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Identification of potential soybean crosses for grain yield in the F_2 generation

Identificação do potencial de cruzamentos de soja para produtividade de grãos na geração F_2

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Abstract: The diallel schemes comprise a powerful strategy for the genetic study of the characters and the ability to match the genotypes, as well as to obtain information at the different stages of a genetic breeding program involving artificial hybridizations. Moreover, it presents importance for the adequate selection of the parents in generations of endogamy after the hybridization. The objective was identifying the potential of soybean crosses to obtain progenies with high grain yield. A partial diallel was carried out, where group I was composed of ten experimental lines with high grain yield, and group II was composed of five genotypes with resistance to white mold, as indicated in literature. Two field experiments were installed to estimate the general and specific combining ability, the first one with the 50 crosses and the second one with the 15 parents (I and II groups). At the R_8 stage, grain yield in kg ha^{-1} of the crosses and the parents was evaluated. The comparison of means between the genotypes and heterosis was also calculated. Broad-sense heritability was estimated considering phenotypic, environmental and genotypic variances. The results indicated superiority of the crosses in comparison to the parents. Heritability was considered high for most crosses evaluated. Diallel analysis was effective in identifying F_2 populations with higher genetic gain potentials.

Keywords: *Glycine max,* heterosis, herdability, partial diallel

Resumo: Os esquemas dialélicos de cruzamentos compreendem uma estratégia poderosa para o estudo genético dos caracteres e capacidade de combinação entre genótipos, bem como para se obter informações nas diferentes etapas de um programa de melhoramento genético envolvendo hibridações artificiais. Além disso, apresenta importância na escolha adequada dos genitores em gerações de endogamia após a hibridação. O objetivo foi identificar cruzamentos potenciais a fim de obter progênies altamente produtivas. Foi utilizado um dialelo parcial em que o grupo I envolveu dez genótipos representados por linhagens de soja experimentais com alta produtividade de grãos e o grupo II foi composto por cinco genótipos de soja com indicações na literatura de possível resistência ao mofo branco. A fim de estimar a capacidade geral e específica de combinação, foram instalados dois experimentos em campo, sendo o primeiro experimento representado por 50 cruzamentos e o segundo experimento pelos 15 genótipos (grupos I II). No estádio R_8, foi avaliada a produtividade de grãos, em kg.ha^{-1}, dos dois experimentos. Foi realizado teste de média entre os genótipos e foi calculada a heterose. A herdabilidade no sentido amplo foi estimada com as variâncias fenotípicas, ambientais e genotípicas. Os resultados indicaram superioridade dos cruzamentos em comparação aos genitores. A herdabilidade foi considerada alta para a maioria dos cruzamentos. A análise dialélica foi eficaz em identificar populações F_2 com maiores potenciais de ganho genético.

Palavras-chaves: *Glycine max*, heterose, herdabilidade, dialelo parcial

Introduction

Soybeans originated in China and there are reports of cultivation dating to about 1500 BC (Qiu and Chang, 2010). It took many years for western civilizations to notice the value of soybeans for food and afterwards, due to its protein value that provides multiple uses for it, there was a formation of an industrial complex destined to processing the grains, directing for production of oil and feed (Liu, 2008).

In Brazil, the introduction of soybeans occurred in the state of Bahia in 1882. Later, new cultivars arised and were introduced in São Paulo and later in Rio Grande do Sul, where soybeans were most successful (Balbinot Junior et al., 2017).

Soybean, *Glycine max* (L.) Merr., is the world's most important oilseed crop. The agricultural sector has predicted the constant yield increase through the improvement of crop management and the use of improved cultivars (Acquaah, 2012). Therefore, soybean breeding programs in Brazil have selected genetic materials with higher yield potential, ensuring productivity increases of 1.5 to 2% per year (Lange and Federizzi 2009, Balbinot Junior et al., 2017). High yield is essential to profitable soybean production, particularly in a highly competitive market.

In breeding programs, the diallel schemes constitute a powerful strategy for the estimation of genetic components, such as the type of gene action and the combining ability among the parents, as well as to obtain information in different stages of a breeding program involving artificial hybridizations. Information on general and specific combining ability effects is very important in making the next phase of a breeding program (Bernardo, 2010).

