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ABSTRACT

in Maize Genotype Selection

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. As such, this study intended to analyze the cause and effect associations between agronomic traits for increasing yield in maize populations cultivated in Espírito Santo. Randomized block design with three replicates. The experiment was conducted in the Instituto Federal de Educação, Ciência e Tecnologia do Espírito Santo campus of Alegre, between October 2017 and October 2018. A total of 16 accessions of field maize from conservation works in eight different municipalities were evaluated, in a randomized 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, the genotypes present genetic variability, showing a significant difference between the genotypes for all the traits analyzed by the F test (P=.05). Insertion height of the first cob, plant height, and final plant stand variables presented heritability (h2) higher than 80%, suggesting that superior genotypes can be achieved. The highest estimate of phenotypic correlation (rp) was found between the insertion height of the first cob with plant height 0.85 and total number of cobs with number of cobs per plant 0.85. For the estimates of genotypic correlation (rg), the highest was of 0.88 between the insertion height of the first cob and the plant height; number of grains per row and number of cobs per plant; total number of cobs and final plant stand. The final plant stand and the mass of one thousand seeds are determinants to directly increase the grain yield.

Association Among Traits by Correlations and Path

Original Research Article

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Keywords: Zea mays L., heritability, genetic parameters, 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];[7];[8]. This is a knowledge that needs to be considered so that the conservation of germplasm of these maize populations is increasingly promoted [9].

With the purpose of exploring favorable alleles in these populations to obtain 34 higher yield values, the study of agronomic traits has been of paramount 35 36 importance in plant breeding, due to the possibility of identifying variability in germplasm and, especially, the chance to select superior accessions for 37 morpho-agronomic traits of interest [10];[11]. In this regard, the association of 38 knowledge on the correlations between agronomic traits allows the breeder 39 to design strategies that ensure a higher probability of obtaining superior 40 materials [12]. 41

Correlation studies between traits can be conducted through simple 42 correlations, combined with the study of the genetic parameters involved, 43 given that the correlations between two traits can be of phenotypic, 44 genotypic, or environmental nature, in which only genotypic correlations 45 associate heritability [13]. Simple correlations, despite being useful, do not 46 allow conclusions to be drawn about cause and effect relationships between 47 them, i.e. they do not comprise the direct and indirect effects of traits on a 48 49 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 50 method [14]. 51

In the state of Espírito Santo, both the Instituto Federal do Espírito Santo 52 (Ifes) and the Instituto Capixaba de Pesquisa e Extensão Rural (Incaper) 53 have been working on studies with maize populations grown in the state, 54 gathering germplasm of these populations and working on breeding 55 strategies so as to increase grain yield in the state [15];[16]. As such, 56 studying correlations between agronomic traits in these maize populations 57 will contribute to the optimization of the strategies used by breeders in the 58 59 state.

In this manner, the purpose of this study was to analyze the cause and effect associations between agronomic traits for increasing yield in populations of

62 maize grown in Espírito Santo.

63 2. MATERIAL AND METHODS

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The experiment was conducted in the Instituto Federal de Educação, Ciência e Tecnologia do Espírito Santo campus of Alegre in 2017. According to the Köppen international classification, the climate of the region is of "Cwa" type, i.e. tropical hot humid, with a cold and dry winter and a hot and rainy summer. The mean temperature of the region is 23.1° C, and the mean total 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 openpollinated populations and have been cultivated for some years by smallholder farmers in their respective locations.

Table 1 - Accessions (populations) of maize evaluated in accordance with
 agronomic traits, in the municipality of Alegre, Espírito Santos state, Brazil,
 and respective municipalities where they were conservated.

