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Inter and Intra Selection Efficiency of Cotton Families (*Gossypium hirsutum* L.)

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Abstract: *Offspring families (F3 and F4) derived from superior crosses were grown at an agricultural farm in Baghdad Governorate\ Iraq (33.05N latitude, 44.32E longitude) for two successive years (2021-2022) by using a Randomized Completely Block Design with three replications to investigate responses for selection for seed cotton yield and its components traits.*

Results showed: Some lines outperformed their parents in yield and its components in both the third and fourth generations. The combinations 2-2, 3-1, and 3-4 demonstrated the best performance and stability in the yield of cotton bolls (135.06 and 145.72), (130.46 and 141.33), and (143.97 and 137.77) for the third and fourth generations, respectively. They also excelled in yield traits compared to other genetic combinations. The coefficients of inbreeding were negative for the number of fruit branches, the number of bolls per plant, and the yield of cotton bolls per plant (-9.33, -21.01, and -14.62, respectively). Genetic divergence indicated that the most distinct genetic combination was line 4-1, which formed a unique group, followed by line 9-2, which included other subgroups. However, group seven, comprising combinations 1-2 and 3-4, stood out with the best performance and highest yield of cotton bolls (139.46 grams per plant), followed by group six, which included combination 3-3 (143.97 grams per plant), and group four, which included combination 2-1 (135.06 grams per plant). These groups can be considered sources for improving the yield traits and their components of cotton bolls. Therefore, it can be concluded that the best performing and productive line was combination 3-4, which was distinguished by a unique group with combination 1-2, making it a promising candidate for selected cotton families.

.**Keywords:** *Cotton families, selection, genetic advanced, cluster analysis*

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1. INTRODUCTION

The stability of seed cotton yield across years is an important goal of agricultural production programs (1). Variations in plant populations can be established through introduced mutation and crossing among genotypes (2). Segregating lines have huge data about their potential genetic ability; therefore, plant breeders should take over and select promising efficient genotypes by applying appropriate methods to estimate genetic parameters (3). Selection depends essentially on the existence of variances among selected populations. Variance components (genetic, environment, and their interactions) affect selection efficiency and change the expected genetic gain from selection for each trait (4,5). Progenies of cotton genotypes must be evaluated to distinguish elite genotypes (6). Many alleles of the ability in potential production can be masked or inhibited by the environments, also the correlations among genes controlling traits and behavior need to be considered for obtaining promising genotypes (7). The yield trait is the selection procedure's most important output resulting from the favorable gene accumulation. (8) found diminishing variances, GCV, and PCV across F2-F4 generations as a result of reducing heterozygosis by the same meaning non-additive gene effects also genotypic environmental interactions can be magnitude differences among observed and predicted genetic advanced from F2-F4 generations. Expected gain from selection differs according to the gene frequency in the population even though the full-sib population showed the importance of genetic advancement and correlation of yield with its components than half-sib families (9). Each selection approach aims to initiate genetic potential improvement in yield ability through increasing the efficiency in physiological activities associated with the increasing of seed cotton yield of the elite genotype (10). Success in selection depends on the type of selection method applied though the Selection index of multi traits simultaneously gave the highest genetic gain from selection and was more efficient which led to improving seed cotton yield and its components to the single traits selection (11). Many methods applied on segregating lines perform significant increases in seed cotton yield and its components compared to the pedigree and single seed descent methods even though most traits were stable except ball weight (12). Application selection among families was more efficient than individual selection at the early generations, while individual plant selection should be followed after family selection (13). The superior family selected even individuals promising to segregate lines of population reformation according to the direction of genome combination. Consequently desired segregates should be involved in effective genes of important traits (seed cotton yield and its components) (14). Genetic parameters (variance components, heritability, and gain from selection) differ significantly and affect selection across generations of segregating lines according to the nature of gene combinations and type of gene in multiple environments. Inter and intra-population selection can be modified to meet the demands of each crop and approaches need to be applied such as individual lines or pedigree methods (15). This equation is sometimes termed the Breeder's equation. It is a statement that the evolutionary change across generations (responses for selection) is proportional to the change caused by directional selection within a generation (Selection differential). Also, the strength of this relationship is determined by the narrow sense heritability (h^2_{ns}) (16).

