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Evaluation Maize Genotypes for Yield and Yield Components and Constructing Selection Index.

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ABSTRACT

This experiment was conducted at farm of field crops department, collage of agriculture, Duhok University in spring 2018 to construct selection index. The results showed that all selection indices include the yield gave relative efficiency equal to those when used the yield only, the increase in efficiency was very low and not important, selection index was a few relative efficiency as a compered with efficiency index which include the yield, therefore, the best selection index was depend on the yield only to select the better indices and some variance components to twenty maize genotypes according to Randomize Complete Block Design with three replication, also the result exhibited that the GCVwas medium for all characters except grain yield while, the PCV was high for grain yield, ear height and 300 grain weight and medium for the rest characters. The GAM gave high values for grain yield, plant and ear height and leaf area, the value range between 22-40 while the others characters showed medium values. On other hand the results showed high heritability broad sense ranged from %80 to %99 for all characters except 300- grain weight.

INTRODUCTION:

Maize is one of important cereal crops, which ranks third after wheat and rice of world. It's a multipurpose crop that provides food for humans, feed for animals especially poultry and livestock. Population improvements of a crop is the primary objective of a plant-breeding program. However, the progress in any breeding program depends a primary upon the genetic diversity and effectiveness of the selection procedure involved.

Corn breeder are generally interested improving more than a single trait at a time, or improving single trait without affecting the performance of others. When single trait selection is practiced and the correlation of that trait with others is high and unfavorable, undesirable correlated responses may occur for those traits not being considered in selection criteria. (Arshad *et al., 2004 and* Sarwat *et al.*,2004). Three methods have been used to simultaneously improve several traits: tandem selecting, independent culling and selecting index. The later, as indicated by Hazel and Lush, (1942) is the most efficient method for improving several quantitative traits simultaneously.

Several types of selection indices have been developed, the first one formally introduced, and probably the most widely known is the so called Smith-Hazel index (Simith,1936 and Hazel,1943), among others that followed are the base and weight-free indices. One of the requirements for using the Smith-Hazel index is estimation of phenotypic and genotypic variance and covariance (Lin,1978 and Baker 1974).Various studies have been carried out selection indices as an effective selection criterion in their programs on different crops (Hallauar et al,.1988); (Eta-Ndu and Openshaw, (1992);

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Rabiei *etal* (2004); Berrardo and YU, (2007); Muhammed and Syed, (2010) and Rafale *et al*., (2017). reported that selection index is procedure to provide a single criterion for selection among genotypes by including combination of several traits and also selection index is to find a linear combination of phenotypic value that maximizes the expected gain in aggregate genotype.

The objective of this study was construct several selection indices among seven traits of corn genotypes and to compare that efficiency with that form the direct selection for grain yield in order to find a simple and useful index to be used in the evolution of 20 in bread lines of corn.

Materials and Methods:

The genetic materials used in this experiment consisted of twenty maizes in bread lines of corn state in table (1). All in bread lines were planted using Randomized Complete Block Design (RCBD) with three replications. The experimental unit consisted of a single row plot of 3m length with plants spaced 0.25 m a part and having 0.75 m distance between rows. The genotypes were planted in 15th of March 2018. Filed was fertilized at planting time with (N.P.k; 27; 27; 0) with rate 400 kg.ha and 200kg.ha of urea (46% N) were added. Weed control and other managements were performed according to plant requirements. Yield traits measured on plot mean (ten plants from each plot) basis were plant height, ear height cm, number of row ear^{-1}, number of grain row^{-1}, 300-grain weight (g), grain yield plant^{-1} (g) and leaf area cm^{2}.

Table 1. Pedigree for maize genotypes using in this study.

No.	Genotype	Source
1	L-831	College of Agriculture / Salhadean University
2	L- 3007	College of Agriculture / Salhadean University
3	L-MSL.4279	College of Agriculture / Salhadean University
4	L-232DSS	College of Agriculture / Salhadean University
5	L-KR640	College of Agriculture / Salhadean University
6	L-PIO375	College of Agriculture / Salhadean University
7	L-538	College of Agriculture / Salhadean University
8	ZP.670	College of Agriculture / Duhok University
9	Ir-F_3	College of Agriculture / Duhok University
10	Max-1	College of Agriculture / Duhok University
11	ZP 607	College of Agriculture / Duhok University
12	Pon-1	College of Agriculture / Duhok University
13	ZP- 197	College of Agriculture / Duhok University
14	ZP-707	College of Agriculture / Duhok University
15	DK- F_1	Central of Agriculture Research Salhadean
16	ZP- 505	Central of Agriculture Research Salhadean
17	Sym-5	College of Agriculture / Duhok
18	DK- F_2	Central of Agriculture Research Salhadean
19	Un44052	Centeral of Agriculture Salhadean
20	Agr-5	Central of Agriculture Research Salhadean

