

Genotypic correlation and path analysis in early and super-early maize genotypes

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ABSTRACT. The aims of this study were to assess the linear relationships between agronomic and nutritional traits and to identify promising traits for indirect selection in early and super-early maturing maize genotypes. Two trials were run in the 2009/2010 agricultural year, each consisting of a randomized block design with three replications. One trial was run on 36 early maturing maize genotypes and the other on 22 super-early maturing genotypes. Six agronomic traits, 11 protein-nutritional traits, and four energetic-nutritional traits were measured. Error normality assumptions were verified using the Kolmogorov-Smirnov test and residual variance homogeneity assumptions using the Levene test. Analysis of variance and the F-test were run for each of the 21 traits. Next, the genotype correlation coefficient matrix was estimated for the 21 traits and each trial. Ridge path analysis was based on values of $k = 0.00$ and $k = 0.10$ on the diagonal of $X'X$ correlation matrix, taking the nutritional traits as principal variables and agronomic traits as explanatory variables. The number of days from sowing to male flowering, the number of days from sowing to female flowering, plant height, ear insertion

height, ear weight and grain yield can be used in indirect selection as indicators of grain nutritional quality.

Key words: *Zea mays* L.; Ridge path analysis; Multicollinearity; Agronomic traits; Nutritional traits; Indirect selection

INTRODUCTION

Maize (*Zea mays* L.) is an important crop throughout the world and has both social and economic repercussions. It is widely used for various applications, but mainly as animal feed. Demand for maize, for both human and animal consumption, is expected to increase. Maize breeding researchers seek to combine increased grain yield with improved nutritional quality, especially regarding protein and energetic content. It is, therefore, of fundamental importance to identify the agronomic and nutritional traits of maize genotypes. Maize grains consist of 7.5% crude protein, 0.24% lysine, 0.18% methionine, 0.18% cysteine, 0.29% threonine, 0.07% tryptophan, 0.42% valine, 0.29% isoleucine, 1.00% leucine, 0.42% phenylalanine, 0.40% arginine, 3.5% ether extract, 1.9% crude fiber (Batal and Dale, 2010), 3438.51 kcal/kg apparent metabolizable energy corrected for nitrogen (Li et al., 2014), and 30% amylose (Hasjim et al., 2009).

Knowledge of the linear association between agronomic and nutritional maize traits could lead to significant advances in genetic breeding programs, especially when defining crossings, with the aim of targeting animal feed to increase efficiency and cut production costs. Associations between traits can be studied by analyzing a linear correlation coefficient ranging from -1 to 1. However, this coefficient measures the degree of relatedness between two traits and does not allow direct and indirect influences to be quantified (Cruz et al., 2012).

Path analysis, proposed by Wright (1921), has been used to understand the causes involved in associations between traits. Using this method, it is possible to obtain information on the direct and indirect effects of traits on a principal variable. Path analysis can also be used to identify traits that can be used in indirectly selecting plants, helping researchers to select superior genotypes in agricultural crops such as maize (Bello et al., 2010; Srećkov et al., 2010; Amini et al., 2013; Mustafa et al., 2014; Filipović et al., 2014; Baretta et al., 2016) and soybean (Silva et al., 2015). In addition to conventional path analysis, ridge path analysis allows all traits to be used, provided that a constant k be added on the diagonal of the matrix correlating the explanatory variables. In ridge path analysis, constant k ranges from 0 to 1, and it is recommended to use the lowest k -value capable of stabilizing path coefficients, i.e., working on the degree of multicollinearity between explanatory variables (Cruz et al., 2012).

Ridge path analysis has been used in studies on canola (Coimbra et al., 2005), maize (Carvalho et al., 2001; El-Taweel et al., 2012; Toebe and Cargnelutti Filho, 2013a,b), peppers (Moreira et al., 2013; Silva et al., 2013), bell peppers (Carvalho et al., 1999), and soybean (Bizeti et al., 2004). Studies conducted by Carvalho et al. (1999, 2001), Bizeti et al. (2004), El-Taweel et al. (2012), and Moreira et al. (2013) have confirmed the effectiveness of ridge path analysis in reducing the adverse effects of multicollinearity.

Studies on the linear association between agronomic and nutritional traits using path analysis have been conducted for crops of castor oil (Torres et al., 2015), maize (Zdunić et al., 2012), and soybean (Haghi et al., 2012). These studies show that there is a linear relationship between traits and that it is possible to indirectly select for promising traits in genetic plant

breeding. However, there are few studies in the literature using ridge path analysis on agronomic and nutritional traits. It is assumed that indirect selection could be used to identify promising agronomic traits for the nutritional quality of maize grains. Since there are no studies that show the real indirect and direct effects of agronomic traits on nutritional traits in the maize crop, the aims of this study were to assess the linear relationships between agronomic and nutritional traits and to identify promising traits for indirect selection in early and super-early maturing maize genotypes.

MATERIAL AND METHODS

Two trials were run during the 2009/2010 agricultural year on maize (*Zea mays* L.) crops grown in the experimental area of the Department of Plant Sciences (29°42'S, 53°49'W and elevation 95 m) of the Federal University of Santa Maria in the Brazilian State of Rio Grande do Sul. Thirty-six early maturing genotypes (trial 1) and 22 super-early maturing genotypes (trial 2) were assessed. The genotypes belonged to the Network of Evaluation of Maize Cultivars of Rio Grande do Sul, coordinated by the State Agricultural Research Foundation (Fundação Estadual de Pesquisa Agropecuária - FEPAGRO).

The trials were designed as randomized block experiments, with three replications. The experimental units consisted of two rows 5 m long, spaced at 0.80 m and with plants spaced at 0.20 m in the row. Seeds were sown manually on October 26, 2009. The plants emerged during the period from November 1st to 3rd, 2009. The plant population was thinned to 62,500 plants/ha. On the day the seeds were sown, basic fertilizer was applied at a rate of 37.5 kg/ha nitrogen (N), 150 kg/ha phosphorus (P₂O₅) and 150 kg/ha potassium (K₂O). Three applications of 200 kg/ha N were applied as topdressing when the plants had developed four, six, and eight expanded leaves, consecutively. The maize ears were harvested on March 15, 2010. The harvests were treated following the technical recommendations for maize.

The following agronomic traits were measured for each field trial, each experimental unit, and each genotype: number of days from sowing to male flowering (MF), number of days from sowing to female flowering (FF; male and female flowering based on 50% of plants in the plot in flower), plant height on harvesting (PH, in cm), ear insertion height on harvesting (EH, in cm; all plants in the plot were measured for plant height and ear insertion height), ear weight (EW, in t/ha), and grain yield at 13% moisture content (GY, in t/ha). Then, a 500-g sample of maize grains from each plot was separated. Each sample was placed in a paper bag and heated in a fan oven until the average moisture content was 10%. After drying, the grains were ground in a micro-mill (MA-630, Marconi) to obtain a particle size between 0.30 and 0.50 mm. After grinding, each sample was placed in a hermetically sealed container pending nutritional analysis. The following protein-nutritional traits were determined for each sample: crude protein (CP), lysine (Lys), methionine (Met), cysteine (Cys), threonine (Thr), tryptophan (Trp), valine (Val), isoleucine (Ile), leucine (Leu), phenylalanine (Phe), and arginine (Arg). The energetic-nutritional traits determined were: apparent metabolizable energy corrected for nitrogen (AMEn, in kcal/kg), ether extract (EE), crude fiber (CF), and amylose (AML), all measured as a percentage of raw material (%RM). The measurements were taken by near-infrared reflectance spectroscopy (NIRS), calibrating the spectrometer using the CEAN 010 analytical procedure (Adisseo Brasil SA). Since the NIRS equipment was not calibrated for determining the maize grain amylose content, this trait was determined using the iodometric method described by Martinez and Cuevas-Perez (1989).

For the agronomic and nutritional traits in each trial, the assumptions of the mathematical model (error normality and homogeneity of residual variances) were tested. Error normality was checked using the Kolmogorov-Smirnov test (Campos, 1983) and homogeneity of residual variances by the Levene test (Steel et al., 1997). Analysis of variance was run, noting the F-test estimate for each genotype (F_G), and selective accuracy (SA) determined by the equation: $SA = (1 - 1 / F_G)^{0.5}$ (Resende and Duarte, 2007). The genotype correlation coefficients (r_g) for the 21 traits were determined.