The study aims to evaluate and estimate the selection efficiency of inter and intra F3 and F4 families for seed cotton yield derived from superior cotton crosses.

2. METHOD

Forty plants were grown for each of nine superior crosses of cotton with their parents in the 2022 season and then selected the best 10% (4 plants for each cross) to grow in the next generation which represents the F4 population of selected plant families by using the plant to row method in 2023 season. The experiment was applied using a Randomized Completely Block Design with three replications for both seasons. Whole plants in the experimental unit (three meters long) were taken to estimate plant height, vegetative and fruiting branches, ball number, ball weight, and seed cotton yield traits. Whole agricultural practices are applied according to recommendations (17). Genetic parameters estimated were: Realized heritability

$(RH^2) = R / S$ (Eqn. 1)

was S: Selection differential of mean trait value between the selected individuals and the entire population (within a generation)

$S = \bar{X}F3s - \bar{X}F3$ (Eqn. 2)

where $\bar{X}F3s$: mean of selected proportion, $\bar{X}F3$= mean of the original population. R: retrospective selection refers to the change in the original population means over a complete generation (across generation) =offspring selected mean- original mean. Also, Inbreeding depression and other formulas computed according to (16) as follows

$(ID) = (F3 - F4/F3) * 100,$ (Eqn. 3)

Expected genetic advanced

$(GA) = i.\delta^2P.RH$ (Eqn. 4)

were i: selection index, δP: phenotypic standard deviation, and RH: realized heritability, genotypic and phenotypic coefficient of variation (GCV and PCV respectively) estimated according to the following formulas

$$g.c.v. = \frac{\sqrt{\sigma^2 g}}{\bar{x}} X100 \quad \text{(Eqn. 5)}$$

and $p.c.v. = \frac{\sqrt{\sigma^2 p}}{\bar{x}} X100$ (Eqn. 6)

Analysis of variance and comparison of means achieved for original population (F3), their best-selected plants, and F4 families according to (18). by using SAS Version 9 software program.

Table 1. Names of crosses of segregating Lines

No.	Crosses	cod number
1(1-4)	(Lashata * Marsoomi)	1/14/1
2(1-4)	(Lashata * Montana)	22/1/1
3(1-4)	(Marsoomi * Ceebro)	1/6/1
4(1-4)	(Marsoomi * Cocker310)	5/4/1
5(1-4)	(Montana * Ceebro)	23/17/1
6(1-4)	(Montana * Cocker310)	3/17/1
7(1-4)	(Ceebro * Cocker310)	11/5/1
8(1-4)	(Ceebro * Cocker310)	12/10/2
9(1-4)	(Cocker310 * Pac-cot)	12/9/1

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3. FINDINGS AND DISCUSSIONS

The inputs (original population: F3, selected parents, and their offspring families) differ from each other significantly indicating the existence of diversity among them. Parents differ significantly from their derived lines according to the significant F test in most studied traits (Plant height, Fruiting branches, No. balls per plant, and seed cotton yield). Also, parents exhibited significant variation from selected and F4 populations (table 2). The differences resulting from the isolations and their descendants across generations are primarily because hybridization occurred between different genotypes and produced new genotypes that have gene combinations that differ from each other in the studied traits (19).

