# ASSOCIATION, VARIATION, HERITABILITY AND PATH COEFFICIENT ANALYSIS OF FIVE F<sub>3</sub> WHEAT FAMILIES UNDER SALINE CONDITIONS

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#### ABSTRACT

Five F<sub>3</sub> selected families of bread wheat were evaluated at Ras Sudr Research Station of (DRC), South-Sinai Governorate in 2000/2001 growing season under salinity conditions of soil and irrigation water (about 9875 and 10000 ppm, respectively). At 90 days after sowing, 10 guarded plants were selected randomly to measure chemical contents in a composite sample of each F<sub>3</sub> family leaves i.e proline (in fresh samples), K/Na ratio, Mg, CI and So<sub>4</sub> (in dry samples). At harvest, fifteen competitive plants from each plot were selected to record observations on plant height, number of spikes / plant, spike length, number of grains / spike, 1000-grain weight and grain yield / plant. Simple correlations, phenotypic & genotypic coefficients of variability, heritability and path analysis were calculated. The obtained results can be summarized as follows:

1. Inter-relationships among the studied characters under such saline conditions

varied in magnitude according to the F<sub>3</sub> population genotypes.

2. Correlations between grain yield / plant and each of the chemical composition of leaves as well as yield components were positive and significant in most cases except for CI content which was negatively correlated to grain yield / plant. For improving grain yield under such saline conditions, the following traits: heavy grains, high number of grains/spike, high content of proline in fresh leaves and low chloride content in dry leaves considered to be a suitable selection criteria.

3. Heritability values varied among traits and between populations studied therefore, selection for the yield attributes may be effective for improving grain yield which had low to moderate (GCV) values among F<sub>3</sub> selected families. Hence, the direct selection for improving yielding ability is not effective and path analysis must be

done to detect the joint effects.

4. The total contribution of each chemical component in leaves showed that proline content was the most powerful determinant of grain yield in S<sub>8</sub>× I<sub>8</sub> F<sub>3</sub> family as it contributed by 20.33%. In general, chemical contents could be arranged over all studied F<sub>3</sub> populations as follows: So<sub>4</sub>, proline, Mg, K / Na and CI.

5. The main source of grain yield variation was 1000- grain weight followed by number of grains / spike and number of spikes / plant in three or more of F<sub>3</sub> families. Such highly contributed traits easily measured and gave a valuable idea for selection to

yield improvement under saline environments.

Keywords: Bread wheat (*Triticum aestivun* L.), Segregating generation, Salinity stress, Phenotypic and genotypic correlations, Variability and heritability, Path coefficient analysis.

#### INTRODUCTION

Improvement cereal crops as wheat under saline conditions is more difficult than breeding under favorable conditions. The greater degree of difficulty is due to increased complexity of genotype-environment interaction

associated with yield and its contributing traits. An effective breeding program for improving wheat under saline conditions such South Sinai depends not only on amount of variability among the diverse genotypes, but also on heritability for the traits under consideration. The breeders can reduce the time required for improving promising genotypes, if they have significant genotypic variability. In this respect, many investigators for breeding wheat genotypes under stress conditions. Moreno-Savilla et al (1995) recorded high variability in some wheat genotypes. Ortiz (1990) and Abd El-Moneim (1993), reported different values of heritability.

Most genetic analyses in wheat concentrate on elucidating the mode of inheritance of characters separately. However, it is equally important to study the genetic relationships between different characters so that the consequences of selection for one character on the performance of another can be predicted. The genetic covariance or its standardized form expresses the degree of genetic relationship between pairs of characters. The correlation coefficient functionally, a significant relationship implies the pleiotropic effect of the same genes or linkage genes controlling the separate characters.