In addition, it is present special importance for the adequate choice of the parents in early generations of endogamy, after hybridization (Falconer and Mackay, 1996). Some studies involving traits of agronomic interest in soybean have provided base material for the soybean improvement program through methodologies of diallel crosses (Gavioli et al., 2008; Cho and Scott, 2000).

In view of the above, the objective with the research was of identifying the potential of soybean crosses to obtain progenies with favorable agronomic characteristics, with emphasis on grain yield.

Materials and Methods

The genetic material used in this research involved 15 soybean genotypes (Table 1) used in a 10 x 5 partial diallel with of 50 crosses (Table 2). Group I was composed of ten parents classified with high yield potential, wide adaptability and resistance to the main diseases and pests, developed by the Department of Genetics, ESALQ-USP. Group II was composed of five genotypes, three commercial cultivars (Caiapônia, EMGOPA 313 and MSOY 6101), an experimental line (A4725RG by Monsanto) and a plant introduction (PI 153.282) with some degree of tolerance to white mold (Table 1).

Table 1. Genealogies from the 15 genotypes

Groups	Genotypes	Genealogy
I	(1) USP 14-01-20	Cristalina x IAC-4
	(2) USP 70.004	(Soc 81-76 x Foster) x (IAC Foscarin 31 x Forrest)
	(3) USP 70.006	Foster x FT 79- 3408
	(4) USP 70.010	(IAC Foscarin 31 x Forrest) x (Foster x FT 79- 3408)
	(5) USP 70.042	(Soc.81-76 x Foster) x Hartwig
	(6) USP 70.057	Kirby x FT-2
	(7) USP 70.080	(Coker x Primavera) x (Viçosa x IAC-10)
	(8) USP 70.108	Hartwig x PI 371.611
	(9) USP 70.109	(IAC-6 x UFV-4) x Hartwig
	(10) USP 93-05.552	GO 81-8.491 x BR 80-15.725-B
II	(11) MSOY6101*	...
	(12) PI153.282*	...
	(13) A4725RG*	...
	(14) EMGOPA 313*	IAC 7 x (Santa Rosa x GO79-3068)
	(15) Caiapônia*	Primavera (OCEPAR 3) x BR 85-6356

*Genotypes with tolerance to white mold.

Table 2. Design of the 10 x 5 partial diallel with 50 crosses between ten parents from Group I and five parents from Group II, with identification numbers varying from 101 to 150

Group II $_{\text{INC*}}$ Group I	(11) MSOY6101	(12) PI153.282	(13) A4725RG	(15) Caiapônia
(1) USP 14-01-20	1x11$_{101}$	1x12$_{102}$	1x13$_{103}$	1x14$_{104}$
(2) USP 70.004	2x11$_{106}$	2x12$_{107}$	2x13$_{108}$	2x14$_{109}$
(3) USP 70.006	3x11$_{111}$	3x12$_{112}$	3x13$_{113}$	3x14$_{114}$
(4) USP 70.010	4x11$_{116}$	4x12$_{117}$	4x13$_{118}$	4x14$_{119}$
(5) USP 70.042	5x11$_{121}$	5x12$_{122}$	5x13$_{123}$	5x14$_{124}$
(6) USP 70.057	6x11$_{126}$	6x12$_{127}$	6x13$_{128}$	6x14$_{129}$
(7) USP 70.080	7x11$_{131}$	7x12$_{132}$	7x13$_{133}$	7x14$_{134}$
(8) USP 70.108	8x11$_{136}$	8x12$_{137}$	8x13$_{138}$	8x14$_{139}$
(9) USP 70.109	9x11$_{141}$	9x12$_{142}$	9x13$_{143}$	9x14$_{144}$
(10) USP 93-05.552	10x11$_{146}$	10x12$_{147}$	10x13$_{148}$	10x14$_{149}$

* INC: Identification Numbers of Crosses: The crosses were enumerated from 101 to 150. The parents were sown in greenhouse at Department of Genetics, ESALQ/USP, in Piracicaba for crossings during the months of January and February of 2011. The hybrid seeds (F_1) were sown in tubes and the seedlings were transplanted to the field in November 2011 in order to obtain sufficient seeds for F_2 generation.