Next, based on the genotype correlation matrix, ridge path analysis under multicollinearity was performed. This analysis involved adding a constant, k ($k = 0.00$ and $k = 0.10$), on the diagonal of the $X'X$ correlation matrix (6×6) between the explanatory variables (agronomic traits). Ridge path analysis under multicollinearity was carried out based on the genotype correlation coefficients matrix. For each trial, ridge path analysis was performed using the protein-nutritional (CP, Lys, Met, Cys, Thr, Trp, Val, Ile, Leu, Phe, and Arg) and energetic-nutritional (AMEn, EE, CF, and AML) traits as the principal variables and the agronomic traits (MF, FF, PH, EH, EW, and GY) as explanatory variables, totaling 60 ridge path analysis operations.

The magnitude of multicollinearity was verified using the variance inflation factor (VIF). VIF values below 10 are considered adequate and indicate the absence of multicollinearity, whereas VIF values of 10 or higher indicate a high degree of multicollinearity (Hair et al., 2009). The statistics were analyzed using the GENES program (Cruz, 2013) and Microsoft Office Excel®.

RESULTS AND DISCUSSION

It was verified that 80.95% (early maturing genotypes) and 95.24% (super-early maturing genotypes) of the traits measured showed normal distribution, and for 100% of the traits measured, residual variances were homogeneous for both early maturing and super-early maturing genotypes. Analysis of variance indicated the existence of variability between the early maturing and super-early maturing genotypes for all traits measured. SA was very high ($SA \geq 0.90$) for 18 traits, high ($0.70 \leq SA < 0.90$) for two traits, and low ($0.50 \leq SA < 0.70$) for one trait in early maturing genotypes. For super-early maturing genotypes, SA was very high ($SA \geq 0.90$) for 18 traits and high ($0.70 \leq SA < 0.90$) for three characters (Table 1).

In overall terms, the results showed that the mathematical assumptions for performing analysis of variance and conducting future studies met the requirements, lending credibility to the trials run.

Estimates of genotype correlation among the 21 traits in early maturing genotypes ranged from $r_g = |0.002|$ to $r_g = |0.993|$ and in super-early maturing genotypes from $r_g = |0.003|$ to $r_g = |0.997|$ (Table 2). Generally, in both early maturing and super-early maturing genotypes, the agronomic traits MF, FF, PH, and EH were positively correlated with all protein-nutritional traits. However, EW and GY agronomic traits were negatively correlated with protein-nutritional traits (Table 2).

MF, FF, PH, and EH were positively correlated with AMEn and EE energetic-nutritional traits in both early maturing and super-early maturing genotypes and EW and GY were negatively correlated (Table 2). Between MF and CF, and between FF and CF, the correlation was negative in early maturing genotypes and non-existent in super-early maturing genotypes. MF, FF, PH, and EH were negatively correlated with the AML trait in early

Table 1. Mean, minimum, and maximum values for selective accuracy (SA), error normality, and homogeneity of residual variances between the 21 traits of 36 early maturing maize genotypes and 22 super-early maturing maize genotypes.

	Early						Super-early					
	Mean	Minimum	Maximum	SA	Z-KS ⁽²⁾	F-test ³	Mean	Minimum	Maximum	SA	Z-KS ²	F-test ³
	Agronomic						Agronomic					
MF ¹	74.28	65.00	88.00	0.94	0.615 ^{ns}	0.500 ^{ns}	72.12	66.00	82.00	0.96	0.998 ^{ns}	0.220 ^{ns}
FF	80.19	69.00	94.00	0.97	0.655 ^{ns}	0.340 ^{ns}	77.18	69.00	87.00	0.98	0.730 ^{ns}	0.260 ^{ns}
PH	187.04	155.32	230.07	0.81	0.623 ^{ns}	0.540 ^{ns}	202.27	178.15	223.51	0.91	0.491 ^{ns}	0.580 ^{ns}
EH	96.33	66.68	132.61	0.90	0.572 ^{ns}	0.610 ^{ns}	104.97	80.08	127.20	0.96	0.750 ^{ns}	0.390 ^{ns}
EW	6.13	2.73	9.69	0.93	0.899 ^{ns}	0.690 ^{ns}	7.27	3.97	9.89	0.92	0.559 ^{ns}	0.340 ^{ns}
GY	5.00	2.15	8.34	0.94	0.741 ^{ns}	0.740 ^{ns}	5.92	3.09	8.23	0.94	0.669 ^{ns}	0.350 ^{ns}
	Protein-nutritional						Protein-nutritional					
CP	7.54	6.68	8.74	0.78	0.533 ^{ns}	0.380 ^{ns}	7.31	6.52	8.07	0.87	0.566 ^{ns}	0.320 ^{ns}
Lys	0.21	0.20	0.23	0.90	1.679*	0.720 ^{ns}	0.22	0.19	0.24	0.90	0.912 ^{ns}	0.380 ^{ns}
Met	0.14	0.13	0.16	0.91	2.153*	0.630 ^{ns}	0.15	0.13	0.17	0.86	1.078 ^{ns}	0.410 ^{ns}
Cys	0.16	0.15	0.18	0.91	2.151*	0.580 ^{ns}	0.16	0.14	0.18	0.93	1.341 ^{ns}	0.380 ^{ns}
Thr	0.21	0.17	0.25	0.90	0.871 ^{ns}	0.280 ^{ns}	0.22	0.17	0.25	0.90	0.808 ^{ns}	0.320 ^{ns}
Trp	0.05	0.04	0.06	0.93	3.358*	0.710 ^{ns}	0.05	0.04	0.06	0.90	1.635*	0.480 ^{ns}
Val	0.30	0.26	0.35	0.95	1.225 ^{ns}	0.580 ^{ns}	0.31	0.27	0.35	0.93	0.715 ^{ns}	0.560 ^{ns}
Ile	0.18	0.15	0.22	0.94	1.008 ^{ns}	0.660 ^{ns}	0.19	0.15	0.22	0.95	0.971 ^{ns}	0.340 ^{ns}
Leu	0.79	0.68	0.95	0.94	0.593 ^{ns}	0.420 ^{ns}	0.84	0.71	0.95	0.93	1.017 ^{ns}	0.720 ^{ns}
Phe	0.27	0.23	0.33	0.96	0.954 ^{ns}	0.560 ^{ns}	0.29	0.23	0.33	0.94	0.677 ^{ns}	0.710 ^{ns}
Arg	0.33	0.30	0.37	0.95	0.915 ^{ns}	0.490 ^{ns}	0.33	0.29	0.37	0.96	0.654 ^{ns}	0.380 ^{ns}
	Energetic-nutritional						Energetic-nutritional					
AMEn	3434.87	3382.00	3479.00	0.93	0.624 ^{ns}	0.540 ^{ns}	3416.05	3332.00	3473.00	0.98	0.396 ^{ns}	0.560 ^{ns}
EE	3.76	3.37	4.18	0.93	0.674 ^{ns}	0.660 ^{ns}	3.72	3.21	4.09	0.96	0.875 ^{ns}	0.870 ^{ns}
CF	1.97	1.58	2.45	0.33	0.521 ^{ns}	0.540 ^{ns}	1.92	1.57	2.18	0.75	0.519 ^{ns}	0.400 ^{ns}
AML	28.96	26.83	31.47	0.90	0.887 ^{ns}	0.450 ^{ns}	28.61	26.04	30.68	0.92	0.776 ^{ns}	0.440 ^{ns}

¹Agronomic traits: MF = number of days from sowing until male flowering; FF = number of days from sowing until female flowering; PH = plant height, in cm; EH = ear insertion height, in cm; EW = ear weight, in t/ha; GY = grain yield, in t/ha; protein-nutritional traits: CP = crude protein, in %RM; Lys = lysine, in %RM; Met = methionine, in %RM; Cys = cysteine, in %RM; Thr = threonine, in %RM; Trp = tryptophan, in %RM; Val = valine, in %RM; Ile = isoleucine, in %RM; Leu = leucine, in %RM; Phe = phenylalanine, in %RM; Arg = arginine, in %RM; and energetic-nutritional traits: AMEn = apparent metabolizable energy corrected for nitrogen, in kcal/kg; EE = ether extract, in %RM; CF = crude fiber, in %RM; AML = amylose, in %RM. ²Kolmogorov Smirnov test values for the normality of the error distribution. ^{ns}Nonsignificant (normal distribution). ³Levene test values for the homogeneity of residual variances. ^{ns}Nonsignificant (homogeneous variances).

maturing genotypes and positively correlated in super-early maturing genotypes. Generally, in both early maturing and super-early maturing genotypes, the correlation between the agronomic traits EW and GY and energetic-nutritional traits was negative. However, CF was positively correlated with EW ($r_g = 0.594$) and GY ($r_g = 0.594$) in early maturing genotypes. In super-early maturing genotypes, there was no correlation between EW and CF ($r_g = 0.008$), and between GY and CF ($r_g = 0.053$) (Table 2). These genotype correlation estimates can be used to verify relationships between agronomic and nutritional traits (protein and energetic) and facilitate improvements in given traits using indirect selection.

