Biometric analysis of *Tripsacum*-maize hybrid populations

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ABSTRACT - *Objective of this research was to evaluate the performance of four base-populations of maize-*Tripsacum *hybrid (T1, T2, T3, and T5), eight populations related to the first (T1B, T2B, T3B, T5B) and second (T1B^2, T2B^2, T3B^2, T5B^2) backcross generations between the four maize-*Tripsacum *hybrid populations, and the maize cultivar BR 205, besides the BR 205 cultivar, the landrace Cachoeira, and two populations: composite Flint and composite Dent. Through biometric analyses, genetic parameters and canonical correlations it was possible to select superior genotypes for the traits flowering, plant height at 90 days, insertion of the highest ear, ear weight, and total grain weight. The average for the yield traits indicated that the four base-populations could be used in breeding programs. Canonical correlations showed that taller plants and plants with a higher insertion of the highest ear have a tendency to bring forth plants with low yield; selection should therefore prioritize shorter genotypes.*

Key words: *Tripsacum*, maize, canonic correlations, genetic parameters.

INTRODUCTION

Maize improvement programs aim at the selection of highly productive cultivars, which are, in general, very demanding in terms of soil fertility and plant protection products. The use of adequate genera is one of the strategies in maize improvement programs that aim to establish more robust cultivars, once the exotic germplasm is an outstanding potential source of genes that confer resistance or tolerance to water stress, diseases and pests and the soil fertility factors (Hallauer 1988).

The genus *Tripsacum* is native to the Occidental Hemisphere and can be found all over the American continent: USA, Mexico, Brazil, Paraguay, and Colombia, consisting of 15 species, according to Kindinger and Dewald (1997). Most of the species can be found in Mexico, which is considered the center of diversity; the known species are perennial, morphologically distinct, adapted to a broad/wide variation of environments and present various cytotypes: diploids (2n=2x=36), triploids (2n=3x=54), tetraploids (2n=4x=72), pentaploids (2n=5x=90) and hexaploids (2n=6x=108) (Leblanc et al. 1995).

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In 1931, Mangelsdorf and Reeves reported the first successful crossing between *Tripsacum* spp and *Zea mays*. Although the genetic recombination between the *Tripsacum* diploid and *Zea mays* is rare, crossings involving *Tripsacum dactyloides (L.)* tetraploids have been successful (Engle et al. 1974). Crossings between maize lines and *Tripsacum* species lead to maize-Tripsacum hybrids, a term first used by Anderson and Erickson in 1941 to describe trait combinations in maize which must have been derived from teosinte or from *Tripsacum* (Engel 1974).

The Centro Internacional de Mejoramiento de Maiz y Trigo - CIMMYT - (International Maize and Wheat Improvement Center) is developing a research project that involves intergeneric crossings between *Tripsacum* and *Zea mays,* aiming at the transference of genes for robustness and apomixis (Leblanc et al. 1995, Kindinger et al. 1996) so that the hybrid vigor hybrid in the cultivated species is retained and thus allows the farmers to store seeds of the best plants to use them in the following crop year, reducing the costs and facilitating the grain yield.

In 1993, maize-*Tripsacum* hybrids were introduced in the germplasm bank of the Universidade Estadual do Norte Fluminense Darcy Ribeiro - UENF (University of the Northern region of the State of Rio de Janeiro), as an alternative in the development of material to be used by the producers in view of the traits of robustness and earliness the genus *Tripsacum* carries. This material was then backcrossed with the common maize BR 205 for four generations for obtaining genotypes adapted to the conditions of climatic adversities of the north and northwestern region of the State of Rio de Janeiro (north and northwestern Fluminense). The development of the present study was therefore considered fit, with the main objective of evaluating the performance of maize-*Tripsacum* hybrid base populations, as well as of backcrossings of maize-*Tripsacum* hybrids with common maize in comparison to the four common maize genotypes, as a first step towards the development of material of interest for the winter crop in common maize yield for the north and northwest Fluminense region.