Table 2. Analysis of variance for selected plants (F3 population) and their offspring (F4 population)

S O V	D F	*Traits*											
		Plant Height (cm)		Vegetative Branchs.Plant-1		Fruiting Branchs.Plant-1		Balls.Plant-1		Ball Weight(g)		Individual Plant Yield (g)	
		Selected	Offspring	Selected	offspring	Selected	Offspring	Selected	Offspring	Selected	Offspring	Selected	Offspring
Rep.	2	2358.9	2406.6	4.1	32.69	19.46	37.75	52.31	10.5	0.775	0.07	2621.67	593.11
Genotypes	35	990.45**	1051.18**	2.92**	3.56**	28.03**	61.27**	69.99**	83.38**	0.65**	30.28**	1835.95**	1900.65**
Error	7	271.9	335.6	0.07	0.44	2.47	1.22	7.55	6.48	0.04	0.28	129.0	151.5

	0	6	3									4	3
Parents VS. selected and offspring plants	1	2208.05**	4394.19**	0.09 ns	0.94 ns	10.78*	36.6**	45.27*	180.08**	0.07 ns	0.13ns	7736.59**	1096.12**

Plant height traits showed variation in selected and their offspring plants (table 3). High plant height (129.9 cm) was in genotype 9-3 which did not differ significantly from other genotypes except 4-3 of the selected F3 population. Also, their offspring family means were similar in 15 genotypes). Maximum plant height 126.63 cm was in 3-3 genotype and have no differences with (3-3, 9-3, 8-2, 8-3, 8-2, 7.1, 6.3, 4-4, 4-1, 4-2, 3-3, 3-1, 2-4, 1-4 and 1-2 genotypes (table 3). Increasing plant height mostly increases nods carrying vegetative and fruiting brunch and determines plant shape. Dwarf plants were in 6-4 (77.3) cm and 5-2 (79.77) cm in offspring families were relevant for mechanical harvesting. No significant differences in vegetative branches either selected or their offspring families. 1-2 and 1-3 genotypes excelled in fruiting branches and balls number per plant (22.19, 27.78, and 22.19, 28.73 respectively) in F3 selected plants. Other than no differences of the last genotypes with 1-1, 7-1, 7-4, and 8-1 in number of fruiting branches. Many F4 families have a large number of fruiting branches (1-4: 22.23, 3-4:20.21, 7-2: 22.66, and 8-2: 22.77). The potential ability in high production of seed cotton yield (137.77 g) of 3-4 genotype among F4 families has a higher number of balls per plant (35.58) than other families. Although the similarity of most genotypes (F4 Families) in ball weight many genotypes (2-2, 2-4, 3-1, 4-2, and 6-1) were superior in seed cotton yield (145.72, 128.99, 141.33, 136.46 and 146.88g respectively). The superior selected parents from the F3 population were in balls per plant and seed cotton yield traits in 2-2, 3-1, 3-4, and 4-1 genotypes. Many F4 families were superior in the number of fruiting branches and balls per plant (1-4, 3-4, 7-2, and 8-2). Also, 3-4, 2-2, 2-4, 3-1, 4-2, and 6-1 genotypes were excelled in seed cotton yield. The continuity of the good performance of the segregate lines is due to their ability and the stability of the genes for the desired traits in expressing themselves (14), and this is evident in 3-4 genotype which can be regarded as a promising genotype.

Table 3. F3-Selected and their offspring family means

Genotypes	***Plant Height (cm)***		***Vegetative Branches per Plant***		***Fruiting Branches per Plant***		***Balls per Plant***		***Balls weight (g)***		***Individual Plant Yield (g)***	
	F3s	F4	F3s	F4	F3s	F4	F3s	F4	F3s	F4	F3s	F4
1,1	90.67	84.13	1	2.95	21.2	19	15.33	19.70	4.5	4.16	115.19	88.672
1,2	83.37	118.81	2.13	3.03	22.23	15.33	27.78	16.7	4.93	4.01	139.23	73.68
1,3	104.63	91.51	1.91	4.04	22.19	16.7	28.73	15.54	4.69	4.21	135.02	72.14

