INBREEDING DEPRESSION AND GENETIC VARIABILITY IN AGRICULTURAL TRAITS AND RESISTANCE TO PLANT PATHOGENS IN EXOTIC MAIZE POPULATIONS

DEPRESSÃO ENDOGÂMICA E VARIABILIDADE GENÉTICA EM CARACTERES AGRONÔMICOS E DE RESISTÊNCIA A FITOPATÓGENOS EM POPULAÇÕES EXÓTICAS DE MILHO

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ABSTRACT: The effect known as depression by inbreeding refers to the reduction on the average value of quantitative traits, related to plant reproduction and physiology, due to the homozygosis of deleterious alleles. This study evaluated the inbreeding depression and the genetic variability of agricultural traits and of the resistance to phytopathogens in inbred families of two exotic maize populations. The experiments were done in the experimental area of the Universidade Federal de Goiás, Regional Jataí, in the second harvest 2015. Fifty and 40 FS_1 of NAP5 and NAP7 populations, respectively, were evaluated interplanting one row with a mixture of base population (family of Germanic siblings) at every ten plots to estimate depression by inbreeding of the traits evaluated. The experimental design was randomized blocks, with three replications. The following traits were evaluated: PH – plant height (cm), EH – ear height (cm), MF – male flowering (days), BP – number of broken plants, LP – number of lodged plants, KW – kernel weigh (kg $plot^{-1}$), ET – resistance to *Exserohilum turcicum*, WS(White Spot) – resistance to *Pantoea ananatis*, CS(Corn Stunt) – resistance to the corn stunt, PP – resistance to *Puccinia polysora* and CZ – resistance to *Cercospora zea-maydis*. The greatest estimates of depression by inbreeding in the agricultural traits were observed for kernel production, with values of 51.2 and 38.9% for the populations NAP5 and NAP7, respectively. Among the traits of resistance to phytopathogens, the greatest estimate was observed for the stunting complex, with values of -58.9% in NAP5 and -74.2% in NAP7. Both populations under study presented genetic potential to be used in breeding programs with recurrent selection and, after some selection cycles, lineages with good agricultural standard and resistance to phytopathogens can be obtained.

KEYWORDS: Leaf diseases. Endogamic families. Genetic parameters. *Zea mays*.

INTRODUCTION

Endogamy is defined as a phenomenon that occurs due to mating between related individuals (CRUZ, 2005). Oftentimes endogamy is undesirable in Hardy-Weinberg equilibrium populations, such as maize, because this type of crossing leads to homozygosis and, in these populations, there are recessive deleterious genes that, in homozygosis, cause harm to plant physiology, decreasing its phenotypic value (MIRANDA FILHO, 2001).

The genetic causes controlling inbreeding depression are not completely known; however, there are some hypotheses to explain them. One of these hypotheses is that favorable genes tend to be dominant or partially dominant; another hypothesis states that the heterozygote has greater phenotypic value than the homozygote (CROW; KIMURA, 1970). Inbreeding depression, in the former, is the rupture of the ideal combination of alleles that control the character under study.

Self-fertilization is the driving mechanism of endogamy, since it allows that common alleles by ancestry be found in the same individual, presenting great importance to obtain lineages. The value of a population as lineage source is highly dependent on inbreeding depression in relation to several characteristics, limiting the potential of obtaining vigorous lineages for subsequent production of hybrids (HALLAUER et al., 2010). In order to obtain lineages with acceptable probability, a breeding program should start with populations with high frequency of favorable alleles of important

traits, while presenting low frequency of undesirable alleles (VENCOVSKY; BARRIGA, 1992). Consequently, when an improved population is subjected to self-fertilization, few deleterious alleles are expressed for a given quantitative trait, resulting in lower estimates by inbreeding depression along the selection cycles, in comparison to the original, non-improved populations.

A study with three semi-exotic maize populations demonstrated that population CRE-01, obtained from a crossing of exotic lineages with a commercial hybrid that had passed through selections to eliminate deleterious genes, presented less inbreeding depression for the traits evaluated in relation to two other populations (OLIVEIRA et al., 2015).

