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Canonical correlations in phenological, morphological, production and tassel traits of maize

Correlações canônicas em caracteres fenológicos, morfológicos, produtivos e de pendão de milho

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ABSTRACT - The objective of this study was to check whether there is linear dependence between phenological, morphological and production traits and tassel traits in maize genotypes. Seven experiments were conducted with 16 maize genotypes, in a randomized block design, with three replicates. Four groups of traits were evaluated: phenological (two), morphological (three), production (four) and tassel (11). Joint analysis of variance and F test at 5% significance level were performed. The matrix of phenotypic correlation coefficients between the traits was estimated and multicollinearity was diagnosed in each group of traits. Associations between the groups of traits were checked by canonical correlation analysis. There is linear dependence between phenological, morphological and production traits and tassel traits in maize genotypes. Phenological (number of days from sowing to 50% of male flowering and number of days from sowing to 50% of female flowering), morphological (plant height and spike height) and production (number of spikes and grain yield) traits are positively associated with tassel traits (tassel branch number and tassel dry matter). Tassel branch number and tassel dry matter can be used for indirect selection of maize plants.

Keywords: *Zea mays* L.. Genotypes. Agronomic performance. Multivariate analysis. Indirect selection.

RESUMO - O objetivo deste estudo foi verificar se há dependência linear entre os caracteres fenológicos, morfológicos e produtivos com os caracteres de pendão em genótipos de milho. Foram conduzidos sete experimentos com 16 genótipos de milho, no delineamento experimental blocos ao acaso, com três repetições. Foram avaliados quatro grupos de caracteres: fenológicos (dois), morfológicos (três), produtivos (quatro) e de pendão (11). A análise de variância conjunta e o teste F a 5% de significância foram realizados. A matriz de coeficientes de correlação fenotípica entre os caracteres foi estimada e realizado o diagnóstico de multicolinearidade, em cada grupo de caracteres. As associações entre os grupos de caracteres foram verificadas por meio da análise de correlação canônica. Há dependência linear entre os caracteres fenológicos, morfológicos e produtivos com os caracteres de pendão em genótipos de milho. Os caracteres fenológicos (número de dias da semeadura até 50% do florescimento masculino e número de dias da semeadura até 50% do florescimento feminino), morfológicos (altura de planta e altura de inserção da espiga) e produtivos (número de espigas e produtividade de grãos) estão associados positivamente aos caracteres de pendão (número de ramificações e matéria seca do pendão). O número de ramificações e a matéria seca do pendão podem ser utilizados para seleção indireta de plantas de milho.

Palavras-chave: *Zea mays* L.. Genótipos. Desempenho agronômico. Análise multivariada. Seleção indireta.

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INTRODUCTION

Maize (*Zea mays* L.) is the most cultivated cereal in the world, with the United States of America, China and Brazil, in this order, being the largest producers. In the 2021/2022 season, the Brazilian area sown with this crop was 21,116.7 million hectares, with grain yield of 5,320 kg ha^{-1}, being the most produced cereal in the country (CONAB, 2022). Maize is used in various sectors of the production chain, with several purposes, such as: in animal feed and staple foods, such as flours, hominy, oil and bread, as well as in the brewing and pharmaceutical industries and even in mining (STRAZZI, 2015).

Due to the economic importance of maize, breeding programs are fundamental to develop genotypes with agronomic characteristics that meet the needs of producers and the demands of the consumer market. Modern maize genotypes have lower plant height and spike height, more erect leaf angle, reduced tassel size (number of branches and mass), shorter duration of the subperiod from tasseling to silking, lower protein content in the grain and higher production potential (DUVICK, 2005).

In maize, a larger size of the tassel can negatively affect grain yield and its components, due to the reduction of solar interception in the canopy of plants (reduction of photosynthesis) and because it acts as a drain of photoassimilates (EDWARDS, 2011; SOUZA et al., 2015). Smaller tassel size is ideal when it comes to production efficiency and shading effect. However, in stress environments (low water availability), where pollen production is reduced, larger tassels are desired, so that pollen production is sufficient for fertilization (PARVEZ, 2007).

Several traits are evaluated in experiments for characterization of maize genotypes, but some traits have low heritability and are difficult to measure. Thus, studying linear associations between traits plays a fundamental role in genetic improvement because they allow the characteristics of agronomic interest to be selected indirectly, that is, without the need to directly measure them. Canonical correlation analysis is an alternative for studying the association between two groups of traits, and the basic idea is the creation of a pair of latent variables that are linear combinations of the variables of the two vectors (p and q) and that the information contained in the pq parameters is concentrated in the correlation between these variables. These latent variables are called canonical variables, and the correlation between them is called canonical correlation (FERREIRA, 2018).

In genetic improvement, canonical correlation analysis is used, for instance, to study shoot *versus* root system traits, agronomic *versus* physiological traits, and primary *versus* secondary traits of yield (CRUZ; REGAZZI; CARNEIRO, 2012). Canonical correlation studies have been conducted in groups of traits in maize, such as: morphological *versus* production traits (SOUZA et al., 2015), phenological *versus* protein nutritional and production *versus* protein nutritional traits (ALVES et al., 2016b), morphological *versus* energy nutritional traits (ALVES et al., 2017), primary *versus* secondary traits (CARVALHO et al., 2017), morpho-agronomic *versus* bromatological traits (CREVELARI et al., 2019), physiological *versus* morphological traits (TROYJACK et al., 2019) and yield components *versus* secondary traits (CARVALHO et al., 2022).

It is assumed that there is a linear association between the groups of phenological, morphological and production traits and tassel traits of maize. Thus, the objective of this study was to check, through canonical correlation analysis, whether there is linear dependence between phenological, morphological, and production traits and tassel traits in maize genotypes.

