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EVALUATION OF SOME PROMISING TEOSINTE HYBRIDS AND THEIR GENETIC BEHAVIOR FOR FODDER YIELD

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ABSTRACT

Although the need for increased production of summer fodder is so keenly felt in Egypt, the plant breeders did not focused much of their attention to improving fodder teosinte. In this study an attempt was made in order to partition the genetic variance to its components for fodder traits through the evaluation of different generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the promising hybrids of teosinte.

Significant differences among crosses for number of tillers per plant, green fodder yield per plant and crude protein percentage were detected in the three cuts. Also, the results revealed that the presence of highly significance among populations within crosses and populations within each cross with respect to all studied traits in three cuts. These results reflected the diversity and the different genetic constitution of parental lines of the studied crosses. Furthermore, years, crosses by years and populations within crosses by years in addition to populations within each cross by years mean squares were significant in most of occasions. This indicates that these populations gave different performances at different environmental conditions. The best combination for fodder yield components was Guatemala × Balsas, which showed the highest means for most of studied traits through the three cuts compared by other two crosses as well as their parents. In this hybrid (Guatemala x Balsas), the values of dominance gene effects were higher in magnitude than the corresponding values of additive gene effects for all studied traits in most of cuts. This finding reflected the presence of heterotic effect and the higher frequency of dominance genes controlling these traits in this cross. Therefore, the means of the F_2 generation appeared to be less than the F_1 hybrids for most of studied fodder traits through the three cuts. Regarding to Rayana x Balsas and Central plateau x Balsas hybrids, F_2 generations appeared to be higher in means than their respective F_1 hybrids in most of studied traits in the three cuts. These results may be due to the presence of transgrassive segregations and the major role of additive as well as additive by additive gene action in the inheritance of fodder yield components with respect to these two hybrids. The means of most backcrosses strongly tended to be toward the respective recurrent parents, reflecting the role of additive and epistasis gene effects. Furthermore, the results showed that most of studied traits were significantly influenced by one or more type of epistasis effects, which included additive × additive, additive × dominance and dominance × dominance gene effects as appeared in the three studied crosses, indicating the role of non-allelic interaction in the genetic expression of fodder traits. Number of tillers per plant was strongly associated with number of leaves per plant, green fodder yield per plant and dry fodder yield per plant at genetic level.

In conclusion, the improvement of fodder yield in teosinte is possible through the direct production of F_1 hybrids, such as Guatemala x Balsas or using these crosses to initiate the selection program for producing superior lines for their combining ability using the number of tillers per plant as morphological marker.

Keywords: Teosinte, Gene Action, Inbreeding Depression, Heterosis

INTRODUCTION

In Egypt as well as other countries, great efforts have been directed towards the improvement of summer fodder crops. Teosinte could provide an answer to overcome the problem of the little production of summer fodder feed for farm animals. Importance of teosinte as a fodder crop can be judged from the fact that, it has the advantage of giving very high yields, due to profuse tillering's capacity which is absent in fodder maize. Besides, it can give three cuts from April to November comparing with only one cut obtained from fodder maize. In addition, teosinte like maize can be safely feed on at any stage of growth (Relwani, 1968). Although, the need for the increased production of summer fodder is so keenly felt in Egypt, the Egyptian plant breeders have not focus much of their attention on improving fodder teosinte.

During the last two decades, information about teosinte has been given by several investigators among them (Smith *et al.*, 1984, Abdel-Twab and Rashed, 1985, Aulicino and Magoja, 1991, Sohoo *et al.*, 1993, Alan and Sundberg 1994, Jode and James, 1996 and Jode *et al.*, 1996) but all available information has contributed to the relationships among teosintes and between teosinte and maize, in addition to the characterization of teosinte for agronomic traits.

Recently, a few authors presented information related to the nature of gene action of fodder yield components (Abd EL-Maksoud *et al.*, 1998) and grain yield components (Abd EL-Maksoud *et al.*, 2001), but these studies were not enough to decide the way to improve teosinte as a new summer fodder crops in Egypt.

A breeding program usually makes use of the information concerning the relative importance of genetic variance components, when the additive gene action represents the main component in the genetic variation, a maximum progress must be expected in the selected character. On the other hand, the presence of a relatively high non-additive gene action indicates that a hybrid program will perform good prospects for the considered character, as a result of the direct relationship between the non-additive gene action and heterosis. Hence, in this study an attempt was made in order to partition the genetic variance to its components for fodder traits through studies on different generations of the promising hybrids of teosinte, which were observed during our previous investigations (Abd EL-Maksoud *et al.*, 1998). In addition, consideration was given to study the possible association existed between some pairs of fodder traits. Such study may help in improving teosinte through hybridization and/or selection.

MATERIALS AND METHODS

Genetic Materials:

The genetic materials used in this investigation included four teosinte races, representing a wide range of diverse geographic origins: Rayana (Damietta, Egypt), Central plateau (Michaocan, Mexico), Guatemala (Jutiapa, Mexico) and Balsas (Central Geurrors, Mexico). These races were obtained from forage crops research section, Agricultural Research Center, Ministry of Agriculture, Giza, Egypt. During the growing season of 1997 at Faculty of Agriculture Research Station, Mansoura Univ., these four races were planted. At the flowering stage all possible crosses excluding reciprocal among these four parental races were hand made according to a half daillel cross mating design. In addition, all parental genotypes were also self pollinated to increase seeds from each one. Seeds of these F_1 hybrids and their parents were sown in 1998 growing season for preliminary evaluation. Three F_1 hybrids were selected according to their superiority for number of tillers per plant (Abd El-Maksoud *et al.*, 1998). These crosses were Rayana × Balsas, Central plateau × Balsas, Guatemala × Balsas. During the growing season of 1999, some flowers from each parent and F_1 plants were self pollinated in order to increase seeds from parental genotypes as well as to produce F_2 generation seeds. Some F_1 plants were also back crossed to their parents in order to obtain BC_1 and BC_2 seeds. In addition, the crosses between these parents were done again in the same manner to increase F_1 seeds.

