

EVALUATION OF BREAD WHEAT GENOTYPES USING SELECTION INDEX

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ABSTRACT

Experiment was carried out at farm of Field Crop Department, College of Agriculture, University of Duhok. Twelve genotypes of bread wheat were sowing in 25/11/2017 to construct selection indices using Randomize Complete Block Design (RCBD) with three replications.

The experiment included six traits studied were plant height (cm), flag leaf area (cm²), No. of grains spike⁻¹, weight of seed spike⁻¹, 1000-grain weight (gm) and grain yield row⁻¹ (gm). The results showed the analysis of variance for six traits was highly significant for plant height, No. of grain spike⁻¹, weight of grains spike, 1000-grain weight and non-significant for flag leaf area. Although the results revealed the combined analysis were highly significant difference for all traits except No. of grain spike⁻¹ and weight of grain spike⁻¹. Also, the results exhibited the best selection index was (L146) which include the traits (grain yield, plant height, 1000-grain weight) and giving relative efficiency 7-29%. Of selection of yield alone. The GCV was medium for all traits and low for flag leaf area while, the PCV was medium for plant height, weight grain spike⁻¹, No. of grain spike⁻¹ and 1000-grain weight, whereas, high for grain yield and low for flag leaf area. Concurring the genetic advance as mean (GAM) the results showed the high value for number of grain spike⁻¹ and weight of grain spike⁻¹ and medium for plant height, 1000-grain weight, grain yield and low for flag leaf area, the value ranged between 5.07 to 20.47%. The heritability was high for all traits and medium for flag leaf area. The results indicated highly significant difference between the wheat genotype in the value of selection index for these which computed depend on the better selection index, grain yield, plant height and 1000-grain weight.

Form this study that the better for genotypes was Abu- graib-1, Research-4, IPA-99 and Sham-6, over all genotypes and could be used this genotypes in breeding program to improve yield of wheat and develop new variety with good productivity and good quality performance to Kurdistan and Iraqi environments.

KEY WORD. Wheat genotypes, yield, yield components, selection index.

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INTRODUCTION

Index selection is one of the fundamentals method for the genetic improvement of traits in crop plants. A theory, which introduced independently by Smith 1936 in plant and Hazel index and has be demonstrated to be more reliable than independent culling level (ICI) and tandem selection(TS) methods in terms of maximizing genetic gain in a crop population. Hazel and Lush,(1942); Cotterill, (1985) and Costal *et al.*,(2008) reported that this approaches the most effective as compared with (ICI) and tandem (TC) selection methods for independent traits while, having at least the same efficiency in the case of correlated traits. Smith(1936) indicated

that the mainly due to their advantage of talking in to account of heritability, the interrelation ship of traits using genetic and phenotypic correlation and the economic values of traits selection for an index which give proper weight to each traits is more efficient than selection for one traits or for several traits independently. Hazel 1943 in animals and Lemer *et al.*, (1947) reported that the method for estimating optimum relative weight for different selection projects, while, Robinson *et. al.*,(1951) have given procedures for estimating genotypic and phenotypic covariance required for construction of a selection index.

Several researchers have been carried the selection indexes in wheat and some other self-fertilized crops has been given by (Pesek and Baker, 1969; Singh *et al.*, 1979; Bhathagar *et al.*,

1982; Wells and Kofoid,1986; Ali,1995; Ahmad and Hamdoo, 2000; Al Guborly *et al* , 2006; Dawod *et al.*, (2010). The objective of this study to construct several selection indices among six traits of wheat and to compare their efficiency with that from direct selection from grain yield and yield components in order to find a simple and useful index to be used in the evolution of twelve wheat genotypes.

MATERIALS AND METHODS

The genetic material used in this study were twelve genotypes of bread wheat Table 1. The all genotypes were planting in 25/11/2017 at the field of College of Agriculture , Duhok University, using Randomized Complete Block Design (RCBD) with three replications, each plot contained three rows, 3 meter long and 0.25 m apart with seeding rate 140 kg/ha⁻¹ .