The progress in research for developing wheat varieties for stress tolerance and good agronomic procedures has not been commensurate with the needs because the narrow base of germplasm used and inadequacy of the selection methods to detect genotypes superior under stress environments. Meantime, many reports identified lines with wide adaptation and ability to withstand the aimed environments outlined using early segregating generations. Hence, many investigators used correlation analysis to ascertain relationships between variables and tested various path analysis models to determine the importance of the yield components contributing to grain yield and found that path analysis is useful [Mitkees et al (1992), Dhanda and Sethi (1996), Deswal et al (1997), Uddin et al (1997), Krishnawat and Sharma (1998), Afiah (1999), Khan et al (1999), Thakur et al (1999), Vijai et al (1999), Dencic et al (2000), Jag-Shoran et al (2000), Krishnawat et al (2000), Shukla et al (2000), and Tammam et al (2000)].

The present study aimed mainly to assess variation, association, heritability and path coefficient analysis for grain yield and its attributes as well as leaves mineral contents of five F<sub>3</sub> bread wheat families grown under saline conditions of Ras Sudr, South Sinai.

## MATERIALS AND METHODS

Six genetically divers wheat genotypes i.e Sakha-8 ( $S_8$ ) as a local variety,  $I_2,I_4,I_5$ ,  $I_7$  and  $I_8$  (introduced from ICARDA) were crossed using Sakha-8 as a male parent with the other ICARDA lines i.e ( $S_8 \times I_2$ ), ( $S_8 \times I_4$ ), ( $S_8 \times I_5$ ), ( $S_8 \times I_7$ )and ( $S_8 \times I_8$ ). The ICARDA line number (No.), origin, entry name and pedigree of the parental wheat genotypes are shown in Table (1). Such salt tolerant genetic materials were chosen after estimating the characters related to salt tolerance in sixteen local and exotic bread wheat genotypes by Hassan (1996).

The crosses were made by hand in winter growing season 1997/1998 at the nursery of Plant Genetic Resources Dept., Desert Research Center (DRC). The F1 hybrid grains and the parental genotypes were sown using randomized complete blocks design with three replications on 10 November 1998 at Ras Sudr Research Station of (DRC), South-Sinai Governorate. The experimental unit consisted of 7 rows i.e 3 rows, for each female parent (I), one row for F<sub>1</sub> hybrid and 3 rows for the male parent (S<sub>8</sub>). At harvesting date, 60 F2 plants were selected from each replicate and threshed and sown separately in the second season (1999 / 1990). Grains of each F2 selected plant were represented by one row 1m long, 20 cm apart and approximately 5 cm between plants (20 plants / row in each replicate). Also, the check variety (Sakha-8), five female parents and F2 bulk populations were grown in three replicates. From each of the 5 crossing F3 sets, the best family was selected according to its superiority in growth behavior, yield and one or more of its attributes. All F<sub>3</sub> selected families were sown in 19 November 2000 following the last experimental procedures. Each experimental unit area was 7.5 m<sup>2</sup> (3 x 2.5 m) consisted of the two parents and its F3 selected family. During this program the genetic materials were evaluated under salinity conditions of soil (ranged from 9600 to 10150 ppm) with 43.8% Ca CO<sub>3</sub> and artesian irrigation water that started by about 8000 ppm (in the first season, 1998/1999) and increased by 1000 ppm every year through out the study (lasted in 2000/2001). Ordinary cultural practices for wheat production under desert conditions were following during each growing seasons. At 90 days after sowing, 10 guarded plants were selected randomly to measure chemical contents in a composite sample of each F3 family leaves i.e proline (in fresh samples), K/Na ratio, Mg, Cl and So<sub>4</sub> (in dry samples). At harvest, fifteen competitive plants from each plot were selected to record observations on plant height, number of spikes / plant, spike length, number of grains / spike, 1000-grain weight and grain yield / plant. Data of the three replications were pooled to use in statistical interpretations for each F3 family.

Biometrical assessment for simple correlations, phenotypic & genotypic coefficients of variability, heritability and path analysis:

Associations among various characters studied were expressed as phenotypic (rp) and genotypic (rg) correlation coefficients. They were calculated with help of the covariance analysis as described by Harvey (1990).

Estimating phenotypic & genotypic coefficients of variability of the studied characters were done according to Comstock and Moll (1963).