Experimental design and procedure:

In the summer of 2000 and 2001 years, 16 entries which included 4 parental lines, 3 F_1 hybrids, 3 F_2, 3 BC_1 and 3 BC_2 generations were evaluated at Faculty of Agriculture Research Station, Mansoura University.

The experimental design used was split plot design with three replications in both years. Each block/replicate consisted of three main plots, which included three crosses. Each main plot was divided to six sub-plots, which included the six generations. Sub-plot size was one row for each parent as well as F_1 hybrids, while it was three rows for each F_2 generation as well as back crosses. Each row was 6 meter long and 0.6 m wide. Hills were spaced 0.3 m apart to insure a constant stand of 20 hills per row. Plants were thinned to one plant per hill. Ordinary cultural practices were followed as usual for the teosinte field in the two seasons. Data recorded on 10 guarded plants, which were chosen randomly from each row in three cuts at two seasons for the following forage traits: number of tillers per plant (NT/P), number of leaves per plant (NL/P), green fodder yield per plant (GFY/P), dry fodder yield per plant (DFY/P) and crude protein percentage (C.P.%). The first cut was taken after 60 days from the day of sowing, the second cut was taken after 30 days from a day of the first cut and the third cut was taken after 30 days from a day of the second cut.

Statistical analysis:

Several analyses of variances were made in order to test the significance of differences among crosses, populations and populations within each cross with respect to all the studied traits according to Steel and Torrie (1980).

The amount of heterosis was determined as the percentage increase of the F_1 hybrids mean over the average of its two parents or above its better parent. While, the inbreeding depression was measured as a percentage deviation of F_2 generation than their the corresponding F_1 hybrids.

The scaling test (A , B and C) were determined according to the formulae outlined by Mather and Jinks (1982) for testing deviations of segregation from the additive and dominance model of gene effects. Then, standard errors of A, B and C are obtained in order to judge the significance of the departures of each calculated value from zero. The standard errors are equal to the square roots of the corresponding variance. "t" values were calculated by dividing the effects of A, B, and C by their respective standard error. These values were compared against tabulated "t" values at 0.05 and 0.01 levels of probability. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. Therefore, the six parameter model is used to estimate various types of gene effects. If the "t" test insignificantly differed from zero, the additive-dominance model is adequate to interpret the nature of gene action.

Six parameter models are m, a, d, aa, ad and dd, these stand for mean effects, additive, dominance, additive × additive, additive × dominance and dominance × dominance gene effects, respectively. These parameters and their variances, standard error and calculated "t" values were estimated according to Gamble's (1962) procedure.

In order to estimate the phenotypic and genotypic correlation between any pair of traits, A covariance analysis between all pairs of studied traits was made from the combined data over all studied crosses according to the procedure out-lined by Singh and Chauldhary (1985) in order to calculation the phenotypic and genotypic correlation coefficients as follow.

$$\text{Phenotypiccorrelation}\ (r_{ph}) = \frac{Cov ph_1 . ph_2}{\sqrt{\sigma^2 ph_1 .\ \sigma^2 ph_2}}$$

$$\text{Genotypiccorrelation}\ (r_g) = \frac{Cov g_1 . g_2}{\sqrt{\sigma^2 g_1 .\ \sigma^2 g_2}}$$

Where:

$Cov\ ph_1 .\ ph_2$ is the phenotypic covariance between any pair of traits.

$Cov\ g_1 . g_2$ = is the genotypic covariance between any pair of traits.

$\sigma^2 ph_1$ and $\sigma^2 ph_2$ = are the phenotypic variance of the first and second traits, respectively.

$\sigma^2 g_1\ and\ \sigma^2 g_2$ = are the genotypic variance of the first and second traits, respectively.

The significant of the phenotypic (r_{ph}) and genotypic (r_g) correlation coefficient were tested by using "t" test at 0.05 and 0.01 levels of probability as described by Steel and Torrie (1980).

- Calculated "t" test values for (r_{ph}) as follow:

$$t_{r_{ph}} = \frac{r_{ph}}{\sqrt{\frac{1-(r_{ph})^2}{n-2}}}$$

- Calculated "t" test values for (r_g) as follow:

$$t_{r_g} = \frac{r_g}{\sqrt{\frac{1-(r_g)^2}{n-2}}}$$

Then, the calculated "t" values were tested against the tabulated "t" values at both levels of probability.

RESULTS AND DISCUSSION

Analyses of variance:

The data which were recorded from the two years for all studied traits were set up in a combined analyses of variance for first, second and third cut and the obtained results are shown in Table 1. The results indicated the presence of significant differences among crosses for number of tillers per plant, green fodder yield per plant and crude protein percentage in the three cuts. While, in the case of dry fodder yield per plant, the differences among crosses was significant only in the second cut. Also, the results revealed that the presence of highly significance among populations within crosses as well as among populations within each cross with respect to all studied traits in three cuts. These results reflected the diversity and the different genetic constitution of parents for these traits in the studied crosses. Therefore, the comparison between genotypic means is valid and the partition of this genotypic variance to its components could be made.

Furthermore, years, crosses by years and populations within crosses by years in addition to population within each cross by years mean squares were significant in most of occasions. This indicates that these populations gave different performances at different environmental conditions. This finding agree with the results obtained by Abd El-Maksoud *et al.*, (1998).

Mean performances of genotypes:

The performances of the studied genotypes appeared to be varied from year to another as well as from cut to another with respect to their means for most of studied traits. Therefore, the means over both years would be more suitable to represent the data. The six populations means of the three crosses from the combined data over both years were determined for the first, second and third cuts and the obtained results are presented in Table 2. The means showed that, although there was no specific parents exhibited highest mean through the three cuts with respect to most of studied traits, the Balsas race (K) was the best in number of tillers/plant (N.T/P) over the three cuts and for number of leaves per plant (NL/P) in the first and second cuts. While, the central plateau race (P) was the highest parent for green fodder yield/plant (GFY/P) and dry fodder yield per plant (DFY/P) for first and third cuts with mean values (237 gm and 49.6 gm) and (652 gm and 90.5 gm), respectively. The Rayana (E) followed by Balsas (K) races were the best parents for crude protein percentage (CP%) in the first cut with the means of 11.4% and 9.8%, respectively. While, Guatemala race (T) was the best parent for crude protein percentage (CP%) with the means values of 7.5% and 6.8% in the second and third cut, respectively.