The results indicate that GY was negatively correlated with protein-nutritional traits in both early maturing and super-early maturing genotypes. Other studies on maize crops have also reported a negative correlation between GY and CP (Idikut et al., 2009; Aliu et al., 2012; Mahesh et al., 2013; Bekele and Rao, 2014), and between GY and grain amino acid composition (Lovatto et al., 2006); this shows that it is not possible to select plants with high grain yield and concomitant high protein quality.

In early maturing genotypes, the correlations between MF and EE, and between FF and EE were positive, with respective values of $r_g = 0.241$ and $r_g = 0.342$. For super-early

Table 2. Estimates of genotype correlation coefficients between the 21 traits of 36 early maturing maize genotypes (above the diagonal) and 22 super-early maturing maize genotype (below the diagonal).

Trait ¹	MF	FF	PH	EH	EW	GY	CP	Lys	Met	Cys	Thr
MF	1	0.875	0.263	0.446	-0.579	-0.554	0.035	0.377	0.342	0.384	0.435
FF	0.900	1	0.279	0.256	-0.733	-0.741	0.020	0.537	0.412	0.473	0.577
PH	0.523	0.501	1	0.464	0.020	0.029	0.280	0.289	0.101	0.457	0.020
EH	0.853	0.805	0.655	1	-0.030	-0.002	0.562	0.367	0.191	0.452	0.159
EW	-0.530	-0.733	-0.181	-0.530	1	0.993	-0.169	-0.562	-0.321	-0.524	-0.741
GY	-0.545	-0.765	-0.186	-0.533	0.992	1	-0.185	-0.619	-0.354	-0.575	-0.783
CP	0.334	0.377	-0.134	0.073	-0.359	-0.361	1	0.383	-0.023	0.486	0.273
Lys	0.368	0.507	-0.003	0.266	-0.706	-0.722	0.640	1	0.760	0.902	0.948
Met	0.571	0.735	0.283	0.552	-0.684	-0.709	0.388	0.832	1	0.643	0.769
Cys	0.620	0.760	0.106	0.427	-0.785	-0.793	0.781	0.856	0.751	1	0.801
Thr	0.606	0.740	0.101	0.377	-0.849	-0.857	0.686	0.950	0.911	0.966	1
Trp	0.581	0.639	-0.056	0.384	-0.852	-0.825	0.654	0.962	0.829	0.962	0.961
Val	0.542	0.723	0.177	0.430	-0.870	-0.870	0.575	0.956	0.956	0.947	0.965
Ile	0.519	0.712	0.156	0.355	-0.861	-0.852	0.612	0.898	0.932	0.937	0.954
Leu	0.478	0.640	0.048	0.291	-0.878	-0.869	0.570	0.846	0.799	0.919	0.867
Phe	0.545	0.684	0.073	0.363	-0.841	-0.835	0.653	0.896	0.876	0.973	0.954
Arg	0.559	0.674	0.137	0.455	-0.682	-0.708	0.664	0.935	0.930	0.971	0.991
AMEn	0.444	0.523	0.429	0.645	-0.152	-0.238	0.178	0.522	0.833	0.469	0.559
EE	0.683	0.725	0.355	0.721	-0.377	-0.442	0.353	0.668	0.846	0.687	0.754
CF	0.047	0.005	0.335	0.048	0.008	0.053	-0.564	-0.349	-0.315	-0.270	-0.403
AML	0.239	0.319	0.206	0.427	-0.141	-0.196	-0.111	-0.105	0.249	-0.055	0.054
	Trp	Val	Ile	Leu	Phe	Arg	AMEn	EE	CF	AML	
MF	0.434	0.340	0.355	0.220	0.324	0.351	0.228	0.241	-0.679	-0.332	
FF	0.558	0.513	0.543	0.408	0.498	0.450	0.207	0.342	-0.834	-0.402	
PH	0.058	0.284	0.110	0.265	0.249	0.290	0.139	0.450	0.140	-0.527	
EH	0.143	0.257	0.106	0.188	0.200	0.452	0.511	0.398	0.008	-0.049	
EW	-0.648	-0.547	-0.626	-0.551	-0.581	-0.614	-0.339	-0.153	0.594	0.262	
GY	-0.710	-0.607	-0.677	-0.612	-0.635	-0.648	-0.324	-0.207	0.594	0.273	
CP	0.348	0.402	0.220	0.464	0.325	0.618	0.155	0.408	-0.045	-0.333	
Lys	0.943	0.844	0.838	0.728	0.869	0.916	0.487	0.607	-0.200	-0.547	
Met	0.741	0.758	0.810	0.577	0.802	0.730	0.533	0.468	-0.318	-0.237	
Cys	0.970	0.946	0.875	0.841	0.919	0.944	0.314	0.743	0.259	-0.530	
Thr	0.979	0.908	0.944	0.806	0.941	0.928	0.347	0.435	0.218	-0.333	
Trp	1	0.964	0.931	0.877	0.961	0.916	0.290	0.654	0.463	-0.368	
Val	0.987	1	0.968	0.915	0.987	0.912	0.226	0.561	0.166	-0.439	
Ile	0.950	0.994	1	0.862	0.970	0.867	0.207	0.486	0.257	-0.350	
Leu	0.908	0.970	0.953	1	0.939	0.805	0.090	0.333	0.349	-0.375	
Phe	0.978	0.997	0.987	0.975	1	0.898	0.242	0.445	0.373	-0.407	
Arg	0.965	0.964	0.928	0.867	0.952	1	0.525	0.628	0.043	-0.392	
AMEn	0.441	0.534	0.449	0.328	0.448	0.664	1	0.536	-0.065	-0.105	
EE	0.680	0.695	0.635	0.509	0.636	0.806	0.945	1	-0.480	-0.415	
CF	-0.304	-0.326	-0.294	-0.310	-0.402	-0.480	-0.413	-0.405	1	0.737	
AML	-0.069	-0.006	-0.025	-0.111	-0.066	0.082	0.645	0.434	-0.660	1	

¹Agronomic traits: MF = number of days from sowing until male flowering; FF = number of days from sowing until female flowering; PH = plant height, in cm; EH = ear insertion height, in cm; EW = ear weight, in t/ha; GY = grain yield, in t/ha; protein-nutritional traits: CP = crude protein, in %RM; Lys = lysine, in %RM; Met = methionine, in %RM; Cys = cysteine, in %RM; Thr = threonine, in %RM; Trp = tryptophan, in %RM; Val = valine, in %RM; Ile = isoleucine, in %RM; Leu = leucine, in %RM; Phe = phenylalanine, in %RM; Arg = arginine, in %RM; and energetic-nutritional traits: AMEn = apparent metabolizable energy corrected for nitrogen, in kcal/kg; EE = ether extract, in %RM; CF = crude fiber, in %RM; AML = amylose, in %RM.

maturing genotypes, the correlation of MF and FF with EE was also positive and of higher magnitude compared to the early maturing genotypes, with respective values of $r_g = 0.683$ and $r_g = 0.725$. A low-magnitude positive correlation between these traits was also reported by Wali et al. (2006) and Chukwu et al. (2015). The correlations between GY and EE were $r_g = -0.207$ and $r_g = -0.442$, respectively, for early maturing and super-early maturing genotypes. Studies conducted by Fabijanac et al. (2006) and Saleem et al. (2008) also reported negative correlations between these traits in maize; this leads us to infer that higher values of MF and

FF result in higher EE, and higher GY results in lower EE in both early maturing and super-early maturing genotypes.

