J.Agric.Chem.and Biotechn., Mansoura Univ.Vol. 8(1): 15- 20 , 2017

Gene Action for Several Important Traits in Some Promising Maize - Teosinte Hybrids Using Generation Mean Analysis

Sakr, H. O.
Forage Research Dept., FCRI, ARC, Egypt.

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 improv fodder teosinte as silage exchange for maize. 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 (P1, P2, F1, F2, BC1, BC2) of the promising maize-teosinte crosses under two locations (El-Serw and Sids). The results indicated the presence of significant differences among crosses for all studied traits. Also, the results revealed the presence of significance of populations within crosses and each cross. The cross SC10 × Rayana (R) was the highest among studied crosses for number of leaves (NL/P) (69.79), number of tillers (NT/P) (6.25), 5 th leaf area (5th LA) (643.56 cm^2) green fodder yield per plant (GFY/p) (3740.0 g) and dry fodder yield per plant (DFY/p) (1191.13 g). While the cross SC 122 × R was the highest for crude protein (CP) (16.52 %), digestible protein (DP) (11.78 %) and total digestible nutrients (TDN) (67.25 %). The F_2 generation of the three crosses in the two locations and their combined were less than corresponding values of F_1 hybrids for all studied traits. This finding reflected the presence of non-additive genetic variance plays the major role in the inheritance of these traits. The results also revealed that, the backcross mean of most of studied crosses tended toward the respective recurrent parent, suggesting the role of additive and dominance gene action effects. Most of studied traits were significantly influenced by one or more type of epistatic effects, which included additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) gene action as appeared in the three studied crosses. In general, green fodder yield per plant (GFY/p) was positively with all other traits. Therefore, it waould be concluded that the production of maize-teosinte hybrids is needed to be used as silage exchange for maize.

Keywords: Epistasis, Additive, Dominance, Zea mays, zea Mexicana(teosinte)

INTRODUCTION

In Egypt as well as other countries, great efforts have been directed towards the improvement of summer fodder crops. Numerous farmers use large area from maize for feeding as silage, so that the national production of grain of maize was decreases. Maize-teosinte crosses could provide an answer to overcome this problem by use maize-teosinte crosses as silage exchange for maize. Importance of maize-teosinte crosses as a fodder crop would be judged from the fact that, it has the advantage of giving very high yields, due to profuse tillering capacity which is absent in fodder maize. Beside it can give three cuts against one cut obtained from fodder maize (Sakr,2009). In addition, maize-teosinte crosses like maize can be safely feed on at any stage of growth. Teomaize crosses have been attempted in the past between teosinte and maize with partial success, but a concerted effort may produce a high yielding and a nutritious variety. In this respect, Chaugale and Chavan (1965) and Chaudhuri and Prasad (1969) reported the successful production of hybrids between maize and teosinte and a considerable amount of hetrosis was observed in most of the hybrids raised by them. On the other hand, Gill and Patil (1985) studied the forage production of maize and their hybrids (maizente) and mentioned that teosinte entries proved to be significantly superior over maizente hybrids and maize for green fodder and dry matter production. During the last three decades, information about the maize-teosintes crosses has been given by several authors (Smith *et al.*1984, Aulicino and Magoja 1991, sohoo *et al*. 1993, Alan and Sundberg 1994, Jode and James 1996). All the available information's have contributed to the relationships among teosintes and between teosintes and maize in addition to the characterization of teosintes for agronomic traits. Barriere *et al*. (1984) studied protein content and agronomic value in progenies from the cross maize × teosintes and reported that the top cross was high in silage (fodder) yield and protein yield/ha. Numerous researchers reported that the variance components of SCA for grain yield and other traits were larger than that due to GCA, indicating the importance of non-additive gene action in the inheritance of these traits; Mostafa et al.(1995), El-Shenawy *et al*. (2003), Aly and Amer (2008) and Barakat and Osman (2008) for grain yield in maize. On the contrary, IIchovska et al. (1995), in maize × teosinte hybrids, Abd El-Maksoud *et al*. (2001), in teosinte and Aly and Mousa (2008)in maize, reported that the additive genetic variance played an important role in the inheritance of plant height, grain yield and other traits. Recently, Sakr (2009), Sakr *et al*. (2009) and Sakr and Mona (2010), presented information about the nature of gene action for green fodder yield in teosinte × maize crosses. 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 would perform good prospects for the considered character, as results of the direct relationship between the non-additive gene action and heterosis. Hence, this study 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 maize-teosinte crosses which were observed during previous investigations (Sakr (2009), Sakr et al. (2009) and Sakr and Mona (2010). 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

Six basic sets of generations namely P1, P2, F1, F2, Bc1 and Bc2 were derived from three contrasting genotypes of maize and teosinte. Three single crosses (commercials) of maize,(*Zea mays L.*) SC10, SC122 and SC128 were crossed as female with local variety of teosinte (Rayana), (*Zea Mexicana L.*) as male produced from Forage Crop Research Department, Field Crops Research Institute, ARC, Egypt. The crosses were SC10 × Rayana (R), SC122 × Rayana (R) and SC128 × Rayana (R) in summer 2012 at El-Serw Research Station . These (F_1) crosses among the accessions were sown in summer 2013, to produce F_2 generation seeds. Some F1 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 2014, two field experiments were carried out at two locations, the first location at El-Serw Research Station, ARC and the second location at Sids Research Station, ARC. In each location, the 16 entries which included 4 parents, 3 F1, 3F2, 3 BC1, and 3BC2 generations were evaluated. The experimental design used was split plot design with three replications in both locations. Each block/replicate consisted of three main plots, which included three crosses. Each main plot was divided into six sub-plots, which included the six generations. Sub-plot size was one row for each parent as well as F1 hybrid, while it was three rows for each F2 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 and maize field in both locations. In the dough stage, data were recorded on 10 guarded plants, which were chosen randomly from each row at two locations for the following forage traits: plant height (Ph), number of leaves per plant (NL/P), number of tillers per plant (NT/P), 5^{th} leaf area (5thLA),(determined according to Owen(1968), using the following formula : maximum length × maximum width × 0.75) green fodder yield (GFY/P) and dry fodder yield (DFY/P). In addition forage quality traits were estimated by chemical analysis for plant samples