MATERIAL AND METHODS

A total of 16 maize (*Zea mays* L.) genotypes were evaluated (Table 1) in seven experiments. The experiments were conducted in the experimental area of the Plant Science Department at the Federal University of Santa Maria, located at 29º42’ S, 53º49’ W and 95 m altitude, in the agricultural years 2015/2016 (environment 1), 2016/2017 (environment 2), 2017/2018 (environment 3), 2019/2020 (environments 4 and 5) and 2020/2021 (environments 6 and 7) (Table 2). According to Köppen’s classification, the regional climate is Cfa, that is, a humid subtropical climate with hot summers and no defined dry season (ALVARES et al., 2013). The soil of the experimental area is classified as *Argissolo Vermelho distrófico arênico* (Ultisol) (SANTOS et al., 2018).

Table 1. Descriptors of 16 maize genotypes regarding technology, company, type, cycle, use, grain, color and investment.

Genotype	Version	Technology(1)	Company	Type(2)	Cycle(3)	Use(4)	Grain	Color(5)	Investment(6)
20A55	PW	PowerCore	Morgan Sementes	TCH	E	G/S	Semi-hard	LO	Medium
30F53	YH	Optimum Intrasect	Pioneer	SCH	E	G/S	Semi-dented	O	High
AG8780	PRO 3	VT PRO 3	Sementes Agroceres	SCH	E	G	Semi-dented	LO	High
AG9025	PRO 3	VT PRO 3	Sementes Agroceres	SCH	SE	G	Semi-dented	LO	High
AM9724	-	Conventional	Melhoramento Agropastoril	SCH	SE	G	Dented	Y/LO	High
AS1666	PRO 3	VT PRO 3	Agroeste	SCH	SE	G	Semi-dented	Y/LO	High
AS1677	PRO 3	VT PRO 3	Agroeste	SCH	SE	G	Semi-dented	LO	High
BM3066	PRO2	VT PRO 2	Biomatrix	SCH	E	G/S	Semi-dented	O	High
DKB 230	PRO 3	VT PRO 3	Dekalb	SCH	SE	G	Semi-dented	Y	High
DKB 290	PRO 3	VT PRO 3	Dekalb	SCH	E	G	Semi-dented	LO	High
MS 2010	-	Conventional	Melhoramento Agropastoril	SCH	E	G	Semi-dented	Y/LO	High
MS 2013	-	Conventional	Melhoramento Agropastoril	SCH	E	G	Semi-hard	LO	High
MS 3022	-	Conventional	Melhoramento Agropastoril	TCH	E	G	Hard	O	Medium
P1630	H	Herculex I	Pioneer	SCH	SE	G	Semi-dented	LO	High
P2530	-	Conventional	Pioneer	SCH	SE	G	Semi-hard	O	High
Status	VIP	Agrisure Viptera	Syngenta Seeds	SCH	E	G	Hard	LO	High

(1) The genetic composition of maize plants is modified and may confer inherent resistance or tolerance in the development of maize hybrids, that is, development of materials with specific characteristics, such as: resistance to attack of pest insects and tolerance to different herbicides. (2) SCH: single-cross hybrid; TCH: triple-cross hybrid. (3) E: early; SE: super-early. (4) G: grain; S: silage. (5) LO: light orange; O: orange; Y: yellow. (6) Financial investment applied in technology and management. Information provided by the Fundação Estadual de Pesquisa Agropecuária (FEPAGRO).

Table 2. Description of sowing dates, meteorological variables and fertilization of the experiments.

Variable	Meteorological data						
	Experiments						
	1	2	3	4	5	6	7
Date of sowing	10/21/2015	11/19/2016	10/31/2017	11/25/2019	12/20/2019	10/28/2020	12/01/2020
Date of grain harvest	03/30/2016	04/07/2017	03/21/2018	04/13/2020	04/13/2020	03/24/2021	04/06/2021
Minimum temperature (°C)	14.36	15.92	16.37	12.43	12.43	17.84	17.84
Average temperature (°C)	22.59	22.92	23.25	23.70	23.84	23.93	23.56
Maximum temperature (°C)	29.45	27.71	29.47	30.78	30.78	36.14	36.14
Rainfall (mm)	1,101.00	906.20	512.00	452.40	424.00	399.20	417.80
Variable	Fertilization (kg ha^{-1})						
	Experiments						
	1	2	3	4	5	6	7
Basal fertilization (N-P-K)	750	400	300	300	300	500	500
Commercial formula	05-20-20	05-20-20	05-20-20	05-20-20	05-20-20	05-20-20	05-20-20
N	37.5	20	15	15	15	25	25
P_2O_5	150	80	60	60	60	100	100
K_2O	150	80	60	60	60	100	100
Top dressing (urea)	270	180	250	180	180	180	180
Applied in stages	V4, V8 and V12	V4 and V8	V4 and V8	V4 and V8	V4 and V8	V4 and V8	V4 and V8

Basal fertilization was carried out on the sowing day in the seven experiments.
N: nitrogen; P: phosphorus; K: potassium.
Plant development stages: V4 (four expanded leaves), V8 (eight expanded leaves) and V12 (twelve expanded leaves).
Meteorological data were obtained from the Automatic Meteorological Station of Santa Maria - RS, provided by the Instituto Nacional de Meteorologia (INMET).

The experimental design used was randomized blocks with three replicates. The plots consisted of two 5-m-long rows at spacing of 0.80 m between rows and 0.20 m between plants in the row, in the seven experiments. Plant density was adjusted by manual thinning to five plants per meter of row, corresponding to 62,500 plants ha^{-1}. The experiments were kept without weeds, pests and diseases.