In the agricultural year 2012/13, two experiments were conducted at Department of Genetics, ESALQ/USP, in Piracicaba (22º42'30 "S, 47º38'10"W, 539 meters altitude) with tropical and semiarid conditions (rainfall 1255 mm, average annual temperature: 20.8°C, minimum 12ºC, maximum 35°C), the soil management in the experiments were according to the recommendations for soybean crop. And insects were controlled with biological and chemical insecticides and weeds with herbicides. The first experiment included the 50 diallel crosses (F_2 generation) and three common checks (CB07-958-B, BRS133 and MSOY8001), with ten replicates; and the second experiment included the 15 parents and the same three common checks, with four replicates. The common checks were useful to obtain the environment variance. In both experiments, the experimental plot had an area of 1.5 m^2.

After harvesting each plant per each plot, the grain yield (GY) in g.plant^{-1} was quantified. The data obtained were transformed to kg.ha^{-1}.

Analyzes of the experimental data of the F_2 plants were performed using the statistical programs R (version 3.4.1) and the GENES (version 2017.26). A residual distribution analysis was performed by residual graphs to verify if the ANOVA assumptions. In addition, the data transformation was verified from the Bartlett and Shapiro-Wilk tests (Snedecor and Cochran, 1989).

With the adjusted means, the analyses of variance were carried out in a random blocks experimental design, represented by the following mathematical model:

$$Y_{ijk} = \mu + g_i + r_j + e_{(ij)} + d_{(ij)k} \qquad (1)$$

Where: Y_{ijk} is the observed value for the plant k of genotype i in the repetition j; μ is the fixed effect of the general mean of the experiment; g_i is the random effect of genotype i; r_j is the random effect of repetition j; $e_{(ij)}$: is the random effect of the experimental residue of the plot that received the genotype i in the repetition j, assuming that the residues are independent and normally distributed with zero mean and variance σ^2; $d_{(ij)k}$ is the random effect of the experimental residue of plant k within plot ij.

For the sources of variation with F-test significant in the ANOVA, the grouping of means proposed by Scott-Knott (Scott and Knott, 1974) was carried out.

The heterosis was estimated according to Vencovsky and Barriga (1992) for each cross, with the necessary adaptation to the F_2 generation, so that the results were expressed at the level of F_1, according to the following expression:

$$h\,(\%) = \left[\frac{2(\overline{F_2} - \overline{G})}{\overline{G}}\right] * 100 \qquad (2)$$

Where: h is the heterosis (%) of the cross; F_2 is the mean of the F_2 plants of the cross; and G is the mean of the parents involved in the cross.

The genotypic variance of each cross was obtained from the difference between the variance within of each crossing (F_2 generation) and the mean of the variances obtained within the checks, estimated in the analysis of variance involving a randomized block design with information within plot.

In order to estimate the broad-sense heritability coefficients, phenotypic, environmental and genotypic variances were obtained according to Bernardo (2010) and are described below:

σ_F^2 is the phenotypic variance obtained from the variance within crosses in F_2 generation. As F_2 plants have high frequency of heterozygous genotypes, this variance has a genetic and an environmental component;

σ_E^2 is the environmental variance estimated from the mean of the variances within the checks used in the experiment. As the checks are homozygous genotypes, this variance is completely environmental;

σ_G^2 is the genotypic variance estimated from the difference between the variance within crosses in the F_2 generation and the variance within the checks. It is assumed that the environmental effect acts in the same way on the checks and F_2 plants.

Therefore, the coefficients of heritability in the broad sense in percentage (h_a^2), were estimated according to the expression:

$$h_a^2 = \frac{\sigma_F^2 - \sigma_E^2}{\sigma_F^2} * 100 \quad = \quad \frac{\sigma_G^2}{\sigma_F^2} * 100 \qquad (3)$$

The general combining abilities of the parents and the specific combining abilities of the crosses were estimated according to method 4 of the Griffing model (1956), adapted for partial diallel by Geraldi and Miranda Filho (1988) by the GENES program, according to the following model:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + e_{ij} \qquad (4)$$

Where Y_{ij} is the mean of the cross involving the parent i of group I and the parent j of group II; μ is the general mean of the diallel; g_i is the effect of the general combining ability of the parent i of group I; g_j is the effect of the general combining ability of the parent j of group II; s_{ij} is the effect of the specific combining ability of the cross between the parents i and j; and e_{ij} is the mean experimental error.

Results and Discussion

From Table 3, it is possible to observe the means of crosses, for grain yield, obtained by the Scott-Knott test.