Table 1: The combined analysis of variance and the mean squares for fodder yield component traits of crosses and their populations at the three cuts.

S.O.V	d.f	N.T/P			N.L/P			GFY/P			DFY/P			C.P%		
		I	II	III	I	II	III	I	II	III	I	II	III	I	II	III
Years (Y)	1	9.6*	837.1**	339.3**	1.8	19283**	2322**	196087**	10816280**	3717308**	332.0	39821**	53492**	2.53**	0.002	0.05
R/Y	4	6.7*	2.9	13.6*	266.9*	321.5	991.6**	8454	116926	82411	179.7	1625	1152	0.13	0.63	0.53*
Crosses (C)	2	24.6**	13.7*	58.7**	591.6**	4565**	566.3**	41369**	491176**	68884**	1234.7	5728*	742.8	6.79**	2.4**	6.28**
C/Y	2	0.4	30.7**	45.7**	97.1	1074	594.6*	24142**	14443	283979**	554.2	1093	4286.1**	0.59**	0.82	0.55*
Rep.W.C*Y(Ea)	8	1.1	2.7	2.2	67.7	353.7	74.2	1090	6530	2632	340.6	840.6	346.6	0.08	0.24	0.10
Pop.W.C.	15	55.0**	99.7**	297.1**	1710**	2029**	8441**	108483**	466513**	369271**	5057.1**	4632**	4992.4**	5.35**	1.90**	1.21**
Pop.W.C1	5	68.3**	106.6**	370.0**	2392**	2055**	7161**	111093**	633291**	531050**	6076.2**	3324.4*	7497.5**	13.32**	1.76**	0.58**
Pop.W.C2	5	13.3**	37.8**	171.2**	507**	989.9**	6875**	83748**	212060**	189915**	1564.1**	4313.4**	2691.5**	1.94**	3.2**	2.04**
Pop.W.C3	5	83.5**	154.8**	350.2**	2230**	2043**	11288**	130608**	554188**	386848**	4530.5**	6258.3**	4788.2**	0.79**	0.7*	1.01**
Pop.W.C *Y	15	2.9	16.6**	46.6**	110.3	907.4**	2084**	26136**	224414**	284066**	1026.4**	2797.4**	4563.9**	0.25	0.59**	0.59**
Pop.W.C1 *Y	5	3.7	17.7**	59.6**	53.4	1163.9**	3157**	17299**	289954**	632275**	1039.3**	3557.9*	10348.7**	0.55*	0.52**	0.52*
Pop.W.C 2*Y	5	2.9	12.1**	45.0**	203.6	616.0*	1034	40658*	153280**	27246**	1514.2**	1453.9*	473.8	0.06	0.52**	0.91**
Pop.W.C3 *Y	5	1.9	19.9**	35.2**	73.96	942.2*	2059.63*	20452*	230007**	192678*	525.81	3380.8**	2869.2*	0.15	0.725*	0.358
Rep. W.P*C (Eb)	60	2.0	2.2	4.9	115.97	250.3	642.1	7568	38900	57239	219.4	666.5	779.8	0.16	0.13	0.145
Rep. W.P*C1	20	2.8	1.5	4.4	118.23	221.43	655.1	3415	55416	75180	104.73	1151.3	958.1	0.15	0.076	0.14
Rep. W.P*C2	20	1.5	2.9	3.8	119.0	223.3	615.9	5713	24541	4051	142.2	370.0	653.5	0.16	0.078	0.128
Rep. W.P*C3	20	1.6	2.2	6.2	110.63	306.1	655.0	13575	36742	56025	411.28	478.2	727.1	0.18	0.235	0.168

*,** Significant at 0.05 and 0.01 levels of probability, respectively

Table 2: The mean performances of genotypes and their standard error for for all studied traits through the three cuts from the data combined over two years for the three studied corsses