Heritability in broad sense (H b) was calculated for all studied characters using Allard equation (1960) as follows:

Heritability in broad sense = Genotypic variation

Phenotypic variation

Path coefficient analysis was used to calculate the coefficient of determination (CD) and percentage of total contribution of leaves chemical components and yield & its attributes on genotypic feature according to Dewey and Lu (1959).

Table (1): ICARDA line number (No.), Origin, Entry name and Pedigree

of the parental wheat genotypes.

No.	Origin	Entry name	Pedigree
140.	Egypt	Sakha 8	PK3418-6S-1SW-0S
2	ICARDA	Rbs/Anza	SWM12008-2AP-1AP-3AP-1AP-0AP
2	ICARDA	SS.1744/7c	SWM11625-15AP-6AP-1AP-0AP
4		Tsi/Vee'S'	CM64335-3AP-1AP-4AP-0AP
5	ICARDA	Maya74/Son	CM58924-1AP-4AP-1AP-0AP
7	ICARDA	Dava'C'/Dua'C'	CM58804-6AP-2AP-1AP-0AP
8	ICARDA	Bove S / Buc S	CIVI36604-0AI -2AI -1AI -0AI

ICARDA; International Center for Agricultural Research in the Dry Areas.

## RESULTS AND DISCUSSIONS

Phenotypic and genotypic associations:

The phenotypic (rp) as well as genotypic (rg) correlation coefficients were estimated from individual F3 plants data of the five wheat crosses; Sakha 8 (S<sub>8</sub>) x ICARDA 2 (I<sub>2</sub>), S<sub>8</sub> x I<sub>4</sub>, S<sub>8</sub> x I<sub>5</sub>, S<sub>8</sub> x I<sub>7</sub> and S<sub>8</sub> x I<sub>8</sub>. Estimates of rp and rg between grain yield and leaves chemical contents are presented in Table (2). Genotypic correlation coefficients were generally higher than their corresponding phenotypic one's, indicating strong inherent associations between grain yield and each of the studied traits. Simple correlation values varied in magnitude and sign of some cases between characters in each F<sub>3</sub> family. These findings are in accordance with those previously obtained by Hurd (1976) and Fischer and Wood (1979). The obtained results in Table (2) revealed that grain yield / plant was positively correlated at both phenotypic and genotypic levels with each of proline content, K / Na ratio and Mg content in F3 families derived from the crosses S8 x I2, S8 x I5 and S8 x I7. Also, grain yield / plant was significantly positive associated with proline content & K / Na ratio and proline & Mg contents in S<sub>8</sub> x I<sub>4</sub> and S<sub>8</sub> x I<sub>8</sub> F<sub>3</sub> families, respectively. Both phenotypic and genotypic correlation coefficients between yielding ability and CI content in leaves were significantly negative in all selected F<sub>3</sub> families studied. So4 content was positively correlated to grain yield in the two F<sub>3</sub> families derived from S<sub>8</sub> x I<sub>7</sub> and S<sub>8</sub> x I<sub>8</sub> crosses. The genotypic association between yielding ability and each of such traits suggesting that genes controlling grain yield / plant are linked with those controlling the correlated traits. The earlier results reported by Hassan (1996) are in partial harmony with these findings.

The associations among grain yield and its contributing characters measured as phenotypic (rp) and genotypic (rg) correlation coefficients are presented in Table (3). It could be seen from the present data that the interrelationships among the studied characters under such saline conditions varied in magnitude according to the F3 population genotypes responded to environment on mean performance of the studied traits. However, in general, the genotypic (rg) correlation coefficients were higher than the phenotypic one's. In this respect, previous studies [Mitkees et.al.(1992), Chaturved and Gupta (1995), Sharma et.al.(1995), Deswal et.al.(1996), Mondal et.al. (1997), Uddin et.al.(1997) and Tammam et.al.(2000)] also reported that grain yield was positively and significantly associated at phenotypic and (or) genotypic level with each of number of spikes/plant, number of kernels/spike, 1000kernel weight and spike length in bread wheat under varying environments.

Table (2): Phenotypic (rp) and genotypic (rg) correlation coefficients between grain yield and each of the chemical contents determined in leaves.