In the seven experiments, the following traits were evaluated: phenological - number of days from sowing to 50% of male flowering (MF, in days) and number of days from sowing to 50% of female flowering (FF, in days); morphological - plant height (PH, in cm; based on the average of five plants per plot), spike height (SH, in cm; based on the average of five plants per plot) and relative position of the spike (RPS=SH/PH); production - number of plants (NP, in plants ha^{-1}), number of spikes (NS, in spikes ha^{-1}), spike index (SI=NS/NP) and grain yield (GY, in Mg ha^{-1}); and tassel (Table 3). Grain moisture was determined and then grain yield (GY in Mg ha^{-1}) was estimated, based on all plants in the plot and after the grain mass was corrected to 13% moisture.

The tassel traits were evaluated at the end of the reproductive stage. For this, 20 tassels per plot were collected in environments 1 and 3 and 11 tassels per plot were collected in the other environments. According to Wartha et al. (2016), 11 tassels are sufficient for estimating the mean with 40% precision and 95% confidence level. After the tassels were collected in the field, they were identified, stored in paper packaging, and dried in an oven at 60 ºC until reaching constant mass. The tassel traits evaluated were: peduncle length, considering the distance between the collar of the flag leaf and the first branch (PL, in cm), branching space length (BSL, in cm), central spike length (CSL, in cm), tassel length (TL=PL+BSL+CSL, in cm), number of primary branches (NPB), number of secondary branches (NSB), tassel branch number (TBN=NPB+NSB), peduncle dry matter, considering the distance between the collar of the flag leaf and the first branch (PDM, in g), branching space dry matter (BSDM, in g), central spike dry matter (CSDM, in g) and tassel dry matter (TDM=PDM+BSDM+CSDM, in g) (Figure 1).

Table 3. Description of phenological, morphological, production and tassel traits evaluated in maize experiments.

Groups	Acronym	Description	Unit
Phenological	MF	Number of days from sowing to 50% of male flowering	days
Phenological	FF	Number of days from sowing to 50% of female flowering	days
Morphological	PH	Plant height, based on five plants per plot	cm
Morphological	SH	Spike height, based on five plants per plot	cm
Morphological	RPS	Relative position of the spike (RPS=SH/PH)	-
Production	NP	Number of plants	plants ha^{-1}
Production	NS	Number of spikes	spikes ha^{-1}
Production	SI	Spike index (SI=NS/NP)	-
Production	GY	Grain yield	Mg ha^{-1}
Tassel	PL	Peduncle length, considering the distance between the collar of the flag leaf and the first branch	cm
Tassel	BSL	Branching space length	cm
Tassel	CSL	Central spike length	cm
Tassel	TL	Tassel length (TL=PL+BSL+CSL)	cm
Tassel	NPB	Number of primary branches	-
Tassel	NSB	Number of secondary branches	-
Tassel	TBN	Tassel branch number (TBN=NPB+NSB)	-
Tassel	PDM	Peduncle dry matter, considering the region between the collar of the flag leaf and the first branch	g
Tassel	BSDM	Branching space dry matter	g
Tassel	CSDM	Central spike dry matter	g
Tassel	TDM	Tassel dry matter (TDM=PDM+BSDM+CSDM)	g

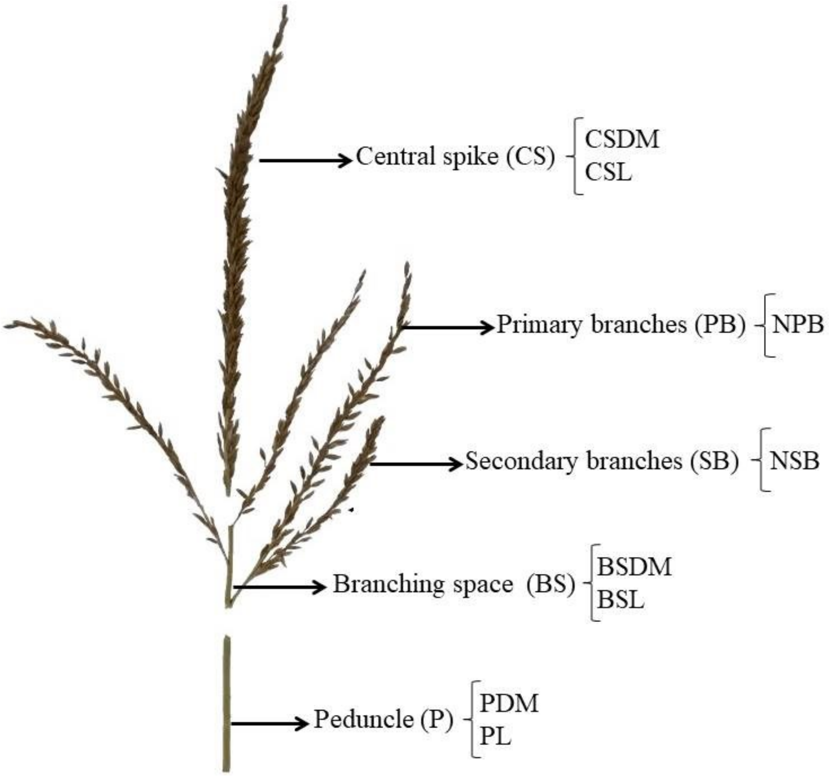

Figure 1. Representation of the traits evaluated in the maize tassel, PL: peduncle length, considering the distance between the collar of the flag leaf and the first branch, in cm; BSL: branching space length, in cm; CSL: central spike length, in cm; TL: tassel length, in cm; NPB: number of primary branches; NSB: number of secondary branches; PDM: peduncle dry matter, considering the distance between the collar of the flag leaf and the first branch, in g; BSDM: branching space dry matter, in g; CSDM: central spike dry matter, in g. Adapted from Wartha et al. (2016).