Table (1): Genotypes using in the experiment

No	Name	Source
1.	Resarch-4	Central of Agriculture Research Duhok
2.	Abu-garib-1	Central of Agriculture Research Abu-graib
3.	IPA-99	IPA
4.	Sham-6	Central of Agriculture Research Duhok
5.	TAWAHI-3	International center of Agriculture Research in Dry Area
6.	Makipak	Central of Agriculture Research Duhok
7.	BABAGA-3	Internal center of Agriculture Research in Dry Area
8.	D-7	Central of Agriculture Research Abu-graib
9.	Azadi	Central of Agriculture Recearch.
10.	IPA-95	IPA
11.	SETTAR-85	Internatioal center of Agriculture Research in Dry Area
12.	Tamoze-2	Central of Agriculture Research Duhok

The field plants was irrigated after planting by sprinkler for about six hours only and then depended upon natural precipitation (the amount

of rain for seven months (December /2017, January, February, march, April, and may/ 2018) were in Table 2.

Table (2): The rainfall for seven month 2017-2018.

Date	Month	Heat		Humidity	Rain
		max.	min.		
2017	November	20.76	7.92	62.37	27.8
	December	56.29	4.835	61.17	9.4
2018	January	13.86	4.158	70.85	73.6
	February	16.2	5.525	74.32	66.4
	March	22.63	9.871	59.01	16
	April	26.47	11.78	55.4	103.5
	May	30.93	17.55	52.6	85.6

Abu- graib-1, Research-4, IPA-99 and Sham-

Fertilizer were applied at rate of 400 kg/ha-1 of Npk (18.30,0 before planting and nitrogen as area at the rate of 200 kg/h. applied at tiller stage and herbicide (pallas) used to control narrow and broad leave weeds at rate of 450 to 500 ml/ha at the stage of 3-4 Leaves. The studied traits were plant height cm, Leaf area cm², number of grains spike-1, spike seed weight, 1000 - grain weight and grain yield. Analysis of variance was carried out according to (Gomez and Gomez, 1984) the estimates of phenotypic and genotypic variances (VP and VG) were obtained by using expected mean square form analysis of variance, the following estimators were calculated.

1. Broad sense heritability (H²) from the ratio of VG and VP

2. Expected genetic advance GA:

$$GA = K(H^2) (\sqrt{VP}) \text{ where } k =$$

Selection differential in standard units and equal 1.75 for 10% selected

(\sqrt{VP}) = phenotypic standard deviation and expected genetic advances as

percent of trait mean $y..$ estimated from equation,

$$GA = (GA)/(Y..) \times 100 \text{ (Assefa et al., 2011).}$$

3. The method of constructing the selection indices were those as outlined by Miller et al.,

1958 which maximize yield the selection index will be of the form

$I = b_1x_1 + b_2x_2 + \dots + b_nx_n$ where x_1, x_2, \dots, x_n are the phenotypic values of the traits and b_1, b_2, \dots, b_n are the relative weights to be applied to each trait, and (b) values obtained from matrix notation as follows $b = p^{-1}g$, where p^{-1} The inverse of the phenotypic variance-covariance matrix, $g(g_1y, g_2y, \dots, g_ny)$ the genotypic covariance of each of the observed characters with yield. The expected genetic advance when selection is based on the selection indices

$$GA = K \sqrt{b_1 \text{ cov } g_1y + b_2 \text{ cov } g_2y + \dots + b_ny}$$

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 3. Showed the analysis of variance for six characters of broad wheat genotypes according to Randomized Complete Block Design method. It was revealed that genotypes mean square was highly significant for all characters except flag leaf area.

Table (3): Analysis of variance for characters of bread wheat genotypes.

S.O.V.	d.f	M.S.					
		Characters					
		Plant height cm	Flag leaf area cm ²	No. grains spike -1	weight of grain spike - 1g	1000 grain weight g	Grain yield row- 1 (g)
Replications	2	9.41	21.63	49.95	0.03	13.19	3498.18
Genotypes	11	202.56 **	25.72ns	173.00 **	0.33 **	83.36 **	6633.61 **
Error	22	19.91	9.45	14.70	0.04	8.70	1874.56
Total	35						