Character	Correlation	F <sub>3</sub> Families								
Onaracter	coefficients	S <sub>8</sub> × I <sub>2</sub>	S <sub>8</sub> × I <sub>4</sub>	S <sub>8</sub> × I <sub>5</sub>	S <sub>8</sub> × I <sub>7</sub>	S <sub>8</sub> × I <sub>8</sub>				
Proline	rp rg	0.605** 0.631**	0.642** 0.695**	0.651** 0.717**	0.717**	0.672**				
K <sup>+</sup> /Na <sup>+</sup>	rp rg	0.617** 0.712**	0.717** 0.752**	0.557* 0.600**	0.618** 0.652**	-0.271 -0.212				
Mg**	rp rg	0.571* 0.600**	0.346 0.342	0.884**	0.762** 0.888**	0.819**				
Cl	rp rg	-0.647** -0.618**	-0.717** -0.616**	-0.662** -0.552*	-0.699** -0.667**	-0.718** -0.700**				
SO4"	rp rg	0.108 0.212	0.217 0.317	0.348 0.412	0.498* 0.552*	0.577* 0.612**				

\* and \*\*: Denote significant at 0.05 and 0.01 levels of probability, respectively.

Table (3): Phenotypic (rp) and genotypic (rg) correlation coefficients between grain yield and each of the yield attributes recorded.

Character	Correlation	F <sub>3</sub> Families							
Onaracter	coefficients	S <sub>8</sub> × I <sub>2</sub>	S <sub>8</sub> × I <sub>4</sub>	S <sub>8</sub> × I <sub>5</sub>	S <sub>8</sub> × I <sub>7</sub>	Sa× Ia			
Spike length (cm)	rp rg	0.572**	0.441 0.450	0.676**	0.400 0.422	0.612**			
No. of spikes/ plant	rp rg	0.376**	0.316	0.411	0.500* 0.510*	0.577*			
No. of grains/ spike	rp rg	0.515* 0.618**	0.517* 0.519*	0.518* 0.545*	0.346 0.417	0.512* 0.534*			
1000 – grain weight	rp rg	0.672** 0.716**	0.400 0.415	0.672**	0.505 0.524*	0.618**			

\* and \*\*: Denote significant at 0.05 and 0.01 levels of probability, respectively.

Data in Table (3) revealed that spike length had positive and significant simple correlation coefficient values with grain yield / plant in Sa x I<sub>2</sub>, S<sub>8</sub> x I<sub>5</sub> and S<sub>8</sub> x I<sub>8</sub> F<sub>3</sub> families. Number of spikes / plant significantly associated with yielding ability in  $S_8 \times I_2$ ,  $S_8 \times I_7$  and  $S_8 \times I_8$  for both phenotypic and genotypic levels. Number of grains/spike showed the same trend in all F3 families studied except that derived from S8 x I7. The thousand grain weight was highly significant and positive correlated to grain yield over the two levels (rp and rg) in  $S_8 \times I_2$ ,  $S_8 \times I_5$  and  $S_8 \times I_8$  while in  $S_8 \times I_7$   $F_3$  family it reached the level of significance in rg only (0.524\*). Generally, the interrelationships of grain yield / plant and chemical composition of leaves (at 90 days after sowing) as well as yield components were positive and significant in most cases except for CI content which was negatively correlated to grain yield / plant. For improving grain yield under saline conditions, the suitable wheat genotypes characterized by some traits as heavy grains, high number of grains/spike, high content of proline in fresh leaves and low chloride content in dry leaves. These findings are more or less in accordance with those reported by Hassan (1996) and Afiah (1999).