Joint analysis of variance and F test at 5% significance level were performed, considering genotype effects as fixed and environment effects as random. Homogeneity of variances was checked by the Hartley's Fmax test, which was calculated by the ratio between the highest and the lowest mean square of residuals of the environments (>MSres/<MSres). When the value found was lower than seven, in experiments with the same number of replicates, joint analysis of variance was carried out to check the significance of genotype (G), environment (E) and G × E interaction effects. When the ratio was greater than seven, the degrees of freedom (DF) were adjusted (CRUZ, 2016). Estimates of mean, coefficient of variation (CV), calculated F for genotype (Fc) and selection accuracy (SA), as described in Resende and Duarte (2007), were recorded for each of the 20 traits (MF, FF, PH, SH, RPS, NP, NS, SI, GY, PL, BSL, CSL, TL, NPB, NSB, TBN, PDM, BSDM, CSDM and TDM).

The matrix of phenotypic correlation coefficients was estimated, and the significance was checked using Student's t-test, at 5% significance level. Multicollinearity was also diagnosed in the phenotypic correlation matrix, within each group of traits (phenological, morphological, production and tassel). The magnitude of multicollinearity within each group of traits was checked by means of the condition number (CN) and interpreted according to the criterion established by Montgomery and Peck (1982).

Canonical correlation analysis was performed between the groups of phenological and tassel traits, morphological and tassel traits, and production and tassel traits. Associations between these groups of traits were interpreted through canonical loadings. The significance of canonical correlations was evaluated by the chi-square test (χ^2) at 5% significance level. Statistical analyses were performed using Genes software (CRUZ, 2016) and Microsoft Office Excel® application.

RESULTS AND DISCUSSION

The joint analysis of variance showed significant effect of genotype on all traits, that is, it was verified that there is genetic variability. For environments, the traits number of plants, number of spikes and spike index showed no significant difference, due to the definition of plant density when the experiments were set up, in addition to thinning, which serves to maintain the number of plants homogeneous. The genotype × environment interaction was not significant only for spike height, demonstrating the effect of genetic variability for almost all traits (Table 4). Studies carried out with the maize crop have also found genetic variability among phenological, morphological, production and tassel traits (SOUZA et al., 2015; ALVES et al., 2016a; ALVES et al., 2016b; ALVES et al., 2017; CARVALHO et al., 2017; XU et al., 2017, KHAN et al., 2018; NASCIMENTO-JÚNIOR; MÔRO; MÔRO, 2018; ÖNER, 2018; CREVELARI et al., 2019; TROYJACK et al., 2019; FERREIRA et al., 2020; CARVALHO et al., 2022).

The coefficient of variation (CV, in %) ranged from 2.59% for the number of days from sowing to 50% of female flowering (FF) to 15.87% for the number of secondary branches (NSB). Based on the classification of Pimentel-Gomes (2009), the CV was medium for five traits (SI, GY, PL, NSB and PDM) and low for the others (Table 4), resulting in medium and high experimental precision, respectively.

Based on the selection accuracy (SA), the experimental precision ranged from high ($0.70 \leq SA < 0.90$) to very high ($SA \geq 0.90$), according to the classes established by Resende and Duarte (2007) (Table 4). Given this broad data set (20 traits evaluated in 16 genotypes in seven environments), the high experimental precision observed and the variability existing among genotypes, it can be inferred that the database is adequate for studying canonical correlations.

The magnitude of phenotypic correlation coefficients ranged from $r=-0.852$ (between branching space length and central spike length) to $r=0.991$ (between number of primary branches and tassel branch number), demonstrating the existence of a negative correlation between some traits and positive correlation between others. Phenological traits showed a positive phenotypic correlation with most tassel traits and, for some traits, the correlation was not significant. The traits MF and FF showed positive and significant phenotypic correlations with the traits NPB, TBN, PDM, BSDM, CSDM and TDM (Table 5). These results show that plants with higher MF and FF are associated with plants with higher NPB, TBN, PDM, BSDM, CSDM and TDM. However, only the traits BSDM and TDM showed positive, significant and high-magnitude correlations with MF and FF, demonstrating that these traits can be used for indirect selection of maize plants, aiming at the selection of BSDM and TDM traits in maize tassels.

Phenotypic correlations were positive between most morphological and tassel traits, but in some cases the correlation was not significant. In addition, the traits PH and SH showed significant and negative phenotypic correlation with CSL; however, these correlations were of low magnitude. For the traits PH and SH, a significant phenotypic correlation was observed with the tassel traits (NPB, NSB, TBN, BSDM and TDM) (Table 5). In addition, TBN was the trait with the highest significant phenotypic correlation with PH ($r=0.652$) and with SH ($r=0.716$), demonstrating that these traits can be used in the indirect selection of plants, aiming at the selection of the TBN characteristic in maize. Positive correlation between morphological traits (PH and SH) and TBN has also been observed by Parvez (2007), Souza et al. (2015) and Prakash et al. (2019) in maize plants.

Table 4. Summary of the joint analysis of variance with the number of degrees of freedom (DF) and the mean square for the sources of variation (Block/Environment, Genotype, Environment, Genotype × Environment and Residual), mean, coefficient of variation (CV), ratio between the highest and the lowest mean square of residuals between the environments (>MSres/<MSres), calculated F value for genotype (Fc) and experimental precision through selective accuracy (SA).