The mean of the crosses (3046 kg.ha^{-1}) was higher than the mean of the parents (2996 kg.ha^{-1}). Four groups (a, b, c and d) were significantly different from each other by the Scott-Knott (SK) test. The highest GY means, were 4413 kg ha^{-1} (Cr.148: USP93-05.552 x A4725RG), 4137 kg ha^{-1} (Cr.102: USP14-01-20 x PI153.282), 4129 kg ha^{-1} (Cr.132: USP70.080 x PI153.282), 4107 kg ha^{-1} (Cr.133: USP 70.080 x A4725RG), 4083 kg ha^{-1} (Cr.149: USP 93-05.552 x EMGOPA313) and 4060 kg ha^{-1} (Cr.134: USP 70.080 x EMGOPA 313). These crosses have their means higher than the parents involved in the corresponding cross. For example,the crosses 102 and 132 involved the parent PI 153282, which presented the lowest average GY (1860 kg.ha^{-1}) among the parents.

The summary of the analysis of variance for the partial diallel in the F_2 generation presented significance for additive and non-additive effects (Table 4).

From analysis variance, was possible observe information regarding the phenotypic variance of each cross for GY. The importance of the phenotypic variance for each crossing is associated with the degree of significance that was found for 14 of 50 crosses. Significance at 5 % was found for one cross, and below 1 % for eleven crosses. The obtained environmental variance was useful to estimate the genotypic variance of each cross and the heritability of GY, presented in Table 5.

Table 3. Summary of the Scott-Knott (SK) test comparing the 50 crosses and the 15 parents means for the grain yield character (GY, kg.ha^{-1})

Parents Means^2		2931 b	1860 c	2896 b	4681 a	2841 b
		MSOY6101	**PI153.282**	**A4725RG**	**EMGOPA313**	**Caiapônia**
3398 b	**USP14-01-20**	**101** 3310 b^1	**102** 4137 a	**103** 3544 b	**104** 3523 b	**105** 3075 c
1928 c	**USP 70.004**	**106** 3286 b	**107** 2061 d	**108** 3222 b	**109** 3117 c	**110** 2124 d
2542 c	**USP 70.006**	**111** 3322 b	**112** 2511 d	**113** 3382 b	**114** 3025 c	**115** 2858 c
3268 b	**USP 70.010**	**116** 3424 b	**117** 2511 d	**118** 3236 b	**119** 2785 c	**120** 2916 c
2547 c	**USP 70.042**	**121** 2955 c	**122** 2632 d	**123** 3455 b	**124** 2981 c	**125** 2488 d
3200 b	**USP 70.057**	**126** 3484 b	**127** 2468 d	**128** 2371 d	**129** 2347 d	**130** 2389 d
3128 b	**USP 70.080**	**131** 2907 c	**132** 4129 a	**133** 4107 a	**134** 4060 a	**135** 3104 c
3268 b	**USP 70.108**	**136** 2943 c	**137** 2471 d	**138** 3199 b	**139** 3260 b	**140** 2398 d
2021 c	**USP 70.109**	**141** 2262 d	**142** 2246 d	**143** 2819 c	**144** 2604 d	**145** 2854 c
4212 a	**USP93-05.552**	**146** 2722 c	**147** 2694 c	**148** 4413 a	**149** 4083 a	**150** 2710 c

[1] Considering letters within the table, averages followed by the same letter belong to the same group by the SK test (p <0.05).
[2] Considering letters in table margins, averages followed by the same letter belong to the same group by the SK test (p <0.05).

Estimates of genotypic variance for GY ranged from -41 in cross number 141 (USP 70.109 x MSOY6101) to 374 in cross 124 (USP 70.042 x EMGOPA313). Crosses involving the USP 70.042 (group I) and EMGOPA313 parents (group II) had higher estimates of variance.

The broad-sense heritability coefficient was useful in estimating the participation of the genetic component in the productive performance of F_2 plants. The estimates of heritability ranged from 11 % to 77 % and were grouped into three different categories according to their magnitude: low ($h_a^2 <$ 40 %), moderate (40 % $< h_a^2 <$ 60 %) and high ($h_a^2 >$ 60 %). High, moderate and low heritability estimates were found at 11, 21 and 13 crossings, respectively. In this way, 33 crosses (66 %) with moderate to high heritability coefficients for GY were found.