Ridge path analysis with constant $k = 0.00$ showed the presence of multicollinearity. Respective VIF values were $0.000 \leq VIF \leq 111.483$ and $0.068 \leq VIF \leq 110.278$ for both early maturing and super-early maturing genotypes (Tables 3 and 4).

Table 3. Estimates of genotypic correlation coefficients and respective estimates of the direct and indirect effect of the explanatory variables based on ridge path analysis performed using values of $k = 0.00$ and path analysis, determination coefficient, and effect of the residual variable for the 36 early maturing maize genotypes.

Effect	Main variable															VIF ¹
	Protein-nutritional										Energetic-nutritional					
	CP	Lys	Met	Cys	Thr	Trp	Val	Ile	Leu	Phe	Arg	AMEn	EE	CF	AML	
Direct of MF on	0.087	0.237	0.250	0.751	0.438	0.892	0.326	0.212	0.332	0.325	0.288	-0.265	0.159	0.687	-0.510	8.716
Indirect of MF via FF on	-0.816	-0.438	-0.033	-1.105	-0.554	-0.918	-0.509	-0.281	-0.758	-0.547	-0.760	-0.128	-0.181	-1.721	0.294	9.226
Indirect of MF via PH on	0.060	0.065	0.001	0.141	0.014	0.040	0.083	0.037	0.104	0.084	0.075	-0.014	0.094	0.141	-0.178	0.110
Indirect of MF via EH on	0.326	0.183	0.073	0.156	0.091	0.047	0.112	0.059	0.097	0.085	0.229	0.302	0.152	0.010	0.165	0.350
Indirect of MF via EW on	-1.647	-2.961	-1.656	-3.447	-2.240	-3.548	-3.009	-2.301	-3.068	-2.720	-2.200	0.368	-2.755	-1.411	0.833	33.723
Indirect of MF via GY on	2.025	3.291	1.707	3.888	2.687	3.921	3.337	2.629	3.512	3.096	2.720	0.065	2.772	1.616	-0.935	34.181
Genotypic correlation (r_g)	0.035	0.377	0.342	0.384	0.435	0.434	0.340	0.355	0.220	0.324	0.351	0.228	0.241	-0.679	0.332	
Direct of FF on	-0.932	-0.501	-0.038	-1.263	-0.634	-1.049	-0.582	-0.322	-0.866	-0.625	-0.869	-0.146	-0.207	-1.968	0.336	12.053
Indirect of FF via MF on	0.076	0.207	0.219	0.657	0.383	0.780	0.285	0.185	0.291	0.285	0.252	-0.232	0.139	0.601	-0.446	6.672
Indirect of FF via PH on	0.064	0.069	0.001	0.150	0.015	0.043	0.088	0.040	0.111	0.089	0.080	-0.015	0.100	0.150	-0.189	0.125
Indirect of FF via EH on	0.187	0.105	0.042	0.090	0.052	0.027	0.064	0.034	0.056	0.049	0.131	0.174	0.088	0.006	0.095	0.115
Indirect of FF via EW on	-2.086	-3.749	-2.097	-4.365	-2.836	-4.492	-3.809	-2.913	-3.885	-3.444	-2.785	0.339	-3.488	-1.787	1.054	54.057
Indirect of FF via GY on	2.711	4.405	2.285	5.204	3.597	5.248	4.466	3.519	4.700	4.144	3.640	0.087	3.710	2.163	-1.251	61.226
Genotypic correlation (r_g)	0.020	0.537	0.412	0.473	0.577	0.558	0.513	0.543	0.408	0.498	0.450	0.207	0.342	-0.834	-0.402	
Direct of PH on	0.228	0.248	0.002	0.537	0.052	0.152	0.317	0.142	0.398	0.319	0.286	-0.052	0.358	0.535	-0.678	1.598
Indirect of PH via MF on	0.023	0.062	0.066	0.197	0.115	0.234	0.086	0.056	0.087	0.085	0.076	-0.070	0.042	0.180	-0.134	0.601
Indirect of PH via FF on	-0.260	-0.140	-0.010	-0.353	-0.177	-0.293	-0.163	-0.090	-0.242	-0.175	-0.243	-0.041	-0.058	-0.550	0.094	0.941
Indirect of PH via EH on	0.339	0.190	0.076	0.162	0.094	0.049	0.117	0.062	0.101	0.088	0.238	0.314	0.158	0.010	0.171	0.377
Indirect of PH via EW on	0.056	0.101	0.057	0.118	0.077	0.121	0.103	0.079	0.105	0.093	0.075	-0.009	0.094	0.048	-0.134	0.040
Indirect of PH via GY on	-0.106	-0.172	-0.089	-0.204	-0.141	-0.205	-0.175	-0.138	-0.184	-0.162	-0.142	-0.003	-0.145	-0.085	0.049	0.089
Genotypic correlation (r_g)	0.280	0.289	0.101	0.457	0.020	0.058	0.284	0.110	0.265	0.249	0.290	0.139	0.450	0.140	-0.527	
Direct of EH on	0.731	0.410	0.164	0.350	0.204	0.106	0.251	0.133	0.217	0.191	0.513	0.678	0.342	0.022	0.369	1.756
Indirect of EH via MF on	0.039	0.106	0.112	0.335	0.195	0.398	0.146	0.094	0.148	0.145	0.128	-0.118	0.071	0.306	-0.228	1.734
Indirect of EH via FF on	-0.239	-0.128	-0.010	-0.324	-0.162	-0.269	-0.149	-0.082	-0.222	-0.160	-0.223	-0.037	-0.053	-0.504	0.086	0.792
Indirect of EH via PH on	0.106	0.115	0.001	0.249	0.024	0.071	0.147	0.066	0.184	0.148	0.133	-0.024	0.166	0.248	-0.314	0.343
Indirect of EH via EW on	-0.084	-0.151	-0.084	-0.176	-0.114	-0.181	-0.153	-0.117	-0.156	-0.139	-0.112	0.014	-0.140	-0.072	0.042	0.091
Indirect of EH via GY on	0.009	0.014	0.007	0.017	0.012	0.017	0.014	0.011	0.015	0.013	0.012	0.000	0.012	0.007	-0.004	0.000
Genotypic correlation (r_g)	0.562	0.367	0.191	0.452	0.159	0.143	0.257	0.106	0.188	0.200	0.452	0.511	0.398	0.008	-0.049	
Direct of EW on	2.846	5.116	2.862	5.956	3.871	6.130	5.198	3.975	5.301	4.700	3.801	-0.462	4.760	2.438	-1.439	100.665
Indirect of EW via MF on	-0.050	-0.137	-0.145	-0.434	-0.253	-0.516	-0.189	-0.122	-0.192	-0.188	-0.166	0.153	-0.092	-0.398	0.295	2.920
Indirect of EW via FF on	0.683	0.367	0.027	0.926	0.464	0.769	0.427	0.236	0.635	0.458	0.637	0.107	1.442	-0.246	6.472	
Indirect of EW via PH on	0.005	0.005	0.000	0.011	0.001	0.003	0.006	0.003	0.008	0.006	0.006	-0.001	0.007	0.011	-0.013	0.001
Indirect of EW via EH on	-0.022	-0.012	-0.005	-0.010	-0.006	-0.003	-0.007	-0.004	-0.006	-0.006	-0.015	-0.020	-0.010	-0.001	-0.011	0.002
Indirect of EW via GY on	-3.630	-5.899	-3.060	-6.970	-4.817	-7.028	-5.981	-4.712	-6.295	-5.550	-4.875	-0.116	-4.968	-2.897	1.676	109.822
Genotypic correlation (r_g)	-0.169	-0.562	-0.321	-0.524	-0.741	-0.648	-0.547	-0.626	-0.551	-0.581	-0.614	-0.339	-0.153	0.594	0.262	
Direct of GY on	-3.658	-5.944	-3.083	-7.022	-4.854	-7.081	-6.026	-4.748	-6.343	-5.592	-4.912	-0.117	-5.006	-2.919	1.688	111.483
Indirect of GY via MF on	-0.048	-0.131	-0.138	-0.416	-0.242	-0.494	-0.181	-0.117	-0.184	-0.180	-0.159	0.147	-0.088	-0.380	0.282	2.672
Indirect of GY via FF on	0.691	0.371	0.028	0.936	0.470	0.777	0.431	0.238	0.642	0.463	0.644	0.108	1.553	1.458	-0.249	6.619
Indirect of GY via PH on	0.007	0.007	0.000	0.016	0.002	0.004	0.009	0.004	0.012	0.009	0.008	-0.002	0.010	0.016	-0.020	0.001
Indirect of GY via EH on	-0.002	-0.001	0.000	-0.001	0.000	0.000	-0.001	0.000	-0.001	0.000	-0.001	-0.002	-0.001	0.000	-0.001	0.000
Indirect of GY via EW on	2.825	5.077	2.840	5.912	3.842	6.084	5.159	3.946	5.261	4.665	3.772	-0.459	4.724	2.420	-1.428	99.165
Genotypic correlation (r_g)	-0.185	-0.619	-0.354	-0.575	-0.783	-0.710	-0.607	-0.677	-0.612	-0.635	-0.648	-0.324	-0.207	0.594	0.273	
Determination coefficient	0.655	0.849	0.274	1.014	0.791	0.882	0.779	0.657	0.823	0.733	0.872	0.443	0.571	0.964	0.457	
Residual variable	0.588	0.388	0.852	0.000	0.457	0.343	0.470	0.586	0.421	0.517	0.358	0.746	0.655	0.189	0.737	