Acessions	GEBs	Origin		
Aliança	-	Muqui-ES		
Asa Branca	IFES Itapina	Itapina-Colatina-ES		
Caiano	$\langle \rangle \vee$	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	lúna-ES		
Palha Roxa	IFES Alegre-ES	Muniz Freire-ES		
Palha Roxa	-	Venda Nova do Imigrante-ES		
Sertanejo	IFES Itapina-ES	Itapina-Colatina-ES		

79 GEBs= Germplasm banks; IFES= Instituto Federal do Espírito Santo;

80 INCAPER= Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão

81 Rural.

In order to implement the evaluation test of the genotypes in the field, it was
 opted for the randomized block design with three replicates, according to the
 following statistical model:

85 X_ij=m+t_i+b_j+e_ij

in which: m = represents the overall mean, ti = treatment effect (genotypes),
bj = block effect, eij = effect of the experimental error.

The experiment comprised 48 experimental units, which were composed of three 4.0 m long lines spaced at 1.00 m between them. The evaluation of agronomic traits was performed on 16 plants within the central line of the plot.

During planting,/sowing 15 seeds per linear meter were uniformly distributed 92 in furrow. At 21 days after sowing (DAS), thinning was performed to establish 93 a population of 5 plants per linear meter of furrow, corresponding to a density 94 of 50,000 plants ha-1 (adapted to Corrêa et al., 2014). The phytosanitary 95 treatments followed the technical recommendations for the cultivation, [18]. 96 97 The maize was naturally dried in the plant, without using desiccants, until it reached the water content of 13%. In February 2018, the harvest was done 98 99 manually.

The agronomic traits evaluated were as follows: I - Plant height (HEI) -100 measured from the base of the stem to the apex of the tassel; II – Insertion 101 height of the first cob (IHC) – measured from the base of the stem to the first 102 cob; III – Total number of cobs (TNC); IV – final plant stand (FPS); V – Plant 103 cob diameter (PCD): VI - Stripped cob length (SCL) - measured from the 104 base to the apex of the cobs; VII – Stripped cob diameter (SCD) – measured 105 in the middle of each cob; VIII - Number of rows of grain per cob (NRC); IX -106 Number of grains per row (NGR); X – Mass of one thousand seeds (MTS); XI 107 - Yield (YIE); XII - Number of cobs per plant (NCP). All the traits under 108 evaluation are descriptors established by Biodiversity International [19] 109

Aside from the 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-liter capacity. Mechanical weeding controlled the weeds at 30 DAS.

For statistical analyses, the phenotypic (rp), genotypic (rg), and environmental (re) correlation analyses and linear regression analysis were performed. For correlations, the following expressions were applied: phenotypic correlations:

120
$$r_F = \frac{MPE_{XY}}{\sqrt{MSG_K MSG_F}};$$

121 genotypic correlations:
122 $r_G = \frac{(MPE_{XY} - PMR_{XY})/r}{\sqrt{\delta g_{d(X)} \delta g_{d(Y)}}} = \frac{\delta g_{(XY)}}{\sqrt{\delta g_{d(X)} \delta g_{d(Y)}}},$
123 and environmental correlations:
124 $r_P = \frac{MPE_{XY}}{\sqrt{MSR_K MSR_Y}}.$
125 in which, MPG_X = mean product between genotypes for traits X and Y;
126 MPG_{XY} = mean square between genotypes for trait X;
127 MSG_X = mean square between genotypes for trait X;
128 MSG_Y = mean square between genotypes for trait X;
129 MSG_X = mean square between residues for trait Y;
130 MSR_X = mean square between residues for trait Y;
131 MSR_X = mean square between residues for trait Y;
132 $\hat{\Phi}_{g(X)}, \hat{\Phi}_{g(Y)}$ = estimators of quadratic components associated with genotypic
133 $variables$ for traits X and Y, respectively.
134
135 The path analysis consisted of studying the direct and indirect effects of the
136 above-mentioned explanatory independent variables (X) on grain yield, main
138 dependent variable (Y). Considering Y to be a complex trait, resulting from
149 the combined action of other traits, the following model can be defined:
141 Y = $\beta_{1X1} + \beta_{2X2} + \cdots \beta_{nXn} + \varepsilon,$
142 in which: $X_{1,X2}, \dots, X_n$ are the explanatory variables,
143 and Y is the main variable (or dependent variables).
144
145 The direct and indirect effects of the explanatory variables are estimated on
146 the main variable. Therefore, $r_{iy} = p_i + \sum_{j=1}^{n} p_{ij} r_{ij}$ in which: correlation
147 between the main variable (Y) and the i-th explanatory variables i_p is j_p direct
148 effect of variable *i* on the main variable.
149 The significance of the genotypic correlation coefficient and the b1 of the
150 regression were evaluated by the "t" test, and the bootstrap with 5000
151 simulations for phenotypic and environmental correlations was applied in
152 accordance with [20].
153
154 In order to verify the collinearity between the traits, a multicollinearity test
155 was conducted, in line with Montgomery an