Table 4. Analysis of variance of the parents of groups I and II and their hybrid combinations for grain yield (GY) by the Griffing method (1956) adapted to a partial diallel

SV	DF	Mean Squares
		GY (g.plant^{-1})
Replications (R)	9	106,02
Crosses	49	2075***
GCA I	9	5131***
GCA II	4	5241***
SCA	36	959,3***
Error between	289	363,4*
Error within	5200	214,8
Plants/Replications/Cr 101	77	179 ^{ns}
Plants/Replications /Cr 102	117	237 ^{ns}
Plants/Replications /Cr 103	107	262 .
Plants/Replications /Cr 104	70	355 **
Plants/Replications /Cr 105	102	204 ^{ns}
Plants/Replications /Cr 106	118	151 ^{ns}
Plants/Replications /Cr 107	22	219 ^{ns}
Plants/Replications /Cr 108	134	193 ^{ns}
Plants/Replications /Cr 109	93	310 **
Plants/Replications /Cr 110	31	127 ^{ns}
Plants/Replications /Cr 111	112	143 ^{ns}
Plants/Replications /Cr 112	66	104 ^{ns}
Plants/Replications /Cr 113	134	208 ^{ns}
Plants/Replications /Cr 114	73	310 **
Plants/Replications /Cr 115	68	206 ^{ns}
Plants/Replications /Cr 116	63	202 ^{ns}
Plants/Replications /Cr 117	66	314 **
Plants/Replications /Cr 118	145	245 ^{ns}
Plants/Replications /Cr 119	109	159 ^{ns}
Plants/Replications /Cr 120	122	231 ^{ns}
Plants/Replications /Cr 121	153	194 ^{ns}
Plants/Replications /Cr 122	61	304 **
Plants/Replications /Cr 123	74	259 ^{ns}
Plants/Replications /Cr 124	94	485***
Plants/Replications /Cr 125	135	180 ^{ns}
Plants/Replications /Cr 126	133	217 ^{ns}
Plants/Replications /Cr 127	155	145 ^{ns}
Plants/Replications /Cr 128	40	245 ^{ns}
Plants/Replications /Cr 129	58	273.
Plants/Replications /Cr 130	42	231 ^{ns}
Plants/Replications /Cr 131	124	201 ^{ns}
Plants/Replications /Cr 132	90	244 ^{ns}
Plants/Replications /Cr 133	100	302 **
Plants/Replications /Cr 134	101	378 ***
Plants/Replications /Cr 135	104	151 ^{ns}
Plants/Replications /Cr 136	87	95,6 ^{ns}
Plants/Replications /Cr 137	140	103 ^{ns}
Plants/Replications /Cr 138	164	154 ^{ns}
Plants/Replications /Cr 139	77	205 ^{ns}
Plants/Replications /Cr 140	88	139 ^{ns}
Plants/Replications /Cr 141	154	69,7 ^{ns}
Plants/Replications /Cr 142	123	99,8 ^{ns}
Plants/Replications /Cr 143	97	207 ^{ns}
Plants/Replications /Cr 144	164	161 ^{ns}
Plants/Replications /Cr 145	143	161 ^{ns}
Plants/Replications /Cr 146	103	367 ***
Plants/Replications /Cr 147	144	124 ^{ns}
Plants/Replications /Cr 148	178	370 ***
Plants/Replications /Cr 149	97	336 ***
Plants/Replications /Cr 150	148	263 *
Error within checks	1007	110,8

ns: no significant; *, **, *** significant at 10 %, 5 %, 1 % e 0,1 % probability, respectively, for the F test . Identification numbers of crosses varying from 101 to 150.

Table 5. Genetic variance estimation (σ^2), heritability (h^2) and heterosis (h %) of crosses in the F_2 generation, for grain yield (GY, kg.ha^{-1})