SV	DF	Mean square	DF	Mean square			
		MF		FF	PH	SH	RPS
Block/Environment	14	7.949	14	9.821	363.966	176.661	0.002
Genotype	15	116.678*	15	180.964*	2,922.912*	3,752.492*	0.033*
Environment	6	1,366.713*	6	1,510.852*	8,703.758*	2,140.027*	0.073*
Genotype × Environment	73	11.039*	90	11.812*	178.839*	103.051^{ns}	0.002*
Residual	164	2.834	210	2.999	122.505	86.037	0.001
Mean		64.652		66.756	215.361	121.966	0.567
CV(%)		2.60		2.59	5.14	7.61	5.66
>MSres/<MSres		10.289		6.824	3.886	2.974	2.529
Fc		10.570		15.320	16.344	36.414	21.807
SA$^{(1)}$		0.952		0.967	0.969	0.986	0.977
Precision		VH		VH	VH	VH	VH

SV	DF	Mean square				
		NP	NS	SI	GY	PL
Block/Environment	14	80,222,284.226	91,973,586.310	0.032	2.165	1.394
Genotype	15	72,683,221.726*	449,674,789.187*	0.162*	26.612*	56.266*
Environment	6	180,845,424.107^{ns}	209,990,389.385^{ns}	0.082^{ns}	208.850*	71.065*
Genotype × Environment	90	30,489,934.689*	91,227,161.872*	0.034*	4.347*	2.689*
Residual	210	17,062,562.004	34,086,681.548	0.011	0.812	0.614
Mean		59,706.101	58,560.268	0.987	7.230	7.394
CV(%)		6.92	9.97	10.50	12.46	10.59
>MSres/<MSres		5.323	4.642	5.377	6.402	2.582
Fc		2.384	4.929	4.801	6.122	20.927
SA(^{1})		0.762	0.893	0.890	0.915	0.976
Precision		H	H	H	VH	VH

SV	DF	Mean square				
		BSL	CSL	TL	NPB	NSB
Block/Environment	14	1.181	4.274	7.528	2.350	0.474
Genotype	15	97.918*	147.109*	87.720*	266.337*	26.808*
Environment	6	23.091*	60.218*	243.583*	49.051*	10.213*
Genotype × Environment	90	2.242*	7.605*	12.295*	2.483*	0.495*
Residual	210	0.522	1.480	2.283	0.910	0.181
Mean		12.558	25.519	45.470	10.862	2.678
CV(%)		5.76	4.77	3.32	8.78	15.87
>MSres/<MSres		2.107	4.865	5.321	3.631	3.336
Fc		43.666	19.343	7.135	107.249	54.157
SA(^{1})		0.988	0.974	0.927	0.995	0.991
Precision		VH	VH	VH	VH	VH

SV	DF	Mean square				
		TBN	PDM	BSDM	CSDM	TDM
Block/Environment	14	3.959	0.002	0.077	0.005	0.122
Genotype	15	434.309*	0.086*	13.065*	0.389*	16.019*
Environment	6	94.631*	0.062*	13.780*	0.469*	19.579*
Genotype × Environment	90	3.972*	0.003*	0.270*	0.013*	0.360*
Residual	210	1.346	0.001	0.051	0.003	0.073
Mean		13.540	0.211	2.287	0.657	3.155
CV(%)		8.57	13.13	9.90	8.82	8.57
>MSres/<MSres		3.656	4.418	4.134	3.393	4.441
Fc		109.346	26.330	48.370	29.453	44.523
SA(^{1})		0.995	0.981	0.990	0.983	0.989
Precision		VH	VH	VH	VH	VH

Traits are described in Table 3.
>MSres/<MSres was greater than seven for the MF trait, so the degrees of freedom (DF) were adjusted (CRUZ, 2016).
*Significant effect by F test at 5% significance level. ^{ns} not significant.
$^{(1)}$ Class limits for selection accuracy (SA), established by Resende and Duarte (2007): VH: very high ($SA \geq 0.90$), H: high ($0.70 \leq SA < 0.90$), and M: moderate ($0.50 \leq SA < 0.70$).

Table 5. Estimates of phenotypic correlation coefficients between phenological, morphological, production and tassel traits measured in 16 maize genotypes.

Trait	MF	FF	PH	SH	RPS	NP	NS	SI	GY	PL
MF	-	0.983*	0.729*	0.713*	0.570*	0.349^{ns}	0.218^{ns}	0.043^{ns}	0.584*	0.390^{ns}
FF			0.768*	0.731*	0.567*	0.375^{ns}	0.284^{ns}	0.094^{ns}	0.651*	0.360^{ns}
PH				0.850*	0.566*	0.358^{ns}	0.538*	0.358^{ns}	0.739*	0.441^{ns}
SH					0.914*	0.424^{ns}	0.540*	0.323^{ns}	0.802*	0.221^{ns}
RPS						0.391^{ns}	0.432^{ns}	0.230^{ns}	0.679*	0.018^{ns}
NP							0.049^{ns}	-0.370^{ns}	0.227^{ns}	0.456^{ns}
NS								0.909*	0.758*	-0.152^{ns}
SI									0.597*	-0.313^{ns}
GY										0.029^{ns}
	BSL	CSL	TL	NPB	NSB	TBN	PDM	BSDM	CSDM	TDM
MF	0.333^{ns}	-0.172^{ns}	0.441^{ns}	0.524*	0.408^{ns}	0.512*	0.569*	0.700*	0.519*	0.755*
FF	0.395^{ns}	-0.201^{ns}	0.445^{ns}	0.578*	0.474^{ns}	0.571*	0.549*	0.767*	0.539*	0.816*
PH	0.521*	-0.500*	0.256^{ns}	0.641*	0.604*	0.652*	0.486^{ns}	0.613*	0.064^{ns}	0.599*
SH	0.424^{ns}	-0.514*	-0.040^{ns}	0.701*	0.674*	0.716*	0.402^{ns}	0.699*	0.143^{ns}	0.683*
RPS	0.256^{ns}	-0.413^{ns}	-0.249^{ns}	0.595*	0.588*	0.612*	0.269^{ns}	0.629*	0.189^{ns}	0.617*
NP	0.273^{ns}	-0.336^{ns}	0.218^{ns}	0.309^{ns}	0.075^{ns}	0.261^{ns}	0.676*	0.319^{ns}	0.137^{ns}	0.359^{ns}
NS	0.663*	-0.715*	-0.347^{ns}	0.633*	0.825*	0.701*	-0.003^{ns}	0.625*	-0.236^{ns}	0.528*
SI	0.505*	-0.538*	-0.414^{ns}	0.447^{ns}	0.731*	0.532*	-0.273^{ns}	0.431^{ns}	-0.307^{ns}	0.321^{ns}
GY	0.616*	-0.526*	-0.006^{ns}	0.813*	0.826*	0.842*	0.193^{ns}	0.833*	0.142^{ns}	0.789*
PL	0.215^{ns}	-0.226^{ns}	0.736*	0.131^{ns}	-0.002^{ns}	0.103^{ns}	0.867*	0.065^{ns}	-0.053^{ns}	0.114^{ns}
	BSL	CSL	TL	NPB	NSB	TBN	PDM	BSDM	CSDM	TDM
BSL		-0.852*	0.126^{ns}	0.725*	0.711*	0.744*	0.393^{ns}	0.615*	-0.373^{ns}	0.526*
CSL			0.214^{ns}	-0.722*	-0.727*	-0.746*	-0.420^{ns}	-0.513*	0.525*	-0.412^{ns}
TL				-0.064^{ns}	-0.192^{ns}	-0.098^{ns}	0.567*	0.037^{ns}	0.244^{ns}	0.113^{ns}
NPB					0.835*	0.991*	0.389^{ns}	0.861*	0.056^{ns}	0.815*
NSB						0.903*	0.163^{ns}	0.842*	-0.092^{ns}	0.758*
TBN							0.345^{ns}	0.884*	0.021^{ns}	0.826*
PDM								0.369^{ns}	0.099^{ns}	0.422^{ns}
BSDM									0.369^{ns}	0.988*
CSDM										0.496^{ns}