Chemical composition (forage quality traits)

Random samples of plants were shopped into 1-2 cm pieces and thoroughly mixed. A 300 g sample of fresh chopped roots was dried in an oven at 40^oC for 2 days and at 70^oC for 3 days. The dried samples were chemically analyzed for crude protein (CP %) and crude fiber (CF %) following the methods of A.O.A.C. (1980), by MAU, Agriculture Chemistry Dep. Faculty of Agriculture, Mansoura University. Total digestible nutrients (TDN %) and digestible crude protein (DCP %) were calculated following equations of Church (1979):

$$\mathbf{DP\ \% = CP \times 0.929 - 3.48,}$$

$$\mathbf{TDN\ \% = 90.36 - 0.29 \times CP - 0.86 \times CF.}$$

Statistical and genetic analyses

Using SAS software (SAS 9.1), analyses of variances were done for six populations (the two parents, F1, F2, Bc1, Bc2) within each cross with respect to all the studied traits. In addition, analysis of variance according to Split Block Design analysis of variance for the studied traits was performed to detect the significant of the observed differences among and within crosses according to Singh and Narayanan, 2000.

Scaling test

The scaling test (A, B and C) and their variances were determined according to the formula 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 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, dominance × dominance gene effects respectively. These parameters and their variances, standard error and calculated "t" values were estimated according to Gamble's (1962) procedure.

RESULTS AND DISCUSSION

Analyses of variance:

The data which were recorded from the two locations (El-Serw and Sids) for all studied traits were set up in a combined analysis of variance and the obtained results are shown in Table 1. Also the data were recorded for forage quality traits were set up in analysis of variance and the obtained results are shown in Table 2. With respect to forage yield and its component the results indicated the presence of significant differences among crosses for all studied traits. Also, the results revealed that the presence of highly significant differences among populations within crosses as well as among populations within each cross with respect to all studied traits. 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 performed.

Furthermore, location, cross by location and population within crosses by locations in addition to population within each cross by location mean squares were significant in most of occasions. This indicates that these populations gave different performances under different environmental conditions. These

findings agree with the results obtained by Abd El-Maksoud et al., (2004). With respect to forage quality, i. e. crude protein (CP), crude fiber (CF), digestible protein (DP), total digestible nutrients (TDN) percentages, presented in Table 3, the results revealed that most generations within all crosses had significant differences for all studied forage quality traits, indicating the existence of genetic variation for these traits. This finding indicates that further partitioning of genetic variance to its components and the comparisons between means are valid test. In fact the development of any plant breeding program is dependent upon the existence of genetic variability. Furthermore, the efficiency of selection and expression of heterosis also depends largely upon the magnitude of genetic variability present in the plant population (Singh and narayanan1993 and Singh and Chaudhary, 1999)

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

SOV	DF	Ph	Nl/plant	Nt/plant	5thLA	Gfy/plant	Dfy/plant
Location (L)	L -1=1	91180**	23776**	34.0**	533322**	32547546**	4517568**
R / L	L(r-1)=4	354	85.8	3.70**	7100**	59828	7630
Crosses (C)	C – 1=2	7653**	7521**	59.70**	266331**	2193469**	237886**
C × L	(c -1)(L-1)= 2	844*	200*	2.20	17771**	621149**	60743**
Rep. within C × L (error a)	L(r -1)(C-1)=8	567*	152**	0.50	504.00	53554	8441*
Pop. Within Crosses	C(p-1)= 15	55028**	19365**	632.80**	281757**	6705066**	809931**
Pop. Within Cross 1	P -1 =5	51726**	20571**	603.60**	383075**	8936251**	1096176**
Pop. Within Cross 2	P -1 =5	76367**	18943**	637.90**	227152**	5464276**	739662**
Pop. Within Cross 3	P -1 =5	36991**	18580**	656.90*	235045**	5714670**	593954**
Pop. Within Crosses × L	C(p-1)(L-1) =15	1971**	1014**	1.70**	12784**	572908**	90150**
Pop. Within Cross 1 × L	(p-1)(L-1)=5	1783**	987.8**	2.70	6082**	446686**	70656**
Pop. Within Cross 2 × L	(p-1)(L-1)=5	3601**	915.1**	1.20**	7923**	463179**	61502**
Pop. Within Cross 3 × L	(p-1)(L-1)=5	529	1141**	1.30**	24348**	808858**	138293**
Rep W Pop. × Crosses(error b)	cL(p-1)(r-1)=60	382	85.4*	2.1**	1216*	40110	6336**
Rep. within Pop. × cross 1	L(p-1)(r-1)=20	276	113.8	2.10*	1049	28670	4582
Rep. within Pop. × cross 2	L(p-1)(r-1)=20	564*	93.5*	2.20**	1681	49346	11160**
Rep. within Pop. × cross 3	L(p-1)(r-1)=20	305	48.7	1.80**	918	42313	3265

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

Table 2. Analysis of variance and mean squares for forage quality traits i. e. crude protein (CP %), crude fiber(CF %), digestible protein(DP%) and total digestible nutrients (TDN%), of crosses and their populations

SOV	DF	CP%	CF %	DP %	TDN %
Reps	r-1=2	0.26	0.58	0.31	10.25**
Crosses (Crs.)	c -1= 2	52.22**	4.63**	36.43**	56.12**
Rep. within Crs (error a)	(r -1)(C-1)=4	1.01	1.09	1.02	1.08
Pop. Within Crosses	C(p-1)= 15	134.34**	40.35**	116.26**	148.71**
Pop. Within Cross 1	P - 1 =5	190.65**	84.89**	160.60**	215.41**
Pop. Within Cross 2	P - 1 =5	81.29**	24.90**	74.32**	92.88**
Pop. Within Cross 3	P - 1 =5	131.09**	11.25**	113.87**	137.84**
Rep W Pop. × Crosses(error b)	c(p-1)(r-1)=30	0.81	0.70	0.56	0.82
Reps. within Pop. × cross 1	(p-1)(r-1)=10	1.62*	0.68	0.96	1.82*
Reps. within Pop. × cross 2	(p-1)(r-1)=10	0.39	0.62	0.40	0.32
Reps. within Pop. × cross 3	(p-1)(r-1)=10	0.41	0.79	0.32	0.32