Heritability and genetic variations:

Estimates of broad sense heritability percentage (Hb%), phenotypic and genotypic variability coefficients for the studied chemical contents of leaves, yield and yield attributes of five F3 families under saline conditions are illustrated in Table (4). Over all the studied F3 families, CI content, So4 content, 1000-grain weight and grain yield / plant had the highest values of Hb% ranging from 70 to 91, 81 to 95, 74 to 96 and 72 to 95%, respectively among the five F3 selected families. However, spike length had the 12 most values (68% to 80%) for broad sense heritability. Proline content had a relatively high and constant (Hb) percentage ranged between 71 and 83% among all the studied F3 families. Data in Table (4) clearly shown that, all characters had high values of broad sense heritability, slightly differences noticed between phenotypic and genotypic coefficients of variability suggesting a small effect of environmental factors on these characters. Also, it is clear that heritability values varied among traits and between populations studied, thus selection for such characters may be effective for improving grain yield of wheat under saline conditions. However, the traits had relatively low values of genotypic coefficient of variability and heritability suggesting little scope for improving grain yield through such traits. The studied characters, which, exhibited great amount of genetic variability, could be considered adequate for improving bread wheat in breeding programs. Moreover, grain yield had low to moderate values among the F3 selected families in this respect. Hence, the direct selection for improving yielding ability not effective and path analysis must be done to detect the joint effects. Several investigators suggested that the knowledge of genetic variability is helpful in selecting a suitable plant type for salt affected regions at Sinai [Fisher and Maurer (1978), Winter et.al.(1988), Abd El-Moneim (1993), Hassan (1996) and Afiah (1999)]

Table (4): Heritability in broad sense (hb), phenotypic (PCV) and genotypic (GCV) variability coefficients for the studied chemical contents of leaves, yield and yield attributes of five F<sub>2</sub> families under saline condition.

	S <sub>8</sub> × I <sub>2</sub>			S <sub>8</sub> × 1 <sub>4</sub>		S <sub>8</sub> × I <sub>5</sub>		S <sub>8</sub> × I <sub>7</sub>		7	S <sub>8</sub> × I <sub>8</sub>				
Characters	Hb	PCV			PCV	_	НЬ	PCV	GCV	Hb	PCV	GCV	Hb	PCV	GCV
1- Chemical conte	nts			- 11-				-358							
Proline	71	30	21	83	71	41	76	45	21	80	23	19	78	44	18
K*/Na*	81	34	25	89	81	66	80	48	21	70	44	17	78	51	22
	91	41	34	84	81	64	69	51	23	76	41	19	80	38	24
Mg <sup>**</sup> Cr	91	36	29	90	75	60	81	41	31	70	24	15	86	46	40
SO4"	95	44	38	88	90	74	81	50	42	84	25	16	81	51	39
2- Yield and yield att	ributes														20.12
Spike length	73	44	40	68	51	40	80	58	37	71	45	22	78	60	38
No. of spikes/ plant	90	29	24	80	21	18	71	64	41	69	44	29	74	45	24
No. of grains /spike	84	84	79	78	60	41	76	54	40	75	41	21	76	46	29
1000- grain weight	96	46	41	86	. 57	47	74	44	41	81	44	25	76	40	24
Grain vield/ plant	95	44	38	76	41	24	72	50	41	84	23	19	80	35	26

# Path coefficient analysis:

The direct and joint effects of studied leaves chemical contents for five  $F_3$  selected families measured as genotypic variations to grain yield/ plant are presented in table (5). The highest direct effect was exerted by proline followed by  $So_4$  content in most  $F_3$  studied families .Regarding the indirect effects on grain yield variations was recorded for, proline via Mg, Mg via  $So_4$  over all  $F_3$  populations. It is evident to mention that, the studied chemical contents accounted by 70, 58.3, 71.6, 72.5 and 77.6 of the total grain yield variations for the  $F_3$  families derived from  $S_8 \times I_2$ ,  $S_8 \times I_4$ ,  $S_8 \times I_5$ ,  $S_8 \times I_7$ . If  $S_8 \times I_8$  wheat crosses respectively. The total contribution of each chemical component in leaves showed that proline content was the most powerful determinant of grain yield in  $S_8 \times I_8$  family as it contributed by 20.33%. In general, the basis of total contribution of the determined chemical contents could be arranged over all studied  $F_3$  populations as follows:  $So_4$ , proline, Mg, K / Na and Cl contents. These findings are in partial harmony with that reported by Hassan (1996).

