

NASCIMENTO, MR; SANTOS, PR; COELHO, FC; JAEGGI, MEPC; COSTA, KDS; SOUZA, MN. 2018. Biometric analysis in maize genotypes suitable for baby corn production in organic farming system. *Horticultura Brasileira* 36: 419-425. DOI - <http://dx.doi.org/10.1590/S0102-053620180322>

Biometric analysis in maize genotypes suitable for baby corn production in organic farming system

Maxwel R Nascimento¹; Paulo Ricardo Santos¹; Fábio C Coelho¹; Mário Euclides PC Jaeggi¹; Kleyton Danilo S Costa²; Mauricio N Souza³

¹Universidade Estadual do Norte Fluminense (UENF), Campos dos Goytacazes-RJ, Brazil; maxwel.rn88@gmail.com; prs_ufal@hotmail.com; fabiocoelhoenf@gmail.com; mariopechara@hotmail.com; ²Instituto Federal de Educação, Ciência e Tecnologia de Alagoas (IFAL), Piranhas-AL, Brazil; kd.agro@gmail.com; ³Instituto Federal de Educação Ciência e Tecnologia do Espírito Santo (IFES), Alegre-ES, Brazil; mauriciosnovaes@yahoo.com.br

ABSTRACT

The aim of this study was to estimate and quantify the degree of association between phytotechnical variables for simultaneous selection of maize genotypes suitable to produce baby corn. Seven genotypes were arranged in field in randomized complete block design with four replicates. Genetic parameters, simple, path and canonical correlations of phytotechnical variables were estimated. The variables production of marketable spikes, length of marketable spikes, final plant stand and plant height showed over 80% heritability and variation index higher than the unity, indicating that superior genotypes can be obtained and selection gains. Significant phenotypic and genotypic correlations were observed for production of marketable spikes, positive and of high magnitude with crude protein, dry mass and final plant stand. However, the direct effect between dry mass and production of marketable spikes was pronounced negative (-0.7085), whereas the phenotypic correlation was positive and showed medium magnitude (0.5343), which should be considered the indirect effect of final plant stand (0.7367), to take advantage of the gains of these two traits. The final plant stand is determinant to increase the production of dry matter and marketable spikes, both direct and indirectly. Given the data, we could identify promising variables for plant breeding which can be indicative to select maize genotypes for baby corn production.

Keywords: *Zea mays*, path analysis, canonical correlation, simultaneous selection.

RESUMO

Análise biométrica em genótipos de milho para produção de minimilho em cultivo orgânico

Objetivou-se estimar e quantificar o grau de associação entre variáveis fitotécnicas para a seleção simultânea de genótipos de milho com aptidão para produção de minimilho. Foram utilizados sete genótipos de milho que foram dispostos no campo em delineamento de blocos casualizados com quatro repetições. Foram estimados parâmetros genéticos, correlações simples, de trilha e canônicas das variáveis fitotécnicas. As variáveis produção de espigas comerciais, comprimento de espigas comerciais, estande final de plantas e altura de plantas apresentaram herdabilidade superiores a 80% e índice de variação superior a unidade, indicando que genótipos superiores podem ser obtidos com ganhos de seleção. Para a produção de espigas comerciais houve correlações fenotípicas e genotípicas significativas, positivas e de alta magnitude com proteína bruta, massa seca e estande final de plantas. No entanto, o efeito direto entre massa seca e produção de espigas comerciais foi negativo (-0,7085), enquanto que a correlação fenotípica foi positiva e de magnitude média (0,5343), o que deve considerar o efeito indireto no estande final de plantas (0,7367), para aproveitar o ganho nessas duas características. O estande final de plantas é determinante para aumento na produção de massa seca e espigas comerciais, tanto direta como indiretamente. Diante dos dados é possível identificar variáveis promissoras para o melhoramento genético de plantas que sejam indicativos de produção de minimilho em genótipos de milho.

Palavras-chave: *Zea mays*, análise de trilha, correlação canônica, seleção simultânea.