160 **3. RESULTS AND DISCUSSION**

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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 prove that, normally, the mathematical assumptions needed to conduct the analysis of variance and further studies were satisfied [23].

167 As a general rule, the genotypes exhibit genetic variability, showing a significant difference for all the traits under analysis, excluding the stem 168 diameter of the plant, by the F test (P=.05) (Table 2). In this regard, [24] 169 observed the variability of field maize, super sweet maize and teosinte maize 170 171 populations, pointing out that the low plant genetic variability leads to lower 172 genetic gain for breeding programs. The experimental coefficients of variation (CV_o%) showed magnitudes ranging from 5.03, for stripped cob 173 diameter, to 25.14%, for plant stem diameter. In turn, the coefficient of 174 genetic variation (CV_{ai} %) varied from 0.0 to 22.51 for the traits plant stem 175 diameter and yield, respectively. These values are basically explained by the 176 177 variability of the genetic material used in the analysis. Research with other 178 cultures shows that high variability of genotypes makes the selection process of superior material easier [25]; [26]; [27]; [28]. 179

As reported by [29], heritability values (h2) 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).

The estimates of phenotypic (rp), genotypic (rg), and environmental (ra) 185 186 correlation are depicted in (Table 2). Hence, among the 55 pairs of combinations for the 12 variables evaluated, 13 had significant (rp), 12 to 1 187 188 or 5% probability by the "t" test, and only one significant to 1% by the bootstrap method with 5000 simulations. There was a positive and high 189 variation from 0.50 to 0.85 for 12 pairs. (rg) also presented 13 significant 190 pairs, but 12 by the bootstrap method with 5000 simulations at 1 or 5% 191 probability, and only one to 5% probability by the "t" test. For this one, there 192 was a positive and high variation from 0.53 to 0.88 for 12 pairs. For (re), 23 193 combinations were significant using the bootstrap method with 5000 194 195 simulations at 1 or 5% probability, varying from 0.4 to 0.88 positive pairs 196 (Table 3).

The highest estimate of (rp) was noticed between the insertion height of the first cob, with plant height 0.85, and the total number of cobs with number of cobs per plant 0.85. The lowest correlations (rp) were 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 seen by [30], which indicate the 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 -0.55. The higher the number of rows, the lower the conversion of photoassimilates into starch [31].

208 Among the estimates of (rg), the highest one was 0.88 between the insertion height of the first cob and the plant height; number of grains per row and 209 number of cobs per plant; total number of cobs; and final plant stand. Also 210 among the positive estimates, the lowest one was found between the 211 insertion height of the first cob and the final plant stand, with 0.53. There was 212 only one significant and high pair, although with a negative value -0.57 213 214 between number of rows of grains per cob and mass of one thousand grains. The genotype selection with a larger diameter and mass of one thousand 215 grains enables obtaining genotypes with a good yield [32]. Moreover, for (re), 216 the highest estimate happened between total number of cobs and number of 217 cobs per plant, with 0.88. Stripped cob length and stripped cob diameter 0.4 218 was the lowest positive and significant value. There was a significant and 219 high pair, however with a negative value between the number of rows of 220 grains per cob and mass of one thousand seeds -0.46, (Table 3). 221