Table (5): Direct and joint effects of studied leaves chemicals contents for the five F<sub>3</sub> families of wheat measured as genetypic variation to grain yield/plant.

Genotypic coefficient of determination (CD) Source of variation S8× 12 S8× 14 S8× 15 S8× 17 S8× 18 Proline 0.0515 0.0392 0.0411 0.0511 0.0671 K/Na ratio 0.0154 0.0201 0.0341 0.0491 0.0161 Mg content 0.0162 0.0273 0.0356 0.0314 0.0261 CI content -0.0167 -0.0199 -0.0248 -0.0317 -0.0417 So4 content 0.1315 0.0175 0.0245 0.0316 Proline X K/Na 0.0384 0.0416 0.0715 0.0551 0.0466 0.0688 Proline X Mg 0.0478 0.0765 0.0651 0.0877 0.0576 Proline X CI 0.0352 0.0215 0.0446 0.0581 C.0682 Proline X So4 0.1116 0.0417 0.0561 0.0381 0.0777 K/Na X Ma 0.0342 0.0315 0.0444 0.0441 0.0576 K/Na X CI 0.0194 0.0182 0.0244 0.0314 0.0781 K/Na X So4 0.0518 0.0679 0.0748 0.0615 0.0419 Ma X CI 0.0352 0.0517 0.0648 0.0716 0.0781 Mg X So4 0.0810 0.0752 0.0848 0.0662 0.0542 CIX SO4 0.0454 0.0432 0.0916 0.0887 0.0772 0.7008 0.5825 0.7163 0.7256 0.7756 Resudial 0.2992 0.4175 0.2837 0.2744 0.2244 Total 1.0000 1.0000 1.0000 1.0000 1.0000 Total contribution % Proline 16.95 14.48 15.16 16.64 20.33 K/Na ratio 8.89 11.45 13.35 14.09 14.29 Mg content 11.52 14.47 16.51 16.62 15.14 CI content 5.09 4.73 8.80 9.32 10.91 So<sub>4</sub> content 27.64 13.12 17.81 15.89 16.90

Table (6) presented the direct and joint effects of studied yield attributes for the selected  $F_3$  families measured as genotypic variations to grain yield /

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plant. All sources of yield variations were positive whereas, largest contribution was detected for number of spikes / plant in most of the studied F<sub>3</sub> families as direct effect. The indirect (joint) effects of different characters recorded towards grain yield revealed that spike length via 1000- grain weight, number of spikes / plant via number of grains/spike, number of spikes/plant via plant height and number of grains/spike via 1000- grain weight had an important positive effects in two or more of the studied F3 families.

Table (6): Direct and joint effects of studied yield attributes for the five F3 families of wheat measured as genotypic variation to

grain vield/plant.

grain yield/plant.	Genoty	nic cceffic	cient of de	terminatio	n (CD)
Source of variation	S <sub>8</sub> × I <sub>2</sub>	S <sub>8</sub> × I <sub>4</sub>	S <sub>8</sub> × I <sub>5</sub>	S <sub>8</sub> × I <sub>7</sub>	S <sub>8</sub> × I <sub>8</sub>
St	0.0016	0.0467	0.0833	0.0981	0.0572
Plant height (cm)	0.0600	0.0761	0.0517	0.0457	0.0615
No. of spikes/plant	0.0603	0.0476	0.0416	0.0335	0.0333
Spike length (cm)	0.0268	0.0417	0.0416	0.0517	0.0492
No. of grains/spike	0.0442	0.0403	0.0918	0.0817	0.0611
1000- grain weight (gm) Plant height × No. of spikes/plant	0.0027	0.0241	0.0715	0.0716	0.0711
Plant height × spike length	0.05;8	0.0710	0.0417	0.0472	0.0476
Plant height × No. of grain/spike	0.0015	0.0512	0.0612	0.0517	0.0617
Plant height × 1000-grain weight	0.0266	0.0517	0.0418	0.0642	0.0571
	0.1092	0.0512	0.0515	0.0572	0.0476
No. of spikes × spike length	0.0512	0.0511	0.0676	0.0511	0.0617
No. of spikes × No. of grains/spike	0.0072	0.1000	0.0572	0.0641	0.0571
No. of spikes × 1000 grain weight					0.0511
Spike length × No. of grains/spike	0.0108	0.0612	0.0417	0.0531	
Spike length × 1000 grain weight	0.1111	0.0981	0.0531	0.0416	0.0551
No. of grains/spike × 1000 grain w.	0.0451	0.0617	0.0417	0.0810	0.0717
R <sup>2</sup>	0.9489	0.8737	0.8443	0.8934	0.8844
Residual	0.0511	0.1263	0.1557	0.1065	0.1156
Total	1.0000	1.0000	1.0000	1.0000	1.0000
Total contribution %	11年11年				1 47.50
Plant height (cm)	4.28	19.57	19.41	21.54	17.59
No. of spikes/plant	14.51	18.93	17.56	16.77	18.02
Spike length (cm)	25.04	14.38	13.55	13.30	13.40
No. of grains/spike	37.14	15.42	14.76	17.01	17.22
1000-grain weight (gm)	13.92	19.07	19.14	20.72	18.16