¹VIF = variance inflation factor. Number of days from sowing until male flowering (MF), number of days from sowing until female flowering (FF), plant height (PH), ear insertion height (EH), ear weight (EW), and grain yield (GY) on the main variables: crude protein (CP), lysine (Lys), methionine (Met), cysteine (Cys), threonine (Thr), tryptophan (Trp), valine (Val), isoleucine (Ile), leucine (Leu), phenylalanine (Phe), and arginine (Arg), apparent metabolizable energy corrected for nitrogen (AMEn), ether extract (EE), crude fiber (CF), and amylose (AML).

VIF ≥ 10 confirms the presence of multicollinearity in the explanatory variable correlation matrix (Hair et al., 2009). Ridge path analysis ($k = 0.00$) overestimated the path coefficient values (direct and indirect effects), with wide variability and, therefore, it was not possible to make appropriate inferences in early maturing and super-early maturing genotypes. Studies based on ridge path analysis ($k = 0.00$) in maize crops by Carvalho et al. (2001) and El-Taweel et al. (2012), and in soybean by Bizeti et al. (2004) also reported that ridge path analysis correlations were violated.

Table 4. Estimates of genotypic correlation coefficients and respective estimates of the direct and indirect effect of the explanatory variables based on ridge path analysis performed using values of $k = 0.00$ and path analysis, determination coefficient, and effect of the residual variable for the 22 super-early maturing maize genotype.

Effect	Main variable															
	Protein-nutritional										Energetic-nutritional					
	CP	Lys	Met	Cys	Thr	Trp	Val	Ile	Leu	Phe	Arg	AMEn	EE	CF	AML	VIF ⁽¹⁾
Direct of MF on	0.475	0.555	-0.334	0.262	0.743	0.925	0.158	0.078	0.589	0.490	0.347	-0.768	-0.159	0.044	-0.767	10.759
Indirect of MF via FF on	0.651	-0.476	0.686	0.690	0.094	-0.214	0.369	0.755	0.028	0.245	0.040	0.199	0.286	0.286	0.160	14.835
Indirect of MF via PH on	-0.128	-0.015	-0.028	-0.072	0.011	-0.129	0.028	0.043	0.033	-0.017	-0.055	-0.061	-0.134	0.279	-0.114	0.567
Indirect of MF via EH on	-0.644	-0.244	0.106	-0.445	-0.660	-0.415	-0.377	-0.626	-0.661	-0.537	-0.090	1.114	0.709	-0.448	0.965	3.762
Indirect of MF via EW on	0.840	-0.600	-0.142	0.701	0.386	1.226	0.666	1.306	0.789	0.879	-0.536	-2.956	-1.917	1.862	-1.957	25.003
Indirect of MF via GY on	-0.860	1.148	0.282	-0.516	0.031	-0.811	-0.301	-1.038	-0.301	-0.516	0.853	2.917	1.897	-1.977	1.953	32.741
Genotypic correlation (r_g)	0.334	0.368	0.571	0.620	0.606	0.581	0.542	0.519	0.478	0.545	0.559	0.444	0.683	0.047	0.239	
Direct of FF on	0.723	-0.529	0.762	0.767	0.105	-0.238	0.410	0.839	0.032	0.272	0.044	0.221	0.318	0.318	0.178	18.311
Indirect of FF via MF on	0.427	0.499	-0.301	0.236	0.669	0.832	0.142	0.070	0.531	0.441	0.312	-0.691	-0.143	0.040	-0.691	8.717
Indirect of FF via PH on	-0.122	-0.014	-0.026	-0.069	0.011	-0.123	0.026	0.041	0.032	-0.017	-0.053	-0.059	-0.128	0.267	-0.109	0.519
Indirect of FF via EH on	-0.608	-0.230	0.100	-0.420	-0.622	-0.392	-0.356	-0.591	-0.624	-0.507	-0.085	1.051	0.669	-0.423	0.910	3.349
Indirect of FF via EW on	1.163	-0.831	-0.197	0.971	0.534	1.697	0.922	1.809	1.092	1.218	-0.743	-4.094	-2.654	2.579	-2.711	47.947
Indirect of FF via GY on	-1.207	1.612	0.397	-0.724	0.043	-1.138	-0.422	-1.457	-0.422	-0.724	1.198	4.095	2.664	-2.776	2.742	64.557
Genotypic correlation (r_g)	0.377	0.507	0.735	0.760	0.740	0.639	0.723	0.712	0.640	0.684	0.674	0.523	0.725	0.005	0.319	
Direct of PH on	-0.244	-0.028	-0.053	-0.138	0.022	-0.246	0.053	0.082	0.063	-0.033	-0.105	-0.117	-0.256	0.533	-0.218	2.069
Indirect of PH via MF on	0.249	0.290	-0.175	0.137	0.389	0.484	0.083	0.041	0.308	0.256	0.182	-0.402	-0.083	0.023	-0.402	2.947
Indirect of PH via FF on	0.362	-0.265	0.382	0.384	0.052	-0.119	0.206	0.420	0.016	0.136	0.022	0.111	0.159	0.159	0.089	4.591
Indirect of PH via EH on	-0.494	-0.187	0.081	-0.341	-0.506	-0.318	-0.290	-0.480	-0.507	-0.412	-0.069	0.854	0.544	-0.344	0.740	2.213
Indirect of PH via EW on	0.288	-0.206	-0.049	0.240	0.132	0.420	0.228	0.447	0.270	0.301	-0.184	-1.012	-0.656	0.638	-0.670	2.934
Indirect of PH via GY on	-0.293	0.392	0.096	-0.176	0.010	-0.277	-0.103	-0.354	-0.103	-0.176	0.291	0.995	0.647	-0.675	0.666	3.816
Genotypic correlation (r_g)	-0.134	-0.003	0.283	0.106	0.101	-0.056	0.177	0.156	0.048	0.073	0.137	0.429	0.355	0.335	0.206	
Direct of EH on	-0.755	-0.286	0.124	-0.522	-0.773	-0.487	-0.442	-0.734	-0.774	-0.629	-0.106	1.305	0.831	-0.525	1.131	5.166
Indirect of EH via MF on	0.405	0.473	-0.285	0.224	0.634	0.789	0.135	0.067	0.503	0.418	0.296	-0.655	-0.136	0.038	-0.655	7.836
Indirect of EH via FF on	0.582	-0.426	0.614	0.618	0.084	-0.192	0.330	0.676	0.025	0.219	0.036	0.178	0.256	0.256	0.143	11.871
Indirect of EH via PH on	-0.160	-0.018	-0.035	-0.090	0.014	-0.161	0.034	0.054	0.041	-0.022	-0.069	-0.077	-0.168	0.349	-0.143	0.886
Indirect of EH via EW on	0.841	-0.601	-0.142	0.702	0.387	1.227	0.667	1.308	0.790	0.881	-0.537	-2.961	-1.920	1.865	-1.960	25.075
Indirect of EH via GY on	-0.841	1.124	0.276	-0.505	0.030	-0.793	-0.294	-1.016	-0.294	-0.505	0.835	2.854	1.857	-1.935	1.911	31.363
Genotypic correlation (r_g)	0.073	0.266	0.552	0.427	0.377	0.384	0.430	0.355	0.291	0.363	0.455	0.645	0.721	0.048	0.427	
Direct of EW on	-1.586	1.134	0.268	-1.324	-0.729	-2.315	-1.258	-2.467	-1.489	-1.661	1.013	5.583	3.620	-3.517	3.697	89.171
Indirect of EW via MF on	-0.251	-0.294	0.177	-0.139	-0.394	-0.490	-0.084	-0.041	-0.312	-0.259	-0.184	0.406	0.084	-0.224	0.406	3.017
Indirect of EW via FF on	-0.530	0.388	-0.559	-0.563	-0.077	0.175	-0.391	-0.615	-0.023	-0.200	-0.032	-0.162	-0.233	-0.233	-0.131	9.846
Indirect of EW via PH on	0.044	0.005	0.010	0.025	-0.004	0.045	0.010	-0.015	-0.011	0.006	0.019	0.021	0.046	-0.097	0.040	0.068
Indirect of EW via EH on	0.400	0.152	-0.066	0.277	0.410	0.258	0.235	0.389	0.411	0.334	0.056	-0.692	-0.441	0.278	-0.600	1.453
Indirect of EW via EW on	1.565	-2.090	-0.514	0.939	-0.056	1.475	0.548	1.889	0.548	0.939	-1.554	-5.309	-3.454	3.599	-3.554	108.502
Indirect of EW via GY on	-0.359	-0.706	-0.684	-0.785	-0.849	-0.852	-0.870	-0.861	-0.878	-0.841	-0.682	-0.152	-0.377	0.008	-0.141	
Genotypic correlation (r_g)	1.578	-2.107	-0.518	0.947	-0.056	1.487	0.552	1.904	0.552	0.947	-1.566	-5.353	-3.482	3.628	-3.583	110.278
Direct of GY on	-0.259	-0.302	0.182	-0.143	-0.405	-0.504	-0.086	-0.043	-0.321	-0.267	-0.189	0.418	0.087	-0.024	0.418	3.194
Indirect of GY via MF on	-0.553	0.405	-0.583	-0.587	-0.080	0.182	-0.314	-0.642	-0.024	-0.208	-0.034	-0.169	-0.243	-0.243	-0.136	10.719
Indirect of GY via FF on	0.045	0.005	0.010	0.026	-0.004	0.046	-0.010	-0.015	-0.012	0.006	0.020	0.022	0.048	-0.099	0.041	0.072
Indirect of GY via PH on	0.402	0.152	-0.066	0.278	0.412	0.260	0.236	0.391	0.413	0.335	0.056	-0.696	-0.443	0.289	-0.603	1.469
Indirect of GY via EH on	-1.574	1.124	0.266	-1.313	-0.723	-2.296	-1.248	-2.447	-1.477	-1.647	1.005	5.538	3.590	-3.488	3.667	87.735
Indirect of GY via EW on	-0.361	-0.722	-0.709	-0.793	-0.857	-0.825	-0.870	-0.852	-0.869	-0.835	-0.708	-0.238	-0.442	0.053	-0.196	
Genotypic correlation (r_g)	0.409	0.582	0.607	0.797	0.906	0.957	0.810	0.892	0.907	0.829	0.580	0.991	0.805	0.322	0.490	
Determination coefficient	0.409	0.582	0.607	0.797	0.906	0.957	0.810	0.892	0.907	0.829	0.580	0.991	0.805	0.322	0.490	
Residual variable	0.769	0.646	0.627	0.451	0.306	0.208	0.435	0.328	0.305	0.413	0.648	0.092	0.441	0.823	0.714	