1,4	88.19	121.46	2.54	3.07	17.1	22.23	26.14	17.18	3.96	4.55	103.34	84.88
2,1	101.56	90.677	1.88	3.32	17.21	17.1	26.41	25.08	4.63	4.57	122.37	121.33
2,2	118.37	83.37	2.84	4.03	19.92	17.21	31.09	28.78	4.33	4.83	135.06	145.72
2,3	95.58	88.19	1.91	3.11	14.59	19.92	24.48	26.14	4.58	3.96	114.3	110.23
2,4	116.34	101.56	1.58	3.04	16.96	14.59	25.09	26.41	3.99	4.63	108.3	128.99
3,1	104.8	118.37	1.9	3.97	16.72	16.96	27.96	31.09	4.48	4.33	130.46	141.33
3,2	82.3	93.047	2.92	3.45	13.46	16.72	21.19	19.55	4.04	3.69	85.55	78.85
3,3	104.64	126.63	4.2	3.40	20.21	13.46	23.5	18.65	4.18	3.58	99.53	73.48
3,4	97.45	95.587	4.09	3.33	18.73	20.21	30.58	35.58	4.63	4.15	143.97	137.77
4,1	88.18	116.34	1.95	3.06	19.95	18.73	27.14	28.02	4.91	3.86	139.7	114.87
4,2	105.14	104.80	1.02	3.06	12.46	19.95	15.28	28.96	3.98	4.48	62.31	136.46
4,3	77.3	82.303	2.16	3.33	15.5	12.46	19.3	21.19	3.99	4.04	77.04	92.32
4,4	108.96	104.64	1.85	2.99	17.43	15.5	21.02	25.58	4.29	3.93	93.24	107.24
5,1	87.84	86.38	5.16	3.32	16.62	17.43	20.68	21.24	4.23	3.8	86.87	87.43
5,2	84	79.77	2.09	3.14	17.46	16.62	18.72	22.3	4.38	3.98	82.42	95.47
5,3	86.83	91.03	2.66	3.16	9.9	17.46	19.96	28.19	4.54	3.92	91.15	117.22
5,4	90.96	97.45	3.19	3.18	14	9.9	20.84	27.48	4.53	4.03	94.4	117.46
6,1	111.06	88.18	1.2	3.29	13.16	14	19.43	29.14	4.59	4.81	93.73	146.88
6,2	106.7	84.74	1.19	3.10	19.62	13.16	19.77	16.55	4.41	3.88	86.94	70.93
6,3	100.5	105.1	1.15	3.2	17.8	19.6	17.5	16.4	4.8	3.7	90.69	68.74

		4		0	1	2	4	1	3	8		
6,4	86.3	77.3	1.2	3.71	17.4	17.81	24.22	19.33	4.53	3.99	110.05	83.84
7,1	95.08	108.96	0.85	3.10	22.66	17.4	18.59	23.02	4.86	4.06	93.67	100.18
7,2	106.13	87.84	2.9	3.69	12.46	22.66	18.77	20.60	4.76	4.23	89.38	93.85
7,3	83.13	84	2.15	2.57	15.4	12.46	20.87	18.72	4.67	4.38	96.12	88.71
7,4	103.9	86.83	1.58	3.06	21.1	15.4	25.25	19.99	4.95	4.54	129.64	97.47
8,1	80.8	90.96	2.29	2.97	22.7	21.1	26.27	20.84	4.55	4.53	119.89	101.12
8,2	122.93	111.06	4.19	3.66	14.43	22.7	26.3	20.43	4.07	4.59	116.47	100.49
8,3	100.83	106.7	1.9	2.85	13.92	14.43	21.48	19.7	4.5	4.41	98.05	93.59
8,4	101.8	100.7	1.85	3.29	11.45	13.92	20.59	19.54	4.62	4.63	95.26	97.19
9,1	97.93	86.3	2.27	3.71	16.64	11.45	23.3	24.22	5.21	4.53	129.53	116.43
9,2	105.9	95.58	1.89	3.37	14.95	16.64	18.4	19.59	5.15	4.76	94.45	99.96
9,3	129.93	106.13	1.15	3.87	19.4	14.95	17.36	18.77	4.5	4.76	81.26	96.06
9,4	97.66	84.13	2.91	3.26	16.7	19.4	22.05	20.66	4.27	4.67	97.85	103.20
LSD(0.05)	51.66	26.84	Ns	Ns	1.79	2.55	4.14	4.47	ns	ns	20.04	18.49