Mean performances of genotypes

The means and standard errors of all studied traits for population within each cross were determined for the first location (Serw), and second location (Sids) and the obtained results are presented in Table 3. The means showed that there was no specific genotype which was superior or inferior for all studied traits at the two locations. However, the performances of these genotypes appeared to be varied from location to another with respect to their means for most of studied traits. Therefore, the means over both locations would be more suitable to represent the data. The six population means of the three crosses from the combined data across both locations, and forage quality traits were determined and the results are presented in Table 4. The mean values showed that the Rayana parent was the highest parent for plant height (Ph) (313.25 cm), number of leaves per plant (NL/p) (88.66), number of tillers per plant (NT/p) (14.58), and green fodder yield per plant (GFY/p) (2447.30 g). While the SC10 parent was the highest parent value for 5th leaf area (5th LA) (681.77 cm^2) and dry fodder yield per plant (DFY/p) (809.79 g). With the respect to forage quality traits, the parent SC128 was the highest parent value for crude protein (CP) (17.02%), crude fiber (CF) (11.39 %), digestible protein (DP) (12.33 %) and total digestible nutrients (TDN) (67.55 %). On the other hand, the results showed that the F_1 crosses which involved at least one of the highest parents with respect to any one of studied traits had the highest mean values for these traits. For instance, the cross SC10 × Rayana (R) was the highest crosses for number of leaves (NL/P) (69.79), number of tillers (NT/P) (6.25), 5 th leaf area (5th LA) (643.56 cm^2) green fodder yield per plant (GFY/p) (3740.0 g) and dry fodder yield per plant (DFY/p) (1191.13 g). While the cross SC 122 × R was highest for crude protein (CP) (16.52 %), digestible protein (DP) (11.78 %) and total digestible nutrients (TDN) (67.25 %). Furthermore, the F2 generations of the three crosses in the two locations and their combined were less than their corresponding values of F1 hybrids for all studied traits. This finding reflected the presence of heterotic effect where the non-additive genetic variance plays the major role in the inheritance of these traits. The results also revealed that, the backcrosses mean of most of studied crosses tended toward the respective recurrent parents in most of studied traits preferred the role of additive and dominance gene action effects.

Table 3. Mean performance of genotypes and their standard error for all studied traits at two locations (Serw and Sids).

		Ph		NL/P		NT/P		5TH LA		GFY/P		DFY/P	
		Serw	Sids	Serw	sids	serw	Sids	serw	Sids	serw	Sids	Serw	Sids
C1	P1	262±2.3	287±-3.7	14.8 ±0.15	15.2±0.15	1.0± 0.001	1.0±0.001	630±6.2	733±7.2	2071±10.6	2789±31.8	678± 8.9	941 ± 5.1
	P2	294±2.4	332±-4.0	70.2 ± 2.22	107 ± 2.50	14.3± 0.4	14.8 ± 0.38	358±8.82	435±5.5	2181±19.2	2712±16.9	567 ± 6.84	709 ± 2.3
	F1	306 ± 3.3	341±4.1	61.4 ± 2.68	78.2 ± 3.33	5.5 ± 0.18	7.0 ± 0.28	583±1.44	703 ± 8.2	3256±24.9	4223±40.5	1016 ± 7.3	1365 ± 8.4
	F2	225 ± 3.3	251±3.8	24.3 ± 1.6	42.3 ± 2.23	2.32 ± 0.21	3.55± 0.25	504±8.11	549 ± 7.9	2192±32.5	2577±49.9	667 ± 10.1	809 ± 20.2
	Bc1	214 ± 3.7	217±5.4	39.0 ± 2.07	43.7 ± 2.83	2.41 ± 0.31	2.50 ± 0.25	625±12.7	690 ± 11.2	1663±35.1	2239±84.5	496 ± 13.2	698 ± 28.1
	Bc2	236 ± 4.3	232±5.1	65.1 ± 1.65	78.3 ± 2.34	5.33 ± 0.27	5.83 ± 0.36	383±5.75	453 ± 9.6	2115±45.1	3067±57.4	634 ± 15.1	1006 ± 30.9
C2	P1	234 ±3.1	259 ± 3.6	14.3 ± 0.22	14.2 ± 0.32	1.0 ± 0.001	1.0 ±0.001	571±5.16	694± 7.1	1894±17.8	2151±11.9	621 ± 10.1	665 ±9.87
	P2	294± 2.4	332 ± 4.0	70.2 ± 2.22	107 ±2.5	14.3± 0.4	14.8 ± 0.38	358±8.82	435±5.5	2181±19.2	2712±16.9	567 ± 6.8	709 ± 2.3
	F1	294± 2.9	365 ± 3.5	31.1 ± 2.15	45.7 ± 3.12	2.71 ± 0.23	3.58± 0.21	527±2.95	556±6.9	3127±13.7	3495±30.2	989 ± 11.42	1173 ± 10.2
	F2	213 ± 3.4	235 ± 5.4	22.7 ± 1.49	32.5 ± 1.48	1.78 ± 0.18	2.56 ± 0.16	403±5.56	503±6.7	2038±29.8	2260±48.3	597 ± 10.42	713 ± 13.0
	Bc1	215 ± 4.2	198 ± 7.5	25.4 ± 2.03	38.8 ± 2.22	1.83 ± 0.22	2.50 ± 0.20	541±7.16	595±8.5	1825±33.2	2745±62.3	512 ± 11.86	852 ± 16.3
	Bc2	236 ± 4.4	226 ±5.4	56.1 ± 1.99	69.2 ± 1.98	4.83 ± 0.2	4.67 ± 0.22	381±7.13	438±8.9	2067±32.5	2483±50.1	680 ± 14.83	814 ± 13.5
C3	P1	231 ±1.9	268 ± 3.9	13.3 ±0.22	13.6 ± 0.14	1.0 ± 0.001	1.0 ±0.001	571±5.16	731±4.0	1874±18.8	2405±37.9	548 ± 13.4	826 ±17.1
	P2	294 ± 2.4	332 ± 4.0	70.2 ± 2.22	107 ± 2.5	14.33± 0.4	14.83 ±0.38	358±8.82	435±5.5	2181±19.2	2712±16.9	567 ± 6.84	709 ± 2.3
	F1	266±3.1	305 ± 6.1	24.3 ± 3.07	38.1 ± 1.76	2.3 ± 0.22	3.17 ± 0.15	490±4.44	478±5.3	3156±24.7	3600±45.1	946 ± 15.9	1075 ± 18.9
	F2	208± 3.3	230 ±4.0	23.9 ± 1.98	26.9 ± 1.73	1.65 ± 0.2	2.07 ± 0.14	431±4.74	442±5.9	2696±41.4	2801±76.6	851 ± 12.3	910 ± 20.2
	Bc1	224 ± 4.1	245 ± 6.1	21.7± 2.54	31.0 ± 1.83	1.83 ± 0.22	2.17 ± 0.15	499±5.36	488±7.2	1864±47.8	2941±103	563 ± 15.6	1005 ± 23.3
	Bc2	227± 4.6	262 ± 5.0	43.8 ± 2.08	58.4 ± 1.32	4.0 ± 0.28	3.50 ± 0.20	371.7	462±8.6	1868±51.6	2299±61.9	550 ± 15.8	726 ± 21.6

