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Diallel analysis and inbreeding depression of hybrid forage corn for agronomic traits and chemical quality

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Abstract

This study aimed to estimate the combining ability and inbreeding depression of corn hybrids for agronomic traits and forage quality. Nine corn hybrids, 36 F1 combinations from a diallel, 9 S1 populations and two checks were evaluated in two experiments in a randomized complete block design with three replications, in the 2009/2010 and 2010/2011 growing seasons. The parents Impacto, CD304 and DKB390 are recommended to form a composite to be subjected to a recurrent selection program aiming to improve forage production. Crosses between Impacto and parents DKB390, P30P34 and P30B39 are promising to increase forage quality by reducing the fiber content and also by increasing the protein content, being recommended for extracting inbred lines and interpopulation improvement. High inbreeding depression for grain yield was detected, indicating that non-additive effects contributed to the inheritance of the trait.

Key words: *Zea mays*, diallelic analysis, breeding.

1. INTRODUCTION

Corn is a reference species in forage production, due to the advantages it offers like the high dry matter yield, high digestibility and excellent acceptance by animals (Oliveira et al., 2007). Worldwide and also in Brazil, about 70% of the corn production is intended for animal feed (Marcondes et al., 2012).

Much of the corn breeding programs in Brazil overlooks the goals of breeding for forage corn, due to the lower volume of seed marketed for this purpose. Hybrids recommended for the silage production are usually the same used in grain production, contributing to the low quality of the Brazilian forage (Marcondes et al., 2012).

The selection of basic populations is a crucial step of a corn breeding program, because these populations are the source of the inbred lines used in hybrid seed production (Hallauer et al., 2010). Currently, corn breeding programs tend to use single commercial hybrids, due to the presence of favorable genes, the wide adaptability, and especially the advanced level of improvement of such cultivars (Oliboni et al., 2013). As there are hundreds of commercial hybrids available for use as a source of germplasm, the choice of the best should consider genetic parameters such as combining ability and inbreeding depression (Chaves et al., 2008).

A promising genotype will not always successfully transfer alleles to its progenies. Diallel crosses can be used to estimate the efficiency of transferring alleles being widely exploited in breeding programs (Miranda & Gorgulho, 2001). Diallel crosses are important because they provide information on the dominant gene action in inheritance of the trait to be improved as well as estimates of combining ability of the parents, heterosis level and subsidies to define the best breeding strategy to be followed by the breeder (Cruz et al., 2012).

Inbreeding depression is the exposure of the individuals in a population to the effects of deleterious recessive genes through selfing or matings between related individuals, causing a reduction of the phenotypic mean in quantitative traits. Inbreeding depression can limit the number of promising lines to be extracted from a certain germplasm and is indicative of the potential of populations for use in breeding (Hallauer et al., 2010).

From estimates of combining ability and inbreeding depression, this study aimed to identify commercial corn hybrids capable to originate segregating populations with higher forage production potential and quality in developing a forage corn breeding program.

2. MATERIAL AND METHOD

Two experiments were conducted in 2009/2010 and 2010/2011 at the Experimental Farm of Iguatemi (23°25' S; 51°57' W), State University of Maringá, in an area with a dystrophic red latosol (Oxisol). The climate is Cfb, according to Koppen classification.

The experiments were a randomized complete block design with three replications. The experimental unit consisted of four rows of 5m, 0.9m spaced apart, with 1m bordering space at the ends. It was evaluated 9 hybrids of different genetic backgrounds, 36 F1 combinations derived from the complete diallel between such hybrids, 9 S1 populations from self fertilization of the parents and two commercial controls (AG5011 and P30F53 single hybrids), totaling 56 treatments.

Fertilization consisted of applying 350 kg ha^{-1} of 4: 14: 8 (N:$P_2O_{5:}K_2O$) + zinc, at sowing, followed by two nitrogen topdressings at the V_4 and V_8 stages, using 35 kg ha^{-1}in both applications. Other cultural practices followed the recommendations of Fancelli & Dourado (2000).