The use of endogamic progenies can be a good strategy for traits that present low heritability, since inbreeding makes available greater genetic variability due to the crossing system, which allows obtaining estimates for the favorable genetic parameters in the selection process. In the breeding perspective, endogamy can be potentially used for the development of lineages with alleles of interest which, subsequently, will be used in the composition of simple, double or triple maize hybrids, or even in recurrent selection involving partially endogamic progenies (S_1, S_2 and S_3), for the development of improved populations (HALLAUER et al., 2010).

Besides improving desirable agricultural traits, the search for sources of resistance to plant pathogens has been one of the main foci of maize breeding programs. Presently, diseases constitute one of the main yield limiting factors and the primary control method is the use of resistant genotypes. However, the search of greater yielding and uniform genotypes resulted in a narrowing of the genetic basis, increasing vulnerability to biotic and abiotic stresses (COTA et al., 2015).

The exotic germplasm can be used both to obtain genotypes with superior agronomic traits and as a source of resistance to diseases of importance for the corn culture, promoting an increase in the genetic variability of this cereal. However, its use in maize breeding programs around the world has been inexpressive (GOODMAN, 2005). The potential of exotic or semi-exotic populations in maize breeding programs has been reported by several authors (OLIVEIRA et al., 2015; MENDES et al., 2015; SILVA et al., 2017; SOUZA et al., 2018). Juliatti et al 2004, 2009 and 2013 showed the possibilities of selection to plant pathogens resistance at endogamic population in maize to main diseases (cercospora leaf spot, common rust and white spot).

This study evaluated inbreeding depression and the genetic potential of agricultural traits and the resistance against plant pathogens (*Exserohilum turcicum* Leonard and Suggs, *Pantoea ananatis* (White Spot), phytoplasm, spiroplasm, *Puccinia polysora* and (Cercospora Leaf Blight) *Cercospora zeae* Tehon and Daniels) in endogamic families of two exotic maize populations.

MATERIAL AND METHODS

The experiments were done from February to July 2015 (second harvest) in Jataí/GO, at the experimental area of Universidade Federal de Goiás, at 17° 52' 53" and 51° 42' 52" W, 676 m above sea level.

Maize populations NAP5 (resistant to *Exerohilum turcicum*) and NAP7 (resistant to *Physopella zeae*) originated from a technical-scientific cooperation Project NAP-Maize (Nucleus of Support to Maize Research), created by the Department of Genetics at ESALQ/USP (Escola Superior de Agricultura "Luiz de Queiroz"/ Universidade de São Paulo) to identify reliable sources of resistance to the major maize leaf diseases. Several public institutions (CNPMS/EMBRAPA, IAC - Instituto Agronômico de Campinas, IAPAR - Instituto Agronômico do Paraná, ESALQ-USP, CENARGEM/EMBRAPA) and private enterprises (empresas Zêneca Sementes, Sementes Colorado, FT Sementes, Sementes Agroceres) joined the program.

One thousand two hundred and seventy three accesses of the BAG (Active Germplasm Bank, CENARGEM/EMBRAPA) were evaluated in the agricultural year 1994/1995 in thirteen locations in the states of Goiás, Mato Grosso, São Paulo and Paraná. Visual evaluations for resistance to five leaf diseases were done, with exclusive selection for each phytopathogens, excluding some accesses with low standards of yield and plant architecture. The number of accesses that entered in the composition of each population were 41 (NAP5) and 34 (NAP7). Each population was formed by an isonumeric seed sample of each selected access.

Endogamic families in each population were obtained by sowing two fields for crossings, each one consisting of 500 seeds. Fifty and 40 endogamic families (FS_1) were obtained from self-pollination of populations NAP5 and NAP7, respectively, for the experiments in Jataí-GO. The experimental design was randomized blocks, with three replications. Each experimental plot consisted of one 2-m long row, and rows were 0.9 meters apart from each other. Plots had 10 plants after thinning. Three plants in the center of the plot were

used to evaluate disease severity for each pathogen. Disease severity evaluations started when the first symptoms appeared, and three evaluations were done with 14 days interval between them.