Table 4. Mean performance of genotypes and their standard error for all studied traits from the data combined over two locations (Serw and Sids). and forage quality traits.

		PH	Nl/p	Nt/p	5thLA	GFY/P	DFY/P	CP%	CF%	DP %	TDN %
SC10×R	P1	275±3.01	15.0±0.15	1.0±0.001	681±6.72	2430±21.23	809±7.0	16.2±0.23	9.1±0.10	11.6±0.22	66.9±0.24
	P2	313±3.22	88.7±2.36	14.6±0.39	396±7.17	2447±18.04	638±4.6	14.4±0.09	10.8±0.07	9.9±0.08	64.9±0.09
	F1	324±3.67	69.8±3.01	6.2±0.23	643±4.83	3740±32.69	1191±7.8	12.2±0.20	11.9±0.14	8.2±0.26	62.6±0.21
	F2	238±3.55	33.3±1.92	2.9±0.23	527±8.00	2385±41.23	738±15.1	7.1±0.25	14.5±0.22	3.2±0.23	57.3±0.26
	Bc1	215±4.58	41.3±2.45	2.4±0.28	657±11.93	1951±59.82	597±20.6	15.3±0.33	8.7±0.14	10.7±0.30	65.9±0.33
	Bc2	234±4.70	71.7±1.99	5.6±0.32	418±7.65	2591±51.25	820±23.0	8.9±0.13	14.3±0.30	5.2±0.23	59.1±0.18
SC122×R	P1	246±3.38	14.2±0.27	1.0±0.001	632±6.12	2022±14.91	643±9.9	14.9±0.17	10.1±0.15	10.4±0.16	65.5±0.19
	P2	313±3.22	88.7±2.36	14.6±0.39	396±7.17	2447±18.04	638±4.6	14.5±0.09	10.8±0.07	9.9±0.08	64.9±0.09
	F1	329±3.21	38.5±2.63	3.1±0.22	542±4.92	3311±21.98	1081±10.8	16.5±0.19	10.8±0.39	11.8±0.25	67.2±0.20
	F2	224±4.41	27.6±1.48	2.2±0.17	453±6.14	2149±39.08	655±11.7	10.6±0.39	11.9±0.31	6.2±0.35	60.9±0.39
	Bc1	206±5.89	32.1±2.12	2.2±0.21	568±7.85	2285±47.77	682±14.1	15.5±0.40	9.9±0.30	10.9±0.37	66.1±0.40
	Bc2	231±4.91	62.6±1.98	4.7±0.21	409±8.06	2275±41.33	747±14.2	11.1±0.30	13.8±0.41	6.8±0.30	61.3±0.35
SC128× R	P1	250±2.95	13.4±0.18	1.0±0.001	651±4.60	2139±28.41	687±15.3	17.0±0.34	11.4±0.22	12.3±0.32	67.5±0.35
	P2	313±3.22	88.7±2.36	14.6±0.39	396±7.17	2447±18.04	638±4.6	14.5±0.09	10.8±0.07	9.94±0.08	64.9±0.09
	F1	286±4.58	31.2±2.41	2.7±0.18	484±4.88	3378±34.91	1010±17.5	11.2±0.31	12.9±0.24	6.92±0.29	61.5±0.32
	F2	219±3.67	25.4±1.85	1.9±0.17	436±5.31	2748±59.00	881±16.2	8.6±0.37	11.9±0.30	4.54±0.35	59.0±0.37
	Bc1	234±5.07	26.3±2.18	2.0±0.18	493±6.29	2402±75.82	784±19.5	15.1±0.41	10.3±0.31	10.57±0.38	65.7±0.41
	Bc2	245±4.80	51.1±1.70	3.7±0.24	416±8.12	2083±56.78	638±18.7	13.3±0.35	12.3±0.30	8.84±0.33	63.7±0.35

Scaling tests and gene action:

To test the presence or absence of epistasis 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 test values are insignificantly differed from zero, the additive, dominance model is adequate to interpret gene effects. Therefore the data for all studied traits are presented in the Table 5 in the first location (Serw), and second location (Sids). The data which were obtained from the two locations were set up in a combined scaling test and the obtained results are shown in Table 6. The results revealed that the scaling test values were significant in any one of the three tests. These findings indicated that the presence of non-allelic interaction and that the six parameter model is valid. The results showed that the estimates of mean effect (m) which reflects the contribution of the overall 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, indicating the contribution of additive, dominance and epistasis gene effects in the genetic expression of these traits. However, SC128 x Rayana (R) crosses showed that additive (a) gene effects were positive or negative significant for 5th LA and green and dry fodder yield/plant. 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 cross. This finding may explain the absence of heterosis, especially over higher parent in these cross in most occasions. Also, dominance gene effects (d) were positive or negative significant with respect to the crosses SC10 x Rayana (R) and SC122 x Rayana (R) for all studied traits except plant height and number of tillers per plant. In this crosses, the values of dominance gene effects (d) were larger in magnitude than the corresponding values of additive gene effects for all studied traits except plant height and number of tillers per plant , indicating the higher frequency of dominance genes in this combination. These findings may explain the presence of heterosis for most studied traits in this crosses. Furthermore, the results showed that most of studied traits were significantly influenced by one or more type of epistasis effects, which included additive x additive (aa), additive x dominance (ad) and dominance x 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 x teosinte hybrids, Jha et al. (1999) and Suneetha et al. (2000) in fodder maize; Manickam and Das (1994) and Kadam et al. (2000) in sorghum.