The half-milk stage (milk line positioned half-way between the tip and the base of the kernel) was adopted as the standard stage for harvesting the plants to obtain forage (Fancelli & Dourado, 2000). To determine the staygreen (SG), five plants were cut at 0.2 m height, for counting the number of senescent leaves. Then, we separated the ears (PE), leaves (PL) and stems (PS) of plants sampled to estimate the percentage of each component. Grain yield (GY) was evaluated in two external rows of each plot, performing the threshing of the ears and the correction of the grain moisture content to 13%.

In the sampling, five plants per plot were cut and chopped with a shredder set to 1.5cm chop length. The green mass (GM) of the treatments was obtained by weighing the chopped material. An homogeneous sample was weighed and dried for the quantification of the dry matter content (AOAC, 1984). Then, the samples were milled in a Wiley mill (1 mm sieve) for the determination of total dry matter at 105 °C (MS). The agronomic traits described above were evaluated in both experiments.

Forage quality evaluations were made only in the first experiment (2009/2010). Total nitrogen was determined by the micro Kjeldahl method. The nitrogen content of each sample was multiplied by 6.25 for quantifying crude protein (PC) (AOAC, 1984). Other forage characteristics were also evaluated: neutral detergent fiber (NDF) (Van Soest et al., 1991) and acid detergent fiber (ADF) (Goering & Van Soest, 1970) and lignin content (NGL) (Van Soest, 1963).

In the analysis of variance, the degrees of freedom for trataments were breakdown into degrees of freedom for the effects of parents, the F1 hybrid combinations, the S1 populations, the controls and the three contrasts: 1) F1 hybrid combinations vs parents; 2) F1 hybrid combinations + parents + S1 generation vs controls; 3) parents + F1 hybrids vs S1 generation. The degrees of freedom for the interaction between treatments × environments were broken down into: parents × environments, F1 hybrid combinations × environments, S1 populations × environments, controls × environments, contrast between (F1 hybrid combinations vs parents) × growing season (F1 hybrid combinations + parents + S1 generation vs controls) × growing season, (parents + F1 hybrids vs S1 generation) × growing season.

In diallel analysis for the forage quality traits, assessed only in the first experiment, the sum of squares of treatments was partitioned for evaluating the effects of general (GCA) and specific (SCA) combining abilities, in accordance to the Method II (parents and F1 hybrids), Model 1 (fixed effect for genotype), according to Griffing (1956). For agronomic traits in both experiments, the joint diallel analysis was carried out by adopting the same method and model described above. The degrees of freedom of the genotype × environment interaction were partitioned into effects of GCA × environments and SCA × environments, according to Vencovsky & Barriga (1992).

On the basis of the average performance of the parents and its respective S_1 populations, we estimated inbreeding depression (ID,%) and the potential of the hybrids as sources of inbred lines ($\hat{u} + \hat{a}$) according to the equations suggested by Vencovsky & Barriga (1992). The statistical and genetic analyses were run with the Genes software (Cruz, 2013).

3. RESULTS AND DISCUSSION

The ratios between maximum and minimum values of residual mean square of the individual analysis of variance were of low magnitude, enabling the use of joint analysis (Banzatto & Kronka, 2013) (Table 1). The significant interaction between treatments and environments for GM, MS, PESP and PL indicates that selection of genotypes

Table 1. Joint analysis of variance of the experiments and of the complete diallel between forage corn hybrids, with the mean square estimates for green mass yield (GM, t ha^{-1}), dry matter yield (DM, t ha^{-1}) and grain yield (GY , t ha^{-1}), stay green (SG, number of senescent leaves), ear percentage (PE,%), stem percentage (PS,%) and leaf percentage (PL,%) in two growing seasons (2009/2010 and 2010/2011)

