***Original Research Article***

# Association Among Agro-morphological Traits by Correlations and Path in Selection of Maize Genotypes

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## ABSTRACT

In the State of Espírito Santo (Brazil), family farmers have grown a number of maize varieties for decades, consisting of open-pollinated populations with valuable importance for the livelihood of smallholder farmers. The study aimed to analyze the cause and effect of associations between agro-morphological traits for increasing yields in maize populations cultivated. A total of 16 maize accessions of in vivo conservation works in eight different locations were evaluated, in a randomized complete block design with three replicates, totaling 48 experimental units. Genetic parameters, genotypic, phenotypic, and environmental correlation were estimated, and a path analysis was conducted. In general, accessions presented enough genetic variability, showing significant differences for all traits analyzed statistically ($P \leq 0.05$). The first cob insertion height with plant height and final plant stand variables presented heritability ($h^2$) higher than 80%, suggesting that superior genotypes could be determined. Highest estimates of phenotypic correlations ($r_p$) were found between the first cob insertion height with plant height and total number of cobs with number of cobs per plant (0.85). For estimates of genotypic correlations ($r_g$), the highest were between (i) the first cob insertion height and plant height; (ii) number of grains per row and number of cobs per plant; (iii) total number of cobs and final plant stand. Maize final plant stand and one thousand seed weight were observed to be traits that could be determinant in grain yield increase.

**Keywords**: *Zea mays* L., heritability, genetic parameter, open-pollination, in vivo germplasm, simultaneous selection.

## 1. INTRODUCTION

Maize (*Zea mays* L.) is one of the most grown cereals worldwide, for its high genetic diversity and wide adaptability [1]. Such a fact, associated with its nutritional characteristics, makes maize also one of the cereals of commercial importance in different countries [2]. Brazil is the third largest maize producer, meaning that the estimated national production for the first 2018/19 harvest is 27.4 million tons and 63.7 million tons for the second one, with a mean yield of 5.2 t ha$^{-1}$ in the last harvest [3].

In the State of Espírito Santo, family farmers have grown a number of maize varieties for decades, consisting of open-pollinated populations with valuable importance for the livelihood of smallholder farmers. Estimated total contribution for the 2019 harvest is 38.0 thousand t, with yield (approximately 2.8 t ha$^{-1}$) being one of the lowest in the country [3].

Open-pollinated populations present lower yield than that of cultivars due to their wide genetic basis [4]; [5]. While such variability does not ensure high yield in the short term, it represents a source of alleles favorable for genetic response to adverse biotic and abiotic factors, conferring greater long-term yield stability to maize populations [6-8]. This is a knowledge that needs to be considered so that the conservation of germplasm of maize could be increasingly promoted [9].

With the purpose of exploring favorable alleles in these populations to obtain higher yield values, the study of agronomic traits has been of paramount importance in plant breeding, due to the possibility of identifying variability in germplasm and, especially, the chance to select superior accessions for morpho-agronomic traits of interest [10-11]. In this regard, the association of knowledge on the correlations between agronomic traits allows the breeder to design strategies that ensure a higher probability of obtaining superior materials [12].

Correlation studies between traits can be conducted through simple correlations, combined with study of genetic parameters involved, given that correlations between two traits can be of phenotypic, genotypic or environmental nature, in which only genotypic correlations were associated with high heritability [13]. Simple correlations, despite being useful, do not allow conclusions to be drawn about cause and effect relationships between them, i.e. they do not comprise the direct and indirect effects of traits on a basic variable. As an alternative, by means of a path analysis, it is possible to analyze these relationships between the variables, according to the Wright method [14].

In the State of Espírito Santo (Brazil), both existing agronomic institutes (Ifes and Incaper) have been working on studies with maize populations grown in the State, gathering relevant germplasm and working on breeding strategies so as to increase grain yield [15]; [16]. As such, studying correlations between agronomic traits in these maize populations will contribute to the optimization of the strategies used by breeders.

The purpose of this study was to analyze the cause and effect associations of agronomic traits for increasing yields in maize populations grown in Espírito Santo.

## 2. MATERIAL AND METHODS

The experiment was conducted in the Federal Institute of Education, Science and Technology of Alegre in 2017. According to the Köppen international classification, the climate of the region is tropical wet and hot with, one the one hand, a cold and dry winter, and on the other hand, a hot and rainy summer. The mean temperature in the region is 23.1ºC, and the mean annual precipitation is 1,341 mm [17].