		N.T/P			N.L/P			GFY/P in gm			DFY/P in gm			C.P%		
		I	II	III	I	II	III	I	II	III	I	II	III	I	II	III
Lines	E	7.6 ±0.2	15.2 ±0.4	20.2 ±0.5	46.0 ±1.3	95.4 ±2.7	125 ±5.5	170 ±7.5	646 ±64	616 ±38	31.9 ±1.5	114 ±11	78.1 ±4.9	11.4 ±0.4	7.4 ±0.1	5.5 ±0.2
	P	9.6 ±0.3	16.9 ±0.6	23.9 ±0.6	59.9 ±1.5	101 ±3.0	149 ±6.3	237 ±13	565 ±43	652 ±25	49.6 ±2.8	106 ±7.2	65.2 ±25	8.78 ±0.2	7.0 ±0.2	5.81 ±0.2
	T	7.3 ±0.3	10.7 ±0.3	15.8 ±0.5	44.9 ±1.6	74.7 ±1.9	95.8 ±4.1	227 ±14	553 13.6	449 ±17	44.0 ±2.7	121 ±3.3	66.4 ±2.7	9.75 ±0.6	7.5 ±0.3	6.8 ±0.3
	K	11.8 ±0.3	22.3 ±0.6	24.0 ±0.6	77.8 ±1.9	128 ±3.5	129 ±5.1	173 ±8.9	452 ±54	359 ±16	33.5 ±1.7	67.0 ±6.1	47.8 ±2.1	9.8 ±0.2	7.3 ±0.2	6.2 ±0.1
E x K	F_1	10 ±0.3	19.6 ±0.6	32.2 ±0.7	61.8 ±1.7	112 ±3.4	186 ±7.9	311 ±13	833 ±53	755 ±26	57.2 ±2.5	117 ±6.8	81.7 ±1.9	10.9 ±0.2	7.5 ±0.2	5.9 ±0.7
	F_2	12.3 ±0.3	24.8 ±0.6	40.7 ±1.4	76.6 ±1.8	130 ±3.2	211 ±9.1	358 ±16	1144 ±44	941 ±54	49.7 ±2.0	127 ±6.7	933 ±5.2	8.8 ±0.2	6.4 ±0.2	6.4 ±0.2
	BC1	9.95 ±0.3	17.2 ±0.8	25.3 ±0.8	61.4 ±1.6	91.6 ±6.3	138 ±5.4	382 ±19	1064 ±71	545 ±27	66.6 ±3.3	118 ±7.7	83.1 ±4.2	8.0 ±0.2	6.6 ±0.2	6.1 ±0.2
	BC2	17.5 ±0.6	25.4 ±0.8	31.8 ±0.7	104±2 .9	133 ±4.6	161 ±4.8	528 ±32	1315 ±60	1182 ±49	118 ±6.5	132 ±6.0	154 ±5.3	6.9 ±0.2	6.5 ±0.2	6.1 ±0.4
P x K	F_1	10.8 ±0.3	15.9 ±0.5	22.6 ±0.6	69.5 ±1.7	94.9 ±2.8	122 ±3.3	401 ±18	513 ±32	618 ±16	67.7 ±3.1	58.3 ±3.2	77.7 ±2.1	9.3 ±0.1	7.1 ±0.2	6.0 ±0.1
	F_2	11.3 ±0.4	21.3 ±1.0	31.7 ±0.9	75.0 ±2.4	111 ±7.1	183 ±6.9	450 ±28	785 ±39	759 ±38	76.6 ±4.9	84.8 ±3.6	80.7 ±3.9	9.0 ±0.4	7.1 ±0.2	6.7 ±0.3
	BC1	10.7 ±0.3	20.2 ±1.0	25.3 ±0.6	68.1 ±1.7	118 ±7.1	139 ±4.2	411 ±23	881 ±44	724 ±24	64.3 ±3.9	131 ±6.4	98.9 ±3.2	8.1 ±0.1	7.4 ±0.1	6.3 ±0.3
	BC2	14.0 ±0.3	20.2 ±0.8	36.1 ±0.7	86.6 ±2.1	111 ±4.5	209 ±5.5	450 ±17	860 ±47	888 ±33	71.7 ±2.7	98.5 ±4.9	108 ±4.2	9.2 ±0.2	5.4 ±0.1	5.0 ±0.1
T x K	F_1	13.7 ±0.5	22.5 ±0.3	35.7 ±0.6	89.3 ±2.6	130 ±3.4	194 ±9.1	546 ±25	1151 ±68	983 ±26	97 ±4.5	143 ±7.2	120 ±2.6	9.9 ±0.1	7.9 ±0.2	6.7 ±1.5
	F_2	12.5 ±0.4	24.0 ±0.6	35.9 ±1.0	81.6 ±2.3	129 ±3.4	211 ±8.7	403 ±17	691 ±31	900 ±34	72.5 ±3.3	82.6 ±4.2	99.4 ±3.7	10.1 ±0.4	7.5 ±0.1	6.8 ±0.2
	BC1	13 ±0.4	19.2 ±0.9	25.3 ±0.9	77.0 ±1.8	110 ±3.5	139 ±4.7	497 ±24	836 ±68	716 ±27	102 ±5.5	15.5 ±9.5	93.9 ±3.4	9.2 ±0.3	7.2 ±0.3	7.5 ±0.2
	BC2	18.9 ±0.6	24.2 ±0.9	24.9 ±0.6	103 ±3.4	130 ±5.2	136 ±5.6	483 ±24	1179 ±76	506 ±17	72.1 ±3.7	146 ±12	56.4 ±1.9	10.1 ±0.2	6.9 ±0.4	6.4 ±0.2

Where E, P, T and K are Rayana, Central plateau, Guatemala and Balsas races, respectively

On the other hand, the results showed that the hybrids which involved at least one of the highest parent for any one of the studied traits had the highest mean values. In general, the best combination for fodder yield components was Guatemala (T) × Balsas (K), which showed the highest means for number of tillers/plant (NT/P), number of leaves/plant (NL/P), green fodder yield/plant (GFY/P) and dry fodder yield per plant in the three cuts and crude protein percentage (CP%) in the second and third cuts compared by other two hybrids as well as their parents. This finding reflected the presence of heterotic effect and the higher frequency of dominance genes controlling these traits in this hybrid. Therefore, it's F_2 generation appeared to be less than the F_1 hybrids means in most of studied fodder traits through the three cuts. Regarding to the other two crosses, F_2 generations appeared to be higher in means than their respective F_1 hybrids in most of studied traits in the three cuts. These results may due to the presence of transgrassive segregations and the major role of additive as well as additive by additive gene action in the inheritance of fodder yield components with respect to these two populations.

'The means also, showed that the highest backcrosses for green fodder yield/plant (GFY/P) and dry fodder yield/plant (DFY/P) in the three cuts were BC_2 of the Rayana (E) × Balsas (K) with mean values of 528 gm, 1315 gm, 1182 gm, respectively for GFY/P and 118 gm, 132 gm and 154 gm, respectively for DFY/P. While, the BC_1 as well as BC_2 of the cross Gyatemala (T) × Balsas (K) were the best for crude protein percentage in the three cuts. Generally, the means of most backcrosses strongly tended to be toward the respective recurrent parents, reflecting the role of additive and epistasis gene effects.