Analysis of variance								
SV	DF	Mean square						
		GM	MS	GY	SG	PE	PS	PL
Block/Seasons	4	849.42	51.73	4.03	1.12	22.42	185.95	121.07
Treatment (T)	(55)	209.30*	35.74*	15.24*	1.69*	11.18^{ns}	20.35*	9.24^{ns}
Season	1	7645*	587*	76.01*	70.67*	35591*	265^{ns}	42002*
Diallel (D)	(44)	135.53*	24.74*	6.17*	1.71*	8.76^{ns}	14.51^{ns}	9.34^{ns}
Parents (G)	8	146.72^{ns}	24.10^{ns}	12.46*	3.40*	7.59^{ns}	13.27^{ns}	10.69^{ns}
F_1	35	118.53*	24.01*	4.90*	1.34*	9.27^{ns}	14.51^{ns}	8.52^{ns}
F_1 *vs* G	1	640.81*	55.55^{ns}	0.032^{ns}	1.14^{ns}	0.07^{ns}	24.22^{ns}	27.10^{ns}
S_1	8	144.26^{ns}	13.96^{ns}	3.50*	1.87*	14.24^{ns}	35.42^{ns}	10.45^{ns}
Control (Test)	1	23.16^{ns}	0.076^{ns}	13.80^{ns}	0.85^{ns}	10.75^{ns}	29.73*	4.72^{ns}
F_1 + G + S_1 *vs* Test	1	7.91^{ns}	0.076^{ns}	10.79^{ns}	0.78^{ns}	65.88^{ns}	86.14*	1.34^{ns}
G + F_1 *vs* S_1	1	4363^{ns}	765^{ns}	514.4*	1.20^{ns}	39.22^{ns}	81.64^{ns}	7.73^{ns}
T × Seasons	(55)	72.03*	12.80*	0.78^{ns}	0.15^{ns}	12.26*	9.46^{ns}	13.63*
D × Seasons	(44)	75.18*	13.49*	0.88^{ns}	0.14^{ns}	11.59*	9.55^{ns}	11.54*
G × Seasons	8	119.97^{ns}	26.97*	2.29*	0.14^{ns}	6.25^{ns}	7.88^{ns}	14.45^{ns}
F_1 × Seasons	35	62.27^{ns}	10.68^{ns}	0.55^{ns}	0.14^{ns}	12.88*	10.19^{ns}	11.07*
(F_1 vs G) × Seasons	1	168.75^{ns}	4.24^{ns}	1.22*	0.066^{ns}	9.22^{ns}	0.80^{ns}	4.63^{ns}
S_1 × Seasons	8	58.22^{ns}	9.34^{ns}	0.36^{ns}	0.21^{ns}	15.81*	11.67^{ns}	26.07*
Test × Seasons	1	43.97^{ns}	0.25^{ns}	0.33^{ns}	0.01^{ns}	19.50*	0.002^{ns}	19.94^{ns}
(F_1 + G + S_1 vs Test) × Seasons	1	71.64^{ns}	5.26^{ns}	0.48^{ns}	0.10^{ns}	15.78^{ns}	0.204^{ns}	12.44^{ns}
(G + F_1 vs S_1) × Seasons	1	72.29^{ns}	30.27*	0.70^{ns}	0.57^{ns}	2.68^{ns}	6.38^{ns}	0.80^{ns}
Error	220	48.46	7.36	0.94	0.28	4.63	7.9384	7.378
Mean	-	55.40	18.54	8.11	2.30	29.35	43.98	26.65
CV (%)	-	12.56	14.62	11.95	23.11	7.33	6.40	10.20
Analysis of variance of the diallel								
SV	**DF**	**Mean Square**						
		GM	**MS**	**GY**	**SG**	**PE**	**PS**	**PL**
Genotype	(44)	135.52*	24.7*	6.17*	1.71*	8.76^{ns}	14.5^{ns}	9.34^{ns}
GCA	8	364.62*	62.8^{ns}	11.56*	6.18*	15.6^{ns}	27.4^{ns}	16.63^{ns}
SCA	36	84.61^{ns}	16.3^{ns}	4.97*	0.71*	7.23^{ns}	11.6^{ns}	7.72^{ns}
Season	1	5832.4	364.51	64.64	60.68	28594	186.3	33395
Genotype × Seasons	(44)	75.17*	13.49*	0.88^{ns}	0.14^{ns}	11.59*	9.55^{ns}	11.54*
GCA × Seasons	8	59.66^{ns}	20.29*	1.37^{ns}	0.36^{ns}	19.47*	16.40*	19.70*
SCA × Seasons	36	78.62*	11.98*	0.77^{ns}	0.09^{ns}	9.84*	8.03^{ns}	9.72^{ns}
Residual mean	176	48.83	7.68	0.86	0.25	4.66	7.90	7.87

* and ^{ns} significant and non-significant by F test ($p<0.05$) respectively.

should be performed in every growing season, because the treatments exhibit specific adaptations for the tested environments.