In the 2017/2018 harvest season, 16 field maize genotypes from conservation work were evaluated in eight different municipalities in the State of Espírito Santo (Table 1). All accessions obtained are described as open-pollinated populations and have been cultivated for some years by smallholder farmers in their respective locations.

Table 1 - Maize accessions (genotypes) evaluated in accordance with agronomic traits, in Alegre (Brazil), and their locations of origin.

| Acessions | GEBs | Origin |
|---|---|---|
| Aliança | - | Muqui-ES |
| Asa Branca | IFES Itapina | Itapina-Colatina-ES |
| Caiano | - | Linhares-ES |
| Caipira | - | Linhares-ES |
| Celina | - | Celina - Alegre-ES |
| BRS Cipotânea | IFES Itapina-ES | Itapina-Colatina-ES |
| BRS Diamantina | IFES Itapina-ES | Itapina-Colatina-ES |
| Emcapa 201 | INCAPER | Viana-ES |
| ES001 | IFES Itapina | Itapina-Colatina-ES |
| Fortaleza | - | Muqui-ES |
| Incaper Capixaba 203 | INCAPER | Viana-ES |
| MA008 | IFES Itapina-ES | Itapina-Colatina-ES |
| Palha Roxa | IFES Alegre-ES | Iúna-ES |
| Palha Roxa | IFES Alegre-ES | Muniz Freire-ES |
| Palha Roxa | - | Venda Nova do Imigrante-ES |
| Sertanejo | IFES Itapina-ES | Itapina-Colatina-ES |

GEBs= Germplasm banks; IFES= Federal Institute of Espírito Santo; INCAPER= Institute of Technical Assistance and Rural Development.

In order to implement the evaluation test of the genotypes in the field, a randomized complete block design with sixteen genotypes (treatments) and three replicates was used according to the following statistical model: $X_{ij} = m + t_i + b_j + e_{ij}$ in which: m = represents the overall mean, $t_i$ = treatment effect (genotypes), $b_j$ = block effect, $e_{ij}$ = effect of the experimental error. The experiment comprised 48 experimental units, each of them being composed of three lines of 4.0 m in length with 1.0 m of inter-row spacing. The evaluation of agronomic traits was performed on 16 plants within the central line of the plot.

During sowing 15 seeds per linear meter were uniformly distributed in furrow. Twenty one days after sowing (DAS), thinning was performed to establish a population of 5 plants per linear meter of furrow, corresponding to a density of 50,000 plants ha$^{-1}$ (adapted to Corrêa *et al*., 2014). Standard maize cultivation practices were followed by pre-emergence herbicide application [18]. The maize grain was naturally dried on plant, without using any desiccant, until it reached 13% moisture content. Manual harvest occurred in February 2018.

Twelve different agronomic traits such as Plant height (HEI), first cob Insertion height (CIH) and Total number of cobs (TNC) were evaluated. HEI was measured from the base to the last flag leaf before tasselling and CIH from the base of the stem to the first cob. All traits under evaluation are descriptors established by Biodiversity International [19].

Aside from conventional treatments to control the fall armyworm (*Spodoptera frugiperda*), leaf sprays were carried out using the Dipel WP biological insecticide, made from *Bacillus thuringiensis*. The quantity used was of 500g ha$^{-1}$ and the applications were made with the aid of a manual knapsack sprayer with a 20 litre capacity. Mechanical weeding was used to control the weeds at 30 DAS.