White spot and helminthosporiosis severity evaluations were done with specific diagrammatic scales (MALAGI et al., 2011; LAZAROTO et al., 2012). Severity of cercosporiosis, polisora rust and the corn stunt were done with the scale developed by Agroceres (1996), used to evaluate most maize leave diseases.

One plot of the base population of each population was inserted at every ten FS_1 plots. An internal border was used to avoid the effect of the competitive effect of the base population with the endogamic lineages, in such a way that for each plot of the base population planted, two rows of that same population were used for protection, and externally to these two rows, two other rows were inserted as borders with a mixture of endogamic lineages. Agricultural management of both experiments was done according to the recommendations for maize (FANCELLI; DOURADO-NETO, 2000).

The characters plant height (PH), ear height (EH), male flowering (MF), number broken plants (BP), number lodged plants (LP), kernel weight (KW), number of plants (NP), resistance to *Exserohilum turcicum* (HT), resistance to *Pantoea*

ananatis (WS), resistance to corn stunt (CS), resistance to *Puccinia polysora* (PR) and resistance to *Cercospora zeae-maydis* (CZ) were evaluated. However, the number of plants was used only to make a correction on kernel weight to the ideal number of plants (10 plants), using the correction by covariance method, suggested by Miranda Filho (VENCOVSKY; BARRIGA, 1992).

The analyses and estimates of statistical-genetic parameters were done with the Program Genes (CRUZ, 2016).

RESULTS AND DISCUSSION

Population NAP7 presented greater averages for most variables of the agricultural traits evaluated (Table 1) than population NAP5, except for BP, which was similar for both populations. The observed averages of PH and KW for both exotic populations were considered low. Consequences of inbreeding are reduction in plant height and ear size and, consequently, in yield (BORÉM; MIRANDA, 2017). The values of KW were 2.01 and 2.09 t ha^{-1} for populations NAP5 and NAP7, respectively. Although the averages of KW for both populations were low, S_1 families with yield greater than four tons were observed, indicating the productive potential of these populations for recurrent selection programs.

Table 1. Averages of base population (m_0), averages of endogamic families (m_1), estimates of depression by endogamy (DP%), contribution of homozygotes ($\mu + a*$) and of heterozygotes ($d*$) and experimental coefficient of variation (CV%) for six agronomic traits in two exotic maize populations. Jataí, 2015

Estimates	PH	EH	MF	BP	LP	KW
	Population NAP5					
m_0	187.4	104.3	59	2	3	4.12
m_1	162.7	92.7	61	1	3	2.01
DP%	13.2	11.1	-3.4	50.0	0	51.2
$(\mu+a*)$	138.0	81.1	63	0	3	-0.10
$d*$	49.4	23.2	-4	2	0	4.22
CV%	11.0	14.7	1.8	79.1	51.3	28.1
	Population NAP7					
m_0	204.1	107.1	60	1	6	3.42
m_1	182.2	96.2	62	1	5	2.09
DP%	10.7	10.2	-3.3	0	16.7	38.9
$(\mu+a*)$	160.3	85.3	64	1	3	0.76
$d*$	43.8	21.8	-4	0	0	2.66
CV %	10.1	13.2	1.9	108.8	41.1	24.3

Traits – PH: plant height (cm); EH: ear height (cm); MF: flowering male (dias); BP: number of broken plants; LP: number of lodged plants; KW: kernel weight (t ha^{-1});

The observed averages of PH, EH and KW of both populations evaluated were lower than those observed in other studies with inbred exotic and semi-exotic maize populations (RODRIGUES, 2013; OLIVEIRA et al., 2015).

The population NAP5 presented the lowest averages of AUDPC (Table 2) for all five diseases evaluated, indicating greater resistance than NAP7. Some S_1 families of the two populations presented high resistance to HT, WS, CS, PR and CZ. This result demonstrates the potential of the exotic populations for use as resistance sources to phytopathogens in maize breeding programs.