		MSOY 6101	PI 153.282	A4725RG	EMGOPA 313	Caiapônia
USP 14-01-20	**INC**	**101**	**102**	**103**	**104**	**105**
	σ^2	69.1	127	151.9	245	93.5
	h^2	38 %	53 %	58 %	69 %	46 %
	h %	9.20	114.72	25.23	-25.57	-2.85
USP 70.004	**INC**	**106**	**107**	**108**	**109**	**110**
	σ^2	40.81	109.18	82.8	199.4	16.9
	h^2	27 %	50 %	43 %	64 %	13 %
	h %	70.51	17.63	67.16	-11.35	-21.85
USP 70.006	**INC**	**111**	**112**	**113**	**114**	**115**
	σ^2	32.6	-6.79	97.7	199.8	95.2
	h^2	23 %	-7 %	47 %	64 %	46 %
	h %	42.79	28.17	48.77	-32.48	12.37
USP 70.010	**INC**	**116**	**117**	**118**	**119**	**120**
	σ^2	91.2	204.1	134.6	48.7	120.6
	h^2	45 %	65 %	55 %	31 %	52 %
	h %	20.94	-4.13	9.99	-59.86	-9.07
USP 70.042	**INC**	**121**	**122**	**123**	**124**	**125**
	σ^2	83.3	193.9	149.1	374.5	69.9
	h^2	43 %	64 %	57 %	77 %	39 %
	h %	15.77	38.89	53.90	-35.03	-15.29
USP 70.057	**INC**	**126**	**127**	**128**	**129**	**130**
	σ^2	107.1	34.7	135	162.2	120.3
	h^2	49 %	24 %	55 %	60 %	52 %
	h %	27.30	-4.90	-44.42	-80.88	-41.81
USP 70.080	**INC**	**131**	**132**	**133**	**134**	**135**
	σ^2	90.9	133.2	191.7	267.7	41
	h^2	45 %	55 %	63 %	71 %	27 %
	h %	-8.09	131.11	72.71	7.97	8.01
USP 70.108	**INC**	**136**	**137**	**138**	**139**	**140**
	σ^2	-15.2	-7.3	43.7	94.9	29
	h^2	-16 %	-7 %	28 %	46 %	21 %
	h %	-10.10	-7.25	7.59	-35.95	-42.99
USP 70.109	**INC**	**141**	**142**	**143**	**144**	**145**
	σ^2	-41.1	-11	96.7	50.7	50.3
	h^2	-59 %	-11 %	47 %	31 %	31 %
	h %	-17.29	31.49	29.33	-44.58	34.80
USP 93-05.552	**INC**	**146**	**147**	**148**	**149**	**150**
	σ^2	256.5	14	259.5	225.3	152.2
	h^2	70 %	11 %	70 %	67 %	58 %
	h %	-47.57	-22.53	48.34	-16.35	-46.31

INC: Identification Numbers of the Crosses.

The heterosis also presented in Table 4 ranged from -81 % at cross 129 (USP70.057 x EMGOPA313) to 131 % at cross 132 (USP70.080 x PI153.282). Overall, 50 % of the crosses showed negative heterosis, nine of a total of 10 crosses involving the EMGOPA 313 parent had negative heterosis, meaning that the averages of these crosses was lower than the average of the parents. The contrary was observed for the A4725RG parent, since the crosses involving this genitor had positive values for heterosis, except the crossing 128 (USP 70.057 x A4725RG).

In relation the combining ability estimates (Table 5), the most potential parents were: USP 70.080 and USP14-01-20 from group I and A4725RG and EMGOPA313 from group II. The parents that contributed to decrease the GY, presenting negative g_i effect were USP70.109 and USP70.057 of group I and Caiapônia and PI153.282 of group II.

Table 6. Estimation of General (GCA) and Specific Combining Ability (SCA) by Griffing method 4, in the F_2 generation, for grain yield (GY, kg.ha^{-1})

GI\GII	**MSOY6101**	**PI153.282**	**A4725RG**	**EMGOPA313**	**Caiapônia**	**CGC (g_{iGI})**
USP 14-01-20	**101** -250.96	**102** 852.24	**103** -329.76	**104** -155.06	**105** -116.46	499.26
USP 70.004	**106** 480.64	**107** -469.16	**108** 103.84	**109** 195.54	**110** -310.86	-256.34
USP 70.006	**111** 259.64	**112** -276.16	**113** 5.84	**114** -154.46	**115** 165.14	0.66
USP 70.010	**116** 406.44	**117** -231.36	**118** -95.36	**119** -348.66	**120** 268.94	-44.14
USP 70.042	**121** 9.64	**122** -37.16	**123** 196.84	**124** -81.46	**125** -87.86	-116.34
USP 70.057	**126** 829.84	**127** 89.00	**128** -596.96	**129** -425.26	**130** 103.34	-406.54
USP 70.080	**131** -797.76	**132** 700.44	**133** 88.44	**134** 239.14	**135** -230.26	643.06
USP 70.108	**136** 45.64	**137** -151.16	**138** -11.16	**139** 245.54	**140** -128.86	-164.34
USP 70.109	**141** -338.16	**142** -78.96	**143** -93.96	**144** -113.26	**145** 624.34	-461.54
USP 93-05.552	**146** -644.96	**147** -397.76	**148** 732.24	**149** 597.94	**150** -287.46	306.26
CGC (g_{iGII})	42.76	-232.44	356.56	159.86	-326.74	