For statistical analyses, the phenotypic ($r_p$), genotypic ($r_g$), and environmental ($r_e$) correlation analyses and linear regression analysis were performed. For correlations, the following expressions were applied: phenotypic correlations: $\mathrm{r_F} = \frac{\mathrm{MPG_{XY}}}{\sqrt{\mathrm{MSG_X\,MSG_Y}}}$; genotypic correlations: $\mathrm{r_G} = \frac{(\mathrm{MPG_{XY}} - \mathrm{PMR_{XY}})/\mathrm{r}}{\sqrt{\hat{\Phi}\mathrm{g_{(X)}}\hat{\Phi}\mathrm{g_{(Y)}}}} = \frac{\hat{\Phi}\mathrm{g_{(XY)}}}{\sqrt{\hat{\Phi}\mathrm{g_{(X)}}\hat{\Phi}\mathrm{g_{(Y)}}}}$, and environmental correlations: $\mathrm{r_p} = \frac{\mathrm{MPG_{XY}}}{\sqrt{\mathrm{MSR_X\,MSR_Y}}}$. in which, $\mathrm{MPG_x}$ = mean product between genotypes for traits X and Y; $\mathrm{MPR_{xy}}$ = mean product between residues for traits; $\mathrm{MSG_x}$ = mean square between genotypes for trait X; $\mathrm{MSG_y}$ = mean square between genotypes for trait Y; $\mathrm{MSR_x}$ = mean square between residues for trait X; $\mathrm{MSR_y}$ = mean square between residues for trait Y; $\hat{\Phi}\mathrm{g_{(XY)}}$ = genotypic covariance estimator; $\hat{\Phi}\mathrm{g_{(X)}}, \hat{\Phi}\mathrm{g_{(Y)}}$ = estimators of quadratic components associated with genotypic variabilities for traits X and Y, respectively.

The path analysis consisted of studying the direct and indirect effects of the above-mentioned explanatory independent variables (X) on grain yield, main dependent variable (Y). Considering Y to be a complex trait, resulting from the combined action of other traits, the following model can be defined:

$Y = \beta_{1X1} + \beta_{2X2} + \cdots \beta_{nXn} + \varepsilon$, in which: $X_1, X_2, \ldots, X_n$ are the explanatory variables, and Y is the main variable (or dependent variable). The direct and indirect effects of the explanatory variables are estimated on the main variable. Therefore, $r_{iy} = p_i + \sum_{j \neq 1}^{n} p_{ij}\, r_{ij}$ in which: correlation between the main variable (Y) and the i-th explanatory variable; $p_i$: direct effect of variable i on the main variable; and $p_j r_{ij}$: indirect effect of variable i by means of variable j on the main variable.

The significance of genotypic correlation coefficient and b1 of the regression were evaluated by the "t" test, and the bootstrap with 5000 simulations for phenotypic and environmental correlations was applied in accordance with Ferreira *et al* [20].

In order to check the co-linearity between traits, a multi co-linearity test was conducted, in line with Montgomery and Peck cited by Cruz *et al* [21]. Subsequently, it was carried out through a split of simple correlation coefficients into direct and indirect effects provided by the trail analysis. For all analyses, computational resources from Gene stat program were used [22].

## 3. RESULTS AND DISCUSSION

All evaluated traits acted in accordance with the assumption of normality of error distribution ($p = .05$) by the Lilliefors test and homogeneity of residual variances ($p = .05$) by the Bartllet test. These results have proved that, normally, the mathematical assumptions needed to conduct the analysis of variance and further studies were satisfied [23].

As a general rule, the genotypes presented enough genetic variability, showing a significant difference for all the traits under analysis, excluding the stem diameter of the plant, by the F test ($P=.05$) (Table 2). In this regard, Almeida *et al* [24] observed the variability of field maize, super sweet maize and teosinte maize populations, pointing out that the low plant genetic variability leads to lower genetic gain for breeding programs. Experimental coefficients of variation ($CV_e$%) showed magnitudes ranging from 5%, for stripped cob diameter, to 25.14%, for plant stem diameter. In turn, the genotypic coefficient variation ($CV_{gi}$%) varied from 0.0 to 22.5% for traits like plant stem diameter and yield, respectively. These values are basically explained by the variability of the genetic material used in the analysis. Research on other crops has shown that high variability among genotypes facilitated the selection process of superior material [25-28].

As reported by Falconer [29], heritability values ($h^2$) above 80% and variation index above unit 1.0 ensure satisfactory selection gains. For the insertion height of the first cob, plant height, and final plant stand, this situation was verified suggesting that, for these variables, superior genotypes can be obtained by means of simple selection methods, such as mass selection (Table 3).

Among 55 pairs of combinations for 12 variables evaluated, 13 had significant ($r_p$), 12 to 1 or 5% probability by the "t" test, and only one significant to 1% by the bootstrap method with 5000 simulations (Table 2). There was a positive and high variation from 0.50 to 0.85 for 12 pairs. ($r_g$) also presented 13 significant pairs, but 12 by the bootstrap method with 5000 simulations at 1 or 5% probability, and only one to 5% probability by the "t" test. For this one, there was a positive and high variation from 0.53 to 0.88 for 12 pairs. For environmental correlations ($r_e$), 23 combinations were significant using the bootstrap method with 5000 simulations at 1 or 5% probability, varying from 0.4 to 0.88 positive pairs (Table 3).