Heterosis and Inbreeding Depression:

The estimated amounts of heterosis and inbreeding depression from the combined data over both years for all fodder traits in the three cuts are shown in Table 3. Although, the cross Guatemala (T) × Balsas (K) exhibited positive and significant heterotic values over mid-parents and/or better parent for number of tillers/plant (NT/P), number of leaves/plant (NL/P), green fodder yield/plant (GFY/P) and dry fodder yield /plant (DFY/P) as well as positive, but insignificant values for crude protein percentage through the three cuts. Heterotic effects were absent in most of occasions with respect to other two crosses; Rayna (E) × Balsas (K) and Central plateau (P) × Balsas (K). The heterotic values over mid-parents in Guatemala (T) × Balsas (K) combination ranged from 1.84% to 172.65% for crude protein percentage (CP%) and green fodder yield/plant in the first cut, respectively. While, these values over better parent ranged from 0.89% to 139.85% for number of tillers per plant (2nd cut) and green fodder yield per plant (1st cut), respectively.

Regarding inbreeding depression, positive values were associated with highly significant and positive heterosis relative to mid-and /or high parent with respect to most of studied traits in the three cuts of the three crosses. This is logic, since the expression of heterosis in F_1 hybrids will be followed by considerable reduction in the F_2 generation performances. The high level of heterosis and reduction due to inbreeding depression in these occasions were taken as evidence of the relative importance of dominance gene effects in these crosses. Significant heterosis and negative inbreeding depression were detected for number of tillers/plant (NT/P), number of leaves/plant (NL/P), and green fodder yield/plant in the three cuts, dry fodder yield/plant in the second and third cuts of the cross Rayana (E) × Balsas (K) as well as some cases in the other two crosses. This observed discrepancy, where the presence of heterosis and absence of inbreeding depression may due to the role of additive and additive by additive gene action and /or may due to the presence of linkage between genes controlling these traits, with respect to this cross. In this respect, Tarumoto (1974) reported that inbreeding depression in F_2 generation appeared largely for sorghum forage yield and Kadam *et al.* (2000) showed that F_2 heterosis values ranged from -36% to 232% among population in sorghum. On the other hand, Khristova *et al.* (1985) found that inbreeding depression in the F_2 was usually much less than the heterosis percentage of the F_1 in the crosses between maize × teosinte.

Table 3: Heterosis over mid-parents (M.P) and high parent (H.P), inbreeding depression (I.D) and potence ratio (P) for all studied traits from the data combined over two years through three cuts

			NT/P	NL/P	GFY/P	DFY/P	C.P.
Rayana × Balsas	H, mp%	I	3.09	-0.24	81.4**	74.92**	2.70
		II	4.58	0.35	51.63	28.64	1.22
		III	45.7**	46..4**	54.68	29.78	-0.17
	H, hp%	I	-15.2	-20.62	80.3*	70.44*	-4.50
		II	-12.10	-12.59	28.9	1.83	0.40
		III	34.16**	43.79**	22.4	4.60	-5.64
	I.D	I	-23.30	-23.9	-14.90	13.11	18.53
		II	-26.27	-15.8	-37.20	-9.25	16.04
		III	-31.10	-13.37	-24.72	-14.11	-9.83
Central plateau × Balsas	H, mp%	I	0.74	0.91	95.50**	62.93**	0.10**
		II	-19.0	-17.50	0.98	-32.91	-0.56
		III	-5.64	-12.0*	22.37	12.36	0.50
	H, hp%	I	-8.80	-10.73	68.94**	36.50	-4.91
		II	-28.92	-26.20	-9.10	-45.40	-2.46
		III	-5.83	-17.80	-5.09	-14.14	-2.74
	I.D	I	-4.9	-7.99	-11.35	-13.36	3.01
		II	-34.38	-17.88	-52.89	-46.18	0.07
		III	-40.11	-49.18	-22.72	-3.79	-11.11
Guatemala × Balsas	H, mp%	I	43.45**	45.50**	172.65**	150.32**	1.84
		II	36.58**	28.57**	128.93**	51.60*	6.63
		III	79.40**	72.60**	143.12**	111.03**	2.30
	H, hp%	I	16.10**	14.80**	139.85**	120.45**	1.74
		II	0.89	1.63	108.09**	17.42	5.35
		III	48.75**	50.03**	118.80**	81.50**	-2.34
	I.D	I	8.75	8.60	16.53	25.25	-1.58
		II	-6.55	-0.57	39.97	42.30	5.45
		III	0.28	-8.60	8.38	17.60	-1.65

***,** Significant at 0.05 and 0.01 levels of probability, respectively**

Scaling tests:

To test the presence or absence of epistatic gene action, the A, B and C scaling tests were applied for all studied traits. The significance of any one of the three tests indicated the presence of non-allelic interaction (epistasis). While, if the scaling tests values are insignificantly differed from zero, the additive, dominance model is adequate to interpret gene effects.

Therefore, the data which were obtained from the two years in three cuts were set up in a combined scaling tests and the obtained results are shown in Table 4.

Table 4: Scaling tests (A, B and C) and their standard errors for all studied traits through three cuts from the data combined over both years for all studied traits.