Forage quality

The results of scaling tests (A, B and C) for crude protein (Cp%), crude fiber (Cf %), digestible protein (Dp %), total digestible nutrients (TDN %)are shown in Table 10. The values of scaling test were significant in all crosses. Also, the results of mean effects parameter (m), which reflects the contribution due to the overall mean (additive) plus the locus effects (dominance) were found to be highly significant for all crosses. The three

crosses showed that additive (a) gene effects were significant positive or negative and for all studied traits, indicating the major role of additive gene effects in these crosses. Also, dominance gene effects(d)were significant positive or negative for all studied traits and the values of dominance gene effects (d) were larger in magnitude than the corresponding values of additive gene effects (a)for most studied traits, indicating the higher frequency of dominance genes in this combinations. Furthermore the results showed that most of forage quality traits were significantly influenced by one or more type of epistasis effects, which included additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) gene action as appeared in the three studied crosses, indicating the role of non-allelic interaction in the genetic expression of forage quality.

Table 5. Scale test and gene action of silag yield and its components at Serw and Sids locations

		PH		NL/P		NT/P		5TH LA		GFY/P		DFY/P	
		Serw	sids	serw	sids	serw	Sids	serw	sids	Serw	sids	Serw	Sids
Sc10× R	A	-140±26.2**	-194±12.1**	1.75±4.95	-5.98±6.56	-1.66±0.63*	0.17±0.31	37.9±26.1	-56.7±24.9*	-2001±75.3**	-2533±176**	-702±28.9**	-909±57.0**
	B	-128±30.4**	-208±11.4**	-1.51±4.80**	-28.6±6.3**	-9.17±0.67**	-11.0±0.6**	-175±14.6**	-231±21.5**	-1208±95.5**	-801±122**	-315±31.8**	-61.9±62.5
	C	-268±15.3**	-195±10.5**	-110±8.65	-109±11.4**	-17.1±0.95**	-13.9±0.7**	-136±34.3**	-379±36.7**	-1996±140**	-3637±218**	-610±44.3**	-1143±82.7**
	m	225±3.34**	251±3.75**	24.3±1.60**	42.3±2.22**	2.32±0.20**	2.1±0.14**	504±8.1**	549±7.9**	2192±32.5**	2577±49.9**	667±10.1**	809±20.2**
	a	-21.9±19.9	-15.6±7.41*	-26.1±2.65**	-34.7±3.7**	-2.91±0.40**	-1.33±0.2**	242±13.9**	236±14.7**	-451±57.2**	-828±102**	-137±20.1**	-308±41.7**
	d	27.7±42.1	-76.5±21.6**	129±8.81**	91.9±12.1**	4.05±1.16**	-1.68±0.78*	87.4±43.1*	209±44.1**	-83.8±175	1775±289**	-13.7±57.5	711±116**
	aa	-0.94±41.9	-107±21.1**	111±8.32**	74.8±11.6**	6.22±1.13**	3.1±0.74**	-1.7±42.7	90.4±43.2*	-1213±173**	302±285	-407±56.9**	171±116
	ad	-6.16±19.9	-6.78±7.81	1.63±2.88	11.3±3.87**	3.75±0.44**	5.6±0.31**	106±14.9**	87.7±15.4**	-396±58.2**	-866±103**	-193±20.8**	-423±41.8**
	dd	270±80.9**	510±34.6**	-111±13.7**	-40.3±18.6*	4.61±1.86*	7.8±1.22**	139±65.4*	198±69.4**	4422±268**	3031±463**	-1424±91.7**	799±186**
Sc122× R	A	-98.0±9.5**	-228±15.9**	5.41±4.59	17.8±5.43**	-0.05±0.50	-3.0±0.56**	-16.4±15.5	-60.3±19.7**	-1371±70.2**	-155±128	-585±28.2**	-135±35.5**
	B	-115±9.65**	-245±11.9**	10.8±5.04*	-14.4±5.62*	-7.38±0.59**	-10.2±0.9**	-123±17.0**	-114±20.0**	-1174±69.2**	-1241±106**	-195±32.5**	-255±29.0**
	C	-263±15.5**	-382±23.2**	-56.1±7.70**	-82.7±8.95**	-13.6±0.91**	-15.6±1.19**	-371±25.2**	-228±31.5**	-2178±125**	-2811±203**	-776±49.1**	-866±56.8**
	m	213±3.4**	235±5.36**	22.7±1.49**	32.5±1.47**	1.78±0.17**	3.6±0.24**	503±5.6**	503±6.7**	2038±29.8**	2260±48.3**	597±10.4**	7133±13.0**
	a	-21.2±6.13**	-27.9±9.26**	-30.7±2.84**	-30.3±2.97**	-3.00±0.30**	-3.3±0.43**	156±10.1**	156±12.4**	-242±46.5**	262±79.9**	-168±18.9**	37.8±21.2
	d	79.7±18.8**	-22.6±28.7	61.1±8.60**	71.1±9.03**	1.24±0.96	1.54±1.35	45.3±30.7**	45.3±37.4	721±152**	2477±252**	389±57.8**	962.5±68.2**
	aa	49.6±18.5**	-91.8±28.3**	72.3±8.25**	86.1±8.38**	6.20±0.92**	2.5±1.31	53.8±30.1**	53.8±36.6*	-368±151**	1414±250**	-4.46±56.4	476±67.1**
	ad	8.76±6.44	8.54±9.65	-2.71±3.05	16.1±3.23**	3.66±0.35**	3.6±0.47**	27.6±11.3**	27.3±13.2*	-98.3±48.3*	543±80.6**	-195±19.9**	59.9±21.7**
	dd	163±29.0**	566±43.7**	-88.5±13.7**	-89.5±14.9**	1.23±1.50	10.7±2.11**	121±47.7	121±58.8	2914±224**	-18.2±379	785±90.4**	-86.3±101
SC128× R	A	-50.75±8.92**	-84.1±14.1**	5.7±5.95	10.3±4.07*	0.33±0.53**	0.42±0.44	-63.2±12.70**	-233±15.9**	-1302±100**	-123±215	-368±37.6**	109±53.1*
	B	-105±10.0**	-113±12.4**	-6.92±5.64	-28.3±4.05**	-8.66±0.74**	-9.07±0.61**	-106±18.12**	10.8±18.9	-1601±107**	-1715±160**	-413±36.2**	-333±47.3**
	C	-226±15.1**	-291±20.9**	-36.4±10.3**	-89.1±6.81**	-13.4±1.06	-12.8±0.88**	-185±23.3**	-354±26.7**	414±174*	-1114±322**	396±60.6**	-43.9±90.8
	m	208±3.3**	230±4.00**	23.9±1.98**	26.9±1.31**	1.65±0.20**	2.6±0.17**	431±4.74**	442±5.88**	2696±41.4**	2801±76.6**	851±12.3**	910±20.1**
	a	-3.75±6.1	-17.4±7.87*	-22.2±3.29**	-27.4±2.26**	-2.17±0.36**	-2.2±0.30**	128±9.30**	26.1±11.3*	-14.2±70.3	642±129**	12.83±22.3	279±31.7**
	d	74.8±18.5**	100±23.4**	17.7±10.8	48.9±7.27**	-0.27±1.16	0.23±0.95	41.05±27.4	27.1±33.2	-2190±218**	317±403	-789±68.9**	127±104
	aa	70.9±18.2**	94.7±22.5**	35.2±10.3**	71.1±6.94**	5.06±1.07**	4.10±0.91**	15.84±26.6	132±32.6**	-3319±217**	-724±400	-1177±66.4**	-179±102
	ad	27.3±6.34**	14.5±8.36	6.30±3.50*	19.3±2.58**	4.49±0.41**	4.74±0.35**	21.68±10.6*	-122±11.8**	149±71.6*	796±130**	22.33±23.5	221±32.9**
	dd	85.2±28.8**	102±37.8**	-33.9±16.7*	-53.1±11.3**	3.27±1.75	4.55±1.49**	153±43.9**	90.4±52.4	6223±331**	2563±608**	1959±107**	402±156*