Total contribution percentages showed that the main source of grain yield variation was 1000- grain weight followed by number of grains / spike and number cf spikes / plant in three or more of F3 families. Such highly contributed traits easily measured and gave a valuable idea for selection to yield improvement under saline environments. Earlier published by [Afiah (1999), Narwal et al. (1999), Rana et al. (1999) and Jag-shoran et al. (2000)] mentioned that number of grains / spike and grain weight had the most direct and joint effects in grain yield variation and considered as important selection criteria for improving bread wheat under saline conditions.

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plant. All sources of yield variations were positive whereas, largest contribution was detected for number of spikes / plant in most of the studied  $F_3$  families as direct effect. The indirect (joint) effects of different characters recorded towards grain yield revealed that spike length via 1000- grain weight, number of spikes / plant via number of grains/spike, number of spikes/plant via plant height and number of grains/spike via 1000- grain weight had an important positive effects in two or more of the studied  $F_3$  families.

Table (6): Direct and joint effects of studied yield attributes for the five  $F_3$  families of wheat measured as genotypic variation to

grain yield/plant.

	Genotypic coefficient of determination (CD)								
Source of variation	S <sub>8</sub> × I <sub>2</sub>	S8× I4	S <sub>8</sub> × I <sub>5</sub>	S8× I7	S8× 18				
Plant height (cm)	0.0016	0.0467	0.0833	0.0981	0.0572				
No. of spikes/plant	0.0600	0.0761	0.0517	0.0457	0.0615				
Spike length (cm)	0.0603	0.0476	0.0416	0.0335	0.0333				
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No. of spikes × spike length	0.1092	0.0512	0.0515	0.0572	0.0476				
No. of spikes × No. of grains/spike	0.0512	0.0511	0.0676	0.0511	0.0617				
No. of spikes × 1000 grain weight	0.0072	0.1000	0.0572	0.0641	0.0571				
Spike length × No. of grains/spike	0.0108	0.0612	0.0417	0.0531	0.0511				
Spike length × 1000 grain weight	0.1111	0.0981	0.0531	0.0416	0.0551				
No. of grains/spike × 1000 grain w.	0.C451	0.0617	0.0417	0.0810	0.0717				
$R^2$	0.9489	0.8737	0.8443	0.8934	0.8844				
Residual	0.0511	0.1263	0.1557	0.1065	0.1156				
Total	1.0000	1.0000	1.0000	1.0000	1.0000				
Total contribution %	5150 B	81-111		14					
Plant height (cm)	4.28	19.57	19.41	21.54	17.59				
No. of spikes/plant	14.51	18.93	17.56	16.77	18.02				
Spike length (cm)	25.04	14.38	13.55	13.30	13.40				
No. of grains/spike	37.14	15.42	14.76	17.01	17.22				
1000-grain weight (gm)	13.92	19.07	19.14	20.72	18.16				

Total contribution percentages showed that the main source of grain yield variation was 1000- grain weight followed by number of grains / spike and number of spikes / plant in three or more of  $F_3$  families. Such highly contributed traits easily measured and gave a valuable idea for selection to yield improvement under saline environments. Earlier published by [Afiah (1999),Narwal et al. (1999), Rana et al. (1999) and Jag-shoran et al. (2000)] mentioned that number of grains / spike and grain weight had the most direct and joint effects in grain yield variation and considered as important selection criteria for improving bread wheat under saline conditions.