The interaction between parents and growing seasons had a significant effect only for MS and GY, indicating a different behavior of the parents in each growing season (Table 1). Interactions of F1 combinations of the diallel over the growing seasons were significant only for PE and PL, showing that assimilate partitioning was influenced by the growing season for such traits (Table 1). The F1 combinations differed ($p < 0.05$) and exceeded, on average, the parents in terms of yield of GM (Table 1). Only the GY was significantly influenced by the effect of "parents vs F1 hybrids x environment" (Table 1). It is interesting to note that the significance of these contrasts allow the inference about the average heterosis of diallel crosses (Gabriel et al., 2009; Oliboni et al., 2013).

The interaction between genotypes and environments is the differential response of a genotype to environmental changes. The nature of the interaction is related to intrinsic factors of the cultivar and of great importance in plant breeding. In general, there is a strong interaction between genotypes and environments in corn, depending on the diversity of the environments and the magnitude of the genetic background (Aguiar et al., 2004; Pfann et al., 2009). These results are supported by the strong interaction between genotypes and environments for traits related to forage production, highlighting the yield of grains and dry matter (Oliboni et al., 2013; Oliveira et al., 2007).

The S1's populations and their interaction with growing seasons significantly influenced ($p<0.05$) the traits PE and PL (Table 1). PE was significantly influenced by the interaction between the controls and the growing seasons (Table 1). The parents and the F1 combinations differed ($p<0.05$) and exceeded, on average, S1 populations as to the GY (Table 1). For the interaction between parents + F1 combinations vs S1 with effects of seasons, only MS showed significant mean square values ($p<0.05$) (Table 1).

The chemical traits PC, NDF, ADF, and LC were significantly affected ($p<0.05$) by parents, F1 combinations and S1 populations, indicating variability between treatments within each group of genotypes (Table 2). The literature on the chemical traits of forage in corn confirms the variability among genotypes for these traits (Chaves et al., 2008; Marcondes et al. 2012; Mendes et al. 2008). The F1 combinations differed ($p<0.05$) and exceeded, on average, the parents as to the PC in the whole plant forage (Table 2). The S1's populations differed ($p<0.05$) and exceeded, on average, parents + F1 combinations for the traits PC and LC (Table 2). Commercial controls differed ($p<0.05$) and exceeded, on average, the other genotypes of the experiment (F1 combinations, parents and S1's populations) as for PC, FDA and LC (Table 2). Only NDF did not reach significant estimates for the previously mentioned contrast, corroborating Pinto et al. (2010).

The general combining ability (GCA) results from the behavior of a given parent upon crosses in which it participated, reflecting the effect of additive genes. Moreover, the specific combining ability (SCA) is the deviation of a hybrid from the expected, based on the GCA of its parents, expressing the effect of non-additive genes. Thus, for plant breeding, the ideal hybrid combination is the one which simultaneously has a high SCA estimate and the presence of at least one parent with high GCA estimate (Cruz et al., 2012).

The traits MS, PE, PS and PL were significantly influenced by the interaction between GCA and growing seasons, demonstrating the influence of growing seasons on phenotypic differences of the parents and suggesting that the best parents should be chosen within each growing seasons (Table 1). The interaction between SCA and growing seasons significantly influenced only GM, MS and PE, indicating that the hybrid combinations behaved differently in different seasons (Table 1). It is noteworthy that GY was significantly influenced by the effects of GCA and SCA, with no interaction of these estimates with the growing seasons evaluated (Table 1). These results differ from some studies reporting the interaction between GCA and SCA with environments (Aguiar et al. 2004; Locatelli et al., 2002).