Received on May 30, 2017; accepted on November 25, 2017

One alternative found in order to diversify production and increase profitability of family farming is growing fields for special maize production, such as baby corn. The baby maize production allows gains superior to the maize for grain production, due to early harvest, lower production cost and the possibility of higher number of

seasons in the same area (Santos *et al.*, 2014). With the advent of processed, industrialized foods in the national market, baby corn has been frequently consumed, providing an increase of the cultivated area for this purpose (Araújo *et al.*, 2010).

Baby corn is considered a vegetable, due to the short time taken from sowing

to harvest, which varies according to planting time, cultivar and cultural practices, which may reach up to 70 days (Santos *et al.*, 2014). Besides the commercialization of baby corn, the producer has as by-product the complete green plant, useful as forage to feed animals and also to be incorporated on soil (mulch), common practice of rural

organic producers (Araújo *et al.*, 2010). One limitation for producers is the small availability of maize genotypes that combine high productivity and quality of marketable baby corn spikes and forage production for animal feeding.

Getting to know nature and magnitude of the associations between the variables of interest is extremely important. The relationships between the variables are, in general, evaluated through estimates and signs of simple correlation coefficients, which quantify the degree of genetic and non-genetic association between two or more characters (Hallauer *et al.*, 2010). These associations may provide indirect gains through selection in correlated characters, mainly under truncation selection on low heritability characters, increasing the efficiency of selection (Cruz *et al.*, 2012).

Although the knowledge of the correlations is of great importance, some care should be considered, since these correlations are not measures of cause and effect. In this case, path analysis helps to understand the real relationships between the variables (Silva *et al.*, 2009), which consists of the study of direct and indirect effects of characters on a basic variable. However, this technique does not allow the evaluation of the interrelationships between two groups of variables determined by a larger number of variables of agronomic importance. Applying canonical correlation technique can be more appropriate to estimate the relationships between two groups of agronomic characters, and it can be used to evaluate relationships of physiological, bromatological and agronomic variables, as well as to help out in selection processes efficiently (Cruz *et al.*, 2012). The great advantage of this technique is the possibility of assisting breeders in the study involving more than one dependent variable, such as plant breeding variables in this study.

Biometric analysis has been performed in this study, on suitable maize genotypes for baby corn production in an organic cropping system using the estimation of genetic parameters, simple, path and canonical

correlation coefficients.

MATERIAL AND METHODS

The experiment was carried out from January to September 2016, in the experimental area of Setor de Horticultura of Instituto Federal de Educação, Ciência e Tecnologia do Espírito Santo (IFES), Campus Alegre.

According to Köppen classification, the local climate is “Cwa”, hot, under humid tropical conditions, with cold dry winters and hot rainy summers, 23.1°C average temperature and 1,341 mm total average rainfall (Lima *et al.*, 2008). The soil was classified as Dystrophic Yellow Latosol type A (Embrapa, 2013).

Maize was manually sown in succession to sunn hemp on May 5, 2016, opening furrows for sowing and organic fertilizing (6 t ha⁻¹) with broiler litter.

Treatments consisted of the maize cultivars: 1) creole Fortaleza (Muqui-ES); 2) creole Alliance (Muqui-ES); 3) BR 106 (control); 4) Capixaba Incaper 203; 5) Eldorado; 6) double hybrid corn BM 207 and 7) EMCAPA 201. Genotypes were arranged in field; the experimental design was randomized blocks, with four replicates totaling 24 experimental plots. Plots, 6.0x3.2 m (19.2 m²), were allocated in four 6-m length lines, spaced 0.80 m. During the evaluation, two central lines were used, discarding 0.5 m of each end, resulting in a useful area of 8 m² (5.0x1.6 m).

Thirty three seeds were homogeneously distributed within the furrow per linear meter. 21 days after sowing (DAS), plants were thinned to establish a population of 17 plants per linear meter of furrow, consisting of a density of 212,500 plants ha⁻¹ [adapted from Corrêa *et al.* (2014)]. During thinning, soil was organic fertilized with broiler litter (6 t ha⁻¹).

Leaves were sprayed with biological insecticide DiPel WP, based on *Bacillus thuringiensis*, to control fall armyworm (*Spodoptera frugiperda*). The spray volume was of 500 g ha⁻¹ and a pressurized costal sprayer, 20 L capacity, was used. Weeds were controlled

manually using a hoe at 30 DAS.