Table 2. Averages of base population (m_0), averages of endogamic families (m_1), estimates of depression by endogamy (DP%), contribution of homozygotes ($\mu + a*$) and of heterozygotes ($d*$) and experimental coefficient of variation (CV%) for area under the disease progress curve (AUDPC) of five diseases in two exotic maize populations. Jataí, 2015

Estimates	[£] Diseases (AUDPC)				
	ET	WS	CS	PR	CZ
Population NAP5					
m_0	277.8	309.1	567.9	280.8	175.8
m_1	396.8	292.6	902.1	255.9	201.1
DP%	-42.8	5.3	-58.9	8.9	-14.4
($\mu+a*$)	515.8	276.1	1236.3	231.0	226.4
$d*$	-238.0	33.0	-668.4	49.8	-50.6
CV%	35.7	32.6	37.6	35.3	40.6
Population NAP7					
m_0	398.1	380.4	594.2	329.0	183.3
m_1	471.7	302.8	1034.8	309.6	223.1
DP%	-18.5	20.4	-74.2	5.9	-21.7
($\mu+a*$)	545.3	225.2	1475.4	290.2	262.9
$d*$	-147.2	155.2	-881.2	38.8	-79.6
CV%	31.8	31.5	28.1	38.6	40.9

[£]: ET – *Exserohilum turcicum*, WS (White Spot) – *Pantoea ananatis*, CS – Corn stunt, PP – *Puccinia polysora* and CZ – *Cercospora zea-maydis*.

According to the classification for experimental coefficients of variation for maize, proposed by Scapim et al. (1995), the trials presented values indicating good experimental precision for most of the traits evaluated, except for estimated values of BP, LP and the resistance to diseases, which had values above 28.1%. These results are due to strong environment effect on these traits, which cannot be controlled. Thus, high coefficients of variation for these traits are accepted and do not compromise the experimental precision. Brito et al. (2011), studying resistance of maize hybrids to cercospora leaf spot (Gray Leaf Spot) and white spot, found coefficient of variation values of 37.0 and 48.2% for these diseases, respectively.

The population NAP5 presented greater estimates of depression by inbreeding (DP%) for most agricultural traits evaluated than population NAP7, except for the trait LP. The DP% estimates for both populations, for the traits PH, EH, MF and AC were low, highlighting that the effects of dominance are less important for them. Bernini et al. (2013), in studies of inbred families, obtained for self-pollination of hybrids, reported low DP% values for PH, EH and MF.

Both populations presented high estimate of DP% for the trait KW, indicating that both of them are sensitive to inbreeding for this trait. Therefore, new cycles of recurrent selection are required for both populations in order to reduce their genetic load and, from the selection of superior genotypes, obtain lineages with excellent agricultural standards. High values of DP% for KW in exotic and semi-exotic maize populations were observed by Rodrigues (2013) and Oliveira et al. (2015). Good and Hallauer (1977) confirmed that production is strongly affected by inbreeding at any degree of homozygosis.

Inbreeding depression…   OLIVEIRA, A. S. et al.

The relative contribution of heterozygotes (d*) was greater than that of homozygotes to BP in the population NAP5. This result implies, indirectly, the existence of genetic heterogeneity in the populations. Taking into account the genetic effects, the estimates of depression by inbreeding are smaller for PH and EH than for the trait kernel production because the effects of gene dominance are less important for these traits (LIMA et al., 1984). High values of contribution by homozygotes (μ + a*) are indicative of the potential of the populations as sources of lineages with high productive potential. The contribution of loci in homozygosis for the traits PH, EH, MF and PH was greater than that of the loci in heterozygosis.

The estimates of μ + a* for KW in both populations are low; thus, in order to effectively extract lineages from them, it is necessary to select the best endogamic families and recombine them for new evaluations, in such a way that the populations will concentrate greater number of favorable alleles, allowing the retrieval of lineages with good productive potential. Maldonado and Miranda Filho (2002) presented similar results to those observed in this study for kernel production.