¹VIF = variance inflation factor. Number of days from sowing until male flowering (MF), number of days from sowing until female flowering (FF), plant height (PH), ear insertion height (EH), ear weight (EW), and grain yield (GY) on the main variables: crude protein (CP), lysine (Lys), methionine (Met), cysteine (Cys), threonine (Thr), tryptophan (Trp), valine (Val), isoleucine (Ile), leucine (Leu), phenylalanine (Phe), and arginine (Arg), apparent metabolizable energy corrected for nitrogen (AMEn), ether extract (EE), crude fiber (CF), and amylose (AML).

To get around this problem of multicollinearity in the correlation matrix, a constant, $k = 0.10$, was added on the diagonal of the $X'X$ matrix, resulting in VIF values below ten in the correlation matrices for early maturing genotypes ($VIF \leq 6.415$) and for super-early maturing genotypes ($VIF \leq 6.556$), indicating the absence of multicollinearity (Tables 5 and 6).

Introducing $k = 0.10$ overcomes correlation matrix multicollinearity problems so that biological inferences can be made for both early maturing and super-early maturing genotypes.

Tables 5 and 6 indicate the direct and indirect effects, via agronomic traits, on protein-nutritional and energetic-nutritional traits for a k -value of $k = 0.10$. Based on the genotype correlation coefficient matrix, for early maturing genotypes, the FF trait showed a negative linear correlation ($r_g = -0.834$) and a direct negative effect (direct effect = -0.821) on CF. PH showed a negative linear correlation ($r_g = -0.527$) and a direct negative effect (direct effect = -0.536) on AML. The EH trait showed a positive linear correlation and a positive direct effect on CP (direct effect = 0.635) and AMEn (direct effect = 0.565). GY showed a negative linear correlation ($-0.783 \leq r_g \leq -0.575$) with the protein-nutritional traits Lys, Cys, Thr, Trp, Val, Ile,

Leu, Phe, and Arg, and a direct negative effect ($-0.619 \leq \text{direct effect} \leq -0.501$) with the same sign and similar magnitude, confirming the cause and effect relationship between GY and Lys, Cys, Thr, Trp, Val, Ile, Leu, Phe, and Arg. The direct effects of MF, FF, and EW on Lys, Cys, Thr, Trp, Val, Ile, Leu, Phe, and Arg were negligible and, therefore, the existing association is explained by greater indirect effects via GY (Table 5).

Table 5. Estimates of genotypic correlation coefficients and respective estimates of the direct and indirect effect of the explanatory variables based on ridge path analysis performed using values of $k = 0.10$ and path analysis, determination coefficient and effect of the residual variable for the 36 early maturing maize genotypes.