The first harvest was carried out three days after the issuance of styles-stigmata, about 70 DAS and after, twice a week, totaling 11 harvests. Spikes were kept in a cold chamber at temperature ranging from 5 to 12°C up to the measure of the variables. All harvests were carried out from 6 to 8:30 in the morning. After that time, air temperature became hotter, which could decrease the humidity of spikes compromising the final product quality.

We evaluated: number of marketable spikes (NEC) (plot average converted to spikes ha⁻¹); production of marketable spikes (PC) (plot average of total mass of spikes, in t ha⁻¹); plant height (ALT) (in cm, measured from the base of the stem up to the apex of the tassel); length of marketable spikes (CE) (in cm); diameter of marketable spikes (DE) (with the aid of a caliper in the center of each spike, in mm); stem diameter (DC) (using a caliper next to the stem basis, in mm); final stand (EST) (counting the number of maize plants of the useful area of the plot, converted to one hectare); shoot dry mass (MS) (t ha⁻¹); number of spikes per plant (NEP) (dividing the total number of spikes by the final stand); crude protein (PB) (percentage of dry mass). To determine marketable production, all spikes of the useful area were unhusked and weighed, being, right after, selected and counted the spikes which corresponded to the marketable standard described by Silva *et al.* (2013).

To evaluate shoot dry mass, three plants of the useful area of each experimental unit were collected. Samples of maize plants were submitted to a dryer with forced air circulation at 65°C for 72 hours and later weighed to obtain dry mass. After weighing, the dry mass was ground using a Willey type mill to determine the percentage of crude protein in the shoot.

The authors used average data of the plot, for the evaluated variables. Initially, the authors carried out the tests of assumptions of the variance analysis to detect if the variables follow a normal distribution and if residual variances are homogeneous. The variables which met the assumptions were submitted to

the variance analysis using statistical model:

$$Y_{ijk} = \mu + g_i + b_k + \bar{\epsilon}_{ijk}$$

Phenotypic, genotypic and environmental variance were estimated, besides heritability, genetic variation coefficient, environmental variation and variation index.

During the association analysis between pairs of variables, the estimators of the simple correlations were: phenotypic, genotypic and environmental correlations. Significances of the phenotypic correlation coefficient were evaluated using the “t” test and for genotypic and environmental correlations, the bootstrap with 5000 simulations was used, according to Ferreira *et al.* (2008).

Through the multicollinearity test we verified the collinearity between traits, according to Montgomery & Peck cited by Cruz *et al.* (2012). Afterwards, the unfolding of the correlation coefficients in direct and indirect effect was done, data obtained using the path analysis. Two strategies were used for the path analysis; first to study the direct and indirect effects of the variables mentioned previously (X), for producing marketable spikes, dependent variable (Y); the second strategy was about studying direct and indirect effects of the explanatory variables (X) in dry mass, dependent variable (Y).

Canonical correlations were used to estimate maximum correlation between linear combinations of characters distributed in two groups: 1) bromatologic variables (MS and PB); 2) agronomic variables (PC, DE, CE and EST). Ponderation variable coefficients in each linear combination (Cruz *et al.*, 2012) were estimated. The null hypothesis significance testing, in which all the possible canonical correlations are null, was evaluated using the χ^2 test. Analyses were carried out using the software GENES (Cruz, 2013).

RESULTS AND DISCUSSION

The number of marketable spikes did not meet the normality assumption of error distribution ($p \leq 0.05$) using Lilliefors test and homogeneity of

residual variances ($p \leq 0.05$) using Bartlett test, whereas the other variables had adjusted to normal distribution and show homogeneous residual variances. These results demonstrated that, in general, the mathematical assumptions required to perform the variance analysis and further studies were met. Average values, as well as genetic parameters for agronomic and forage variables, are presented in Table 1.

Overall, the variables show genetic variability, with exception of the diameter of marketable spikes (DE), length of marketable spikes (CE), and crude protein (PB), which did not show any significant difference for the genotypes using F test ($p \leq 0.05$).