The chemical traits of the forage, ADF and LC were significantly influenced by additive effects. On the other

Table 2. Analysis of variance of the experiment and of the complete diallel between forage corn hybrids for protein content (PC, %), neutral detergent fiber (NDF,%), acid detergent fiber (ADF,%) and lignin content (LC, %) obtained in the first experiment (2009/2010)

Analysis of variance of the experiment					
SV	**DF**	**Mean Square**			
		PC	**NDF**	**ADF**	**LC**
Blocks	2	3.58	29.43	25.78	1.38
Treatments (T)	55	0.97*	27.63*	11.89*	3.42*
Diallel (D)	(44)	0.58*	22.60*	11.70*	3.50*
Parents (G)	8	0.92*	30.61*	16.05*	2.35*
F_1	35	0.48*	20.73*	11.04*	3.85*
F_1 vs G	1	1.48*	23.90^{ns}	0.30^{ns}	0.37^{ns}
S_1	8	1.72*	47.60*	15.34*	2.55*
Controls (Test)	1	2.42*	31.64*	8.01^{ns}	4.92*
F_1+G+S_1 *vs* T	1	3.08*	94.03*	2.83^{ns}	4.90*
G + F_1 *vs* S_1	1	8.23*	18.55^{ns}	5.43^{ns}	4.02*
Residual	110	0.31	8.02	6.62	0.92
CV (%)		7.97	4.24	8.90	12.89
Mean		7.03	66.81	28.92	7.42
Analysis of variance of the diallel					
SV	**DF**	**Mean Square**			
		PC	**NDF**	**ADF**	**LC**
Genotype	(44)	0.59*	22.60*	11.71*	3.50*
GCA	8	0.29^{ns}	22.24^{ns}	22.96*	7.41*
SCA	36	0.65*	22.68*	9.21^{ns}	2.63*
Residual	88	0.31	8.02	6.62	0.92

* and ^{ns} significant and non-significant by F test ($p<0.05$) respectively.

hand, the non-additive effects were significant for PC NDF and LC indicating the possibility to explore the allelic complementation in crossings (Table 2).

Forage corn breeding usually aims at obtaining hybrids that combine high forage yield and high digestibility of the fibrous part of plants (Ferreira et al., 2007; Marcondes et al. 2012). Such hybrids shall be achieved from parents with highly positive GCA estimates for the traits GM, MS, GY, PE, PL and PC, unlike that required for SG, PS, NDF and ADF.

For the trait MS, the parents with suitable GCA estimates for breeding were DKB390, Impacto and Cargo for the first experiment, and 2B710, DKB390, Cargo and P50R50 for the second experiment (Table 3). The parents most appropriate to increase the PE were Impacto, P30B39 and CD308 for 2009 and Cargo, Impacto and DKB390 (Table 3) for the second growing season. For PL, the hybrids Impacto, 2B710 and Cargo were the parents with the most appropriate estimates of GCA in the first experiment. In the second experiment, the hybrids Cargo and DKB390 were the only parents that showed no interesting GCA estimates for increasing PL, since they tended to reduce the percentage of leaves in crosses (Table 3). The hybrid Impacto was the only parent that obtained in the first experiment with appropriate GCA estimate for PS (Table 3).

The parents Impacto and DKB 390 stood out for their estimates of GCA for GY, showing a higher frequency of alleles favorable of additive effects (Table 3). The parent DKB390 had the highest estimate of GCA for GM, being suitable for forage corn breeding programs. This condition probably results from the presence of alleles favorable for both GY and GM so as to increase the energy contribution of the forage (Table 3). The best parents for the improvement of SG were CD304, CD308 and 2B710, as they presented highly negative estimates of GCA, contributing to reduce the number of senescent leaves in the progeny (Table 3).

The lack of significance of additive effects for PC and NDF indicated that, in general, there was not a parent contributing more than others to the expression of these traits in their progeny (Table 2). Regarding the FDA and LC, the parent Impacto showed negative estimates of GCA of high magnitude, contributing to reduce the content fiber and lignin of their progeny, possibly reflecting the greater frequency of genes favorable to such traits (Table 3).