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الارتباط ومعامل الاختلاف والكفاءة التوريثية ومعامل المرور لخمسة من عائلات الجيل الثالث في القمح تحت الظروف الملحية احمد ابراهيم حسن و سامي عبد العزيز عافية وحدة تربية النباتات – قسم الأصول الوراثية النباتية – مركز بحوث الصحراء – المطرية القاهرة

تهدف هذه الدراسة الى تقييم خمسة عائلات منتخبة فى الجيل الثالث الهجين مسن قصح الخبز تحت الظروف الملحية (حوالى ٩٨٧٥ جزء فى المليون بالتربة و ١٠٠٠٠ جزء فى المليون بحياه الرى) السائدة بمحطة البحوث التابعة لمركز بحوث الصحراء - جنوب سيناء خلال موسم النمو ٢٠٠١/٢٠٠٠. حيث تم اخذ عينة مركبة من أوراق عشرة نباتات عشوائبا من كل عائلة بعد ٩٠٠٠ يوم من الزراعة لتقدير نسبة البرولين والبوتاسيوم والصوديوم والماغنسيوم والكوريث والكبريتات كما تم تسجيل بيانات خمسة عشر نباتا منتخبا من كل مكررة عند الحصاد لصفات: طول النبات - عدد سنابل النبات - طول محور السنبلة - عدد حبوب السنبلة - وزن ١٠٠٠ حبة ومحصول النبات الفردى.

تم تقدير معاملات الارتباط والاختلاف على المستوى الورائسي والمظهري والكفاءة التوريثية وتحليل معامل المرور لبيانات كل عائلة منتخبة على حده ويمكن تلخيص اهم النتائج فسي الاتي:

١- اختلفت قيمة معاملات الارتباط بين الصفات تحت الدراسة باختلاف التراكيب الوراثية لعشائر

٣- تباينت قيم معامل التوريث عبر الصفات المدروسة وبين عشائر الجيل الثالث المنتخبة وعليه فيمكن تحسين المحصول من خلال الصفات الاكثر مساهمة بعد تحليل معامل المرور حيث كان معامل الاختلاف الوراثي منخفضا او متوسطا بالنسبة لمحصول الحبوب بالنبات مما يقلل من اهمية الانتخاب المباشر لمحصول النبات الفردي.

٤- بدراسة مجموع المساهمات الكلية (مباشرة وغير مباشرة) لمكونات الاوراق الكيميائية كان المحتوى من البرولين من اقوى محددات المحصول في عشيرة الجيل الثالث المنتخبة من انعز الات المجين سخا ٨ × ايكاردا ٨ حيث ساهم بنسبة ٢٠,٣٢% ولكن بنظرة عامة السي كافة العشائر تحت الدراسة يمكن ترتيب المكونات الكيميائية حسب درجة مساهمتها في محصول الحبوب على النحو التالى: نسبة الكبريتات يليها البرولين ثم الماغنسيوم ثم نسبة البوتاسيوم الى الصوديوم (K/Na) وأخيرا الكلوريد.

د- كان المكون الرئيسي في اختلافات محصول النبات من الحبوب هو وزن ١٠٠٠ حبة متبوعط بعدد حبوب السنبلة ثم عدد سنابل النبات في ثلاثة او اكثر من عائلات الجيل الشالث تحت الدراسة وعليه يمكن اعتبار هذه الصفات سيلة القياس من الدلائل الانتخابية الميمة لتحسين المحصول تحت الظروف الملحية.