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

The mean performance of genotypes for all characters was presented in Table 4. For plant height the results in the same table exhibited, the highest value was recorded by genotypes 9 which were (87.43 cm) and the lowest value was (57.81 cm) was obtained by genotype 3. For flag leaf area, the genotypes (1) had the largest leaf area (53.28cm²) while, the smallest value (44.17 cm²) recorded by genotype 5. Also, in the same table the maximum number of grain spike-1 (66.88) was noticed in genotypes 12 whereas, the genotypes 5

gave the minimum number of grain spike-1 which was 47.46. Regarding to weight of grain spike, genotype 12 showed highest value (2.78) while the genotype 9 had the lowest value (1.63). For 1000-grain weight, the genotypes 7 recorded the maximum value (52.33g) while, the genotypes 3 exhibited the minimum value (34.07g). In traits grain yield row the genotypes (1) and (2) was superiority over all genotypes giving 302.60 gm and 299.33 g respectively while, the genotype 12 gave the lowest value 168.13g. From the results

above the genotype (1) had maximum leaf area and the flag leaf plays a very important role in grain filling in small grain crops such as wheat because of its position on the column. It is the top most leaf and as such it intercepts quite a lot of radiation. Assimilation translocation from the flag leaf (source) to the panicle (reproduction sink) is

enhanced by proximity of the flag leaf to the sink. When the flag leaf of a small grain cereal crop is lost or destroyed, grain yield is lost as a result. Many researchers pointed to some results such as Bhatthagar *et. al.*, 1982 and wells and Kofoid, 1986.

Table (4): Means for characters of bread wheat genotypes.

Genotypes	Mean					
	Characters					
	Plant height cm	Flag leaf area cm ²	No. grains spike -1	weight of grain spike -1g	1000 grain weight g	Grain yield row-1
1.	70.10 cd	53.28 a	55.70 bcd	2.31 bcd	41.55 c	302.60 a
2.	75.60 bc	48.97 abc	62.57 ab	2.18 cde	34.89 de	299.33 a
3.	57.81 e	50.21 ab	57.32 bc	1.94 def	34.07 e	250.23 abcd
4.	69.00 cd	47.40 abc	47.58 e	1.80 ef	37.76 cde	253.23 abc
5.	68.83 cd	44.17 c	47.46 e	2.24 bcd	47.26 b	223.00 abcd
6.	81.36 ab	52.25 a	54.86 cd	2.38 abc	43.39 bc	170.00 d
7.	72.05 cd	47.88 abc	50.12 de	2.62 ab	52.33 a	223.53 abcd
8.	63.58 de	49.21 abc	61.03 abc	2.44 abc	40.04 cd	268.53 ab
9.	87.43 a	49.12 abc	40.23 f	1.63 f	40.68 c	172.23 cd
10.	76.55 bc	45.92 bc	60.30 abc	2.12 cde	35.18 de	258.17 ab
11.	63.50 de	45.14 bc	58.53 bc	2.45 abc	42.03 bc	212.50 bcd
12.	63.50 de	44.45 bc	66.88 a	2.78 a	41.69 c	168.13 d

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

Table 5. Showed the combine analysis for characters of bread wheat genotypes. In this table used six characters in selection index in all possibility. The results in the same table exhibited highly significant difference for all characters except traits (No. of grain spike-1 and weight of grain spike-1) when using traits or more

characters. To constructed of selection index, the results exhibited, the choice of different Striates was necessary to pick the index having fewer traits with better grain. Similar results were obtained by other researchers Alguborly *et al.*, 2006, Dawod *et al.*, 2010, Zine *et al.*, 2018.

Table (5): Combined analysis for characters of bread wheat genotypes

S.O.V	d.f	M S							
		Characters							
		1x2	1x3	1x4	1x5	1x6	2x3	2x4	2x5
Rep.	2	54.57	23.39	22.17	58.10	3210.66	102.73	52.21	18.02
Genotype	11	185.92**	259.97**	24.81*	94.80**	6899.77**	208.50**	182.66**	168.84**
Error	22	21.56	41.38	9.52	20.71	1974.30	52.19	16.09	26.06
Total	35								

2x6	3x4	3x5	3x6	4x5	4x6	5x6
4367.79	10.40	2.91	3851.54	12.56	3511.98	3087.30
7336.59**	197.54**	314.03**	6092.67ns	89.05**	6620.77**	6117.29*
2001.78	20.88	31.61	2096.19	9.63	1882.44	1957.82

based on the various selection index and genetic efficiencies over direct selection for yield and six of these tested indices are presented in Table 6. The predictive genetic advanced in yield 4 indices at 10% selection intensity range from 7.892 to 32.5 as compared with a predictive advanced of 7.89 for direct selection on yield. The predicted selection grain in efficiency from use of the indices range from 25.63089 to 107.2943 for flag leaf area and leaf area with 1000- grain weight. From the results in the same table, the best selection index was L1.46 (which include the

grain weight, giving relative efficiency of 7.29% of the selection of yield alone. Therefore, this index was adopted in the differentiation between wheat genotypes.