Increased severity of the diseases HT, CS and CZ were observed after one generation of self-pollination, indicating a negative effect of inbreeding, making both exotic populations more sensitive to these three diseases. The estimates of DP% varied from -58.9 to 8.9 for NAP5 and from -74.2 to 20.4 for NAP7. The AUDPC of CS was variable and presented the greatest DP% in both populations evaluated. The effect of inbreeding for WS and PP reduced severity, conferring greater resistance to these phytopathogens. Values of DP% between 14.6 and 26.8 for CS were observed by Oliveira et al. (2015) in three semi-exotic maize populations selected as resistance source to the pathogens of the corn stunt disease.

The contribution of loci in homozygosis (additive effects) was greater than those in heterozygosis (deviations due to dominance) for the reduction of disease severity of WS and PP in both populations, while for the diseases HT, CS and CZ, the contribution of loci in heterozygosis was more expressive in the reaction of resistance to these phytopathogens. Therefore, endogamic families in both populations were more resistant to WS and PP than the base population, while the base population was more resistant to the phytopathogens HT, CS and CZ due to the greater contribution of the loci in heterozygosis in relation to those in homozygosis for these.

Success in selective process depends on the existence of genetic variability for agricultural traits and resistance to phytopathogens in the breeding programs with focus on genetic resistance to diseases. Based on the results of the analyses of variance of the traits evaluated in both maize populations (Tables 3 and 4), significant differences were observed among S_1 families for all traits evaluated, except for CS in population NAP5 and for BP, LP and CZ in NAP7, which were not significant. Consequently, there is genetic variability for the agricultural traits and the expression of resistance to the diseases evaluated in both exotic maize populations, with the possibility of obtaining gains through genetic breeding and, thus, producing better adapted and resistant maize populations for the production of lineages.

Although the results of the analysis of variance are important as indicators of the potential of a given population and of the experimental precision, it still is insufficient for the breeder because it does not provide the magnitude of the available genotypic variability (CRUZ et al., 2014). Therefore, estimating genetic variance along with other components becomes indispensable for the studies of genetic breeding.

Population NAP5 presented greater genetic variability for the traits PH, EH, BP, LP, WS and CZ (Tables 5 and 6) than NAP7, while the later presented greater estimates for the traits MF, KW, HT and CS than the former. Population NAP7 presents greater genetic potential for the trait KW since, although average yield of both populations is similar, NAP7 presented greater genetic variability than NAP5 and genetic gains are more promising in populations with greater variability. The selection of families more resistant to CZ is more promising in population NAP5; however, the same selection in NAP7 for this trait will be ineffective since this population does not present genetic variability to promote genetic gains. Similarly, population NAP5 did not present genetic variability for CS, making the population NAP7 more adequate for the selection of more resistant families.

Studies of endogamic families in four exotic maize populations reported values of genetic variance for PH between 88.69 and 326.01 and for EH between 90.82 and 112.53 (RODRIGUES, 2013). Oliveira et al. (2015) reported estimates of genetic variance for KW in endogamic families of three semi-exotic families between 190.2 and 227.5.

The estimates of broad sense heritability coefficient for the agricultural traits of family averages were equal to or greater than 0.7 for PH, EH, MF and KW in population NAP5 and for EH, MF and KW in NAP7. Heritability estimates equal

Inbreeding depression…   OLIVEIRA, A. S. et al.

to or greater than 0.7 favor the selection process with greater genetic gains. Heritability estimates for traits related to resistance to phytopathogens were between 0.55(PP-NAP7) and 0.85 (WS-NAP5). Such heritability magnitude indicate that the major

variability cause presented by the populations was due to genetic effects, and acceptable genetic gains can be obtained with the selective process of progenies that are more resistant to these pathogens.