Effect	Main variable															
	Protein-nutritional										Energetic-nutritional					
	CP	Lys	Met	Cys	Thr	Trp	Val	Ile	Leu	Phe	Arg	AMEn	EE	CF	AML	VIF ¹
Direct of MF on	-0.312	-0.291	-0.022	-0.168	-0.110	-0.041	-0.264	-0.209	-0.340	-0.247	-0.248	-0.155	-0.246	-0.132	-0.142	3.542
Indirect of MF via FF on	-0.233	0.198	0.238	-0.029	0.088	0.102	0.183	0.211	0.060	0.133	-0.058	-0.125	0.272	-0.718	-0.076	2.820
Indirect of MF via PH on	0.037	0.039	-0.006	0.088	-0.010	0.000	0.051	0.017	0.064	0.051	0.044	-0.007	0.072	0.084	-0.141	0.084
Indirect of MF via EH on	0.283	0.149	0.058	0.153	0.078	0.053	0.093	0.042	0.083	0.072	0.200	0.252	0.124	0.052	0.116	0.266
Indirect of MF via EW on	0.073	0.005	-0.049	0.025	0.091	-0.001	0.001	0.038	0.043	0.034	0.115	0.149	-0.123	0.000	-0.006	1.716
Indirect of MF via GY on	0.218	0.306	0.124	0.332	0.308	0.325	0.302	0.277	0.343	0.305	0.323	0.130	0.167	0.048	-0.068	1.625
Genotypic correlation (r_g)	0.035	0.377	0.342	0.384	0.435	0.434	0.340	0.355	0.220	0.324	0.351	0.228	0.241	-0.679	-0.332	
Direct of FF on	-0.266	0.226	0.272	-0.034	0.101	0.117	0.209	0.241	0.069	0.152	-0.067	-0.143	0.311	-0.821	-0.087	4.458
Indirect of FF via MF on	-0.273	-0.255	-0.019	-0.147	-0.096	-0.036	-0.231	-0.183	-0.297	-0.216	-0.217	-0.136	-0.215	-0.115	-0.124	2.241
Indirect of FF via PH on	0.039	0.041	-0.006	0.094	-0.010	0.000	0.054	0.018	0.068	0.054	0.047	-0.008	0.077	0.090	-0.150	0.095
Indirect of FF via EH on	0.163	0.086	0.033	0.088	0.045	0.030	0.053	0.024	0.048	0.041	0.115	0.145	0.071	0.030	0.067	0.088
Indirect of FF via EW on	0.092	0.006	-0.062	0.032	0.115	-0.001	0.002	0.048	0.055	0.043	0.145	0.189	-0.156	0.000	-0.008	2.751
Indirect of FF via GY on	0.291	0.410	0.166	0.444	0.412	0.436	0.405	0.371	0.459	0.408	0.432	0.174	0.223	0.065	-0.092	2.912
Genotypic correlation (r_g)	0.020	0.537	0.412	0.473	0.577	0.558	0.513	0.543	0.408	0.498	0.450	0.207	0.342	-0.834	-0.402	
Direct of PH on	0.141	0.148	-0.023	0.336	-0.037	-0.001	0.195	0.063	0.243	0.194	0.169	-0.028	0.275	0.321	-0.536	1.465
Indirect of PH via MF on	-0.082	-0.077	-0.006	-0.044	-0.029	-0.011	-0.069	-0.055	-0.089	-0.065	-0.065	-0.041	-0.065	-0.035	-0.037	0.202
Indirect of PH via FF on	-0.074	0.063	0.076	-0.009	0.028	0.033	0.058	0.067	0.019	0.042	-0.019	-0.040	0.087	-0.229	-0.024	0.288
Indirect of PH via EH on	0.294	0.155	0.060	0.159	0.081	0.055	0.097	0.044	0.087	0.075	0.208	0.262	0.129	0.054	0.121	0.287
Indirect of PH via EW on	-0.002	0.000	0.002	-0.001	-0.003	0.000	0.000	-0.001	-0.001	-0.001	-0.004	-0.005	0.004	0.000	0.000	0.002
Indirect of PH via GY on	-0.011	-0.016	-0.007	-0.017	-0.016	-0.017	-0.016	-0.015	-0.018	-0.016	-0.017	-0.007	-0.009	-0.003	0.004	0.004
Genotypic correlation (r_g)	0.280	0.289	0.101	0.457	0.020	0.058	0.284	0.110	0.265	0.249	0.290	0.139	0.450	0.140	-0.527	
Direct of EH on	0.635	0.335	0.130	0.343	0.176	0.118	0.208	0.095	0.187	0.161	0.449	0.565	0.278	0.117	0.260	1.615
Indirect of EH via MF on	-0.139	-0.130	-0.010	-0.075	-0.049	-0.018	-0.118	-0.093	-0.152	-0.110	-0.111	-0.069	-0.110	-0.059	-0.063	0.583
Indirect of EH via FF on	-0.068	0.058	0.070	-0.009	0.026	0.030	0.054	0.062	0.018	0.039	-0.017	-0.037	0.080	-0.210	-0.022	0.242
Indirect of EH via PH on	0.065	0.069	-0.010	0.156	-0.017	-0.001	0.090	0.029	0.113	0.090	0.079	-0.013	0.128	0.149	-0.248	0.260
Indirect of EH via EW on	0.004	0.000	-0.002	0.001	0.005	0.000	0.000	0.002	0.002	0.002	0.006	0.008	-0.006	0.000	0.000	0.005
Indirect of EH via GY on	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.000
Genotypic correlation (r_g)	0.562	0.367	0.191	0.452	0.159	0.143	0.257	0.106	0.188	0.200	0.452	0.511	0.398	0.008	-0.049	
Direct of EW on	-0.126	-0.008	0.084	-0.043	-0.157	0.001	-0.002	-0.065	-0.075	-0.059	-0.198	-0.258	0.213	0.000	0.010	6.198
Indirect of EW via MF on	0.181	0.169	0.013	0.098	0.064	0.024	0.153	0.121	0.197	0.143	0.143	0.090	0.142	0.076	0.082	0.981
Indirect of EW via FF on	0.195	-0.166	-0.199	0.025	-0.074	-0.086	-0.153	-0.176	-0.050	-0.111	0.049	0.105	-0.228	0.062	0.064	1.978
Indirect of EW via PH on	0.003	0.003	0.000	0.007	-0.001	0.000	0.004	0.001	0.005	0.004	0.003	-0.001	0.005	0.006	-0.011	0.000
Indirect of EW via EH on	-0.019	-0.010	-0.004	-0.010	-0.005	-0.003	-0.006	-0.003	-0.006	-0.005	-0.013	-0.017	-0.008	-0.003	-0.008	0.001
Indirect of EW via EW on	-0.390	-0.549	-0.223	-0.595	-0.552	-0.583	-0.542	-0.497	-0.614	-0.547	-0.579	-0.233	-0.299	-0.087	0.123	5.223
Genotypic correlation (r_g)	-0.169	-0.562	-0.321	-0.524	-0.741	-0.648	-0.547	-0.626	-0.551	-0.581	-0.614	-0.339	-0.153	0.594	0.262	
Direct of GY on	-0.393	-0.553	-0.224	-0.599	-0.557	-0.588	-0.546	-0.501	-0.619	-0.551	-0.583	-0.234	-0.301	-0.087	0.124	6.415
Indirect of GY via MF on	0.173	0.161	0.012	0.093	0.061	0.023	0.146	0.116	0.188	0.137	0.137	0.086	0.136	0.073	0.079	0.898
Indirect of GY via FF on	0.197	-0.167	-0.202	0.025	-0.075	-0.087	-0.155	-0.178	-0.051	-0.113	0.050	0.106	-0.230	0.609	0.065	2.023
Indirect of GY via PH on	0.004	0.004	-0.001	0.010	-0.001	0.000	0.006	0.002	0.007	0.006	0.005	-0.001	0.008	0.009	-0.016	0.001
Indirect of GY via EH on	-0.002	-0.001	0.000	-0.001	0.000	0.000	-0.001	0.000	0.000	0.000	-0.001	-0.001	-0.001	0.000	-0.001	0.000
Indirect of GY via EW on	-0.125	-0.008	0.084	-0.043	-0.156	0.001	-0.002	-0.065	-0.074	-0.058	-0.197	-0.256	0.211	0.000	0.010	5.046
Genotypic correlation (r_g)	-0.185	-0.619	-0.354	-0.575	-0.783	-0.710	-0.607	-0.677	-0.612	-0.635	-0.648	-0.324	-0.207	0.594	0.273	
Determination coefficient	0.474	0.524	0.179	0.596	0.590	0.481	0.459	0.454	0.473	0.461	0.634	0.383	0.311	0.768	0.388	
Residual variable	0.725	0.690	0.906	0.636	0.641	0.721	0.735	0.739	0.726	0.734	0.605	0.785	0.830	0.481	0.782	

¹VIF = variance inflation factor. Number of days from sowing until male flowering (MF), number of days from sowing until female flowering (FF), plant height (PH), ear insertion height (EH), ear weight (EW), and grain yield (GY) on the main variables: crude protein (CP), lysine (Lys), methionine (Met), cysteine (Cys), threonine (Thr), tryptophan (Trp), valine (Val), isoleucine (Ile), leucine (Leu), phenylalanine (Phe), and arginine (Arg), apparent metabolizable energy corrected for nitrogen (AMEn), ether extract (EE), crude fiber (CF), and amylose (AML).

