 124.9922, followed by the selection index I_{12} for the two traits of the number of fruiting branches and the number of bolls per plant, which amounted to 124.8954, unlike the two selection indices I_3 and I_{34}, which took the lowest selection index for each they reached -20.720 and -20.6235, respectively.

As for the expected genetic advance, it was the best for the index I_{1234}, which includes the number of fruiting branches, the number of bolls per plant, boll weight, and Seed cotton yield per plant, which took a value of 8.7753. The expected genetic advance of the selections indices I_4 and I_1 for Seed cotton yield per plant only, as well as for the number of fruiting branches only, each of them reached 0.2721 and 1.0926, respectively.

As for the relative efficiency, the selection index I_2 outperformed the traits of the number of bolls per plant, as the relative efficiency reached 3109.95, which is one of the single selection indexes. As for the selection index for two traits, the index I_{12} excelled for the number of fruiting branches and the number of bolls per plant, the index I_{23} for the number of fruiting branches and boll weight, and the index I_{24} for the number of bolls per plant and Seed cotton yield per plant, for which the relative efficiency was 3135.75, 3198.38, and 3111.57, respectively.

As for the selection index for three traits, I_{123} for the number of fruiting branches, the number of bolls per plant, and boll weight, which amounted to 3223.48, and the index I_{124} for the number of fruiting branches, the number of bolls per plant, and Seed cotton yield per plant, whose value amounted to 3137.37, and the selection index I_{234}, which includes the number of bolls per plant, boll weight, and Seed cotton yield per plant, whose value amounted to 3199.92, as for the selection index, which includes four traits, I_{1234}, which are the number of fruiting branches, the number of bolls per plant, boll weight, and Seed cotton yield per plant, as the relative efficiency for it was 3225.02.

The notice in these results is that selection for the yield or direct selection remains one of the most important influencing factors that can be relied upon for the differentiation between genotypes and any other evidence whose efficiency exceeds 100% is considered sufficient than that which includes the yield alone, selection evidence that includes the least number of traits is preferred, the highest relative efficiency, these results are consistent with a some of researchers, which [17], [18], [19]and [20], as they found among the selection index of the components of the yield.

Table (6) selection evidence, expected genetic improvement, and relative efficiency of yield traits and some components

No. of selection index	Value of selection index	Expected genetic advance	Relative efficiency %
I_1	4.9090	1.0926	401.54
I_2	119.9863	8.4622	3109.95
I_3	-20.720	2.0321	746.82
I_4	0.0968	0.2721	100.00
I_{12}	124.8954	8.5324	3135.75
I_{13}	-15.8114	2.3072	847.92
I_{14}	5.0059	1.1260	413.81
I_{23}	99.2659	8.7028	3198.38
I_{24}	120.0832	8.4666	3111.57
I_{34}	-20.6235	2.0503	753.50
I_{123}	104.1749	8.7711	3223.48
I_{124}	124.9922	8.5368	3137.37
I_{234}	99.3628	8.7070	3199.92
I_{134}	-15.7145	2.3232	853.80
I_{1234}	104.2718	8.7753	3225.02

Conclusion

The Montana and Coker 310 genotype shows the superiority of No. of fruiting branches, No. of balls per plant, boll weight, and Seed cotton yield per plant. While for fertilizer levels, it exceeded (200) for some studied traits, as for the distances between the lines, the distance exceeds 60 cm for the studied traits.

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مجلة جامعة كركوك للعلوم الزراعية

الاداء، الادلة الانتخابية لستة تراكيب وراثية من القطن للحاصل وبعض مكوناته

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- البحث مستل من رسالة ماجستير للباحث الاول .

المستخلص

اجريت تجربة عاملية في محطة البحوث / موقع داقوق الواقعة على بعد 40 كم جنوب كركوك على خط طول 28 – 44° شرقاً وخط عرض 8 – 35° شمالاً وفقا لتصميم القطاعات العشوائية الكاملة، باستخدام ستة تراكيب وراثية من القطن وثلاث مستويات من سماد البوتاسيوم ومسافتين بين الخطوط، حللت البيانات كتجربة عاملية لدراسة تحليل التباين والمقارنة بين المتوسطات حسب اختبار دنكن متعدد المدى عند مستوى احتمال 5% لدراسة جميع الصفات المدروسة، اظهر التركيبين الوراثيين مونتانا وكوكر 310 تفوق معنوي لصفة عدد الافرع الثمرية بمتوسط بلغ (8.15) والتركيب كوكر 310 لصفة عدد الجوز بالنبات بمتوسط بلغ (17.81) والتركيب الوراثي مونتانا لمتوسط وزن الجوزة بمتوسط بلغ (4.85) والتركيب الوراثي كوكر 310 لصفة حاصل القطن الزهر في النبات بمتوسط بلغ (87.26)). بينما تفوق المستوى (200) كغم. هـ –1 لصفة عدد الافرع الثمرية بمتوسط بلغ (8.29) وعدد الجوز بالنبات بلغ(17.66) ومتوسط وزن الجوزة بمتوسط بلغ (4.86) وحاصل القطن الزهر بالنبات بمتوسط بلغ (84.36). اما مسافات الزراعة فكانت المسافة 60 سم بين الخطوط متفوقا في حاصل القطن الزهر بمتوسط بلغ (83.99). اما افضل دليل انتخابي فكان (عدد الجوز بالنبات وحاصل القطن الزهر الذي بلغ (124.9922) وتحسين وراثي متوقع كان 1234I الذي تضمن (عدد الافرع الثمرية وعدد الجوز بالنبات ومتوسط وزن الجوزة وحاصل القطن الزهر)الذي بلغ (8.7753) واعلى كفاءة نسبية للدليل 2I الذي تضمن (عدد الجوز بالنبات) اذ بلغ (3109.95)).

الكلمات مفتاحية: ادلة انتخابية، الاداء، القطن، تراكيب وراثية.