F3s:F3 selected plants, F4: offspring F3s

The responses to selection and selection differential are important two factors that affect realized heritability and expected genetic gain from the selection. Selection differential among selected plants and the original population tends to be positive and has increased in vegetative branches, fruiting branches, balls no. per plant and seed cotton yield (0.082, 1.24, 2.96, 0.009, and 15.767 g respectively) (table 4). Plant height decreased slightly (-2.26) for the selection focused on the economic yield. Responses to selection estimate differences in phenotypic means of offspring and the entire of their parents. It was negative in plant height (-0.61) and positive and few in vegetative branches (0.076), fruiting branches (0.962), and ball weight (0.007). Selection led to improvement in seed cotton yield and balls number per plant across generation through the high responses of selection in the two traits (13.22 and 2.17 respectively. Population means increased or decreased traits across generations. Selection applied on the best superior genotypes of the F3 population which has 105.06 g per plant though the original population has 89.3 g. Balls number behaved similarly to yield trait through increased value in F4 generation which has an important role in increasing seed cotton yield. It's obvious from the higher ratio of responses to selection (2.17) than other traits except for seed cotton yield. Differences in intra-families need to be distinguished through the genomic and phenotypic coefficient of variation estimates, which are moderate to high in most traits. However, genotypic variations have a large amount of phenotypic differences. The proportional importance of genotypic and phenotypic refers to the divergence in segregated lines (8). Hybrid vigor acts against Inbreeding depression which correlates with the diversity among lines (20) therefore, negative inbreeding depression coefficients in fruiting branches, balls number and seed cotton yield (-9.33, -21.91 and -14.62 respectively). which parallels with inbred vigor in that the first comes from dominance gene action while the second comes from additive gene action in cotton (3).

Table 4. Realized heritability, inbreeding depression, and genetic advanced for the original population (F3Selected) and their offspring (F4-population).

Generation and genetic parameters	*Plant height*	*Veg. Branch.*	*Fruit Bra.*	*Balls No.*	*Balls Weight*	*Plant yield*
Mean of Original Populations (F3)	100.8	2.13	15.64	19.85	4.5	89.3
Means of Selected Plants (F3)	98.54	2.21	16.882	22.81	4.50	105.06
Means Offspring Families	98.01	2.13	17.1	24.2	4.23	102.36
Genotypic variance of selected plants	239.49	0.95	8.52	20.81	0.20	568.97
Genotypic variance of offspring	112.74	0.96	8.68	21.20	0.19	671.22
Phenotypic Variance of Selected Plants	511.45	1.02	10.99	28.36	0.24	698.01
Phenotypic Variance of offspring	415.88	1.04	11.2	28.89	0.23	800.48
Realized Heritability	0.27	0.92	0.77	0.73	0.82	0.83
Genetic Advanced of Selected plants (%)	18.91	74.82	26.79	30.15	16.08	36.07
Genetic Advanced of offspring plants (%)	9.92	77.92	26.69	28.69	16.48	40.79
Genotypic Coefficient of Variation (Selected plants)	15.70	44.05	17.28	20	10	22.70
Genotypic Coefficient of Variation (offspring plants)	10.83	46.07	17.22	19.02	10.30	25.31
Phenotypic Coefficient of Variance (selected plants)	22.95	45.64	19.63	23.34	10.93	25.14
Phenotypic Coefficient of Variance(offspring plants)	20.8	47.95	19.57	22.21	11.33	27.64
Selection differential	-2.26	0.08	1.24	2.96	0.009	15.76
Response to selection from one cycle	-0.61	0.07	0.96	2.17	0.007	13.22
Inbreeding depression	2.76	0	-9.33	-21.91	6	-14.62