[L146 = 0.168 (grain yield)- 0.2569 (plant height-399) (1000- grain weight)] and followed in importance the index L 2345, L 2345, L 345, L 465, L 2346, L 346 and L 1245, the indices and at last, it is noted that all the indices which empty of the yield trait were less efficient than the selection for a yield alone

Index	GA	Efficiency	Index	GA	efficiency	Index	GA	efficiency
I1	30.79471	100%	I123	30.81365	100.0615	I12	31.18572	101.2697
I123456	32.91425	106.8828	I124	31.48977	102.2571	I13	30.80007	100.0174
I12345	32.63007	105.96	I125	31.13849	101.1164	I14	31.4603	102.1614
I12346	32.54803	105.6936	I126	31.43497	102.0791	I15	31.08497	100.9426
I12356	31.48626	102.2457	I134	31.54546	102.0962	I16	31.40722	101.989
I12456	32.59656	105.8512	I135	31.45057	102.1298	I23	24.4456	79.38247
I13456	32.7873	106.4706	I136	31.43683	102.0852	I24	22.85758	74.22567
I23456	30.77444	99.93418	I145	32.45211	105.3821	I25	10.12143	32.86743
I1234	31.57122	102.5216	I146	33.04096	107.2943	I26	18.2465	59.25206
I1235	31.48569	102.2438	I156	31.44022	102.0962	I34	17.08294	55.47362
I1236	31.47936	102.2233	I234	20.74147	67.354	I35	19.8848	64.57213
I1345	32.61084	105.8975	I235	20.49438	66.55163	I36	19.03958	61.82744
I1346	32.53676	105.657	I236	19.67885	63.90335	I45	23.70674	76.98316
I1456	32.58062	105.7994	I245	25.40645	82.50264	I46	24.28784	78.87017
I2345	27.20532	88.34413	I246	25.72787	83.54639	I56	19.00968	61.73034
I2346	26.43373	85.83854	I256	19.60678	63.66931			
I2456	26.7544	86.87986	I345	26.0057	84.4486			
I1245	32.46946	105.4384	I346	25.19878	81.82828			
I1246	32.15719	104.4244	I356	22.66044	73.5855			
I1256	31.48135	102.2297	I456	25.53236	82.91151			
I1356	31.4584	102.1552						
I2356	23.63642	76.75481						
I3456	28.95658	94.03102						
I2	7.892958	25.63089						
I3	8.149872	26.46517						
I4	17.08218	55.47115						
I5	9.411918	30.56342						
I6	19.00888	61.72774						

characters, and low for flag leaf area. While, the pcv was medium for plant hight, weight of grain spike-1 , number of grain spike-1 and 1000- grain weight whereas, was high for grain yield and low for flag leaf area.

Regarding to heritability was high for all characters and medium for flag leaf area and grain yield. The results in the same table showed GAMY. Was high for weight grain spike-1 and number of grain spike-1 and medium for plant height, 1000-grain weight and grain yield and low

for flag leaf area. The weight grain spike-1 and number of grain spike-1 exhibited high broad sense heritability and associated with high genetic advance as mean. From this results can be useful of these characters to improving the yield in bread wheat after putting in program of wheat breeding. These results was in agreement with obtained by Robinson *et al.* 1951; Johansson *et al.*, 1955, Sarwar *et al.*2004, Al-Gubory *et al.*, 2006, Hussin *et al.* 2010, Dawood *et al.*, 2015 and Sebastia *et al.*, 2019

Table (7): Variance components, heritability and genetic advance for characters bread wheat genotype