MATERIAL AND METHODS

The genetic material used in the present study consisted of four maize-*Tripsacum* hybrid base populations: a) maize-*Tripsacum* hybrid T1 (T1), b) maize-*Tripsacum* hybrid 2 (T2), c) maize-*Tripsacum* hybrid 3 (T3),

and d) maize-*Tripsacum* hybrid 5 (T5), which had been introduced in Brazil in 1987, originated from Illinois (Von Bülow 1979); besides eight genotypes related to the first (T1B, T2B, T3B, and T5B) and second (T1B^2, T2B^2, T3B^2 and T5B^2) generations of backcrossings of the four base populations of maize-*Tripsacum* hybrids with the common maize cultivar BR 205; cultivar BR 205; a common maize landrace - Cachoeira (CAC); and two common maize genotypes - "flint" (composite Flint - CF) and "dent" - (composite Dent - CD).

The experiment was conducted at the Estação Experimental da PESAGRO-RIO – Unity Experimental Fields of the Goytacazes, RJ, from October 1999 to February 2000, using the randomized block design in four replications. The plots consisted in 5 m double rows, amounting to 48 individuals. Eighteen traits were evaluated of which eight were morphological and nine yield-related, observed in 21 randomly chosen individuals of each plot.

The evaluated traits were: a) flowering period (FLO) - number of days from planting to the emission of the female flower of at least 50% of the plants of the treatment per plot in days; b) plant height after 45 days (H45) - computed by the distance from the ground to the plant tops 45 days after planting in meters; c) plant height at 65 days (H65) - computed by the distance from the ground to the plant tops 65 days after planting in meters; d) plant height at 90 days (H90) - computed by the distance from the ground to the plant tops 90 days after planting in meters; e) insertion height of the highest ear (IHE) - computed by the distance from the ground to the point of insertion of the highest ear in meters; f) length of the tassel (TAL) - computed by the length from the point of insertion of the tassel in the stem to the top of the plant when completely ripe in centimeters; g) number of tillers (NTI) - number of ears growing from the same node; and h) prolificity (PRO) - number of ears growing on the same plant from different buds.

The evaluated yield traits were: a) total final number of plants (FNP) - number of plants that grew and that reached the end of the cycle; b) number of broken ears (BRO) - number of ears that were not supported in the stem and hung down; c) number of lodged ears (NLE) - number of broken plants under the wind or their own weight; d) number of ears poorly hulled (PHE) - ears with partially exposed grains; e) total number of ears (NEP) - harvested ears including the diseased ones and those with pests; f) total number of diseased ears (NDE) - ears with disease symptoms; g) total number of ears with pests (EPE) - number of ears in which pests were detected; h) weight of ears per plot (WEP) - weight of all ears in each plot, in kilogram; i) grain weight (TGW) - total grain weight of all

ears of each plot, in kilograms; and j) weight of 100 grains (W100) - weight of 100 grains of each plot in grams.

The analysis of variance was carried out with the objective of testing the hypothesis H_0: $G_1 = G_2 = ... = G_k$, by means of an evaluation of the 16 genotypes, based on the data obtained from the plot means for the 17 evaluated traits.

The estimated genetic parameters were:
Phenotypic variance

$$\sigma_f^2 = \frac{MSG}{r} ,$$

Coefficient of experimental variation in percent

$$CV_e(\%) = 100 \frac{\sqrt{MSE}}{m} ,$$

Coefficient of genotypic variation in percent

$$CV_g(\%) = 100 \frac{\sqrt{\phi_g}}{m} ,$$

Variation index

$$VI = \frac{CV_g}{CV_e} , \text{ and}$$

Coefficient of genotypic determination

$$H^2 = \frac{\phi_g}{\sigma_f^2}$$

In the analysis of correlation, the presence of colinearity produces diverse effects in the canonical procedures due to the high estimates of phenotypic or genotypic correlations among the studied traits, making the results little precise (Carvalho et al. 1999). Thus, in the present study, we chose to use only traits with no colinearity.

The technique of canonical correlations was used to estimate the maximal correlation between linear combinations of traits distributed in two groups: secondary (H90 and IHE) and (WEP, TGW and W100). The loading factors of the traits in each linear combination were also estimated.