The highest s_{ij} values were found in the crosses 102 (USP14-01-20 x PI153.282), 126 (USP 70.057 x MSOY6101), 148 (USP93-05.552 x A4725RG), 132 (USP70.080 x PI153.282) and 145 (USP70.109 x Caiapônia). Only crosses 148, 102 and 132 are among those crosses with the highest GY means, which can be explained by the participation of at least one parent with high yield potential. In addition, the heterosis of these three crosses was extremely high (98 %).

The mean of the crosses was higher than the parent means, indicating that it is possible to obtain progenies superior to the parents, that is, transgressive genotypes for GY. Similar result was found in the work of Pandini, Vello and Lopes (2001), in which more than half of the crosses presented mean GY higher than the parents. The high grain yield observed in the best crosses can be explained by the favorable combination of the alleles in the parents. For example, crosses involving the parent EMGOPA313 have shown that the parent in question has a good GCA estimative and transmits well to offspring.

Diallel analysis was effective in identifying F_2 populations with higher genetic gain potentials. In a practical point of view, a breeding program has benefits with the information about the estimates of general combining ability (GCA) and specific combining ability (SCA). The first refers to the mean performance of a parent in hybrid combinations, while the second refers those cases in which certain combinations are shown to be relatively better or worse than that could be expected based on the average performance of the parents (Resende et al., 2016).

There was significance for GCS and SCA, as well as founded by Daronch et al. (2014) and Rocha, Pereira and Vello (2018). The additive variance, expressed by the mean of GCA, is comparatively higher than the non-additive variance, similar fact was observed by Oliveira et al. (2014). This denotes, therefore, that the best strategy is the use of intrapopulation improvement (Falconer and Mackay, 1996).

Crosses with high genetic variance may have variability to be explored in the search for superior genotypes. Although most crosses showed high heritability, this result does not match to the quantitative nature of the character, a fact that can be explained by the presence of gene dominance, which may be a considerable impediment to selection in early generations (Vencovsky and Barriga, 1992). These high values can be compared with the GY heritability in topcrosses of high genetic diversity (Yokomizo et al., 2000). Some negative heritability values were obtained when the estimate of the environmental variation was higher than the genetic one.

The knowledge of heterosis is important for a pre-selection of crosses, since more heterotic crosses are associated with greater divergence between the parents (Friedrichs et al., 2016). When heterosis is present for quantitative traits such as seed yield, it may indicate that the parents contrast sufficiently so that the diversity between the parents can be captured in a transgressive recombinant progeny (Taliercio et al., 2017). In the F_1 generation, Colombari Filho et al. (2010) found heterosis ranging from 6 to 57 %. Chaudhary and Singh (1974) also found values above 68 %.

The USP70.080 and USP14-01-20 parents also presented higher GCA values on the study of Oliveira et al. (2014). These parents may be useful to form a new base population for the selection of productive and superior genotypes in segregating generations. According to Cho and Scott (2000), the parents with the highest GCA values are related to the most productive combinations. Since the GCA is composed mainly from additive variance and additive epistatic variance, it may contribute significantly to the variance of GCA estimates (Bhullar et al., 1979).

The use of the partial diallel in the F_2 generation for grain yield may be a good strategy to associate with marked assisted selection in the F_3 generation to reduce de number of crosses or plants to be analyzed with the markers (Yang et al., 2015).

Conclusion

In general, three crosses (148, 102 and 132) had the best performance for grain yield, where, possibly, there was a complementarity of the loci generating a better than that expected combination based on the GCA of the respective parents. These three crosses could be use especially to investigate the reaction for white mold. Diallel analysis was effective in identifying F_2 populations with higher genetic gain potentials.

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