Character	VG	VE	VP	GcV%	PCV	H%	GA	GAM%
Plant height	60.8	19.91	80.75	10.97	12.64	75.0	11.85	16.67%
Flag leaf area	5.42	9.45	14.87	4.83	8.00	36	2.44	5.07%
Weight of grain gm	0.095	0.048	0.143	13.75	16.88	66	0.43	0.91%
Number of grain	53.1	14.70	67.80	13.19	14.19	78	11.30	20.47%
1000-grain wt.grain	27.88	9.70	37.58	12.90	14.98	74	7.98	19.52%
Grain yield	1586.35	1874.56	3460.91	17.06	25.20	45	46.59	19.95%

VG- Variance genotypes, VE- Variance environment, VP- Variance of phenotypic, GcV- Genotypic coefficient variance, PCV- Phenotypic coefficient variance, H- Heritability broad sense, GA- Genetic advance, GAM- Genetic advance as mean.

The results in Table 8 and 9. revealed the analysis of variance between the wheat genotypes, the results showed highly significant between the genotypes in the values of selection index for these

which computed depend on the better selection index which consist yield, plant height and 1000-grain weight. From the results of comparison between the means of genotypes, the highest mean index reached 17.056 for genotype 2 and with out significant with some genotypes and significant with others. Therefore this genotype was the better and followed by genotype (1) and genotype (3) and (8).

Table (8): analysis variance to test significant of selection indices values differences among genotypes.

Source	df	Sum of square	Mean square	F value	Pr. > F
Replication	2	227.04	113.52	2.68	0.091
Genotype	11	3191.28	290.11	6.84	<.0001
Error	22	933.47	42.43		
Total	35	14351.79			

Table (9): Analysis variance of index fo each genotype

Genotypes	Mean	Genotypes	Mean
1	16.36 a	7	-1.75 def
2	17.05 a	8	12.90 abc
3	13.68 ab	9	-9.69 f
4	9.84 abcd	10	9.76 abcd
5	1.05 cdef	11	2.69 bcde
6	-9.59 f	12	-5.48 fe

Finally it was concluded from this study that the better four genotypes respectively was 2, 1, and 3 and surpassed genotype over all genotypes

and could be used this genotypes in breeding programs to improved yield of wheat and develop new variety with good productivity and good

quality performance to Kurdistan and Iraqi environments.

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هه لسه نگاندا توخمین میراتی ژ گه نمی نانی بکارئینانا ته کنیکا ریه ری هه لبرارتنی

پوخته

ئه ف قه کولینه هاته ئه نجامدان ل زه قین پشکا ده رانه تین کینگه یی کولیزا چاندنی ، زانکویا دهوک. چارده توخمین میراتی هاتنه چاندن ل 25-11-2017 بو چیکرنا ریه ری هه لیزاردنا جاواز بکارئینانا دزاینا کهرتی نا هه مه رهنگی سیی جارکی. ئه قی قه کولینی خاندنا شه ش سالوخه تا بخو قه گرد ئه وژی بلندایا روه کی ، روه ری به لکی ، هژمارا دندکا/ گولی ، کیشا دندکا / گولی ، کیشا هزار (1000) دندکا ، به ری گهنمی/ خیح.

پشتی شرو قه کرنا جاواز ئه نجام دیار بوون جاوازی هه ی دنا قبه را بلندایا روه کی و هژمارا دندکا، کیشا دندکا/ گولی، کیشا هزار (1000) دندکا. و جاوازی نه بوو دنا قبه را روه ری به لگی. هه روه سا شرو قه کرنا بکوم بو سالوخه تا دیار بو جاوازیه کا مه زن یا هه یی بو هه می سالوخه تا ژبلی هژمارا دندکا / گولی، کیشا دندکا / گولی ، و باشتترین ریه ری هه لیزارتنی ل (146) ئه وین سالوخه تی بری دندکا ، بلندایا روه کی ، کیشا (1000) دندکا بخو قه کرت وشیانین بریزا %7.29 به راورد کرن دگه ل ریه ری هه لیزارتنا به ری بتنی.