Table 3. Mean squares of the analysis of variance of agronomic traits in endogamic families (FS$_1$) of two exotic maize populations. Jataí (GO), 2015

Source	[1]d.f.	[£,(2)]PH	[£,(2)]EH	[£]MF	[£]BP	[£]LP	[£,(2)]KW
Population NAP-5							
Replication	2	19.448	10.790	0.050	0.010	0.124	0.490
Progenies	49	11.934**	7.531**	0.041**	0.028**	0.043*	3.453**
Error	98	3.184	1.856	0.012	0.011	0.027	1.039
Population NAP-7							
Replication	2	38.039	10.232	0.001	0.014	0.068	0.253
Progenies	39	9.995**	5.897**	0.156**	0.017[NS]	0.053 [NS]	6.807**
Error	78	3.370	1.611	0.014	0.011	0.041	0.833

[£]: PH: plant height (cm); EH: ear height (cm); MF: male flowering (days); BP: broken plants; LP: lodged plants; KW: kernel weight (g plant^{-1}) corrected for number of plants; [1]: degrees of freedom; [2]: variance values divided by 10^2; [**,*,NS]: significant at 1%, 5% and not significant by F-test, respectively.

Table 4. Mean squares of the analysis of variance of resistance to phytopathogens in S$_1$ families in two exotic maize populations. Jataí, 2015

Source	[1]d.f.	[£,(2)E]ET	[£,(2)]WS	[£,(2)]CS	[£,(2)]PP	[£,(2)]CZ
Population NAP-5						
Replication	2	51.734	27.965	318.808	4.427	28.062
Progenies	49	62.219**	59.985**	168.165[NS]	25.549**	17.085**
Error	98	20.109	9.090	114.949	8.151	6.670
Population NAP-7						
Replication	2	226.352	3.196	247.603	73.527	4.286
Progenies	39	105.734**	49.939**	226.589**	31.741**	12.014[NS]
Error	78	22.502	9.120	84.437	14.246	8.341

[£]: ET – *Exserohilum turcicum*, WS – *Pantoea ananatis*, CS – Corn stunt, PP – *Puccinia polysora* and CZ– *Cercospora zea-maydis*; [1]: degrees of freedom; [2]: variance values divided by 10^3; [*,NS]: significant at 1% and not significant by F-test, respectively.

Table 5. Estimates of genotypic variance (σ_G^2), of heritability based on Family averages (h_m^2), of the coefficient of genetic variation (CVg%) and of the variation index (θ) for six agronomic traits of S$_1$ families of two exotic maize populations. Jataí, 2015

Estimates	[£] Traits					
	PH	EH	MF	BP	LP	KW
	Population NAP5					
σ_G^2	291.69	189.15	0.94	0.66	0.52	80.47
h_m^2	0.73	0.75	0.70	0.64	0.36	0.70
CV$_g$%	10.50	14.84	1.60	60.51	22.39	24.77
Θ	0.96	1.01	0.87	0.77	0.44	0.88
	Population NAP7					
σ_G^2	220.85	142.88	4.74	-	-	199.10
h_m^2	0.66	0.73	0.91	-	-	0.88
CV$_g$%	8.16	12.43	3.54	-	-	37.46
Θ	0.81	0.94	1.84	-	-	1.55

[£] Traits – AP: plant height (cm); AE: ear height (cm); FM: tasseling (days); PQ: number of broken plants; AC: number of lodged plants; PG: kernel weight (g plant^{-1});

Table 6. Estimates of genotypic variance (σ_G^2), heritability based on family average (h_m^2), of the genetic variation coefficient (CVg%) and of the variation index (θ) for resistance to phytopathogens in S_1 families of two exotic maize populations. Jataí, 2015.

Estimates	₤ Diseases (AUDPC)				
	[1]E ET	[1] WS	[1] CS	[1] PP	[1] CZ
	Population NAP5				
σ_G^2	14.037	16.965	-	5.799	3.472
h_m^2	0.68	0.85	-	0.68	0.61
CV$_g$%	29.86	44.51	-	29.76	29.30
Θ	0.84	1.37	-	0.84	0.72
	Population NAP7				
σ_G^2	27.744	13.606	47.384	5.832	-
h_m^2	0.79	0.82	0.63	0.55	-
CV$_g$%	35.31	38.53	21.04	24.67	-
Θ	1.11	1.22	0.75	0.64	-

₤: ET – *Exserohilum turcicum*, WS – *Pantoea ananatis*, CS – Corn stunt, PP – *Puccinia polysora* and CZ – *Cercospora zea-maydis*; [1]: variance values multiplied by 10^3.