According to Cruz (2001) a canonical correlation is one that maximizes the relation between the linear combinations X_1 and Y_1, where

$X_1 = a_1x_1 + a_2x_2 + ... + a_px_p$; and
$Y_1 = b_1y_1 + b_2y_2 + ... + b_qy_q$, which is estimated based on the matrixes:
R_{11} = p x q, matrix of correlation between the traits of group I;
R_{22} = p x q, matrix of correlation between the traits of group II;
R_{12} = p x q, matrix of correlation between the traits of groups I and II.

The first canonical correlation is estimated by the square root of the greatest eigenvalue of matrix $R_{11}^{-1} R_{12} R_{22}^{-1} R_{12}'$. The first canonical pair ($X_1 = a'x$ and $Y_1 = b'x$) is obtained considering that "a" is the first eigenvector of $R_{11}^{-1} R_{12} R_{22}^{-1} R_{12}'$, or equivalently, $a = R_{11}^{-1} R_{12} b$. Furthermore, "b" is the first eigenvector of $R_{11}^{-1} R_{12} R_{22}^{-1} R_{12}'$, or analogously $b = R_{22}^{-1} R_{12}' a$ (Cruz 2001). The other correlations between **p** and **q**, in equal or lower number, are estimated by the eigenvalues and eigenvectors of the described expressions, corresponding to the order of the estimated correlation. The software Genes (Cruz 2001) was used for the data analysis.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance of the 17 evaluated traits (Tables 1 and 2) evidenced significant differences by means of the F test (P < 0.01) among the genotypes for the following traits: flowering period, height of plant after 90 days, insertion height of the highest ear, total final number of plants, number of broken ears, ear weight per plot, grain weight and weight of 100 grains, indicating expressive genetic variability among the 16 analyzed genotypes.

The trait total number of ears with pests was excluded from the analyses since no occurrence of pests was detected in any of the treatments. These results were probably more associated to the unfavorable climatic conditions for an occurrence and the ideal moment for harvest than because of the aspect of genetic resistance against pests conferred by *Tripsacum*, as reported by De Wet (1979), since the same performance was observed in all treatments, including maize-*Tripsacum* hybrids and maizes.

The traits number of tillers, prolificity, number of broken ears, number of lodged plants, number of poorly hulled ears and number of diseased ears presented coefficients of high variations that varied from 64.53 to 135.40 % (Tables 1 and 2). This result could be more associated to the inconsistence of the trait expression than to the environment effect since only sporadic cases were observed, leading to somewhat reduced means. Considering that such traits are not desirable for the development of varieties, the favorable results for the characterization of genotypes of interest for improvement programs can be interpreted.

Estimates of genetic parameters

The estimated genetic parameters for the 17 analyzed traits, important for inferences on selection strategies, are displayed in the Tables 1 and 2. The coefficient of genotypic determination was over 80% for the traits flowering period, plant height at 90 days, insertion height of the highest ear, number of broken ears, ear weight per plot and grain weight. A variation index below 1% for the traits total number of ears, number of poorly hulled ears and final plant stand was observed; and a genotypic determination coefficient below 50% for the traits insertion

Table 1. Summary of analysis of variance for eight traits related to 16 genotypes

Causes of variation	df	Mean squares							
		FLO[1]	H45	H65	H90	IHE	TAL	NTI	PRO
Block	03	17.687	0.285	0.154	0.076	0.051	0.018	8.932	0.354
Genotype	15	50.86**	0.017*	0.030*	0.054**	0.069**	0.008	9.170	4.000
Error	45	5.643	0.008	0.009	0.007	0.095	0.005	5.788	2.176
		Means							
highest		45.50	1.46	2.70	2.84	1.60	0.43	5.00	3.50
lowest		25.00	1.20	2.34	2.42	1.10	0.29	1.00	0.25
general		39.97	1.35	2.45	2.55	1.25	0.34	1.95	1.28
MSD		7.08	0.26	0.30	0.24	0.29	0.21	7.17	4.40
		Genetic parameters							
CV_e		5.94	6.41	4.03	3.21	7.80	20.67	123.18	115.14
σ_f^2		12.720	0.004	0.007	0.013	0.017	0.002	2.290	1.000
CV_g		8.41	3.63	2.93	4.25	9.78	7.85	47.11	52.64
H^2		88.90	56.13	67.91	87.50	86.28	36.57	36.91	45.53
VI		1.41	0.57	0.73	1.32	1.25	0.38	0.38	0.46