The insertion height of the first cob indicated negative correlations (rg) with 222 stripped cob length of -0.19, stripped cob diameter of -0.32, and number of 223 rows of grains per cob of -0.54; and positive correlations with number of 224 225 grains per row of 0.28, number of cobs per plant 0.47, mass of one thousand seeds of 0.09, and yield of 0.29, still not significant in all cases (Table 3). In 226 accordance with [21] a non-significant or low magnitude correlation 227 coefficient does not suggest lack of relationship between two variables, but 228 absence of a linear relationship between them. 229

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Table 2. Estimates of genetic parameters for phytotechnical traits of 16 maize genotypes in the municipality of

Alegre, Espirito Santo state, Brazil, 2017

							N	lean squ	ares				
SV	D F	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* *	13.15n s	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
						G	enetic pa	rameters	;				
($\sigma_{\rm f}^2$)		0.03	0.05	4.38	0.93	5.69	1.35	9.54	67811.92	31060.69	0.00	1474.20	1483.06
(σ_{e}^{2})		0.00	0.00	4.44	0.45	1.48	0.28	4.48	14956.99	4858.25	0.00	326.68	358.44
(σ_{g}^{2})		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}_{g}^{2})		90.57	87.17	0.0	51.0 5	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 _{qi} %)		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 _{q/} /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
(<i>r</i>)		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	15.6 1	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.

237 Genotypic variance (σ_q^2), residual variance (σ_e^2), phenotypic variance (σ_f^2), heritability (\hat{h}_q^2), 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.

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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 are those that most contribute 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 248 grain weight per cob, is a difficult task for plant breeders, considering that the 249 genes on which these traits are conditioned, have often negative correlations 250 in genotypes [33]. The significance between the stripped cob diameter and 251 the mass of one thousand seeds in the phenotypic and genotypic 252 correlations, with values of 0.70 and 0.77, respectively, demonstrate that 253 254 large cobs have a larger number of rows; nevertheless, the cob size is a relevant trait for a larger number of grains, contributing to a greater grain 255 weight per cobs. 256

The variable insertion height of the first cob showed a positive phenotypic and genotypic correlation coefficient with regard to yield, with 0.31 and 0.29 respectively (Table 3). As stated by [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.

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Table 3. Phenotypic (r_p) , genotypic (r_g) , and environmental (r_e) correlations among 12 phytotechnical traits of 16 maize accessions in the municipality of Alegre, Espirito Santo state, Brazil, 2017

Variable s	Correlatio n	HEI	SCL	SCD	NRC	NGR	NTE	TNC	NCP	MTS	YIE
	(r _p)	0.85**	-0.05	-0.25	-0.45	0.25	0.55 +	0.51*	0.41	0.09	0.31
IHC	(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+ +
	(r _p)		0.33	-0.00	-0.35	0.40	0.36	0.37	0.24	0.27	0.35
HEI	(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+
	(r _p)			0.50*	0.11	0.33	-0.09	-0.15	0.01	0.50*	0.32
SCL	(r _g)			0.59	0.22	-0.07	-0.20	-0.26	-0.05	0.59	0.20
	(r _e)			0.4+ +	-0.08	+	0.09	0.06	0.11	0.39+ + 0.70**	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	+	0.00