The highest estimate of ($r_p$ = 0.85) was noticed between the first cob insertion height and the total number of cobs with number of cobs per plant. Lowest correlations ($r_p$) were observed between stripped cob length with stripped cob diameter 0.50 and stripped cob length and mass of one thousand seeds 0.50, being significant estimates by the "t" test. These results corroborate the ones reported by Souza, *et al* [30], which indicate variable cob height as the most influential in yield variation and of greater relevance in indirect selection for yield. Number of rows of grains per cob and mass of one thousand seeds showed significant and high value, though negative (rp= -0.55). The higher the number of rows, the lower the conversion of photoassimilates into starch [31].

Among estimates of ($r_g$), the highest one was 0.88 between the first cob insertion height and plant height. Within positive estimates, the lowest one was found between the first cob insertion height and final plant stand, with 0.53. There was only one significant and high pair, although with a negative value (rg= -0.57) between number of rows of grains per cob and mass of one thousand grains. The genotype selection with a larger diameter and one thousand grain weight enables to obtain genotypes with a good yield [32]. Moreover, regarding ($r_e$), the highest estimate happened between total number of cobs and number of cobs per plant, with 0.88. Stripped cob length and stripped cob diameter 0.4 was the lowest positive and significant value. There was a significant and high pair, however, with a negative value between the number of grain rows per cob and one thousand seed weight (rg= -0.46), (Table 3).

The first cob insertion height indicated negative correlations ($r_g$) with stripped cob length of (-0.19), stripped cob diameter of (-0.32), and number of rows of grains per cob of (-0.54). Positive correlations were observed with number of grains per row 0.28, number of cobs per plant 0.47, one thousand seed weight 0.09 and yield 0.29, but still not significant in all cases (Table 3). In accordance with Cruz *et al* [21], a non-significant or low magnitude correlation coefficient does not suggest lack of relationship between two variables, but absence of a linear relationship between them.

Table 2. Estimates of genetic parameters for agro-morphological traits of 16 maize genotypes in Alegre, Brazil.

| SV | Mean squares | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | DF | IHC | HEI | PCD | SCL | SCD | NRC | NGR | TNC | FPS | NCP | MTS | YIE |
| Blocks | 2 | 0.01 | 0.00 | 0.59 | 1.49 | 2.26 | 0.36 | 19.20 | 134548.68 | 48868.35 | 0.01 | 1722.67 | 829.53 |
| Varieties | 15 | 0.10** | 0.15** | 13.15ns | 2.80* | 17.09** | 4.06** | 28.63* | 203435.78** | 93182.08** | 0.02** | 4422.62** | 4449.19** |
| Residue | 30 | 0.00 | 0.01 | 13.32 | 1.37 | 4.46 | 0.86 | 13.44 | 44870.97 | 14574.77 | 0.01 | 980.06 | 1075.33 |
| | Genetic parameters | | | | | | | | | | | | |
| $(\sigma^2_f)$ | | 0.03 | 0.05 | 4.38 | 0.93 | 5.69 | 1.35 | 9.54 | 67811.92 | 31060.69 | 0.00 | 1474.20 | 1483.06 |
| $(\sigma^2_e)$ | | 0.00 | 0.00 | 4.44 | 0.45 | 1.48 | 0.28 | 4.48 | 14956.99 | 4858.25 | 0.00 | 326.68 | 358.44 |
| $(\sigma^2_g)$ | | 0.03 | 0.04 | 0.0 | 0.47 | 4.20 | 1.06 | 5.06 | 52854.93 | 26202.43 | 0.00 | 1147.52 | 1124.62 |
| $(\hat{h}^2_g)$ | | 90.57 | 87.17 | 0.0 | 51.05 | 73.87 | 78.74 | 53.04 | 77.94 | 84.35 | 64.80 | 77.83 | 75.83 |
| $(CV_e\%)$ | | 9.30 | 6.11 | 25.14 | 7.50 | 5.03 | 7.41 | 11.42 | 16.00 | 7.59 | 12.35 | 11.14 | 22.01 |
| $(CV_{gi}\%)$ | | 16.66 | 9.20 | 0.0 | 4.42 | 4.88 | 8.24 | 7.00 | 17.37 | 10.17 | 9.67 | 12.05 | 22.51 |
| $(CV_{gi}/CV_e)$ | | 1.78 | 1.50 | 0.0 | 0.58 | 0.97 | 1.11 | 0.61 | 1.08 | 1.34 | 0.78 | 1.08 | 1.02 |
| $(r)$ | | 0.95 | 0.93 | 0.0 | 0.71 | 0.85 | 0.88 | 0.72 | 0.88 | 0.91 | 0.80 | 0.88 | 0.87 |
| Overall | | 1.05 | 2.30 | 14.51 | 15.61 | 41.98 | 12.54 | 32.10 | 41840.27 | 50289.35 | 0.82 | 281.01 | 4709.72 |