فاکته ری جاوازی میراتی دیار کر به ایی نا قینجی بو هه می سالوخه تا و به ایی کیم بو روه ری به لکی ده ماندمدا به ایی فاکته ری جاوازی ده رقه نا قینجی بوو بلندایا روه کی، کیشا دندکا/ گولی، هه لیزارتنا دندکا/ گولی ، کیشا (1000) دندکا ، به ایی بلندبوو بو به ری دندکا، به ایی کیم بو روه ری به لگی. ده رنه جامی میراتی یی هژمارا نا قینجی ئه وژی هه رهوسا یا بلند بوو بو هژمارا دندکا/ گولی، کیشا دندکا/ گولی، نا قینجی بوو بو بلندایا روه کی و کیشا هزار دندکا و به ری دندکا و یا کیمبوو بو روه ری به لگی ، %5.07 - %20.47 .

ده می هژمارتتا ریزا قه گو هاستنا میراتی بو اتا فره بو سالوخه تین هاتیه خاندنی یا بلند بو بو هه می نا قبه را توخمین میراتی بشبه ستن باشتترین ریه ری هه لیزارتنی ئه وی پیک هاتی ژ به ری دندکا و بلندایا روه کی و کیشا (1000) دندکا.

ژ قی قه کولینی دیار بوو کو باشتترین توخمین میراتی (بحوپ 4 ، اباو 99، شام 6) و جوریه یناوی. ئه شین ئه قان توخما بو پروگرامین په روه رده کرنا پیشیخستنا بکاربنین بو گه ش و هه وا کوردستانا – عیراقی.

تقیم تراکیب وراثیه من حنطه الخبز باستخدام تقنية دليل الانتخاب

الخلاصة

طبقت تجربة في حقل قسم المحاصيل الحقلية / كلية الزراعة جامعة دهوك. زرع اثنا عشر تركيبا وراثيا في 25/11/2017 لانشاء ادلة انتخاب مختلفة باستخدام تصميم القطاعات العشوائية وبثلاثة مكررات واشتملت التجربة على دراسة ستة صفات وهي ارتفاع النبات مساحة ورقة العلم وعدد الحبوب في السنبله ووزن حبوب السنبله ووزن 1000 حبة وحاصل الحبوب خط.

اظهرت نتائج تحليل التباين وجود فروقات معنوية لارتفاع النبات وعدد الحبوب في السنبله ووزن حبوب السنبله ووزن 1000 حبة وفرقات وغير معنوية لمساحة ورقة العلم . كما اظهر التحليل التجميحي للصفات فروقات عالية المعنوية لجميع الصفات باستثناء عدد الحبوب في السنبله ووزن حبوب السنبله , وكان افضل دليل انتخابي ل 146 الذي اشتمل على حاصل الحبوب وارتفاع النبات ووزن 1000 حبة واعطاء كفاءة نسبية 7.29% بالمقارنة مع دليل الانتخاب للحاصل لوحده . اظهر معامل التباين الوراثي قيم متوسطه لجميع الصفات وقيمة واطئة لمساحة ورقة العلم بينما كانت قيم معامل التباين المظهري متوسط لارتفاع النبات, وزن حبوب السنبله وعدد الحبوب في السنبله ووزن 1000 حبة وقيمة عالية لحاصل الحبوب وواطئة لمساحة ورقة العلم. اما التحصيل الوراثي منسوباً الى المتوسط الحسابي فهو الاخر كان عاليا لعدد الحبوب في السنبله ووزن حبوب السنبله ومتوسط القيمة لارتفاع النبات ووزن 1000 حبة وحاصل الحبوب وواطئاً لمساحة ورقة العلم, وتراوحت قيمته بين 5.07 الى 20.47%, وعند حساب نسبة التوريث بالمعنى الواسع للصفات المدروسة فكانت عالية لجميع الصفات ومتوسطة لمساحة ورقة العلم كما بينت النتائج وجود فروقات عالية المعنوية بين التراكيب الوراثية بالاعتماد على احسن دليل انتخابي والذي هو كان مكوناً من حاصل الحبوب وارتفاع النبات ووزن 1000 حبة.

من هذه الدراسة يتبين ان افضل التراكيب الوراثية كان ابو غريب-1 وبحوث-4 وابعاء-99 وشام-6 ونوعيته ويمكن وضع هذه التراكيب في برنامج لتحسين حاصلها تحت ظروف اقليم كردستان والعراق