Analysis of variance and covariance for all traits by following the procedures described by (Gomez and Gomez,1984) and estimates of phenotypic and genotypic variance (VP and VG) and covariance (VP co P x y) and (VG co G x y) were obtained by using expected mean square form analysis of variance and covariance, the following estimators were calculated:

1. Broad sense heritability (H^2) from the ratio of VG/VP
2. Expected genetic advance GA:

GA= K(H^2) ($\sqrt{VP}$) where k= Selection intensity = 1.76 at 10% selected

($\sqrt{VP}$) = phenotypic standard deviation. The expected genetic advances as percent of trait mean y^{-} estimated from equation.

$GA = \frac{GA}{Y_{..}}$X 100).(Assefa *et al.*, (2011).

3. The method of constructing the selection indicates were those as outlined by Miller *et al.*, (1958) which maximize yield the selection index will be of the form
$1= b_1x1 + b_2\ x_2....+bnxn$ where x_1, x_2... x_n are the phenotypic values of the traits and b_1, b_2....b_n are the relative weights to be applied to each trait, and (b) values obtained from metrix notation as follows $b= p^{-1}g$, where p^{-1} The inverse of the phenotypic variance- covariance matrix, $g(g_1y,g\ 2\ y.....gny)$: the genotypic covariance of each of the observed characters with yield. The expected genetic advance when selection is based on the selection indices

$GA= K\sqrt{b1}\ \ cov\ g_1y + b_2\ cov\ g_2y + ...+bngy$

4. Selection indices values from each genotype is each replicate were estimated using the more efficient selection index, then analysis variance carried out from these values, and comparison between the genotypes means by Dancans Multiple Range Test (DMRT).

RESULTS AND DISCUSSIONS

Table 2. Exhibited the analysis of variance for seven traits of inbreed lines of maize according to randomize complete blocks design method, it was shown that genotypes mean square was highly significant differences among maize genotypes for plant and ear height, leaf area, number of rows ear^{-1}, number of grain row^{-1} and grain yield plant $^{-1}$ except 300-grain weight.

Table 2: Analysis of variance for characters maize genotypes.

S.O.V.	d.f	Ms						
		Characters						
		Plant height cm	Ear height cm	Leaf area cm^2	No. of rows ear^{-1}.	N0. of grains row^{-1}	300 grain weight g.	Grain weight $plan^{t-1}$ g.
Replications	2	3.10	9.11	969.57	0.45	0.80	1446648.66	85.85
Genotypes	19	2859.21 **	875.42 **	28297.48 **	8.00 **	76.68 **	1467055.63	3092.70 **
Error	38	65.58	22.36	1670.83	0.69	18.25	1461398.81	40.27
Total	59							

*** , **significant difference at level 0.05 and 0.01 respectively.**

The result in Table 3. revealed the mean performance of twenty genotypes, the Tallest plant among all genotypes was noticed in genotypes 2 ,17,18 and 20 with value range 200 to 208.33 cm, while the shortest plant with 113.33cm was recorded by genotypes (7). For ear height the maximum value exhibited by genotype 17 with value 105 cm Also, in the same table, the largest leaf area was exhibited in genotypes 12 with 849.87 cm^2 while genotype 7 had the smallest value with value 486.10 cm^2. Regarding to number rows ear^{-1} and number of kernels row^{-1}, genotypes 11, 16, gave the highest value range-between 16 to 16.67 respectively, and 42.33 for number of kernels row^{-1} whereas, the genotype (5) and (10) gave the minimum value with 26.33 and 25 respectively. Concerning to yield $plant^{-1}$, for grain weight plant $^{-1}$ the genotypes 16 had the highest value with 198.75g, the genotype 14 gave the lowest value with 90.73g. from the result above the genotype (16) was superior comparison with other genotypes because it gaves the highest yield components (number of rows ear^{-1} and number of kernels row^1).

Table 3. Means studied characters of maize genotypes.