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

Table 6. scale test and gene action of yield and its components over two location and forage quality traits.

		Ph	NL/P	NT/P	5thLA	GFY/P	DFY/P	CP%	CF %	DP %	TDN %
Sc10× R	A	-167±20.4**	-2.11±5.81	-0.74±0.49	-9.40±25.5	-2267±135**	-805±45.2**	2.11±0.73**	-3.56± 1.0**	1.64± 0.67*	2.38± 0.73**
	B	-168±22.9**	-15.0±5.6*	-10.1±0.62**	-203±18.4**	-1004±110**	-188±49.6**	-8.74±0.34**	5.88± 2.0**	-7.76± 0.50**	-9.37 ± 0.41**
	C	-281±16.7**	-110±10.1**	-15.5±0.85**	-257±35.5**	-2816±183**	-876±66.3**	-26.5± 1.10**	14.4± 0.92**	-25.3 ± 1.0**	-27.9 ± 1.16**
	m	238±3.55**	33.3±1.94**	2.2±0.17**	527±8.0**	2385±42.1**	738±15.9**	7.14±0.25**	14.5 ± 0.22**	3.15 ± 0.22**	57.3 ± 0.26**
	a	-18.7±14.9	-30.4±3.20**	-2.12±0.33**	239±14.3**	-639±82.7**	-223±32.8**	6.32± 0.36**	-5.6 ± 1.12**	5.53 ± 0.38**	6.86 ± 0.37**
	d	-24.4±33.4	110±10.6**	1.18±0.99	148±43.6**	845±239**	349±91.9**	16.7± 1.24 **	-10.1± 2.40**	16.6 ± 0.19**	17.6 ± 1.32**
	aa	-54.3±33.2	92.9±10.1**	4.64±0.96**	44.3±42.9	-455±236	-117±91.5	19.9 ± 1.22**	-12.0 ± 2.4**	19.2 ± 1.17**	20.9 ± 1.29**
	ad	0.31±15.1	6.5±3.41	4.67±0.38**	97.2±15.2**	-631±84.1**	-308±33.1**	5.42 ± 0.37**	-4.72 ±1.12**	4.70 ± 0.40**	5.87 ± 0.40**
	dd	390±62.2**	-75.8±16.32**	6.19±1.57**	168±67.4*	3727±378**	1112±146.9**	-13.3± 1.80**	9.72 ± 4.56*	-13.1± 1.80**	-13.9 ± 1.89**
Sc122× R	A	-163±13.1**	11.6±5.03*	-1.52±0.53**	-38.3±17.7*	-763±103**	-360±32.1**	-0.47 ± 0.84	-1.02± 0.7	-0.36 ± 0.81	-0.60 ± 0.85
	B	-180±10.9**	-1.8±5.34	-8.77±0.74**	119±18.6**	-1208±89.6**	-225±30.8**	8.73 ± 0.67**	5.97 ± 0.89**	-8.03 ± 0.66**	-9.53 ± 0.76**
	C	-322±19.7**	-69.4±8.35**	-14.6±1.05**	-300±28.5**	-2494±169**	-821±53.1**	-19.9 ± 1.61**	5.05 ± 1.44**	-19.1 ± 1.51**	-21.0 ± 1.66**
	m	224±4.50**	27.6±1.48**	2.7±0.21**	453±6.2**	2149±40.2**	655±11.8**	10.6 ± 0.39**	11.9 ± 0.30**	6.2 ±0.35 **	61.0 ± 0.40**
	a	-24.5±7.85**	-30.5±2.90**	-3.16±0.37**	158±11.3**	10.29±65.4	-65.2±20.1**	4.35 ± 0.51**	-3.83 ± 0.50**	4.04 ± 0.48**	4.72 ± 0.54**
	d	28.5±24.2	66.1±8.82**	1.39±1.17	170±34.2**	1599±208**	676±63.2**	12.5 ± 1.87**	0.24 ± 1.60	12.4 ± 1.73**	12.9 ± 1.95**
	aa	-21.1±23.9	79.2±8.31**	4.33±1.13**	142±33.5**	523±207**	236±61.9**	10.7 ± 1.85**	-0.10 ± 1.55	10.7 ± 1.70**	10.9 ± 1.93**
	ad	8.65±8.21	6.71±3.14*	3.62±0.41**	40.4±12.3**	222±66.5**	-67.7±20.9**	4.13 ± 0.52**	-3.5 ± 0.5**	3.83 ± 0.5**	4.5 ± 0.55**
	dd	365±37.1**	-89.0±14.3**	5.97±1.83**	14.6±53.5	1448±311**	349±96.4**	-1.50± 2.60	-4.85 ± 2.43	-2.36 ± 2.44	-0.76±2.72
SC128× R	A	-67.4±11.8**	8.01±5.10	0.37±0.47	-148±14.4**	-712±168**	-129±46.0**	2.03 ± 0.94*	-3.70 ± 0.71**	1.89 ± 0.86*	2.35 ± 0.95*
	B	-109±11.3**	-17.6±4.91**	-8.86±0.66**	-47.8±18.5*	-1658±136**	-373±42.1**	0.88 ± 0.76	0.90 ± 0.62	0.82 ± 0.70	0.84 ± 0.80
	C	-259±18.2**	-62.8±8.72**	-13.1±0.94**	-270±25.1**	-349±259	176±77.2*	-19.3 ± 1.65**	-0.54 ± 1.26	-17.9± 1.53**	-19.6 ± 1.66**
	m	219±3.68**	25.4±1.68**	2.10±0.18**	436±5.3**	2748±61.6**	881±16.7**	8.64 ± 0.37**	11.9 ± 0.28**	4.54 ± 0.35**	59.0 ±0.37**
	a	-10.6±-7.1	-24.8±2.82**	-2.17±0.33**	77.1±10.3**	319±103**	146±27.4**	1.86 ± 0.54**	-2.01 ± 0.42**	1.73 ± 0.50**	2.04 ± 0.55**
	d	87.4±21.1**	33.3±9.21**	-0.25±1.04	34.1±30.4	-936±324**	-331±88.6**	17.7± 1.87**	-0.45 ± 1.44	16.4± 1.73**	18.0±3 **
	aa	82.8±20.4**	53.1±8.8**	4.58±1.0**	73.9±29.7	-2021±322**	-678±86.5**	22.2 ± 1.84**	-2.26 ± 1.41	20.7± 1.70**	22.8 ± 1.85**
	ad	20.9±7.42**	12.8±3.1**	4.62±0.38**	50.2±11.2**	472±105**	121±28.6**	0.57 ± 0.56	-2.30 ± 0.44**	0.53 ± 0.52	0.75 ± 0.57
	dd	93.9±33.6**	-43.5±14.3**	3.91±1.62	122±48.3*	4393±489**	1181±134**	-25.1± 2.71**	5.06 ±2.11*	-23.4± 2.50**	-25.9± 2.75**