The significant interaction between SCA and growing seasons for the traits GM, MS and PE indicates that the

Table 3. Estimates of general combining ability (GCA) of corn hybrids used as parents in diallel crosses for the traits dry mass (MS, t ha^{-1}), ear percentage (PE,%), stem percentage (PS, %) and leaf percentage (PL,%), plant height (PH) and ear height (EH), green mass (GM t ha^{-1}), grain yield (GY, t ha^{-1}), stay green (SG, number of senescent leaves) , number of senescent leaves), protein content (PC%), neutral detergent fiber (NDF,%) and acid detergent (FDA,%), lignin (LC,%), mineral matter (MM%) and organic matter (OM,%)

Parents	GCA							
	MS		PE		PS		PL	
	2009	2010	2009	2010	2009	2010	2009	2010
Impacto	1.0	–0.82	1.30	0.24	–2.37	0.01	1.07	–0.26
Cargo	1.20	0.70	–0.69	1.02	0.14	0.20	0.54	–1.23
P30B39	0.09	–4.63	1.04	–0.38	–0.29	–0.34	–0.75	0.72
P30P34	–0.41	–0.06	–0.41	–0.22	0.92	–0.17	–0.50	0.40
P30R50	–0.62	0.12	–0.04	–0.28	0.60	0.71	–0.55	–0.42
CD304	–1.28	–1.82	–0.54	–1.0	0.54	0.47	–0.002	0.52
CD308	–1.34	–0.91	0.83	–0.02	–0.58	–0.60	–0.24	0.62
2B710	–0.24	1.92	–1.0	–0.02	0.11	–0.78	0.90	0.80
DKB390	1.61	1.31	–0.47	0.67	0.93	0.49	–0.45	–1.16
DP ($\hat{g}_i$)	0.52		0.51		0.47		0.51	
DP ($\hat{g}_i – \hat{g}_j$)	0.78		0.76		0.70		0.77	

Parents	GCA						
	GM	GY	SG	PC	NDF	ADF	LC
Impacto	–0.98	0.60	0.02	–0.09	0.09	–1.78	–1.01
Cargo	0.18	0.19	0.02	0.02	–0.23	0.37	–0.30
P30B39	–0.39	0.28	–0.004	–0.11	1.35	0.37	0.25
P30P34	1.17	–0.26	–0.003	0.11	–1.61	–0.14	0.14
P30R50	0.70	0.11	0.01	0.07	0.009	0.06	–0.30
CD304	–3.56	–0.58	–0.054	0.03	–0.35	–0.21	0.49
CD308	–2.80	–0.56	–0.055	–0.05	–0.36	0.89	0.06
2B710	1.38	–0.17	–0.016	0.12	0.58	–0.53	0.22
DKB390	4.31	0.38	0.083	–0.09	0.52	0.97	0.43
DP ($\hat{g}_i$)	0.89	0.13	0.07	0.09	0.46	0.42	0.15
DP ($\hat{g}_i – \hat{g}_j$)	1.34	0.20	0.10	0.13	0.69	0.63	0.23

selection of the best hybrids should be made within each growing season. For both variables, GM and MS, the choice of the best hybrids is driven by the presence of the parent DKB390, which showed appropriate GCA estimates for the two traits in both seasons. Thus, the best hybrid combinations for GM were CD308 × DKB390 (growing season 2009 SCA: 3.61 t ha^{-1}; growing season 2010 SCA: 7.84 t ha^{-1}) and CD304 × DKB390 (growing season 2009 SCA: 3.06 t ha^{-1}; growing season 2010 SCA: 5.96 t ha^{-1}). For MS, the prominent hybrid combinations were 2B710 × DKB390 (growing season 2009 SCA: 2.19 t ha^{-1}; growing season 2010 SCA: 5.04 t ha^{-1}) and CD308 × DKB390 (growing season 2009 SCA: 1.68 t ha^{-1}; growing season 2010 SCA: 3.36 t ha^{-1}).

For the trait PE, estimates of GCA and SCA had high interaction with the environment. Thus, for the first season, the parents with higher estimates of GCA were Impacto, P30B39 and CD308. The hybrid combinations with higher estimate of SCA in 2009 were Cargo × CD308 (5.39%), P30B39 × CD304 (1.90%), P30B39 × P30R50 (1.58%) and P30B39 × P30P34 (1.53%). For the second season, the parents with the highest estimates of GCA were Cargo, Impacto and DKB390. For this same growing season, the best hybrids were Cargo × DKB390 (3.12%), CD308 × DKB390 (1.76%), Impact × P30B39 (0.77%) and Cargo × P30B39 (0.65%).