Traits are described in Table 3.
*Value of phenotypic correlation coefficient greater than |0.497| is significant at 5% significance level by Student's t-test, with 14 degrees of freedom. ^{ns} not significant.

Production traits showed a positive correlation with tassel traits (BSL, NPB, NSB, TBN, BSDM and TDM). However, in some cases the correlation was not significant (Table 5). The traits NS, SI and GY showed negative and significant phenotypic correlations with CSL, i.e., if the interest is to increase NS, SI and GY, CSL should be reduced, or vice versa. The production traits NS and GY showed significant phenotypic correlations with BSL, NPB, NSB, TBN, BSDM and TDM, indicating that the increase of these traits results in the increase in the number of spikes and grain yield in the selection of maize genotypes. A positive linear association between GY and TBN was observed by Prakash et al. (2019). Öner (2018) found a positive linear association between NS and TBN. The results obtained by Öner (2018) and Prakash et al. (2019) were similar to those obtained in the present study. In addition, Khan et al. (2018) report that the number of grains per spike is an important yield component and can significantly contribute to grain yield, and this trait showed a positive and significant correlation with MF, FF, PH and TL.

Estimates of phenotypic correlation coefficients show that there is a linear association between phenological, morphological, production and tassel traits in maize. Therefore, it is possible to use these results for improving traits through indirect selection of plants. Correlation coefficients are used in the quantification of the magnitude and direction of influences between two traits. However, with only this information it is not possible to make inferences about the relationship between two groups of traits, which must be performed through linear combinations between the characteristics that make up each group (CRUZ; REGAZZI; CARNEIRO, 2012).

Regarding the diagnosis of multicollinearity, the group of phenological traits (MF and FF) had a condition number (CN) equal to 113.29 (Table 6), with multicollinearity classified as moderate according to the classification of Montgomery and Peck (1982). The exclusion of variables is an alternative for reducing the degree of multicollinearity, and this practice has been performed in maize by Alves et al. (2016a), Alves et al. (2016b), Alves et al. (2017) and Crevelari et al. (2019), whereas in studies carried out by Carvalho et al. (2017), Troyjack et al. (2019) and Carvalho et al. (2022) there was no need for exclusion, as the trait groups showed weak multicollinearity. However, due to the need for two or more traits in each group to perform the canonical correlation analysis, it was decided to maintain the two phenological traits. Severe multicollinearity was observed in the groups of morphological (CN=3,478.57), production (CN=2,051.28) and tassel (CN=1,174,830.56) traits. In these groups, it was necessary to eliminate the traits relative position of the spike (RPS) and spike index (SI), as well as eight tassel traits (PL, BSL, CSL, NPB, NSB, PDM, BSDM and CSDM) (Table 6). Canonical correlation analyses were performed with the traits that remained in the groups of phenological (MF and FF), morphological (PH and SH), production (NP, NS and GY) and tassel (TL, TBN and TDM) traits.

Table 6. Multicollinearity diagnosis, based on the condition number, for the four groups of traits (phenological, morphological, production and tassel) evaluated in 16 maize genotypes.

	Phenological	Morphological	Production	Tassel
Nº of traits in the group	2	3	4	11
Traits in the group	MF and FF	PH, SH and RPS	NP, NS, SI and GY	PL, BSL, CSL, TL, NPB, NSB, TBN, PDM, BSDM, CSDM and TDM
Initial CN	113.29	3,478.57	2,051.28	1,174,830.56
Excluded traits	None	RPS	SI	PL, BSL, CSL, NPB, NSB, PDM, BSDM and CSDM
Final CN	113.29	12.36	8.18	12.38
Remaining traits	MF and FF	PH and SH	NP, NS and GY	TL, TBN and TDM

Traits are described in Table 3.
Classification of the condition number (CN) according to Montgomery and Peck (1982): CN<100 = weak multicollinearity; 100<CN<1,000 = moderate to strong multicollinearity; and CN>1,000 = severe multicollinearity.