Genotypes	Characters Mean						
	Plant height cm	**Ear height cm**	**Leaf area cm^2**	**No. of rows ear^{-1}.**	**N0. of grains row^{-1}**	**300 grain weight g.**	**Grain weight plant^{-1} g.**
1	161.00 e	90.00 edc	655.83egf	12.67 d e	27.00 e fd	105.50 b	124.02 i h
2	208.33 a	105.00 a	685.60efd	14.00 d c	30.33 e fdc	87.80 b	117.57 ih j
3	123.33 g f	94.67 bdc	813.70 b a	14.00 d c	34.33 e dc	85.20 b	138.92 g
4	135.00 f	70.00 h i	655.87egf	12.33 e	27.00 e f d	81.00 b	95.25 k
5	161.33 e	71.67hg i	611.17 g f	12.00 e	26.33 e f	101.70 b	111.69 j
6	162.67 e	71.67hg i	627.03 g f	15.00 b c	26.33 e f	100.20 b	112.93 i j
7	113.33 g	43.00 j	486.10 h	14.67 b c	36.00 b c	88.00 b	170.45 c d
8	116.00 g	48.33 j	493.63 h	14.00 d c	34.00 e d c	75.50 b	113.28 i j
9	178.33c b d	93.00 d c	771.33b c	12.67 d e	31.33e fdc	90.80 b	126.62 h
10	181.67c b	86.67 edf	814.47 b a	14.00 d c	25.00 f	88.40 b	124.67 i h
11	184.00 b	79.00 g f	742.03bcd	16. a	42.33 b a	90.20 b	176.41 c b
12	163.67 e d	71.67hg i	849.87 a	16.67 a	33.00 ef d c	96.80 b	170.26 c d
13	168.33c e d	81.67 e f	741.00bcd	14.67 b c	29.33 e f dc	54.40 b	93.41 k
14	208.33 a	102.33 ba	719.47ecd	16.00 b a	34.00 e d c	48.60 b	90.73 k
15	165.00 e d	86.67 edf	684.07efd	16.00 b a	34.00 e dc	64.80 b	116.08i h j
16	120.00 g	65.00 i	599.13 g	16.67 a	43.67 a	81.10 b	198.75 a
17	201.67 a	105.00 a	649.00egf	16.67 a	37.67 b a c	112.32 a	184.77 b
18	208.33 a	98.33 bac	656.03egf	16.67 a	35.00 b d c	88.30 b	159.88 e d
19	173.67cebd	81.67 e f	770.20 b c	16.67 a	32.67e f d c	86.60 b	148.11 g f
20	200.00 a	78.33 hgf	670.17egfd	16.00 b a	32.67e f d c	86.90 b	153.23 e f

Means bearing different letters within each column differ significantly at 0.05 level.

The combine analysis for character of maize genotypes was presented in Table 4. In this table used seven characters in selection index in all possibility. The results were significant for all studied characters amount genotypes except (1x5), (2x5) (3x5) (4x5), (5x6) and (5x7). From the result above, the selection index for genotypes was low efficiency and effected on the other genotypes in the same table. Similar results were recorded by Hallaur etal., (1988), Berhardo and Yu.(2007) and Arshad. *et al* (2001).

Table 4. Combine analysis of characters' maize genotypes.

		M S						
S.O.V	d.f	1x2	1x3	1x4	1x5	1x6	1x7	2x3
Rep.	2	318.74	39.28	1511.86	1448429.7	93.30	70.13	16.40
Treat.	19	5687.65**	3548.18**	30512.8 **	1518952.1	3292.31**	3888.73**	6064.12**
Error	38	112.05	56.01	1723.01	1463541.4	43.83	68.91	87.37
Total	59							

*** , **significant difference at 0.05 and 0.01 level respectively.**

The predicted advance in yield from selection based on the various selection index and genetic efficiency over direct selection for yield for six of these tested indices are presented in Table 5. The predicted genetic advance in yield for indices at 10% selection intensity range from 0.0 to 55.07554 as compared with a predicted advance of 55.07554 from direct selection yield. The predicted selection gain in efficiency from use of the indices ranged from 100.0261 grain yield to 4.613442. All the indices tested excluded the yield had a relative efficiency more than the results in the same table indicate that all selection indices include the yield trail gave 100% efficiency equal to those when used the yield only, the increase in efficiency was very low and not important, while the selection index which was with no grain yield few relative efficiency as compared with efficiency index which include the yield, there for the better selection indices depend on the yield only to select the better genotypes and the indices was L_1=09619(grain yield). These results were in agreement with the result obtained by Eta-Ndu. and Openshaw. 1992. and Rabie *et al* .,2004.