IHC - insertion height of the first cob; HEI – plant height; PCD - plant cob diameter; SCL - stripped cob length; SCD - stripped cob diameter; NRC - number of rows of grain per cob; NGR - number of grains per row; TNC – total number of cobs; FPS - final plant stand; NCP - number of cobs per plant; MTS - mass of one thousand seeds; YIE – yield.

Genotypic variance $(\sigma^2_g)$, residual variance $(\sigma^2_e)$, phenotypic variance $(\sigma^2_f)$, heritability $(\hat{h}^2_g)$, coefficient of genotypic variation $(CV_{gi}\%)$, coefficient of residual variation $(CV_e\%)$, coefficient of relative variation, considering $(CV_{gi}/CV_e)$, coefficient of correlation $(r)$ and mean. $^*$, $^{**}$ and ns = significant at 5 and 1% probability and non-significant, respectively.

The phenotypic and genotypic correlations between the number of rows of grains per cob and mass of one thousand seeds were predominantly significant and negative, however, of less than (-0.60) magnitude (Table 3). The larger number of rows in a cob tends to reduce the grain size, thereby influencing the seed weight in a negative way. Cob volume and grain volume were those that most contributors to increasing the mean cob weight in production components, for super sweet maize populations [10].

The simultaneous selection of traits, such as number of grains per cob and grain weight per cob, is a difficult task for plant breeders, considering that the genes on which these traits are conditioned, have often negative correlations in genotypes [33]. The significance between the stripped cob diameter and one thousand seed weight in the phenotypic and genotypic correlations, with values of 0.70 and 0.77, respectively, demonstrate that large cobs have a larger number of rows. Nevertheless, cob size is a relevant trait for a larger number of grains, contributing to a greater grain weight per cob.

The first cob insertion height showed positive phenotypic and genotypic correlation coefficients regarding maize yield, with 0.31 and 0.29 respectively (Table 3). As stated Lorentz *et al* [34], when the correlation coefficient is positive, but the direct effect is negative, or when the value is insignificant, indirect effects cause the correlation. The variable stripped cob diameter also showed positive values by means of phenotypic and genotypic correlations, of 0.42 and 0.36, respectively, in relation to yield.

Table 3. Phenotypic ($r_p$), genotypic ($r_g$), and environmental ($r_e$) correlations among 12 agro-morphological traits of 16 maize accessions in Alegre, Brazil.