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

REFERENCES

Abd El-Maksoud, M. M.; M. S. Hamada and M. E. Hagag (2001). Heterosis and combining ability for grain yield components and crude protein percentage in interspecific hybrids of teosinte. J. Agric. Sci. Mansoura Univ., 26(7): 4261-4270

Abd El-Maksoud, M. M., A. Z. Abd El-Haliem and H. O. Sakr 2004. Evaluation of some promising teosinte hybrids and their genetic behavior for fodder yield. J. Agric. Sci. Mansoura Univ., 29(1): 97-111.

Alan, R. O. and M. D. Sundberg (1994). Inflorescence development in a perennial teosinte: Zea perennis (POACEAE), Amer. J. Bot., 81(5):598- 608.

Aly, R.S.H and E.A. Amer (2008). Combining ability and type of gene action for grain yield and some other traits using line × tester analysis in newly yellow maize inbred lines(*Zea mays L.*).J. Agric. Sci. Mansoura Univ., 33(7): 4993–5003.

Aly, R.S.H. and S.Th.M. Mousa (2008). Estimation of combining ability for newly developed white inbred lines of maize (*Zea mays L.*) via line × tester analysis Egypt. J. Appli. Sci, 23(2B): 554 — 564.

A.O.A.C. (1980). Official Methods of Analysis. Association of Analytical Chemists, 13ed. Washington DC., USA.

Aulicino-MB; Magoja-JL. (1991). Variability and heterosis in maize-Baisas teosinte and maize-Guatemala teosinte hybrids. Maize-Genetics Cooperation-News-Letter. 65,43-44.

Barakat A.A. and M.M.A Osman (2008). Combining ability estimates of maize inbreed lines by top crosses for grain yield and other traits. J. Agric. Sci. Mansoura Univ., 33(9): 6291-6302.

Barriere-Y; Montalant-Y and Boyat-A (1984). Study of protein content and agronomic value in progenies from the cross maize × teosinte. Agronomie. 4: 5,417-422, 10 ref.

Chaudhuri, A.p. and B. Prasad (1969) Maize-teosinte hybrid for fodder. Indian J. Agric sci. 39(6):467-472.

Chaugale, D.S. and V.M. Chavan (1965). A new maize hybrid for fodder Poona Coll. Mag. 56:33-36.

Church, D.C. (1979). Livestock Feeds and Feeding. 4th Ed. Pp. 79 O&B Books. Inc: Corvallis, Dragon 97330, USA.

El-Shenawy, A. A.; E. A. Amer and H. E. Mosa (2003). Estimation of combining ability of newly developed inbred lines of maize by (line × tester) analysis. J. Agric. Res. Tanta Univ., 29(1): 50-63.

Gamble, E.E. (1962). Gene effects in corn (Zea mays L.) Separation and relative importance of gene effects for yield. Canadian J. of Plant Sci., 42(2): 339-348.

Gill, A.S. and B.D Patil (1985). Forage production potential of Maizente, teosinte and Maize Agic.sci. Digest, 5(1): 44-45

IIchovska-M; Khristova-P, and khristov-K (1995). Evaluation of the combining ability of maize lines obtained by genetic transformation . Rasteniev"dni-Nauki. 32:9-10, 53-55: 6ref.