Table (5) Predicted index, genetic advance and efficiency for characters' maize genotypes.

index	GA	efficiency	index	GA	efficiency	index	GA	efficiency	index	GA	efficiency
1	55.0611	100%	1234	55.0636	100.0045	123	55.0628	100.003	12	55.0617	100.0011
2	2.46841	4.483031	1235	55.0725	100.0205	124	55.0619	100.0013	13	55.0612	100.0001
3	9.66265	17.54893	1236	55.0629	100.0032	125	55.0725	100.0206	14	55.0615	100.0006
4	2.54021	4.613442	1237	55.0631	100.0035	126	55.0619	100.0014	15	55.0716	100.0189
5	11.3247	20.56761	1245	55.0742	100.0236	127	55.0621	100.0017	16	55.0618	100.0012
6	31.2852	56.81908	1246	55.0620	100.0015	134	55.0619	100.0012	17	55.0615	100.0005
7	33.8546	61.48541	1247	55.0623	100.002	135	55.0722	100.02	23	7.7061	13.99552
1234567	55.0753	100.0258	1256	55.0730	100.0214	136	55.0617	100.0009	24	3.07071	5.576897
123456	55.0747	100.0246	1257	55.0729	100.0213	137	55.0615	100.0005	25	14.5167	26.36467
123457	55.0755	100.0261	1267	55.0622	100.0018	145	55.0722	100.02	26	33.4301	60.71443
123467	55.0641	100.0053	1345	55.0741	100.0235	146	55.0618	100.0011	27	33.8995	61.56692
123567	55.0731	100.0218	1346	55.0622	100.0018	147	55.0620	100.0014	34	7.05644	12.81563
134567	55.0751	100.0254	1347	55.0623	100.0021	156	55.0716	100.019	35	0	0
124567	55.0749	100.025	1356	55.0722	100.0199	157	55.0719	100.0195	36	0	0
234567	39.6309	71.97618	1357	55.0724	100.0204	167	55.0618	100.0011	37	34.0374	61.81743
12345	55.0746	100.0244	1367	55.0619	100.0012	234	7.87581	14.30373	45	11.4677	20.82727
12346	55.0636	100.0045	1456	55.0721	100.0198	235	14.8094	26.89619	46	32.3609	58.77265
12347	55.0641	100.0053	1457	55.0727	100.0209	236	33.5409	60.91566	47	33.9541	61.66608
12356	55.0728	100.0212	1467	55.0621	100.0016	237	34.0535	61.84663	56	31.5988	57.38859
12357	55.0729	100.0213	1567	55.0720	100.0196	245	14.6759	26.65386	57	34.6490	62.92814
12367	55.0631	100.0035	2345	15.2457	27.68863	246	6.08135	11.04472	67	37.6490	68.37662
12456	55.0744	100.0241	2346	33.8049	61.39519	247	34.0662	61.86968			
12457	55.0750	100.025	2347	34.4677	62.59885	256	35.1695	63.87339			
12467	55.0623	100.0021	2356	35.1713	63.87679	257	35.1884	63.90775			
12567	55.0733	100.022	2357	12.2987	22.3364	267	38.5745	70.05748			
13456	55.0743	100.0237	2367	27.1983	49.39641	345	14.6796	26.66048			
13457	55.0749	100.0248	2456	13.8527	25.15879	346	33.0970	60.10954			
13467	55.0625	100.0024	2457	12.7111	23.08543	347	34.4392	62.54705			
13567	55.0749	100.0248	2467	27.1648	49.33562	356	33.4244	60.70417			
14567	55.0728	100.0211	2567	29.1652	52.96869	357	34.9730	63.51653			
23456	35.2714	64.05855	3456	12.0444	21.87454	367	38.3445	69.63976			
23457	35.8158	65.04718	3457	12.5466	22.78672	456	32.5470	59.11067			
23467	38.6099	70.12175	3467	26.3367	47.83168	457	34.7758	63.15837			
23567	39.5937	71.90862	3567	27.1088	49.23395	467	37.8476	68.7374			
24567	39.6283	71.97138	4567	25.6507	46.58581	567	38.0072	69.02719			
34567	38.7476	70.37187									

Table 6. Show the estimation of variance components (genetic, environmental and phenotype) , heritability and genetic advance to the characters used as criterion of selection. The Gcv was medium for all characters except green yield while the Pcv was high for grain yield ear height and 300- grain weight and medium for the rest trait, the results exhibited that the genetic advance as mean gave high values for grain weight plant^{-1}, plant and ear height and leaf area and the value ranged between 22 to 40. While , the rest characters have medium values. For broad sense heritability, the same table show high broad sense heritability and ranged from 80% to 99% for all characters except 300 kernel weight and VG, Genetic variance, VE, Environment variance, VP, Phenotypic variance, GCV, Genetic coefficient variance, PCV, Phenotypic coefficient variance, GAM, Genetic advance as mean, H, Heritability, GA, Genetic advance.