Crosses	Scale	Cut	N.T/P	N.L/P	GFY/P	DFY/P	C.P.%
(E) * (K)	A	I	2.3±0.69**	14.9±3.86**	33.9±40.05	44±6.9**	-6.14±0.64**
		II	-0.4±2.01	-24.6±13.2	649.7±155.0**	5.3±20.13	-1.65±0.42**
		III	-1.7±1.75	-34.5±14.45**	-280.8±72.3**	6.35±9.7	0.81±0.47
	B	I	13.2±1.17**	69.25±6.3**	532.9±64.1**	145.9±13.3**	-6.79±0.46**
		II	8.9±1.7**	27.0±10.3**	1345±129.7**	80±14.5**	-1.83±0.44**
		III	7.35±1.65**	7.4±13.0	1250.6±86.5**	179.9±9.3**	0.1±0.73
	C	I	9.8±1.3**	58.85±8.1**	425.8±70.9**	19.1±9.2**	-7.46±1.03**
		II	22.5±2.8**	71.9±15.2**	1450±220.9**	94.1±32.5**	-3.94±0.86**
		III	54.4±4.75**	218.2±39.2**	1280±214.02**	83.8±20.9**	2.31±0.71**
(P) * (K)	A	I	1.1±0.76	6.9±3.98	184.1±5.7**	11.3±8.6	-1.94±0.32*
		II	7.7±2.1**	40.9±14.76**	683±100.7**	96.9±15.1**	0.6±0.37
		III	3.95±1.8*	6.7±10.9	177.8±54.9**	29.54±7.35**	0.78±0.64
	B	I	5.35±0.75**	35.65±4.8**	287.9±39.5**	42.3±6.5**	-0.74±0.52
		II	2.3±1.8	-1.0±10.1	754.4±99.9**	60.5±11.6**	-3.63±0.41**
		III	25.5±1.6**	166.8±12.6**	799.7±70.05**	91.88±8.6**	-2.28±0.29**
	C	I	2.35±1.78	33.15±10.4**	548.3±113.3**	88±19.9**	-1.15±1.31
		II	14.4±2.5**	27.7±13.77	1096±168.2**	37.5±18.2*	-0.12±1.04
		III	33.45±3.7**	207.9±28.5**	788.8±155.7**	29.02±16.6	2.67±1.22*
(T) * (K)	A	I	5±0.91**	19.75±7.2**	220.3±56.6**	63.1±11.9**	-1.23±0.77
		II	5.2±1.89**	15.0±11.86	-31.7±150.4	-34.1±20.5	-0.98±0.67
		III	-0.8±1.75	-10.8±13.5	0.6±59.0	1.1±7.65	1.51±0.45**
	B	I	12.3±1.3**	48.8±7.5**	209.3±56.8**	13.65±8.8	0.68±0.41
		II	3.5±1.99	0.8±11.41	754.1±171.9**	72.5±25.5**	-1.4±0.76
		III	-9.95±1.35**	-50.85±14.95**	-330.5±40.0**	-55.4±5.15**	-0.06±0.45
	C	I	3.3±1.76**	34.55±10.7**	81.5±89.7	18.6±16.2	1.04±1.63
		II	18.1±2.8**	53.7±16.6**	-544.2±180.0**	-156±22.5**	-0.74±0.73
		III	32.35±4.2**	231.8±37.7**	827.9±139.2**	42.4±15.95**	1.33±0.92

***,** Significant at 0.05 and 0.01 levels of probability, respectively.**
Where: E, P, T and K are Rayana, Central plateau, Guatemala and Balsas races, respectively.

The results revealed that the scaling test values insignificantly differed from zero for 3rd cross [Guatemala (T) × Balsas (K)] with respect to crude protein percentage. These findings indicated that the absence of epistasis and the additive-dominance model is adequate to interpret gene effects in this cross for this trait. While the six parameter model is valid to explain the nature of gene action for other cases.

Types of gene action:

The results presented in Table 5, showed that the estimates of mean effect (m) which reflects the contribution of the over all mean plus the locus effects and the interaction of the fixed loci was found to be highly significant for all studied fodder traits with respect to the three hybrids in the three cuts, indicating the contribution of additive, dominance and epistatic gene effects in the genetic expression of these traits. However, Rayana (E) × Balsas (K) and Central plateau (P) × Balsas (K) crosses showed that additive (a) gene effects were positive or negative significant for all studied traits in most of cuts. These values were higher in magnitude than the corresponding values of dominance gene effects (d) in most occasions, indicating the major role of additive gene effects in these two crosses.

Table 5: Type of gene action for all studied traits through the three cuts from the data combined over two years for the three studied corsses.