	(r.)		0.40					0.47+	0.61+
	(re)		+	0.12	0.21	0.31	0.08	+ 0.55*	+
	(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
NRC				0.40	0.00	0.10	0.40	-	0.25
	(r _e)			0.45	0.05	0.00	0.00	0.46+	
	(-)			0.15	0.05	0.09	0.00	+ 0.19	0.67**
	(ľ _p)				0.48	0.30	0.51*	0.05	0.05
NGR	(r _g)				0.79	0.5	0.88+ +	0.35	0.85+
	(r.)					0.40		-0.09	0.38+
	(.e)				-0.09	-0.10	-0.02	0.04	0.81**
	(r _p)					0.84**	0.85**	0.01	0.01
TNC	(r _g)					0.88+ +	0.86+	0.00	0.83+
	(\mathbf{r})					0.68+	0.88+	0.18	0.74+
	(I _e)					+	+	0.00	+
	(r _p)						0.44	0.09	0.74
FPS	(r _a)							0.06	0.78+
	(-9)						0.51	0.23	+ 0 58+
	(r _e)						0.26	0.20	+
	(r _p)							0.00	0.66**
NCP	(r.)							-0.02	0.69+
NOI	('g)							0.09	0.61+
	(r _e)							0.00	+
	(r _p)								0.43
MTO	(r)								0.43
1112	(Ig)								0.40
	(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 - mass of one thousand seeds; YIE – yield. *, ** and ns = significative at 5 and 1% probability and no significative, respectively, by the t test. *, ** = significative at 1 and 5%, respectively, by the bootstrap method with 5000 simulations.

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276 Before performing the path analysis, a multicollinearity analysis was conducted among the variables [21]. Genotypic correlation matrices were 277 278 submitted to the diagnosis of multicollinearity on the basis of the number of 279 conditions. The elimination of the variables stem diameter of the plant and number of cobs per plant was required in view of the severe multicollinearity, 280 107,826.62. For the remaining variables, insertion height of the first cob; 281 282 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 283 stand; mass of one thousand seeds; and yield, the number of conditions was 284 742.19, which enabled classifying them from moderate to strong, not 285 affecting the path analysis statistics. It was decided to use, in this study, only 286

the variables with no collinearity, given that, in strong or severe multicollinearity, 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 290 using grain yield as the main variable. The coefficient of determination (R^2) in 291 the path analysis model displayed a value of 0.9236 and residual effects 292 lower than 0.0143. As such, the model showed the cause and effect 293 294 relationship between the explanatory variables and grain yield. The satisfactory use of path coefficients is directly linked to the composition of 295 causal diagrams, which should be listed to the most important variables in 296 the expression of the main variable [35] The diagram applied enabled to 297 explain 92.36% (R^2) of the variation in grain yield (Table 4). 298

299 In accordance with [30], in five hybrid maize lines, the weight of 100 grains was the variable yield, which generated the greatest direct effect on grain 300 yield, being the most indicated for indirect selection regarding yield. Greater 301 direct effect and greater total correlation on grain yield point to a great 302 303 contribution to increase yield [36]. The highest values of direct effects on grain yield were seen for the mass of one thousand seeds, with 0.8079, 304 followed by the final plant stand, with 0.5850, and total number of cobs, with 305 0.4359, while the stripped cob diameter displayed negative direct effect and 306 307 high magnitude, with -0.5173, and positive phenotypic correlation of mean magnitude, 0.42, with the indirect effect being considered on the mass of one 308 309 thousand seeds, 0.6266, in the conditions in which the experiment was 310 carried out (Table 4).

311 The direct effect between the variable insertion height of the first cob and 312 yield was negative, -0.6416, while the phenotypic correlation was positive 313 and with a mean magnitude of 0.31, which should take into account the indirect effect in the final plant stand 0.3150 to benefit from the gain in these 314 315 two traits (Table 4). As stated by [23], the final plant stand is critical to 316 increase the production of dry mass and commercial cobs, both directly and 317 indirectly. This is not the case in [36], who reported a positive value for the trait insertion height of the cobs in the harvest with the yield, even though 318 319 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 320 yield. Also in agreement with [37], the plant height in the harvest can be 321 322 considered for indirect selection, because of the positive linear relationship 323 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 [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, [31] achieved a greater correlation between the number of grains per row and yield 0.586.