Table (6). Variance component, heritability and genetic advance for characters maize genotypes.

Characters	VG	VE	VP	GCV%	PCV	H%	GA	GAM%
plant height	929.54	65.59	995.13	18	19	98	51.63	31
Ear height	284.35	22.36	306.71	21	22	93	28.35	35
Leaf area	8875.55	1670.83	10546.38	14	15	92	151.82	22
300 g wt.	1885.6	1461398.81	1463284.4	18	502	84	0.00	0.00
No. row ear	2.43	0.69	3.12	10	12	0.092	2.39	16
No. grain row	19.47	18.25	37.72	13.5	19	77	5.15	16
gr. Wt. plant	1017.47	40.27	1057.74	23	24	61	54.95	40

The analysis of variance to test the significant of selection indices values differences among genotypes was presented in Table (7). Depending on superior selection index (I 123457), index value for each genotype was estimated in each replicate, and then the data of all genotypes analyzed using randomized complete block design, same table was showed from F-test that genotypes mean square was highly significant this main significant differences is selection index means values among genotypes.. Table 8. Analysis of variance to test significant of selection indices.

Table (7) analysis variance to test significant of selection indices differences values among genotypes.

Source	Df	Sum of square	Mean square	F value	Pr. > F
Replication	2	158.88162	79.44081	2.13	0.1326
Genotype	19	54369.01308	2861.52700	76.79	< .0001
Error	38	1415.99575	37.26305		
Total	59	55943.89045			

The results in Table 8. showed the difference between all genotypes using Duncan's Multiple Rang- Test and also the same table exhibited that the highest mean selection index was 191.174 for genotypes with ZP-505 significant difference over all other genotypes, followed by symams and ZP-607 while ZP-707 and ZP-197 in this study located at the seqeueuel 20 and 19 respectively.

Table 8. Analysis variance of index for each genotype

Genotypes	Mean	Genotypes	Mean
1	119.292 ih	11	169.686 cb
2	113.087 ihj	12	163.770 cd
3	133.627 g	13	89.854 k
4	91.621 k	14	87.276 k
5	107.438 j	15	111.657 ihj
6	108.631 ij	16	191.174 a
7	163.956 cd	17	177.727 b
8	108.961 ij	18	153.789 ed
9	121.793 h	19	142.467 gf
10	119.923 ih	20	147.389 ef

Finally it was concluded from this study that the better the genotypes respectively ZP-607,ZP-568 and symami and the surpassed 20 genotypes that these genotypes could be used in breeding programs to improve yield at maize genotypes and develop new hybrid with good productivity and good quality performance to Iraqi environments.

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تقيم تراكيب وراثية من الذرة الصفراء من خلال تقنية دليل الانتخاب

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جامعة دهوك – كلية علوم الهندسة الزراعية

المستخلص

طبقت التجربة في حقل قسم المحاصيل الحقلية في كلية الزراعة جامعة دهوك لموسم الربيعي لعام 2018 لأنشاء ادلة انتخاب مختلفة, اظهرت النتائج ان جميع ادلة الانتخاب التي اشتملت على الحاصل اعطت كفاءة نسبية مساوية لو استخدم دليل الحاصل لوحده وكانت قيمة الكفاءة لهذه الادلة لوحدها واطئة و غير مهمة بالمقارنة عند استخدام هذه الادلة مع الحاصل و لذا يعتبر دليل الحاصل افضل مؤشر يمكن الاعتماد عليه في عملية الانتخاب كما اظهرت النتائج ان قيمة معامل التباين الوراثي كان عاليا لجميع الصفات ما عدا حاصل الحبوب في حين كان معامل التباين عاليا لحاصل الحبوب و ارتفاع النبات و وزن 300 حبة و متوسطا لبقية الصفات الاخرى. أما التحصيل ألوراثي منسوبا الى المتوسط الحسابي فهو لأخر كان عاليا للحاصل وارتفاع النبات والعرنوص والمساحة الورقية وتراوحت قيمته بين 22–40% في حين أظهرت الصفات الأخرى قيم متوسطة كما كانت نسبة التوريث بالمعنى الواسع عالية وتراوحت قيمها بين 80–99% لجميع الصفات بأستثناء وزن 300 حبة.

الكلمات المفتاحية: تقييم، تراكيب وراثية، الذرة الصفراء، دليل الانتخاب.