Dispersion of populations under investigation showed diversity depending on the relationship between the genotypes, distinguishing them into two different groups to the greatest extent compared to the other genotypes which were divided into smaller closer groups (Figure 1). The genotypes 4-1 and 9-2 represent the differences between the genetic genotypes in a clustered manner and include measurements up to 25 units. It is noted that the genotypes 4-1 and 9-2 distinguished themselves with the highest unit of measurement of differences, which indicates an increase in degrees of dissimilarity and differences from the rest of the other genotypes. Additionally, the connecting lines between the genotypes indicate the merging of two or more states within the same genetic dimension. The figure also shows the distribution of the genotypes into several main groups and secondary subgroups. It contained two main groups: the first included genotype 4-1, while the second included secondary and subordinate groups. The first subgroup included genotypes 9-2, and the second included several subordinate groups, including the sub-subgroup that contains genotypes 8-1 and 2-3, and other subordinate group that includes genotypes 2-1. Other genotypes were clustered into groups under another subcategory. From the above, we note that the genetic genotype 4-1 was distinguished by a special group, followed by genotype 9-2, and then genotypes 8-1 and 3-2 in the subcategory, and also genotype 2-1. This indicates the maximum degree of genetic differences for these genotypes and the low similarity with the other genotypes due to the differences in their genetic dimensions, in addition to the small number of groups that include more than one genotype. The increased branching of the secondary groups of other genotypes confirms the genetic relationship between them compared to the groups that include unique genotypes with maximum genetic dimensions. When comparing the averages of the groups in Table 5, we note that the sixth group, which included genotype 3-3 were characterized by the highest rate for the plant yield trait (143.97 gram.plant^{-1}) and the number of pods per plant (30.58 pods), followed by genotypes 3-4 and 1-2 within the seventh group, which gave 139.465 gram.plant^{-1} and a pod count of 28.26 pod.plant-1. These genotypes are promising in improving the yield of cotton, in addition to their importance as a source for transferring desirable traits of the yield and its components using hybridization programs. The fourth group, which included composition 2-1, had the highest average number of bolls (31.09 bolls.plant-1), while the highest average boll weight (5.21 grams) was found in compositions 4 and 8 within the eighth group. Furthermore, the highest average number of fruiting branches (22.7) was in the fifth group, which included compositions 4-7. From the above, it can be concluded that the progenies derived from 3 and 1 genotypes

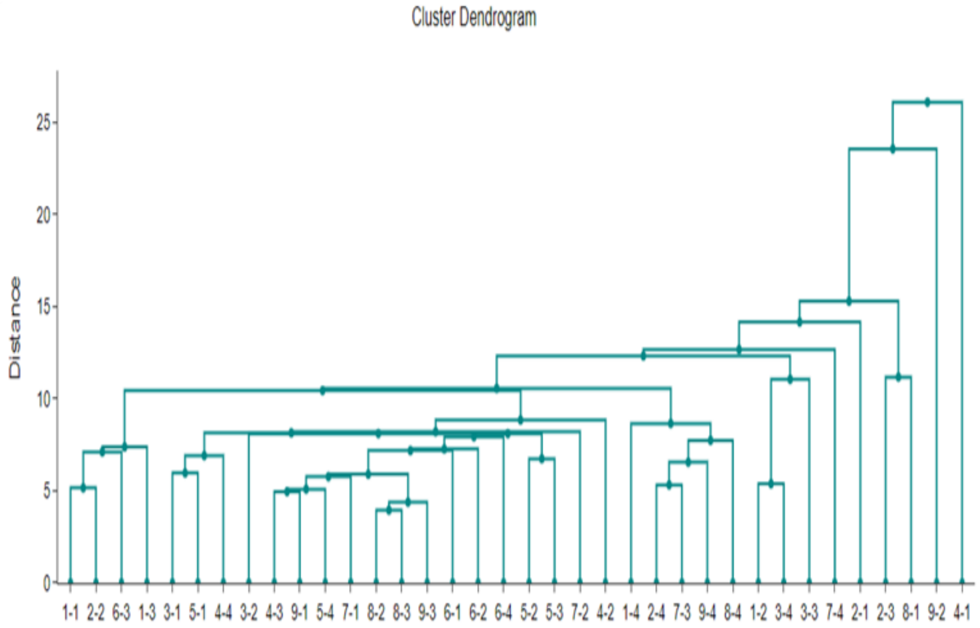

Figure 1. Dendrogram for the studied genotypes

showed good performance in some individuals, and they were distinguished by unique groups (1-2 and 3-4), followed by forth group (2-1) and six group (3-3) , each belonging to different groups with different genetic dimensions. They can be considered promising compositions for improving seed cotton yield through single plant selection in late generations (F4 and F5) which is more effective in identifying desired genotypes (21), as well as a source for transferring their good traits through hybridization.