| Variables | Correlation | HEI | SCL | SCD | NRC | NGR | NTE | TNC | NCP | MTS | YIE |
|---|---|---|---|---|---|---|---|---|---|---|---|
| IHC | ($r_p$) | 0.85** | -0.05 | -0.25 | -0.45 | 0.25 | 0.55+ | 0.51* | 0.41 | 0.09 | 0.31 |
| | ($r_g$) | 0.88++ | -0.19 | -0.32 | -0.54 | 0.28 | 0.58+ | 0.53+ | 0.47 | 0.09 | 0.29 |
| | ($r_e$) | 0.62++ | 0.33+ | 0.06 | 0.02 | 0.29+ | 0.39+ | 0.38+ | 0.28+ | 0.08 | 0.47++ |
| HEI | ($r_p$) | | 0.33 | -0.00 | -0.35 | 0.40 | 0.36 | 0.37 | 0.24 | 0.27 | 0.35 |
| | ($r_g$) | | 0.40 | -0.03 | -0.45 | 0.50 | 0.41 | 0.40 | 0.3 | 0.33 | 0.37 |
| | ($r_e$) | | 0.26 | 0.15 | 0.12 | 0.26 | 0.15 | 0.16 | 0.10 | 0.00 | 0.28+ |
| SCL | ($r_p$) | | | 0.50* | 0.11 | 0.33 | -0.09 | -0.15 | 0.01 | 0.50* | 0.32 |
| | ($r_g$) | | | 0.59 | 0.22 | -0.07 | -0.20 | -0.26 | -0.05 | 0.59 | 0.20 |
| | ($r_e$) | | | 0.4++ | -0.08 | 0.77++ | 0.09 | 0.06 | 0.11 | 0.39++ | 0.57++ |
| SCD | ($r_p$) | | | | 0.02 | 0.19 | -0.05 | 0.13 | -0.18 | 0.70** | 0.42 |
| | ($r_g$) | | | | -0.08 | 0.24 | -0.14 | 0.08 | -0.30 | 0.77++ | 0.36 |
| | ($r_e$) | | | | 0.40+ | 0.12 | 0.21 | 0.31 | 0.08 | 0.47++ | 0.61++ |
| NRC | ($r_p$) | | | | | -0.26 | -0.28 | -0.13 | -0.33 | -0.55* | -0.19 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | $(r_g)$ | -0.49 | -0.38 | -0.18 | -0.46 | -0.57* | -0.32 |
| | $(r_e)$ | 0.15 | 0.05 | 0.09 | 0.00 | -0.46++ | 0.25 |
| | $(r_p)$ | | 0.48 | 0.30 | 0.51* | 0.19 | 0.67** |
| NGR | $(r_g)$ | | 0.79+ | 0.5 | 0.88++ | 0.35 | 0.85+ |
| | $(r_e)$ | | -0.09 | -0.10 | -0.02 | -0.09 | 0.38+ |
| | $(r_p)$ | | | 0.84** | 0.85** | 0.04 | 0.81** |
| TNC | $(r_g)$ | | | 0.88++ | 0.86++ | 0.00 | 0.83++ |
| | $(r_e)$ | | | 0.68++ | 0.88++ | 0.18 | 0.74++ |
| | $(r_p)$ | | | | 0.44 | 0.09 | 0.74 |
| FPS | $(r_g)$ | | | | 0.51 | 0.06 | 0.78++ |
| | $(r_e)$ | | | | 0.26 | 0.23 | 0.58++ |
| | $(r_p)$ | | | | | 0.00 | 0.66** |
| NCP | $(r_g)$ | | | | | -0.02 | 0.69+ |
| | $(r_e)$ | | | | | 0.09 | 0.61++ |
| | $(r_p)$ | | | | | | 0.43 |
| MTS | $(r_g)$ | | | | | | 0.43 |
| | $(r_e)$ | | | | | | 0.42++ |

HEI – plant height; SCL - stripped cob length; SCD - stripped cob diameter; NRC - number of rows of grain per cob; NGR - number of grains per row; TNC – total number of cobs; FPS - final plant stand; NCP - number of cobs per plant; MTS - one thousand seed weight; YIE – yield. $^{*}$, $^{**}$ and ns = significant at 5 and 1% probability and no significant, respectively, by the t test. $^{+}$, $^{++}$ = significant at 1 and 5%, respectively, by the bootstrap method with 5000 simulations.

Before performing the path analysis, a multi co-linearity analysis was conducted among the variables [21]. Genotypic correlation matrices were submitted to the diagnosis of multi co-linearity on the basis of the number of conditions. The elimination of the variables stem diameter of the plant and number of cobs per plant was required in view of the severe multi co-linearity, 107,826.62. For the remaining variables, insertion height of the first cob; plant height; stripped cob length; stripped cob diameter; number of rows of grains per cob; number of grains per row; total number of cobs; final plant stand; one thousand seed weight; and yield, the number of conditions was 742.19, which enabled classifying them from moderate to strong, not affecting the path analysis statistics. It was decided to use, in this study, only the variables with no collinearity, given that, in strong or severe multi co-linearity, the variances associated with path coefficients are likely to reach high values [12].