When heritability values are superior to 80% and variation index is superior to the unit, satisfactory selection gains can be obtained (Falconer, 1987). This situation was observed for the production of marketable spikes (PC), length of marketable spikes (CE), final plant stand (EST) and plant height (ALT) (Table 1), showing that superior genotypes for these variables can be obtained through simple methods of selection, such as mass selection. However, even considering that the heritability is not so low for the other variables; the authors do not exclude the possibility of using genotypic recurrent

selection, in order to obtain superior gains, although this strategy has not been used in maize genotypes suitable for maize production yet.

The estimates of phenotypic (r_p), genotypic (r_g) and environmental (r_a) correlations are shown in Table 1. Thus, among the 36 pairs of combinations for the nine evaluated variables, only thirteen presented significant r_g , ranging from 1 to 5% probability, being six high positive, ranging from 0.02 to 0.92 (Table 2). Positive genotypic correlations show that selection aiming any gain for one trait will cause the same effect on another.

The highest estimate of r_f was noticed between length of marketable spikes and plant height (ALT), 0.90, and the lowest, 0.07, between length of marketable spikes and crude protein, being significant and non-significant estimates verified using “t” test, respectively. Among the r_g estimates, the highest was 0.92 between dry mass and crude protein and the lowest was observed between length of marketable spikes and crude protein, which was 0.02. And for r_a the highest estimate was 0.67, noticed between plant height and crude protein, and the lowest, between plant final stand and crude protein of -0.03.

For production of marketable spikes,

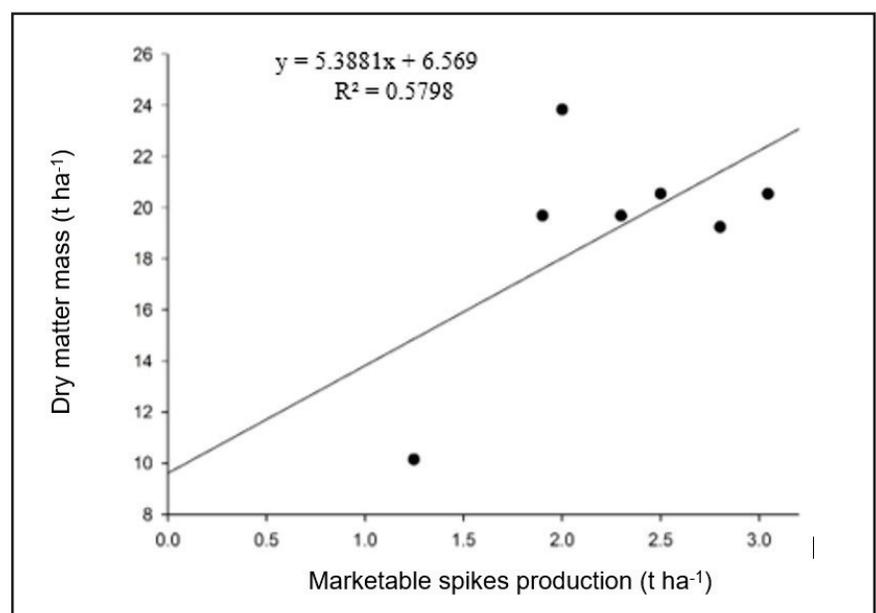


Figure 1. Linear regression between marketable spikes (PC) and dry mass (MS) production. Alegre, IFES, 2016.

Table 1. Estimates of genetic parameters, for production of marketable spikes (PC), length of marketable spikes (CE), diameter of marketable spikes (DE), stem diameter (DC), final stand (EST), shoot dry mass (MS), plant height (ALT), number of spike per plant (NEP) and crude protein (PB), evaluating seven maize genotypes for baby corn production in organic farming system. Alegre, IFES, 2016.

Variables	$\sigma_g^2/ $	σ_e^2	σ_f^2	\hat{h}_g^2	CV _g %	CV _e %	IV	Average
PC	0.34	0.03	0.38	91.82	26.66	15.91	1.67	2.21 t ha ⁻¹
CE	0.22	0.03	0.26	85.36	6.29	5.21	1.21	7.59 cm
DE	0.03	0.02	0.05	43.34	1.09	2.49	0.43	13.39 mm
DC	1.41	0.95	2.36	59.61	6.39	10.53	0.60	18.56 mm
EST	1495.32	206.64	1700.95	87.85	27.29	20.30	1.34	141,616 plants ha ⁻¹
MS	13.80	4.10	17.91	77.07	19.44	21.21	0.91	19.10 t ha ⁻¹
NEP	0.08	0.02	0.11	74.52	13.31	15.56	0.85	2.20 u
ALT	887.44	140.83	1028.27	86.30	10.59	8.44	1.25	281.18 cm
PB	0.09	0.05	0.14	61.31	25.58	40.64	0.62	5.79%