[1]Traits as coded in material and methods
* and **, P < 0.05 and P < 0.01, respectively

Table 2. Summary of analysis of variance for nine traits related to 16 genotypes

Causes of variation	df	Mean squares								
		FNP[1]	BRO	NLE	PHE	NEP	NDE	WEP	TGW	W100
Block	03	4.50	17.19	10.10	9.77	8.93	21.79	1.21	1.22	24.86
Genotype	15	16.12**	17.36**	2.17	14.23	108.10*	92.25	3.86*	3.54**	23.12**
Error	45	4.86	3.22	1.45	6.77	36.31	93.70	0.42	0.58	5.35
		Means								
highest		53.00	10.00	7.00	12.00	68.00	16.00	7.80	6.60	37.92
lowest		36.00	1.00	0	0	30.00	2.00	2.20	0.50	21.84
general		47.19	2.78	0.89	3.11	46.89	9.44	5.89	4.74	30.9
MSD		6.57	5.35	3.59	7.75	17.96	28.85	1.93	2.27	6.89
		Genetic parameters								
CV_e		4.67	64.53	135.40	83.65	12.85	102.57	10.97	16.11	7.49
σ_f^2		4.03	4.34	0.54	3.57	27.02	23.06	0.97	0.88	5.78
CV_g		3.56	67.60	47.34	44.14	9.03	-	15.74	18.14	6.82
H^2		69.87	81.45	32.84	52.68	66.41	-	89.17	83.52	76.84
VI		0.76	1.05	0.35	0.53	0.70	-	1.43	1.13	0.91

[1]Traits as coded in material and methods
* and **, P < 0.05 and P < 0.01, respectively

height of the highest ear and number of poorly hulled ears.

These results allow conclusions on the possibility of identifying superior genotypes for five traits: FLO, H90, IHE, EW, and TGW. This statement is based on the expression of the coefficient of experimental variation below 10%, on the variation index above 1.0 and on the genotypic determination coefficient over 60%, expressing a greater potential of genetic than phenotypic contribution. For these traits, simple selection methods would be sufficient to obtain satisfactory gains in the segregant generations.

Estimates of phenotypic means

The base populations of maize-*Tripsacum* hybrids present a potential for use in improvement programs, once the main yield traits revealed superior means, as could be seen principally in the populations originated by the crossing with BR 205 (Table 3).

Table 3. Mean test for three traits evaluated in 16 genotypes

Genotypes	WEP[1]	TGW	W100
T1/4	3.775^e	3.025^d	26.257^c
T 2	6.125^{abcd}	4.950^{abcd}	32.225^{abc}
T 3	5.675^{abcde}	3.500^{bcd}	29.695^{abc}
T 5	4.925^{cde}	3.975^{abcd}	30.932^{abc}
T1B	6.775^{abc}	5.650^{ab}	29.440^{abc}
T2B	6.875^{ab}	5.675^{ab}	36.060^a
T3B	6.775^{abc}	5.600^{abc}	34.157^{ab}
T5B	6.650^{abc}	5.500^{abc}	30.142^{abc}
T1B^2	5.775^{abcd}	4.800^{abcd}	31.282^{abc}
T2B^2	5.425^{abcde}	4.400^{abcd}	28.770^{bc}
T3B^2	5.475^{abcde}	4.500^{abcd}	30.807^{abc}
T5B^2	7.000^a	5.825^a	32.402^{abc}
BR 205	7.050^a	5.900^a	32.975^{abc}
CF	6.350^{abcd}	5.050^{abcd}	28.400^{bc}
CD	5.025^{bcde}	4.100^{abcd}	29.015^{bc}
CAC	4.550^{de}	3.350^{cd}	31.860^{abc}

Values followed by the same letters on each column do not differ significantly by Tukey test at 5% probability
[1]Traits as coded in material and methods

According to Magelsdorf and Reeves (1931), the introgression of *Tripsacum* genes in maize is mainly accumulated in the recessive form and depends on the condition of heterozygosis for its maintenance. The expression of traits with high heterozygosis in the intergeneric hybrids or in maize-*Tripsacum* hybrids is therefore to be expected. On the other hand, the loss of vigor and the excessive segregation can be induced by endogamic processes, which is the probable reason why the populations of maize-*Tripsacum* hybrids originated from the crossing between the base populations and BR 205 generally presented superior means to those resulting from backcross genotypes.