Table 4 depicts the direct and indirect effects of the explanatory variables using grain yield as the main variable. The coefficient of determination ($R^2$) in the path analysis model displayed a value of 0.92 and residual effects lower than 0.014. As such, the model showed the cause and effect relationship between the explanatory variables and grain yield. The satisfactory use of path coefficients is directly linked to the composition of causal diagrams, which should be listed to the most important variables in the expression of the main variable [35]. The diagram applied enabled to explain 92% ($R^2$) of the variation in grain yield (Table 4).

In accordance with Souza *et al* [30], in five hybrid maize lines, the weight of 100 grains was the variable yield, which generated the greatest direct effect on grain yield, being the most indicated for indirect selection regarding yield. Greater direct effect and greater total correlation on grain yield point a great contribution to increase yield [36]. The highest values of direct effects on grain yield were seen for one thousand seed weight, with 0.81, followed by the final plant stand, with 0.58, and total number of cobs, with 0.43, while the stripped cob diameter displayed negative direct effect and high magnitude, with (-0.52), and positive phenotypic correlation of mean magnitude, 0.42, with the indirect effect being considered on the mass of one thousand seeds, 0.63, in the conditions in which the experiment was carried out (Table 4).

The direct effect between the variable insertion height of the first cob and yield was negative, (-0.64), while the phenotypic correlation was positive and with a mean magnitude of 0.31, which should take into account the indirect effect in the final plant stand 0.31 to benefit from the gain in these two traits (Table 4). As stated by Nascimento *et al* [23], the final plant stand is critical to increase the production of dry mass and commercial cobs, both directly and indirectly. This is not the case in Kleinpaul *et al* [37], who reported a positive value for the trait insertion height of the cobs in the harvest with the yield, even though they had worked with precocious cycle maize cultivars. In this case, a direct selection on the causal factor effect may not be efficient to improve the trait yield. Also in agreement with Kleinpaul *et al* [37], the plant height in the harvest can be considered for indirect selection, because of the positive linear relationship with yield.

The low correlation observed between the insertion height of the first cob and the stripped cob diameter with the grain yield was caused by the negative indirect effects via the stripped cob length, number of rows of grains per cob, plant height, and total number of cobs, with very low values similar to the ones reported by [23]. Conversely, when a direct effect displays positive results, indirect effects are responsible for the lack of correlation [38]. In this way, for the indirect selection of more productive genotypes, the trait yield should be related, with positive effects, through the desired trait. As mentioned by Nemati *et al* [11], the negative correlation between different phenotypic traits is assigned to different genes that are controlling these traits such is the existing negative correlation between grains per cob and grain thickness.

For indirect effects with negative values, the simultaneous selection in an indirect way leads to a low efficiency, [36]. In contrast, the positive values for the direct effects of primary components on grain yield are good predictors of genetic correlation according [39] and [40].

The indirect selection for increasing of the traits number of grains and number of rows is efficient in increasing the grain weight [33]. Indirect selection may result in faster genetic progress than direct selection of the desired trait, [41] In an experiment with open-pollinated varieties, Balbinot Jr *et al* [31] achieved a greater correlation between the number of grains per row and yield 0.586.

Table 4. Direct and indirect effects of agro-morphological traits of 16 maize varieties in Alegre, Brazil.

| Variable | Effect | Via | Coefficients |
|---|---|---|---|
| IHC | Direct | YIE | -0.6416 |
| | Indirect | HEI | 0.1744 |
| | | SCL | -0.0072 |
| | | SCD | 0.1686 |
| | | NRC | -0.1190 |
| | | NGR | 0.0688 |
| | | TNC | 0.2558 |
| | | FPS | 0.3150 |
| | | MTS | 0.0796 |
| | Total | | 0.2946 |
| HEI | Direct | YIE | 0.1979 |
| | | AIHC | -0.5656 |
| | | SCL | 0.0153 |
| | | SCD | 0.0202 |
| | | NRC | -0.0999 |
| | | NGR | 0.1227 |
| | | TNC | 0.1791 |
| | | FPS | 0.2390 |
| | | MTS | 0.2696 |
| | Total | | 0.3786 |
| SCL | Direct | YIE | 0.0382 |
| | Indirect | IHC | 0.1224 |
| | | HEI | 0.0796 |
| | | SCD | -0.3068 |