¹Genotypic variation (σ_g^2), residual variances (σ_e^2), phenotypic variance (σ_f^2), heritability (\hat{h}_g^2), coefficient of genotypic variation (CV_g%), coefficient of residual variation (CV_e%), coefficient of relative variation considering (CV_g/CV_e = IV) and overall average.

r_f and r_g were significant, positive and high magnitude for crude protein, dry mass and final plant stand. Between production of marketable spikes and plant final stand, r_g was 0.81, showing that increasing planting density may result in gains of marketable spikes production. Moreover, plants with higher accumulation of dry mass and crude protein in the shoot area show higher production of baby corn marketable spikes (Table 2).

The positive correlation between production of marketable spikes and dry mass was also observed through a linear adjustment of the equation (Figure 1), corroborating the correlation analysis, despite the low magnitude (Table 2). The angular coefficient was significant by F test at 1% probability. For the equation on the line, the authors noticed that when an increase of t ha⁻¹ in the production of marketable baby corn spikes is verified, an average increase of 5.39 t ha⁻¹ in dry mass can be noticed. The determination coefficient (R^2) was 0.5798, which means that 57.98% in the range of the production of marketable spikes can be explained by dry mass production in the shoot area.

Production of marketable spikes showed negative r_g correlations with number of marketable spikes per plant (-0.32), plant height (-0.08) and stem diameter (-0.50), and positive with

length (0.11) and diameter of marketable spikes (0.81); however, all these correlations are non-significant (Table 2). Cruz *et al.* (2012) reported that one non-significant correlation coefficient or one correlation coefficient showing low magnitude do not mean lack of relationship between two variables, but absence of linear relationship between these variables.

Among traits of great interest in maize genotypes suitable for baby corn production and biomass, the production of marketable spikes, dry mass and crude protein stand out.

Before performing the path analysis, the multicollinearity test was done among variables (Cruz *et al.*, 2012). Phenotypic correlation matrices were submitted to multicollinearity diagnosis based on the condition number, using all variables, pointing out that the value obtained for number of conditions was 12.242, showing severe multicollinearity. Thus, the variables NEC, NEP, ALT and DC had to be eliminated. Using the variables PC, CE, DE, EST MS and PB, the authors observed value 122.21 for number of conditions, which allows classifying as moderate, not causing great damage to the statistics of path analysis. According to Coimbra *et al.* (2005), in the presence of strong or severe multicollinearity, variances associated to path coefficients can reach

too high values, which result in several effects on canonical procedures, making the results inaccurate and assuming absurd values or without any coherence with the studied biological phenomenon. Thus, for this study, the authors decided to use only variables showing no collinearity.

Table 4 presents direct and indirect effects of explanatory variables using strategy as the main variable, taking turns choosing the production of marketable spikes (PC) and dry mass as basic variables. Determination coefficients (R^2) in path analysis models were superior to 0.82 and the residual effects lower than 0.42. Thus, the models showed cause and effect relationship between the explanatory variables and production of marketable baby corn spikes and dry mass. Using the path coefficients successfully is directly linked to the composition of casual diagrams, which should be formed with the knowledge of the breeder about variables which are the most important in the expression of the main variable (Silva *et al.*, 2009). The used diagrams allowed explaining 82.92% (R^2) of variation in production of marketable baby corn and 90.31% (R^2) of variation in dry mass (Table 3).

The highest values of direct effects of marketable spikes production were observed for plant final stand

Table 2. Phenotypic (r_p), genotypic (r_g) and environmental (r_e) correlations among nine phytotechnical characteristics evaluating seven maize genotypes for baby corn production in organic farming system. Alegre, IFES, 2016.