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Table 4. Direct and indirect effects of agronomic variables of maize from 16
 varieties of maize in the municipality of Alegre, Espirito Santo state, Brazil,
 2017

Variable	Effect	Via	Coefficients
	Direct	YIE	-0.6416
		HEI	0.1744
		SCL	-0.0072
\sim		SCD	0.1686
IHC	Indiract	NRC	-0.1190
	Indirect	NGR	0.0688
		TNC	0.2558
		FPS	0.3150
		MTS	0.0796
	Total		0.2946
	Direct	YIE	0.1979
\mathcal{A}		AIHC	-0.5656
		SCL	0.0153
HEI		SCD	0.0202
		NRC	-0.0999
		NGR	0.1227

		TNC	0.1791
		FPS	0.2390
		MTS	0.2696
	Total		0.3786
	Direct	YIE	0.0382
		IHC	0.1224
		HEI	0.0796
		SCD	-0.3068
SCL		NRC	0.0489
	Indirect	NGR	-0.0174
		TNC	-0.0885
		FPS	-0.1573
\sim		MTS	0.4822
	Total		0.2015
	Direct	YIE	-0.5173
		IHC	0.2091
		HEI	-0.0077
		SCL	0.0226
SCD	Indirect	NRC	-0.0187
		NGR	0.0588
		TNC	-0.0641
		FPS	0.0508

		MTS	0.6266
	Total		0.3602
	Direct	YIE	0.2202
		IHC	0.3468
		HEI	-0.0898
		SCL	0.0084
NCR	Indirect	SCD	0.0440
		NGR	-0.1189
		NTE	-0.1659
		FPS	-0.1090
		MTS	-0.4641
	Total		-0.3283
	Direct	YIE	0.2417
		IHC	-0.1827
		HEI	0.1004
		SCL	-0.0027
	Indiroct	SCD	-0.1260
NGR	mairect	NRC	-0.1083
		TNC	0.3478
		FPS	0.2943
		MTS	0.2894
	Total		0.8539
	Direct	YIE	0.4359
		IHC	-0.3765
		HEI	0.0813
		SCL	-0.0077
	Indiraat	SCD	0.0761
INC	mairect	NRC	-0.0838
		NGR	0.1928
		FPS	0.5153
		MTS	0.0046
	Total		0.838
FPS	Direct	YIE	0.5850

		IHC	-0.3455
		HEI	0.0808
	Indirect	SCL	-0.0102
		SCD	-0.0449
		NRC	-0.0410
		NGR	0.1216
		TNC	0.3840
		MTS	0.0543
	Total		0.7842
	Direct	YIE	0.8079
		IHC	-0.0632
		HEI	0.0660
		SCL	0.0228
MTO	Indiract	SCD	-0.4012
IVI I S	munect	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.

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356 4. CONCLUSION

The genetic variability identified in local breeds enables the selection of genotypes to be used in genetic breeding programs, given that the traits under evaluation showed a genotypic correlation of greater magnitude than the phenotypic one, indicating genetic effects whether of an additive, epistatic or dominance nature, exceeding the contribution of environmental origin.

The gain in the traits stripped cob diameter, which presented an indirect effect with mass of one thousand seeds, positive and with high magnitude, as well as the indirect effect of the variable insertion height of the first cob in the final plant stand, should be exploited. The final plant stand and the mass of one thousand seeds are determinants to directly increase the grain yield.

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379 **COMPETING INTERESTS**

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

383 AUTHORS' CONTRIBUTIONS

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385 'Author Richardson Sales Rocha' designed the study and performed the statistical analysis, 'Author Maxwel Rodrigues Nascimento' managed the 386 analyses of the study, 'Author José Tiago Barroso Chagas' and "Author 387 388 Rafael Nunes De Almeida" managed the literature searches, "Author Paulo Ricardo Dos Santos" and "Author Camila Queiroz Da Silva Sanfim De 389 Sant'anna" supporting at the experimental design and traits evaluations, 390 "Author Derivaldo Pureza Da Cruz" and "Author Kleyton Danilo Da Silva 391 Costa" suggests path analysis, "Author Geraldo De Amaral Gravina" and 392 "Author Rogério Figueiredo Daher" review the manuscript and suggests 393 394 some alterations. All authors read and approved the final manuscript."

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