| | | | |
|---|---|---|---|
| | | NRC | 0.0489 |
| | | NGR | -0.0174 |
| | | TNC | -0.0885 |
| | | FPS | -0.1573 |
| | | MTS | 0.4822 |
| | Total | | 0.2015 |
| SCD | Direct | YIE | -0.5173 |
| | Indirect | IHC | 0.2091 |
| | | HEI | -0.0077 |
| | | SCL | 0.0226 |
| | | NRC | -0.0187 |
| | | NGR | 0.0588 |
| | | TNC | -0.0641 |
| | | FPS | 0.0508 |
| | | MTS | 0.6266 |
| | Total | | 0.3602 |
| NCR | Direct | YIE | 0.2202 |
| | Indirect | IHC | 0.3468 |
| | | HEI | -0.0898 |
| | | SCL | 0.0084 |
| | | SCD | 0.0440 |
| | | NGR | -0.1189 |
| | | NTE | -0.1659 |
| | | FPS | -0.1090 |
| | | MTS | -0.4641 |
| | Total | | -0.3283 |
| NGR | Direct | YIE | 0.2417 |
| | Indirect | IHC | -0.1827 |
| | | HEI | 0.1004 |
| | | SCL | -0.0027 |
| | | SCD | -0.1260 |
| | | NRC | -0.1083 |
| | | TNC | 0.3478 |
| | | FPS | 0.2943 |
| | | MTS | 0.2894 |
| | Total | | 0.8539 |
| TNC | Direct | YIE | 0.4359 |
| | Indirect | IHC | -0.3765 |
| | | HEI | 0.0813 |
| | | SCL | -0.0077 |
| | | SCD | 0.0761 |
| | | NRC | -0.0838 |

|  |  |  |  |
|---|---|---|---|
|  |  | NGR | 0.1928 |
|  |  | FPS | 0.5153 |
|  |  | MTS | 0.0046 |
|  | Total |  | 0.838 |
| FPS | Direct | YIE | 0.5850 |
|  | Indirect | IHC | -0.3455 |
|  |  | HEI | 0.0808 |
|  |  | SCL | -0.0102 |
|  |  | SCD | -0.0449 |
|  |  | NRC | -0.0410 |
|  |  | NGR | 0.1216 |
|  |  | TNC | 0.3840 |
|  |  | MTS | 0.0543 |
|  | Total |  | 0.7842 |
| MTS | Direct | YIE | 0.8079 |
|  | Indirect | IHC | -0.0632 |
|  |  | HEI | 0.0660 |
|  |  | SCL | 0.0228 |
|  |  | SCD | -0.4012 |
|  |  | NRC | -0.1265 |
|  |  | NGR | 0.0865 |
|  |  | TNC | 0.0024 |
|  |  | FPS | 0.0393 |
|  | Total |  | 0.4342 |
| Coefficient of Determination |  |  | 0.9632 |
| Effect of residual variable |  |  | 0.0143 |

IHC - insertion height of the first cob; HEI – plant height; SCL - stripped cob length; SCD - stripped cob diameter; ; NRC - number of rows of grain per cob; NGR - number of grains per row; TNC – total number of cobs; FPS – final plant stand; MTS - mass of one thousand seeds; YIE – yield.

## 4. CONCLUSION

The genetic variability identified in local cultivars allowed the selection of maize genotypes to be used in breeding programs. Agro-morphological traits evaluated showed genotypic correlations of greater magnitude than the phenotypic ones, indicating genetic different effects of additive, epistatic or dominance nature. These effects exceeded variations of environmental origin.

A gain of high magnitude on traits like stripped cob diameter which presented an indirect effect with one thousand seed weight as well as the indirect effect of first cob insertion height in final plant height, should be exploited. The final plant stand in maize and one thousand seed weight were determinant in grain yield increase.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist in this study.

## AUTHORS' CONTRIBUTIONS

"Author Richardson Sales Rocha' designed the study and performed the statistical analysis, 'Author Maxwel Rodrigues Nascimento'' managed the analyses of the study, 'Author José Tiago Barroso Chagas' and "Author Rafael Nunes De Almeida" managed the literature searches, "Author Paulo Ricardo Dos Santos" and "Author Camila Queiroz Da Silva Sanfim De Sant'anna" supporting at the experimental design and traits evaluations, "Author Derivaldo Pureza Da Cruz" and "Author Kleyton Danilo Da Silva Costa" suggests path analysis, "Author Geraldo De Amaral Gravina" and "Author Rogério Figueiredo Daher" review the manuscript and suggests some alterations. All authors read and approved the final manuscript".

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