Variables	Correlation	CE ¹	DE	EST	NEP	ALT	DC	MS	PB
PC ¹		0.15	0.56	0.71*	-0.19	-0.03	-0.30	0.53**	0.48**
CE			-0.36	-0.24	0.16	0.90**	0.70	0.32	0.07
DE				0.48	-0.35	-0.21	-0.70	0.08	0.13
EST	(r_p)				-0.72	-0.45	-0.71	0.73**	0.87**
NEP						0.19	0.70	-0.66	-0.66
ALT							0.66	0.12	-0.17
DC								-0.17	-0.36
MS									0.88**
PC		0.11	0.81	0.81 ⁺⁺	-0.32	-0.08	-0.50	0.64 ⁺⁺	0.62 ⁺⁺
CE			-0.78	-0.25	0.13	0.96	0.81	0.32	0.02 ⁺⁺
DE				0.85	-0.86	-0.63 ⁺	-0.91 ⁺⁺	-0.08	-0.57
EST	(r_g)				-0.77	-0.44	-0.82	0.77 ⁺⁺	0.90 ⁺⁺
NEP						0.08	0.73	-0.77	-0.85 ⁺⁺
ALT							0.70	0.10	-0.34 ⁺⁺
DC								-0.26	-0.64 ⁺⁺
MS									0.92 ⁺⁺
PC		0.52 ⁺	0.23	-0.18	0.49 ⁺⁺	0.35	0.40 ⁺	0.08	0.11
CE			0.41 ⁺	-0.21	0.31	0.56 ⁺	0.48 ⁺	0.29	0.51 ⁺⁺
DE				-0.15	0.34 ⁺⁺	0.62 ⁺⁺	0.36 ⁺	0.32	0.67 ⁺
EST	(r_e)				-0.57 ⁺⁺	-0.48 ⁺	-0.52 ⁺⁺	0.59 ⁺⁺	-0.03
NEP						0.63 ⁺⁺	0.66 ⁺⁺	-0.30 ⁺	0.05
ALT							0.66 ⁺⁺	0.19	0.67 ⁺⁺
DC								0.02	0.38 ⁺
MS									0.61 ⁺⁺

¹Production of marketable spikes (PC), length of marketable spikes (CE), diameter of marketable spikes (DE), stem diameter (DC), final stand (EST), shoot dry mass (MS), plant height (ALT), number of spike per plant (NEP) and crude protein (PB). *, ** = significant at 5 and 1% probability, respectively, by t test. +, ++ = significant at 1 and 5%, respectively, using bootstrap with 5000 simulations.

(1.0250), length (0.7454) and diameter of marketable spikes (0.3620), whereas dry mass presented negative direct effect and high magnitude (-0.7085) (Table 3). The phenotypic correlation coefficient between plant final stand and production of marketable spikes (0.7118) was similar to the direct effect (1.0250), in magnitude and signal. This correlation explains the true existing association. In this case, a direct selection on causal factor effect mentioned will be efficient to improve the production of marketable spikes.

On the other hand, when one phenotypic correlation coefficient is negligible, but the direct effect shows high positive, the indirect effects are responsible for lack of correlation (Vencovsky & Barriga, 1992). In this case, indirect causal factors, diameter of marketable spikes (-0.1315), plant final stand (-0.2489), dry mass (-0.2268), and crude protein (0.0202), should also deserve special attention for the selection process. This happens in relation to length and production of marketable spikes (direct effect = 0.7454

and phenotypic correlation = 0.1583).

The direct effect between dry mass and production of marketable spikes was pronounced negative (-0.7085), but phenotypic correlation was positive and medium magnitude (0.5343). In this case, one restrictive selective scheme should be applied in order to consider desirable indirect effects, especially plant final stand (0.7367), to take advantage of these two traits which are the most important for the indication of maize genotypes for baby corn production.

When the strategy of dry mass variable as basic variable is used, the authors noticed that plant final stand is determinant for increase of dry mass production, since this variable showed the highest values of direct effects (0.6917). Likewise the phenotypic correlation coefficient between plant final stand and production of marketable

spikes was similar to the direct effect, magnitude and signal, the same happened to the plant final stand and dry mass, which explains the true existing association. However, considering the direct selection of plant final stand instead of dry mass, results in a decrease in production of marketable baby corn spikes (indirect effect = -0.2862).