Crosses			N.T/P	N.L/P	GFY/P	DFY/P	C.P.%
Rayana x Balsas	m	I	12.3±0.27**	76.6±1.74**	358±16.1**	49.7±1.9**	8.84±0.2**
		II	24.8±0.6**	130.2±3.2**	1144±44.5**	127.5±6.5**	6.42±0.19**
		III	40.7±1.12**	211.5±8.9**	941±50.7**	93.3±4.9**	6.44±0.15**
	a	I	-7.55±0.62**	-43.05±3.3**	-145±36.1**	-51.7±7.3**	1.12±0.29**
		II	-8.2±1.2**	-42.3±7.7**	-250±85.5**	-13.4±9.7	0.15±0.26
		III	-6.45±0.97**	-23.25±7.3**	-636±53.6**	-71.6±6.6**	0.02±0.41
	d	I	6±1.69**	25.12±9.9*	510.3±98**	195.3±16.7**	-5.18±1.08**
		II	-13.2±3.5**	-69.1±20.6**	467.8±258	17.2±34.4	0.55±0.95
		III	-38.6±5.01**	-186±39.5**	-43.8±231.8	121.2±24.0**	1.44±1.09
	aa	I	5.7±1.65**	25.3±9.64**	389±96.9**	170.8±16.5**	-5.47±1.04**
		II	-14.0±3.5**	-69.5±20.1	184.2±249.2	-8.8±33.1	0.46±0.94
		III	-48.7±4.97**	-245±38.6**	-310.7±229.4	102.4±23.8**	-1.4±1.08
	ad	I	-5.45±0.65**	-27.2±3.5**	-125±36.6**	-50.9±7.3	0.33±0.38
		II	-4.6±1.3**	-25.8±8.0**	-347±94.4**	-37.3±11.5**	0.08±0.28
		III	-4.53±1.1**	-20.95±8.2*	-765±57.7**	-86.8±7.13**	0.35±0.43
	dd	I	-21.2±2.8**	-109±15.5**	-1204±161**	-360.6±30.5**	18.4±1.6**
		II	5.5±5.7	67.1±34.5	-2179±409**	-76.5±51	3.02±1.36*
		III	-43.1±6.3**	272±49.2**	-659±303.1*	-288.6±33.8**	0.49±1.83
Central plateu x Balsas	m	I	11.3±0.4**	75±2.4**	450±26.6**	76.6±4.7**	8.99±0.32**
		II	21.3±0.5**	111.8±2.9**	785±36.3**	84.8±3.6**	7.11±0.22**
		III	31.6±0.86**	183.2±6.7**	759±37.5**	80.7±3.9**	6.69±0.29**
	a	I	-3.25±0.44**	-18.5±2.67**	-38.8±28.2	-7.4±4.5	-1.1±0.28**
		II	0.0±1.4	7.45±8.4	20.6±61.3	32.5±8.1**	1.97±0.18**
		III	-10.8±1.1**	-70.2±6.9**	-164±41.7**	-9.8±5.2	1.33±0.3**
	d	I	4.2±1.86*	14.9±11.1	100.7±125.3	-8.3±21.7	-1.52±1.42
		II	-8.12±3.5*	-7.9±20.9	345±194.7	85.7±22.2**	-2.9±0.9**
		III	-7.21±4.1	-51.22±30.7	301.7±174.2	100.9±19.1**	-4.1±1.5**
	aa	I	4.1±1.82*	9.4±10.9	-76.5±123.8	-34.4±21.5	-1.53±1.42
		II	-4.4±3.4	12.3±20.5	340±190.0	119.9±21.5**	-2.9±0.95**
		III	-4±4.1	-34.5±30.3	188.6±172.8	92.4±18.9**	-4.2±1.43**
	ad	I	-2.12±0.5**	-14.4±2.9**	-51.6±29.6	-15.5±4.9**	-0.61±0.31
		II	2.7±1.4	20.9±8.8*	-35.7±68.8	18.2±9.3	2.11±0.22**
		III	-10.78±1.4**	-80.0±7.9**	-310±44.4**	-31.2±5.6**	1.53±0.34**
	dd	I	-10.55±2.5**	-51.9±14.9**	-395±165.9*	-19.2±28.3	4.21±1.77*
		II	-5.5±5.9	-52.2±36.4	-1778±297**	-277.3±37.1**	5.94±1.26**
		III	-25.45±5.7**	-138±40.2**	-1166±230**	-213.8±26.9**	5.66±1.93**
Guatemala x Balsas	m	I	12.5±1.12**	81.55±2.8**	403±17.9**	72.5±3.3**	10.1±0.37**
		II	24±0.6**	129.5±3.6**	691±30.3**	82.6±4.03**	7.45±0.12**
		III	35.8±0.99**	211.6±8.3**	900±33.9**	99.35±3.7**	6.8±0.18**
	a	I	-5.9±1.55**	-26.1±3.8**	13.7±34.7	30±6.4**	-0.96±0.32
		II	-5.0±1.3**	-19.8±7.7**	-342±1015**	-31.4±15.0*	0.3±0.44
		III	0.45±0.96	3.1±7.15	210±32.8**	37.55±3.9**	1.09±0.26**
	d	I	18.5±5.92**	66.8±12.3**	674±103.9**	116.5±19.04**	-1.42±1.66
		II	-3.4±3.6	-8.8±21.5	1915±246**	237.5±35.8**	-1.15±1.08
		III	-27.3±4.54**	-211±37.5**	-578±151**	-33.3±16.9*	0.76±0.99
	aa	I	14.0±5.44**	34±11.95**	348±99.8**	58.2±18.4**	-1.59±1.63
		II	-9.4±3.5**	-37.9±21.1	1266±237**	194.4±34.8**	-
		III	-43.1±4.46**	-293±36.4**	-1157±150**	-96.7±16.7**	-
	ad	I	-3.65±2.36	-14.5±4.1**	5.5±35.8	24.7±6.7**	-0.96±0.43*
		II	0.82±1.3	7.1±7.9	-392±104**	-53.3±15.5**	-
		III	4.57±1.1**	20.02±7.9*	165±34.9**	28.3±4.2**	-
	dd	I	-31.3±8.96**	-102±18.8**	-777±165**	-134.9±30.5**	2.13±2.09
		II	-3.75±5.8	22.1±34.9	-1989±446**	-232±64.9**	-
		III	53.85±5.9**	355±48.3**	1487±191**	151.0±22.3**	-

***,** Significant at 0.05 and 0.01 levels of probalility, respectively**

This finding may explain the absence of heterosis, especially over higher parent in these crosses in most of occasions. Also, dominance gene effects (d) were positive or negative significant with respect to the cross Guatemala (T) × Balsas (K) for all studied traits except for number of tillers/plant and number of leaves/plant in the 2nd cut, and crude protein percentage (three cuts). In this cross, the values of dominance gene effects (d) were larger in magnitude than the corresponding values of additive gene effects (a) for all studied traits in most of cuts, indicating the higher frequency of dominance genes in this combination. These findings may explain the presence of heterosis for most of studied traits in this cross. Furthermore, the results showed that most of studied traits were significantly influenced by one or more type of epistatic effects, which included additive × additive (aa), additive × dominance (ad) and dominance × dominance (dd) gene action as appeared in the three studied crosses, indicating the role of non-allelic interaction in the genetic expression of fodder traits. These results are in agreement with the results obtained by Todorova and Lidanski (1985) in maize × teosinte hybrids; Mohamed *et al.* (1999); Jha *et al.* (1999) and Suneetha *et al.* (2000) in fodder maize; Manickam and Das (1994) and Kadam *et al.* (2000) in sorghum.

Genotypic and phenotypic correlation:

The information about the degree of association among different traits of teosinte is of great importance for breeders. The coefficient of genotypic correlation provide a measure of the genetic association between pairs of traits to identify the traits which could be used as indicator for improvement of other traits through the selection programs. The genotypic and phenotypic covariance's between each pair of studied traits were calculated for all crosses and their parental races. Subsequently, the genotypic and phenotypic correlation's among all studied traits were estimated and the obtained results are shown in Table 6. Significant positive genotypic and phenotypic correlations were observed between number of tillers/plant (NT/P) and each of number of leaves/plant, green fodder yield/plant and dry fodder yield/plant (DFY/P). Dry fodder yield per plant was positively associated with each of number of leaves/plant and green fodder yield per plant at genotypic and phenotypic levels. In general, the coefficient of genotypic correlations were larger in magnitudes than the corresponding values of phenotypic correlations indicating that these pairs of traits are strongly genetically associated to each other. Therefore, the selection for one of these traits will be associated with the improvement of the other traits during the selection program. These results are in agreement with Jha *et al.* (1998); Singh and Dash (2000) in fodder maize; Anup and Vijayakumar (2000) in sorghum.