The observed values of heritability coefficient for the traits PH and EH in this study were similar to those found by Oliveira et al. (2015) in endogamic families of semi-exotic maize populations. Population NAP5 presented lower values of KW than those observed by Rodrigues (2013) while population NAP7 presented similar values to those found by the same author in S_1 families of exotic maize populations.

The relation between CVg and CVe (index θ), represents one more information for the breeder in relation to progeny selection (VENCOVSKY, 1987). As an example, Vencovsky and Barriga (1992), suggest that values of this index above 1.0 indicate a favorable condition for selection of progenies of half-siblings.

Population NAP5 presented indices above 1 for the traits EH and WS. The traits MF, KW, HT and WS from population NAP7 also presented indices above 1. Such results indicate favorable condition for the selection of progenies with desirable agricultural traits and selection of sources of resistance to these diseases.

Despite the comparisons of the indices of this study with those reported by Vencovsky and Barriga (1992), it is important to highlight that the present study evaluated S_1 families and that genetic variance among these families tend to greater than that of half-sibling families, affecting the index of variation.

It is possible to obtain populations with short cycle, good kernel yield and presenting resistance to the main phytopathogens of maiz from the selection of superior progenies from the populations studies, since these presented excellent genetic potential to be exploited in recurrent selection programs.

CONCLUSIONS

The exotic populations presented high depression by endogamy, and it was not possible to use them to extract lineages before doing cycles of recurrent selection.

Both exotic populations presented genetic potential to be explored in breeding programs with recurrent selection, to obtain superior genotypes and resistant to main maize plant pathogens (*Exserohilum turcicum*, WS(White Spot) – resistance to *Pantoea ananatis*, CS(Corn Stunt) – resistance to the corn stunt, PP – resistance to *Puccinia polysora* and CZ(gray leaf spot) – resistance to *Cercospora zea-maydis*.).

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RESUMO: O efeito denominado depressão por endogamia refere-se à redução do valor médio dos caracteres quantitativos, relacionados com a reprodução e a fisiologia da planta, devido ao estado de homozigose dos alelos deletérios. O objetivo deste trabalho foi avaliar a depressão por endogamia e a variabilidade genética de caracteres agronômicos e de resistência a fitopatógenos em famílias endogâmicas de duas populações exóticas de milho. Os experimentos foram realizados na área experimental da Universidade Federal de Goiás, Regional Jataí, na safrinha 2015. Foram avaliadas 50 e 40 FS$_1$ das populações NAP5 e NAP7, respectivamente, intercalando a cada dez parcelas uma linha com a mistura da população base (família de irmãos germanos) para estimar a depressão por endogamia dos caracteres avaliados. Os experimentos foram instalados em delineamento de blocos casualizados, com três repetições. Foram avaliados os seguintes caracteres: PH – altura de planta (cm), EH – altura de espiga (cm), MF – florescimento masculino (dias), BP – número de plantas quebradas, LP – número de plantas acamadas, KW – produção de grãos (kg parcela^{-1}), ET - resistência a *Exserohilum turcicum*, WS (White Spot) - resistência a *Pantoea ananatis*, CS (Corn Stunt) - resistência ao complexo de enfezamento, PP - resistência a *Puccinia polysora* e CZ - resistência a *Cercospora zea-maydis*. As maiores estimativas de depressão por endogamia nos caracteres agronômicos foram observadas para produção de grãos, com valores de 51,2 e 38,9% para as populações NAP5 e NAP7, respectivamente. Nos caracteres de resistência a fitopatógenos, a maior estimativa foi observada para o complexo de enfezamento, com valores de -58,9% na NAP5 e -74,2% na NAP7. As duas populações em estudo apresentaram potencial genético para serem utilizadas em programas de melhoramento com seleção recorrente e após alguns ciclos de seleção extrair linhagens com bom padrão agronômico e resistentes a fitopatógenos.

PALAVRAS-CHAVE: Doenças foliares. Famílias endogâmicas. Parâmetros genéticos, *Zea mays*.

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