In relation to canonical correlations (Table 4), the studied groups of dry mass and crude protein, production of marketable spikes, length of marketable spikes, diameter of marketable spikes and plant final stand showed correlations different from zero using the chi-square test, at 1% probability (0.96) for the first canonical pair, whereas for the second canonical pair did not show any statistical significance at 5% probability (0.68^{ns}). Given the above, through initial analysis, based on the first canonical pair, we concluded that the studied groups are not independent, since a linear dependence among these variables can be noticed. Thus, it is possible to identify promising traits in plant breeding for baby corn production.

Significant correlation between bromatologic and agronomic variables shows that, when a greater plant final stand and higher production of marketable spikes, higher dry mass and higher crude protein content can be verified, the results show that, through indirect selection, based on the plant final stand and production of marketable spikes, the authors can select maize genotypes for forage production.

Notably the plant final stand is the variable which the most determine both direct and indirectly the production of marketable baby corn spikes and the bromatologic characteristics of maize genotypes. Actually, these results suggest that further studies to test different planting densities, in order to determine the optimal plant density for higher productivity and shoot dry mass accumulation, are necessary.

These results, as well as all the facts discussed, show clearly that the study on only simple correlations is little information for studying the degrees of association and interrelation of baby corn production and biomass production. Using only the path analysis and canonical correlations allow a more clear interpretation of the existing association between two or variable groups and the interference that others exert on this association.

Since studies on associations among characteristics such as simple, path and canonical correlations, in order to verify

Table 3. Direct and indirect effects of explanatory variables in production of marketable spikes (PC), direct and indirect effects of agronomic variables in dry mass (MS), evaluating seven maize genotypes for baby corn production in organic farming system. Alegre, IFES, 2016.

Variable	Direct	Via	PC ¹	Variable	Direct	Via	MS ¹
	Indirect		0.7454		Indirect		-0.4021
CE	Effect	DE	-0.1315	PC	Effect	CE	0.0879
		EST	-0.2489			DE	0.0551
		MS	-0.2268			EST	0.4931
		PB	0.0202			PB	0.3002
		Total	0.1583			Total	0.5343
	Direct		0.3620		Direct		0.5558
DE	Indirect	CE	-0.2708	CE	Indirect	PC	-0.0636
		EST	0.4858			DE	-0.0354
		MS	-0.0488			EST	-0.1720
		PB	0.0372			PB	0.0354
		Total	0.5653			Total	0.3202
	Direct		1.0250		Direct		0.0974
EST	Indirect	CE	-0.185	DE	Indirect	PC	-0.2273
		DE	0.1754			CE	-0.2020
		MS	-0.5206			EST	0.3357
		PB	0.2394			PB	0.0652
		Total	0.7118			Total	0.069
	Direct		-0.7085		Direct		0.6927
MS	Indirect	CE	0.2386	EST	Indirect	PC	-0.2862
		DE	0.0249			CE	-0.1380
		EST	0.7367			DE	0.0472
		PB	0.2442			PB	0.4190
		Total	0.5343			Total	0.7348
	Direct		0.2732		Direct		0.4780
PB	Indirect	CE	0.0552	PB	Indirect	PC	-0.2525
		DE	0.0493			CE	0.0412
		EST	0.8788			DE	0.0132
		MS	-0.6286			EST	0.6072
		Total	0.6280			Total	0.8873
Determination coefficient			0.8292	Determination coefficient			0.9031
Residual effect			0.4131	Residual effect			0.3112

¹Production of marketable spikes (PC), length of marketable spikes (CE), diameter of marketable spikes (DE), stem diameter (DC), final stand (EST), shoot dry mass (MS), plant height (ALT), number of spike per plant (NEP) and crude protein (PB).

Table 4. Correlations and coefficients of canonical pairs estimated using evaluation of seven maize genotypes for groups of agronomic and bromatological variables in organic farming system. Alegre, IFES, 2016.