For GY, the best hybrid combinations were 2B710 × DKB390 (1.30 t ha^{-1}), Cargo × DKB390 (0.82 t ha^{-1}), Impacto × P30P34 (0.72 t ha^{-1}) and CD304 × DKB390 (0.63). In this case, there was a complement of genes from both parents in the cross, resulting in an increase in the average of this trait resulting from the non-additive gene action.

To improve the SG trait, the best crosses were P30R50 × CD304 (–0.57 leaves) and CD304 × DKB390 (–0.55 leaves). These were the only crosses that expressed gene complementation to reduce the number of senescent leaves per plant. For PS, the best hybrid combinations were Impacto × DKB390 (–1.1%) and Impacto × CD308 (–0.78%), by concurrently showing negative estimates of GCA and the presence of the hybrid Impacto as parent. For PL, the best hybrid combinations were P30B39 × 2B710 (1.13%) Impacto × DKB390 (1.0%) and CD308 × 2B710 (0.94%).

The parents 2B710 and P30P34 stood out as to the estimates of GCA for PC. The combination P30B39 × P30P34 (1.11%) was the most appropriate for breeding to increase TRP content. The parent P30P39 stood out as to the estimate of GCA for NDF, and the combinations P30B39 × DKB390 (1.37%), Impacto × P30B39 (0.95%) and Cargo × P30B39 (0.52%) showed the highest estimates of SCA. For LNG, the parent Impacto contributed most to reduce the fiber content, with negative GCA estimate, contributing to increase the digestibility and quality of food. Therefore, the best hybrids containing this parent were Impacto × DKB390 (–1.08%), Impacto × Cargo (-0.82%), Impacto × CD308 (–0.67%) and Impacto × P30B39 (–0.40%).

The presence of favorable alleles and the low frequency of deleterious recessive alleles are fundamental for the selection of promising germplasm as a source of breeding lines (Hallauer et al., 2010). Therefore, the estimates of inbreeding depression (ID) and û + â are indicative of the potential of a population in relation to the demand for superior lines, helping the breeder in choosing the best segregating populations (Vencovsky & Barriga, 1992). Thus, the smaller the ID of the population, the smaller the contribution of dominance effects on the means and consequently the greater the estimates û + â (Cruz et al., 2012).

The significance of the effect of interactions between the environments and the performance of S1 families in relation to the traits PE and PL indicates that the best progeny should be selected in each respective season (Table 1). In both seasons, the estimates of ID and (û + â) indicated that the best genotypes to compose source populations for the PE trait were the hybrids Impacto, P30B39 and 2B710 (Table 4). Similarly, for the PL, estimates of (û + â) suggest that the self-pollinated progenies from the hybrids Impacto and DKB390 are better than others (Table 4).

A good silage corn hybrid must have a high production of green mass and high proportion of grains in the ensiled material (Marcondes et al., 2012). Based on these attributes, the hybrids Impacto, DKB390 and CD304 can be selected to compose elite populations for extracting lines for the traits GM and MS due to the relatively low ID and high û + â estimates for such traits (Table 4).

There was a strong inbreeding depression for GY due to the absence of negative estimates, indicating the superiority of hybrids in relation to S1 populations (Table 4). The loss of vigor resulting from self-fertilization ranged from 12.2% to 47.80%. The hybrids 2B710, Impacto and DKB390 expressed a higher frequency of favorable alleles for GY (Table 4). Still, such hybrids showed high estimates of û + â, qualifying them to compose populations source of superior lines for GY (Table 4). The results coincide with studies that show a wide variation in the levels of inbreeding depression for grain yield in corn (Bernini & Paterniani, 2012; Bernini et al., 2013; Pacheco et al., 2002). This variation stems from differences in the levels of dominance between the traits, different allele frequencies and degree of relatedness between individuals in the population (Hallauer et al., 2010).

The P30P34 and P30B39 hybrids obtained the two highest estimates of û + â for the PC, and were the most recommended for the extraction of lines. The hybrids Impacto, 2B710 and CD304 are the most promising for the traits NDF and LC, due to the lower predicted fiber content in their lines. Regarding the FDA trait, it may be recommended the hybrids P30R50 and DKB390 (Table 4).