Table 5. Mean of studied trait groups according to cluster analysis

Group number	*Genotypes*	*Traits*					
		Plant Height (cm)	Vegetative Branchs.Plant-1	Fruiting Branchs.Plant-1	Balls.Plant-1	Ball Weight (g)	plant yield
1	4,1	105.14	1.02	12.46	16.41	3.78	62.31
2	9,2	129.93	1.15	19.4	18.69	4.33	81.26
3	8,1+2,3	121.135	2.885	15.695	28.675	3.915	112.38
4	2,1	118.37	2.84	19.92	31.09	4.33	135.06
5	7,4	80.8	2.29	22.7	26.27	4.55	119.89
6	3,3	97.45	4.09	18.73	35.58	4.03	143.97
7	3,4+1,2	85.775	2.04	21.09	28.96	4.82	139.46
8	8,4	97.93	2.07	16.64	25.38	5.11	129.53
9	9,4	104.63	1.91	22.19	28.73	4.69	135.02
10	7,3+2,4	104.35	1.74	18.91	28.105	4.615	130.05
11	1,4	101.56	1.88	17.21	26.41	4.63	122.37
12	4,2	77.3	2.16	15.5	19.33	3.99	77.04
13	7,2	83.13	2.15	15.4	20.66	4.67	96.12
14	5,3+5,2	88.895	2.925	11.95	20.415	4.535	92.775
15	6,4	95.58	0.85	22.66	19.59	4.76	93.67
16	6,2	100.7	1.15	17.81	19.54	4.63	90.69
17	6,1	106.7	1.19	19.62	19.7	4.41	86.94
18	9,3	97.66	2.91	16.7	24.05	4.07	97.85
19	8,3+8,2	101.315	1.875	12.685	21	4.595	96.655
20	7,1	106.13	2.9	12.46	18.77	4.76	89.38
21	5,4	111.06	1.2	13.16	20.43	4.59	93.73
22	9,1+4,3	107.43	1.87	16.19	20.71	4.605	93.84
23	3,2	104.64	4.2	20.21	25.58	3.93	99.53
24	4,4	87.84	5.16	16.62	20.6	4.23	86.87

25	5,1+3,1	83.15	2.505	15.46	19.955	4.21	83.985
26	1,3	88.19	2.54	17.1	26.14	3.96	103.34
27	6,3	86.3	0.9	17.4	24.22	4.53	110.05
28	2,2+1,1	93.125	1.455	14.96	26.28	4.36	114.74

The results of divergence among cotton genotypes were in greater amount in inter-cluster than intra cluster refers to the wide range of dissimilarity of studied genotypes. The genotypes with different genetic dimensions indicate the presence of wide segregates that can be utilized to improve yield traits through selection and hybridization of superior genotypes. The genotypes with greater genetic dimensions within the same cluster or nearby clusters can lead to higher genetic improvement and selection yield (22).

4. CONCLUSION

The genetic dimension diagram of the selected genotypes shows their distribution into many different groups; however, the degree of variation was diverse depending on the relationship between the genotypes, which were distinctly separated into two different groups to a greater extent compared to the other genotypes, which were divided into smaller, closely related groups (Figure 1). The cluster analysis provided important information about the degree of similarity between the genotypes by estimating genetic dimensions, as it identified the superior genotypes within the same cluster, which are important for genetic improvement through hybridization followed by selection. It also highlighted the genetically distant genotypes, which serve as a source of beneficial variations.

Authors' contributions

D S M performed the experiment and wrote the manuscript.

Compliance with ethical standards

Conflict of interest

The author declares no conflict of interest.

Ethical issues: None

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