In the three analyses performed (phenological *versus* tassel, morphological *versus* tassel and production *versus* tassel), the first canonical correlation was significant. Thus, it can be inferred that there is linear dependence between the groups of traits and that it is possible to identify promising traits for the genetic improvement of plants (Table 7). Significant canonical correlations have also been observed in groups of maize traits, for example by Souza et al. (2015), Alves et al. (2016a), Alves et al. (2016b), Alves et al. (2017), Carvalho et al. (2017), Nascimento-Júnior, Môro and Môro (2018), Crevelari et al. (2019), Troyjack et al. (2019), Ferreira et al. (2020) and Carvalho et al. (2022).

Canonical correlation analysis showed that the first canonical pair between groups I (phenological traits) and group II (tassel traits) was significant ($\hat{\rho}$=0.917). In the first canonical pair, it was found that the correlation between the first canonical variables was due to the high correlation of MF and FF with the first canonical variable in group I and of TBN and TDM with the canonical variable of group II (Table 7). Thus, it can be inferred that phenological traits (MF and FF) can be used for indirect selection of tassel traits (TBN and TDM) in maize crop.

In the analysis between the groups of morphological and tassel traits, the correlation of the first canonical pair was significant ($\hat{\rho}$=0.739). The traits PH and SH are strongly related to the first canonical variable for the group of morphological traits. Again, the traits TBN and TDM showed the highest values of canonical loading for the first canonical pair (Table 7). The results obtained in the first canonical pair show that it is possible, through indirect selection, to improve tassel traits (TBN and TDM) based on morphological traits (PH and SH) in maize plants.

Canonical correlation of high magnitude for the first canonical pair was also verified in the analysis performed with the production and tassel traits ($\hat{\rho}$=0.867). In the first group (production traits), the highest estimates of canonical loading were verified for the traits NS and GY. Thus, these can be used for indirect selection of tassel characteristics of maize. For traits of group II, the highest canonical loadings were verified for TBN and TDM. Thus, tassel traits, TBN and TDM, are ones that are strongly associated with the first canonical variable for this group and are responsible for the association with the other groups of traits, represented by the phenological (MF and FF), morphological (PH and SH) and production (NS and GY) traits (Table 7).

Table 7. Canonical loadings of phenological and tassel traits, morphological and tassel traits, and production and tassel traits, of the canonical correlations ($\hat{\rho}$), significance and degrees of freedom in 16 maize genotypes in seven experiments.

Trait	Analysis 1 (Phenological *versus* Tassel) Canonical loadings		
	1	2	
Group I	Phenological		
MF	0.912	0.410	
FF	0.972	0.233	
Group II	Tassel		
TL	0.467	0.709	
TBN	0.672	-0.718	
TDM	0.930	-0.325	
Canonical correlation ($\hat{\rho}$)	0.917*	0.171 ^{ns}	
χ^2	22.446	0.357	
Degrees of freedom	6	2	
Trait	Analysis 2 (Morphological *versus* Tassel) Canonical loadings		
	1	2	
Group I	Morphological		
PH	0.940	0.340	
SH	0.979	-0.206	
Group II	Tassel		
TL	0.100	0.880	
TBN	0.971	-0.109	
TDM	0.913	-0.171	
Canonical correlation ($\hat{\rho}$)	0.739*	0.624 ^{ns}	
χ^2	15.405	5.915	
Degrees of freedom	6	2	
Trait	Analysis 3 (Production *versus* Tassel) Canonical loadings		
	1	2	3
Group I	Production		
NP	0.362	-0.429	0.827
NS	0.757	0.650	0.064
GY	0.989	0.029	-0.144
Group II	Tassel		
TL	0.008	-0.943	-0.334
TBN	0.977	0.162	-0.141
TDM	0.927	-0.221	0.305
Canonical correlation ($\hat{\rho}$)	0.867*	0.572 ^{ns}	0.056 ^{ns}
χ^2	20.621	4.589	0.037
Degrees of freedom	9	4	1

Traits are described in Table 3.
* Significant by chi-square test (χ^2) at 5% significance level. ^{ns} not significant.

Xu et al. (2017) describe that maize tassels have undergone profound morphological changes (length and number of branches) during the domestication and breeding processes. The same authors report that the traits tassel length and tassel branch number are the factors that determine tassel size, and these traits were used for selection by maize breeding programs. These authors also describe that the evolution of these characteristics was initiated by the selection of some important mutations and by the additional refinement of many modified *loci* with small effects.

According to Duvick (2005), lower tassel branch number has been a trend observed in commercial maize hybrids. Edwards (2011) reports that tassel branch number decreased from 21 to eight after 17 selection cycles. Yordanov (2019) studied 55 maize hybrids and observed that 50% of the most productive hybrids had from 6 to 9 branches, highlighting that the number of branches should be considered for maize selection. Parvez (2007) reports that selecting tassels with erect branches, without compromising their size, ensures sufficient pollen for fertilization, and this can compensate for the reduction of grain yield.

In addition, Duvick (2005) reports that the changes confer higher agronomic efficiency, such as: lower plant height and spike height, more erect leaf angle, reduction of tassel size (number of branches, length and mass), shorter duration of the subperiod from tasseling to silking, lower protein content in the grain and higher production potential. The same author describes that the selection of hybrids/strains with these characteristics may have occurred indirectly, that is, they result from the selection to increase grain yield. The characteristics mentioned above favored an increase in grain yield, as they improve the efficiency of transforming sunlight, CO_2 and soil nutrients into plant constituents.