In conclusion, from the previous results related to the gene action and the performances of the three populations, it could indicated that the improvement of fodder yield in teosinte is possible through the direct production of F_1 hybrids, such as Guatemala x Balsas or using these hybrids to initiate the selection program for producing superior lines for their combining ability using the number of tillers per plant as morphological marker.

Table 6: Genotypic (above diagonal) and phenotypic (blow diagonal) correlations for each pairs of all studied traits combined over the three cuts during the first and second years.

	NT/P	NL/P	GFY/P	DFY/P	C.P%
NT/P		1.00**	0.74**	0.50*	-0.34
NL/P	0.90**		0.76**	0.50*	-0.30
GFY/P	0.67**	0.49*		0.99**	-0.52
DFY/P	0.42	0.42	0.81**		-0.39
C.P%	-0.21	-0.16	-0.03	-0.12	

***,** Significant at 0.05 and 0.01 levels of probability, respectively.**

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تقييم بعض هجن الذرة الريانة المبشرة وسلوكها الوراثى فى محصول العلف الأخضر

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برغم أن هناك حاجة ملحة إلى زيادة إنتاج الأعلاف الخضراء صيفا فى مصر إلا أن مربى النبات لم يهتموا الإهتمام الكافى بتحسين الأعلاف الخضراء الصيفية الغير تقليدية مثل الذرة الريانة – وحيث أن المعلومات الكافية عن الفعل الجينى لها أهمية لغرض إتاحة الفرصة لمعرفة الوسيلة المثلى لتحسين مكونات العلف الأخضر فإن من أهداف هذا البحث تقسيم التباين الوراثى لمكوناته لصفات محصول العلف الأخضر من خلال تقييم عدد من الأجيال المختلفة (الآباء – الجيل الأول – الجيل الثانى – الجيلين الرجعيين) لهجن الذرة الريانة المبشرة والتى لوحظت من خلال الأبحاث السابقة.

والنتائج المتحصل عليها امكن تلخيصها فيما يلى :-

أظهرت النتائج أن الهجن المدروسة تختلف معنويا فى عدد الأشطاء للنبات الواحد ، محصول العلف الأخضر للنبات ونسبة البروتين الخام خلال الثلاث حشات وإيضا أشارت النتائج ان العشائر داخل الهجن والعشائر داخل الهجين الواحد أظهرت إختلافا عالى المعنوية فى كل الصفات المدروسة والخاصة بمكونات العلف الخضر خلال الثلاث حشات. مما يشير إلى ان هناك إختلافا بين المكونات الوراثية للاباء الداخلة فى تكوين هذه الهجن ، وأكثر من ذلك فإن متوسط المربعات للمواسم والتداخل بين الهجن والمواسم بالإضافة إلى العشائر داخل الهجن والمواسم كانت معنوية فى معظم الحالات وهذا يشير إلى أن هذه التراكيب الوراثية تسلك سلوكا" مختلفا" مع الظروف البيئية المختلفة.

كان الهجين Guatemala x Balsas هو أفضل الهجن فى مكونات محصول العلف الأخضر حيث أعطى اعلى متوسط للصفات المدروسة خلال الثلاث حشات مقارنة بالهجيين الآخرين وآبائها وفى هذا الهجين كان تأثير الفعل الجينى السيادى أكبر من الفعل الجينى الإضافى لمكونات محصول العلف الأخضر فى معظم الحشات مما يشير إلى زيادة تكرار الجينات ذات الفعل الجينى السيادى فى آباء هذا الهجين وهذا يفسر وجود قوة هجين خاصة عند مقارنة الجيل الأول بأفضل الأباء وفى هذا الهجين لوحظ أنخفاض معنوى ناتج عن التربية الداخلية بمقارنة الجيل الثانى بالجيل الأول مما يؤكد دور الفعل الجينى السيادى فى توريث هذه الصفات فى هذا الهجين.

أما بالنسبة للهجن Rayana x Balsas ، Central plateau x Balsas كان متوسطات الجيل الثانى أعلى من متوسطات الجيل الأول لمعظم الصفات المدروسة خلال الثلاث حشات مما يشير إلى وجود إنعزال متجاوز الحدود فى الأجيال الأنعزالية راجع إلى الدور الرئيسى الذى يلعبه الفعل الجينى الإضافى والتداخل بين الإضافة x الإضافة فى توريث هذه الصفات فى هذين الهجنيين. ولذلك كان متوسط الهجن الرجعية يسير فى إتجاه الآباء الرجعية مما يؤكد دور كل من الفعل الجينى المضيف والتفوق. وبالتالى نتائج تحليل التباين الوراثى أشارت إلى أن معظم الصفات المدروسة كانت تتأثر بواحد على الأقل من طرز الفعل الجينى التفوقى والذى يشمل إضافة x إضافة ، إضافة x سيادة ، وسيادة x سيادة.

كان هناك إرتباط وراثى ومعنوى بين صفة عدد الأشطاء للنبات وكل من عدد الأوراق للنبات ، محصول العلف الأخضر للنبات ، محصول العلف الجاف للنبات. ويمكن أن تستخلص من هذه النتائج أنه من الممكن تحسين محصول العلف فى الذرة الريانة من خلال الإنتاج المباشر للهجن باستخدام Guatemala x Balsas أو إستخدام هذه الهجن كمصدر لإنتخاب سلالات مميزة بقدرتها العالية على التآلف إعتمادا" على عدد الأشطاء للنبات كعلامة مظهرية.