Table 4. Estimation of inbreeding depression (ID,%) and of (û + â) of corn hybrids for ear percentage (PE,%) and leaf percentage (PL,%), dry mass (DM, t ha^{-1}), green mass (GM, t ha^{-1}), grain yield (GY, t ha^{-1}), stay green (SG, number of senescent leaves), stem percentage (PS,%), protein content (PC%), neutral detergent fiber (NDF,%), acid detergent fiber (ADF,%) and lignin content (LC,%)

Parent	PE				PL				GM		MS		GY	
	2009		2010		2009		2010							
	û+â	ID	û+â	ID	û+â	ID	û+â	ID	û+â	ID	û+â	ID	û+â	ID
Impacto	**4.1**	**2.6**	**20.8**	**–2.1**	**18**	**–2.1**	**34.09**	**5.3**	**51.1**	**–0.3**	**17.8**	**0.7**	**3.1**	**34.9**
Cargo	30.5	9.6	16.9	9.1	14.5	8.1	32.74	4.9	35.3	18	10.6	23.9	1.4	41.5
P30B39	43.2	–2.9	14.1	11.8	12.8	4.5	48.73	–11	44	11.8	7.1	32.4	0.9	45.8
P30P34	35.7	6.3	16	7.5	12.6	8.7	31.04	12.2	39.1	16.3	10.4	21.5	1.6	40.9
P30R50	37	2.0	20.1	–4.4	14.2	3.5	31.83	7.8	41.2	12.7	12.5	15.6	0.4	47.8
CD304	38.1	0.04	15.4	6.4	8.6	27	44.08	–9.5	34.8	9.6	13.7	3.6	1.6	38.7
CD308	33.4	8.5	19.7	–2.7	14.6	2.4	36.80	4.0	32	18.8	10.1	18.5	0.9	44.4
2B710	43.1	–3.5	21.9	–18	13.6	7.8	34.41	10.2	35.7	17.3	15.1	8.7	4.3	12.2
DKB390	31.2	11.4	18.3	3.1	18.1	–14	33.68	2.7	50.3	7.4	9.7	26.5	2.9	34.9

Parent	SG		PS		PRT		NDF		ADF		LC	
	û+â	ID	û+â	ID	û+â	ID	û+â	ID	û+â	ID	û+â	ID
Impacto	1.5	–7.5	43	–2.9	5.5	9	76.7	–4.9	30.2	–7.1	6.9	–1.2
Cargo	3.5	–40.1	52.6	–9.9	7.7	–7.1	67	0.5	24.7	12.1	10.2	–34.7
P30B39	0.9	30.4	40.5	3.4	9.1	–25.1	50.9	14.7	27.1	4.4	6.8	4.3
P30P34	1.6	18.3	52.3	–12.3	10.7	–24.8	60.3	0.2	28.5	–3.7	8.8	–12.8
P30R50	3.2	–5.2	48.4	–3.8	6.7	4.54	63.2	2.8	32.8	–5.4	7.2	0.9
CD304	1.9	21.1	46.8	–3.1	7.6	–4.8	66.1	1.4	29.2	–2.3	7	10.4
CD308	2.6	–20.9	47.7	–5.7	8.9	–10.9	63.2	3.9	28.5	4.7	8.5	1.2
2B710	2.8	–20.9	43.5	–1.6	6.9	6.1	70.3	–0.07	27.4	–2.6	5.6	11.2
DKB390	0.8	32.8	49.4	–4.6	7.7	–0.9	62	3.8	40.4	–22	11.4	–27.2

4. CONCLUSION

The hybrid Impacto is recommended to reduce the content of acid detergent fiber and lignin, in addition to promoting the percentages of leaves and ears of the forage. The combinations of the parent Impacto with the parents DKB390, P30P34 and P30B39 are recommended for extracting lines or interpopulation breeding aimed to reduce the amount of fiber and increase protein content. The hybrid combinations 2B710 × DKB390 and CD304 × DKB390 are prominent in traits related to forage productivity. With respect to grain yield, high inbreeding depression observed indicated that non-additives genes played a key role in its inheritance.

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