Based on the phenotypic correlation matrix and canonical correlation analyses, it can be inferred that there is linear dependence between the groups of phenological, morphological and production traits and tassel traits. The traits tassel branch number and tassel dry matter can be used for indirect selection of maize plants, since they showed a strong correlation with traits of agronomic interest that are important in genetic improvement.

CONCLUSIONS

The significant canonical correlations between the groups of traits, phenological and tassel, morphological and tassel, and production and tassel, indicate that the groups are dependent.

Phenological (number of days from sowing to 50% of male flowering and number of days from sowing to 50% of female flowering), morphological (plant height and spike height) and production (number of spikes and grain yield) traits are positively associated with tassel traits (tassel branch number and tassel dry matter).

Tassel branch number and tassel dry matter can be used for indirect selection of maize plants.

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REFERENCES

ALVARES, C. A. et al. Köppen's climate classification map for Brazil. **Meteorologische Zeitschrift**, 22: 711-728, 2013.

ALVES, B. M. et al. Correlações canônicas entre caracteres agronômicos e nutricionais proteicos e energéticos em genótipos de milho. **Revista Brasileira de Milho e Sorgo**, 15: 171-185, 2016a.

ALVES, B. M. et al. Linear associations among phenological, morphological, productive, and energetic-nutritional traits in corn. **Pesquisa Agropecuária Brasileira**, 52: 26-35, 2017.

ALVES, B. M. et al. Linear relations among phenological, morphological, productive and protein-nutritional traits in early maturing and super-early maturing maize genotypes. **Journal of Cereal Science**, 70: 229-239, 2016b.

CARVALHO, I. R. et al. Components of variance and inter-relation of important traits for maize (*Zea mays*) breeding. **Australian Journal of Crop Science**, 11: 982-988, 2017.

CARVALHO, I. R. et al. Canonical interrelationships in morphological characters, yield and nutritional composests of corn. **Agronomy Science and Biotechnology**, 8: 1-17, 2022.

CONAB - Companhia Nacional de Abastecimento. **Acompanhamento da Safra Brasileira de Grãos**, Brasília, DF, safra 2021/22, sexto levantamento, março 2022. Disponível em: <https://www.conab.gov.br>. Acesso em: 10 abr. 2022.

CREVELARI, J. A. et al. Canonical correlation for morphoagronomic and bromatological traits in silage corn genotypes. **Bragantia**, 1: 1-13, 2019.

CRUZ, C. D. Genes Software - extended and integrated with the R, Matlab and Selegen. **Acta Scientiarum Agronomy**, 38: 547-552, 2016.

CRUZ, C. D.; REGAZZI, A. J.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. 4. ed. Viçosa, MG: UFV, 2012. 514 p.

DUVICK, D. The contribution of breeding to yield advances in maize (*Zea mays* L.). **Advances in Agronomy**, 86: 83-145, 2005.

EDWARDS, J. Changes in plant morphology in response to recurrent selection in the iowa stiff stalk synthetic maize population. **Crop Science**, 51: 2352-2361, 2011.

FERREIRA, L. L. Multivariate and canonical models applied to corn: benefits of green manure with *Vigna unguiculate*. **Holos**, 7: e9737, 2020.

FERREIRA, D. F. **Estatística multivariada**. 3. ed. Revisada e Ampliada. Lavras, MG: Editora UFLA, 2018. 624 p.

KHAN, A. S. et al. Heritability and correlation analysis of morphological and yield traits in Maize. **Journal of Plant Biology and Crop Research**, 2: 1-8, 2018.

MONTGOMERY, D. C.; PECK, E. A. **Introduction to linear regression analysis**. New York: John Wiley & Sons, 1982. 504 p.

NASCIMENTO-JÚNIOR, I.; MÔRO, G. V.; MÔRO, F. V. Indirect selection of maize genotypes based on associations between root agronomic and anatomical characters. **Chilean Journal of Agricultural Research**, 78: 39-47, 2018.

ÖNER, F. Assessment of genetic variation in turkish local maize genotypes using multivariate discriminant analysis. **Applied Ecology and Environmental Research**, 16: 1369-1380, 2018.

PARVEZ, A. S. Genetic analysis of tassel and ear characters in maize (*Zea mays* L.) using triple test cross. **Asian Journal of Plant Sciences**, 6: 881-883, 2007.

PIMENTEL-GOMES, F. **Curso de estatística experimental**. 15. Ed. Piracicaba, SP: Esalq, 2009. 451 p.

PRAKASH, R. et al. Genetic variability, character association and path analysis for yield and yield component traits in maize (*Zea mays* L.). **Electronic Journal of Plant Breeding**, 10: 518-524, 2019.

RESENDE, M. D. V.; DUARTE, J. B. Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical**, 37: 182-194, 2007.

SANTOS, H. G. et al. **Sistema brasileiro de classificação de solos**. 5. ed. Brasília, DF: Embrapa, 2018. 356 p.

SOUZA, V. Q. et al. Variance components and association between corn hybrids morpho-agronomic characters. **Científica**, 43: 246-253, 2015.

STRAZZI, S. Derivados do milho são usados em mais de 150 diferentes produtos industriais. **Visão Agrícola**, 13: 146-150, 2015.

TROYJACK, C. et al. Multivariate characterization and canonical interrelations for the productive performance of open pollinated corn genotypes. **Genetics and Molecular Research**, 18: 1-12, 2019.

XU, G. et al. Complex genetic architecture underlies maize tassel domestication. **New Phytologist**, 214: 852-864, 2017.

YORDANOV, G. Study on inheritance and dependence with grain yield on the size and tassel branch numbers in high yielding corn hybrids**. Journal of Mountain Agriculture on the Balkans**, 22: 36-45, 2019.

WARTHA, C. A. et al. Sample sizes to estimate mean values for tassel traits in maize genotypes. **Genetics and Molecular Research**, 15: 1-13, 2016.