Variables	Coefficients of canonical pairs	
	1°	2°
Forage		
MS ¹	0.9460	0.3241
PB	0.9888	-0.1486
Bromatological		
PC	0.6349	-0.2069
CE	0.1607	0.7762
DE	0.1222	-0.1914
EST	0.8826	-0.3230
Canonical correlation (r)	0.96**	0.68 ^{ns}
χ^2	58.82	11.25
Degrees of freedom	8	3

¹production of marketable spikes (PC), length of marketable spikes (CE), diameter of marketable spikes (DE), stem diameter (DC), final stand (EST), shoot dry mass (MS), plant height (ALT), number of spike per plant (NEP) and crude protein (PB). *Significant using chi-square test, at 5% error probability.

direct, indirect and linear dependence effects among phytotechnical variables to produce baby corn in organic system is scarce, the authors recommend further studies using more genotypes, in other places, including more variables such as phenological, morphological and bromatological characteristics. Considering breeding programs, these results show that, if breeders are interested in selecting genotypes suitable to produce baby corn, larger plant stand and higher production of marketable spikes are indicative for higher production of forage and crude protein. It means that besides the production of baby corn, the producer obtains from the rest of the maize plant, the biomass with higher accumulation of

dry mass and high crude protein content which can be used in feeding small herds of ruminants.

REFERENCES

- ARAÚJO, VS; EKCLUND, CRB; COELHO, FB; CUNHA, RCV; LOMBARDI, CT; AGUIAR, RS. 2010. Teor de proteína bruta e produtividade da forragem de milho utilizando resíduos da cultura de minimilho em sistema de plantio direto. *Revista Brasileira de Milho e Sorgo* 9: 266-276.
- COIMBRA, JLM; BENIN, G; VIEIRA, EA; OLIVEIRA, AC; CARVALHO, FIF; GUIDOLIN, AF; SOARES, AP. 2005. Consequências da multicolinearidade sobre a análise de trilha em canola. *Ciência Rural* 35: 347-352.
- CORRÊA, AL; ABOUD, ACS; GUERRA, JGM; AGUIAR, LA; RIBEIRO, RLD. 2014. Adubação verde com crotalaria consorciada ao minimilho antecedendo a couve-folha sob manejo orgânico. *Ceres* 61: 956-963.
- CRUZ, CD. 2013. GENES: a software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum* 35: 271-276.
- CRUZ, CD; REGAZZI, AJ; CARNEIRO, PCS. 2012. *Modelos biométricos aplicados ao melhoramento genético*. Viçosa: UFV. 514p.
- EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA. 2013. Centro Nacional de Pesquisa do Solo. *Sistema brasileiro de classificação de solos*. 3. ed. Rio de Janeiro: Embrapa Solos. 335p.
- FALCONER, DS. 1987. *Introduction to quantitative genetics*. New York: Longman. 489p.
- FERREIRA, A; CRUZ, CD; VASCONCELOS, ES; NASCIMENTO, M; RIBEIRO, MF; SILVA, MF. 2008. Utilização de bootstrap não-paramétrico para avaliação de correlações fenotípicas, genotípicas e ambientais. *Acta Scientiarum* 30: 647-663.
- HALLAUER, AR; CARENA, MJ; MIRANDA FILHO, JB. 2010. *Quantitative Genetics in Maize Breeding*. New York: Springer. 663p.
- LIMA, JSS; SILVA, AS; OLIVEIRA, RB; CECÍLIO, RA; XAVIER, AC. 2008. Variabilidade temporal da precipitação mensal em Alegre-ES. *Revista Ciências Agronômicas* 39: 327-332.
- SANTOS, RF; INOUE, TT; SCAPIM, CA; CLOVIS, LR; MOTERLE, LM; SARAIVA, FCS. 2014. Produtividade do minimilho em função das adubações nitrogenadas e potássica. *Ceres* 61: 121-129.
- SILVA, FL; PEDROZO, CA; BARBOSA, MHP; RESENDE, MDV; PETERNELLI, LA; COSTA, PMA; VIEIRA, MS. 2009. Análise de trilha para os 394 componentes de produção de cana-de-açúcar via blup. *Ceres* 56: 308-314.
- SILVA, PSL; ARAÚJO JÚNIOR, BB; OLIVEIRA, VR; PONTES, FST; OLIVEIRA, OF. 2013. Effects of nitrogen application on corn yield after harvesting the apical ear as baby corn. *Horticultura Brasileira* 31: 419-425.
- VENCOVSKY, R; BARRIGA, P. 1992. *Genética biométrica no fitomelhoramento*. Ribeirão Preto: Sociedade Brasileira de Genética. 496p.