Popi et al. (2000) evaluated the system of improvement designated HOPE (hierarchical open-ended population enrichment), based on the recurrent selection method and observed that after 15 years the system provided a non-traditional germplasm source in maize improvement programs. According to Hallauer et al. (1988), the method of recurrent selection offers the best procedure of adaptation for exotic germplasm in maize improvement programs and is also the most appropriate for the maintenance of the genetic structure of allogamous species. The recurrent selection method or its modifications are an option for the development of varieties based on the populations of maize-*Tripsacum* hybrids, among which the base populations T2, T3, and T5 and the maize genotypes BR 205 and Composite *Flint* were outstanding.

Canonical correlations between secondary and yield traits

The presence of colinearity, in consequence of the high phenotypic or genotypic correlation estimates among the traits or linear trait combinations produces adverse effects in the canonical procedures, making the results useless (Carvalho et al. 1999). Therefore, the analysis of canonical correlations allows a unifying quantification of the association among variable groups composed of linear combinations of the various traits that constitute them. The traits with no undesirable colinearity effects, which are appropriate for the implementation of the analytical procedure are presented in Table 4, displayed in two groups. In Group I, the secondary traits are related: H90 and IHE; Group II contains the traits related to the yield: WEP; TGW; and W100.

Table 4. Correlations and canonical pairs estimated between two secondary traits (Group I) and three related to yield (Group II), evaluated in 16 genotypes

	Canonical pairs - Group I	
	Loading factor	
	1^a VC	2^a VC
H90[1]	0.16099499	-0.1191488
IHE	5.95040138	8.36612582
	Canonical pairs - Group II	
WEP	-0.2636395	-0.07897628
TGW	-0.08187649	-0.06850362
W100	-0.05241834	0.06506045
r	0.09836958*	0.02960856*

[1]Traits as coded in material and methods
r = canonical correlation evaluated by the chi square test (χ^2_t = 18.5, df=6)
* = significant at the level of 5% of probability by the χ^2. test

Because of the presence of correlations different of zero (Table 4) the evaluated groups can be considered independent. In relation to the first correlations, it can be concluded that H90, IHE, WEP, as well as W100 and the TGW. From the physiological point of view, this may be due to a deviation in the yield metabolism for physiological plant processes. Anyway, these results are interesting when taking into consideration that in the north and northwestern Fluminense regions one of the problems that farmers face is plant lodging.

The results of this study allow the conclusion that the base populations of maize-*Tripsacum* hybrids offer a potential for improvement programs, once the principal yield trait, EWP, TGW and W100 presented higher means, as could be seen, principally, in the populations engendered by the first backcrossing of the maize-*Tripsacum* hybrids with BR 205.

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Análise biométrica de populações híbridas de *Tripsacum*-milho

RESUMO - *O objetivo desta pesquisa foi avaliar a performance de quatro populações-base de tripsacóides (T1, T2, T3 e T5), oito populações relativas à primeira (T1B, T2B, T3B, e T5B) e segunda (T1B^2, T2B^2, T3B^2 e T5B^2) gerações de retrocruzamentos das quatro populações de tripsacóides com a cultivar de milho comum BR 205, além da cultivar BR 205, da cultivar cabocla de milho - Cachoeira (CAC), e de duas populações - composto* Flint *(CF) e composto* Dent *(CD). Baseado na análise biométrica, nos parâmetros genéticos e nas correlações canônicas foi possível selecionar genótipos superiores para as características floração, altura de plantas ao 90 dias, altura de inserção da espiga superior, peso de espigas e peso total de grãos. As médias para características de produção indicaram que as quatro populações-base de tripsacóides podem ser usadas em futuros programas de melhoramento. As correlações canônicas mostraram que plantas mais altas e com maior inserção da espiga superior tendem a produzir plantas com menor produção; assim, deve-se priorizar genótipos de porte inferiores.*

Palavras-chave: *Tripsacum*, milho, correlações canônicas, parâmetros genéticos.

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