Jinks, J. L. and R. M. Jones (1958). Estimation of the components of heterosis. Genetics, 43: 223-224.

Jode, W.E. and G.C. James (1996). Teosinte cytoplasmic genomes. II. Performance of maize hybrids with teosinte cytoplasms. Crop Sci., 36: 1092-1098.

Khristova. L;l. Hristov: L. Todcreve: T Lidanski. and I. Hristova. (1985) Inheritance of economic characters in Intergeneric hybrids of maize with teosinte Genetika-l-Selktsiya., 18 (4): 341 -347.

Mather, K. and J L. Jinks (1982). Biometrical Genetic. Great Britin, Univ. Press, 3rd Ed, 396 pp.

Mostafa, M.A.; F. A. Salama and A. A. Abdel-Aziz (1995). Combining ability of white maize population with inbred testers. J. Agric. Sci., Mansoura Univ., 20(1): 143-149.

Owen, P. C. (1968). A measuring scale for areas of cereal leaves. Exp. Agric., 1(4):275-278.

Sakr, H.O, (2009). Combining ability and type of gene action for green fodder yield and it's components in some teosinte maize hybrids. J. Agric. Sci. Mansoura Univ., 34 (12): 10825 – 10836.

Sakr, H.O., E.M.Zayed and R.S.H Aly (2009). Molecular and genetic analysis of the cross between maize and teosinte. Egypt. J. plant Breed. 13:251-267.

Sakr, H.O. and Mona Ghazy.M.F. (2010). Combining ability and type of gene action for grain yield and some other traits using line × tester analysis in teosinte inbred lines. J. Agric. Chemistry and Biotechnology, Mans. Univ., Vol. 1(9): 457 – 470.

Singh, P. and S. S. Narayanan, 1993. Biometrical Techniques in Plant Breeding. 1 st Edn., Kalayani Publishers, New Dehli, India.

Singh, P. and S. S. Narayanan, 2000. Biometrical Techniques in Plant Breeding.

Kalayani Publishers, New Dehli, India, pp: 17-36.

Singh, R. K. and B. D. Choudhary (1977). Biometrical method in quantitative genetic analysis. Kalyani Pub., New Delhi, India.

Singh, R. K. and B. D. Choudhary (1985). Biometrical methods in quantitative genetic analysis. Kalyani Pub. New Delhi - Ludhiana. 3rd ed.

Singh, J. M. .and B. Dash (2000). Analysis of genetic variability and character association in maize (Zea *mays L.).* Environment and Ecology, 18, 2:503-505.

Smith, J. S. C.; M. M. Goodman and C. W. Stuber (1984). Variation within teosinte. HI. Numerical analysis of allozyme data. Economic Botany. 38(1): 97-113.

Sohoo, M.S.; B.L. Bhardwaj and S.M. Beri (1993). Heterosis for some fodder characters in a maize x teosinte cross. Short Comun., Symp. Heterosis Breeding in Crop Plants, Theory and Application, 72-73.

Todorova, L. and T. Lidanski (1985). Inheritance of quantitative characters in hybrids of maize with teosinte. Genetika-I-Selsktsiya., 18, 2:99-110.

الفعل الجيني لصفات العلف في بعض الهجن المبشرة لهجن الشامية في الريانة بإستخدام تحليل متوسط الجيل

حسام الدين عثمان صقر

قسم بحوث محاصيل العلف – معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية – مصر

بالرغم من ان هناك حاجة ماسة ومتزايدة من انتاج الأعلاف الخضراء الصيفية في مصر إلا ان مربو النبات لم يهتموا كثيرا نحو تحسين الأذرة الريانة كمحصول علف(كسيلاج)بديلا للأذرة الشامية التي تعتبر من أحد محاصيل الحبوب الإستراتيجية. في هذه الدراسة تم عمل تقسيم لمكونات التباين الوراثي لصفات محصول العلف من خلال دراسة عدد من الأجيال المختلفة لهجن الأذرة الشامية × الريانة تحت ظروف بيئية مختلفة(محطة بحوث السرو بمحافظة دمياط ومحطة بحوث سدس بمحافظة بني سويف) ويمكن تلخيص النتائج فيما يلي: دلت النتائج علي وجود فروق معنوية بين الهجن لكل الصفات المدروسة وكذلك وجود فروق عالية المعنوية بين العشائر داخل الهجن وبين العشائر داخل كل هجين لكل الصفات المدروسة وهذا يشير الي ان هناك اختلاف بين المكونات الوراثية للآباء المشتركة في تكوين هذه الهجن وبالتالي يمكن المقارنة بين متوسطات هذه التراكيب وتقسيم التباين الوراثي كانت متوسطات المربعات للمواقع والتداخل بين الهجن والمواقع والعشائر بالإضافة الي العشائر داخل الهجين والمواقع معنوية في معظم الحالات وهذا يشير الي ان هذه التراكيب تسلك سلوكا مختلفا بإختلاف الظرف البيئية كان الهجين "فردي 10 × ريانة " أعلي الهجن ، اذ حقق أعلي متوسط للصفات عدد الأوراق – عدد الخلفات- مساحة الورقة الخامسة – المحصول الأخضر والجاف، بينما كان الهجين "فردي 122 × ريانة" أعلي الهجن في نسبة البروتين الخام ونسبة بروتين الهضم وكذلك العناصر الكلية المهضومة . كانت متوسطات صفات الجيل الثاني كانت أقل من متوسطات الجيل الأول وهذا يدل علي وجود تأثير لقوة الهجين والفعل الجيني غير المضيف لتوريث الصفات كانت متوسطات الهجن الرجعية تميل نحو متوسطات الآباء الرجعية وهو مايعكس عن وجود تأثير الفعل الجيني السيادي والمضيف كانت قيم تأثير المتوسطات عالية المعنوية لكل الهجن في كل الصفات وهذا يشير الي ان هناك مساهمة لكل من الفعل الجيني المضيف والسيادي والتفوقي في التعبير الجيني لهذه الصفات وان الفعل الجيني السيادي يلعب الدور الأكبر في التوريث للهجينين "فردي 10 × ريانة" و"فردي 122 × ريانة".