In super-early maturing genotypes, MF showed a positive linear correlation ($r_g = 0.581$) and positive direct effect (direct effect = 0.491) on Trp. FF showed a positive linear correlation ($r_g = 0.725$) and a positive direct effect (direct effect = 0.493) on EE. PH showed a positive linear correlation ($r_g = 0.335$) and a positive direct effect (direct effect = 0.448) on CF. EH showed a positive linear correlation and positive direct effects on AMEn (direct effect = 0.656), on EE (direct effect = 0.453), and on AML (direct effect = 0.576). The greatest direct negative effects were observed for the EW trait, with a negative linear correlation ($-0.878 \leq r_g \leq -0.841$) on Trp, Val, Ile, Leu, and Phe ($-0.509 \leq \text{direct effect} \leq -0.399$). GY showed a

negative linear correlation ($r_g = -0.722$) and a direct negative effect (direct effect = -0.399) on Lys (Table 6).

Table 6. Estimates of genotypic correlation coefficients and respective estimates of the direct and indirect effect of the explanatory variables based on ridge path analysis performed using values of $k = 0.10$ and path analysis, determination coefficient, and effect of the residual variable for the 22 super-early maturing maize genotype.

Effect	Main variable																AMEn	EE	CF	AML	VIF ¹
	Protein-nutritional											Energetic-nutritional									
	CP	Lys	Met	Cys	Thr	Trp	Val	Ile	Leu	Phe	Arg	AMEn	EE	CF	AML						
Direct of MF on	0.399	0.141	-0.037	0.286	0.382	0.491	0.133	0.168	0.275	0.298	0.180	-0.363	0.021	0.098	-0.362	4.324					
Indirect of MF via FF on	0.284	0.056	0.368	0.342	0.209	-0.054	0.200	0.265	0.096	0.156	0.241	0.451	0.444	-0.150	0.271	3.619					
Indirect of MF via PH on	-0.124	-0.056	-0.005	-0.069	-0.033	-0.143	0.007	0.023	-0.016	-0.043	-0.063	-0.002	-0.080	0.234	-0.051	0.410					
Indirect of MF via EH on	-0.352	-0.150	0.052	-0.234	-0.351	-0.152	-0.196	-0.336	-0.351	-0.271	-0.050	0.560	0.387	-0.179	0.491	2.161					
Indirect of MF via EW on	0.073	0.146	0.066	0.149	0.189	0.269	0.211	0.238	0.256	0.222	0.075	-0.264	-0.165	0.124	-0.158	1.397					
Indirect of MF via GY on	0.014	0.218	0.130	0.118	0.172	0.121	0.175	0.144	0.190	0.153	0.158	0.098	0.074	-0.090	0.083	1.609					
Genotypic correlation (r_g)	0.334	0.368	0.571	0.620	0.606	0.581	0.542	0.519	0.478	0.545	0.559	0.444	0.683	0.047	0.239						
Direct of FF on	0.316	0.062	0.409	0.380	0.232	-0.061	0.222	0.294	0.107	0.173	0.267	0.501	0.493	-0.166	0.301	5.404					
Indirect of FF via MF on	0.359	0.127	-0.033	0.257	0.344	0.442	0.120	0.152	0.247	0.268	0.162	-0.327	0.019	0.088	-0.326	2.895					
Indirect of FF via PH on	-0.118	-0.053	-0.004	-0.066	-0.032	-0.137	0.007	0.022	-0.015	-0.041	-0.060	-0.002	-0.077	0.224	-0.049	0.375					
Indirect of FF via EH on	-0.332	-0.141	0.049	-0.220	-0.332	-0.143	-0.185	-0.317	-0.331	-0.256	-0.047	0.529	0.365	-0.169	0.464	1.923					
Indirect of FF via EW on	0.101	0.202	0.091	0.206	0.262	0.373	0.292	0.330	0.355	0.307	0.104	-0.366	-0.229	0.172	-0.218	2.679					
Indirect of FF via GY on	0.020	0.305	0.183	0.165	0.242	0.170	0.245	0.202	0.267	0.215	0.221	0.137	0.104	-0.127	0.117	3.172					
Genotypic correlation (r_g)	0.377	0.507	0.735	0.760	0.740	0.639	0.723	0.712	0.640	0.684	0.674	0.523	0.725	0.005	0.319						
Direct of PH on	-0.237	-0.106	-0.009	-0.133	-0.064	-0.273	0.013	0.043	-0.030	-0.082	-0.120	-0.004	-0.153	0.448	-0.097	1.812					
Indirect of PH via MF on	0.209	0.074	-0.019	0.150	0.200	0.257	0.070	0.088	0.144	0.156	0.094	-0.190	0.011	0.051	-0.190	0.979					
Indirect of PH via FF on	0.158	0.031	0.205	0.190	0.116	-0.030	0.111	0.147	0.054	0.087	0.134	0.251	0.247	-0.083	0.151	1.120					
Indirect of PH via EH on	-0.270	-0.115	0.040	-0.179	-0.269	-0.116	-0.151	-0.258	-0.269	-0.208	-0.038	0.430	0.297	-0.137	0.377	1.271					
Indirect of PH via EW on	0.025	0.050	0.022	0.051	0.065	0.092	0.072	0.082	0.088	0.076	0.026	-0.090	-0.057	0.042	-0.054	0.164					
Indirect of PH via GY on	0.005	0.074	0.044	0.040	0.059	0.041	0.060	0.049	0.065	0.052	0.054	0.033	0.025	-0.031	0.028	0.187					
Genotypic correlation (r_g)	-0.134	-0.003	0.283	0.106	0.101	-0.056	0.177	0.156	0.048	0.073	0.137	0.429	0.355	0.335	0.206						
Direct of EH on	-0.412	-0.176	0.061	-0.274	-0.412	-0.178	-0.230	-0.394	-0.411	-0.318	-0.058	0.656	0.453	-0.209	0.576	3.590					
Indirect of EH via MF on	0.340	0.120	-0.032	0.244	0.326	0.419	0.114	0.144	0.234	0.254	0.154	-0.310	0.018	0.083	-0.309	2.603					
Indirect of EH via FF on	0.254	0.050	0.329	0.306	0.187	-0.049	0.179	0.237	0.086	0.139	0.215	0.403	0.397	-0.134	0.243	2.896					
Indirect of EH via PH on	-0.155	-0.070	-0.006	-0.087	-0.042	-0.179	0.009	0.028	-0.019	-0.054	-0.079	-0.003	-0.100	0.293	-0.064	0.641					
Indirect of EH via EW on	0.073	0.146	0.066	0.149	0.189	0.270	0.211	0.239	0.256	0.222	0.075	-0.264	-0.165	0.124	-0.158	1.401					
Indirect of EH via GY on	0.014	0.213	0.128	0.115	0.169	0.119	0.171	0.141	0.186	0.150	0.154	0.096	0.072	-0.089	0.082	1.541					
Genotypic correlation (r_g)	0.073	0.266	0.552	0.427	0.377	0.384	0.430	0.355	0.291	0.363	0.455	0.645	0.721	0.048	0.427						
Direct of EW on	-0.138	-0.275	-0.124	-0.282	-0.357	-0.509	-0.399	-0.450	-0.484	-0.419	-0.142	0.499	0.312	-0.234	0.298	6.029					
Indirect of EW via MF on	-0.211	-0.074	0.020	-0.151	-0.202	-0.260	-0.071	-0.089	-0.145	-0.158	-0.095	0.192	-0.011	-0.052	0.192	1.002					
Indirect of EW via FF on	-0.231	-0.046	-0.300	-0.279	-0.170	0.044	-0.163	-0.216	-0.078	-0.127	-0.196	-0.367	-0.362	0.122	-0.221	2.402					
Indirect of EW via PH on	0.043	0.019	0.002	0.024	0.012	0.049	-0.002	-0.008	0.005	0.015	0.022	0.001	0.028	-0.081	0.018	0.409					
Indirect of EW via EH on	0.219	0.093	-0.032	0.145	0.218	0.094	0.122	0.209	0.218	0.169	0.031	-0.348	-0.240	0.111	-0.305	0.834					
Indirect of EW via GY on	-0.026	-0.396	-0.237	-0.214	-0.314	-0.221	-0.318	-0.262	-0.346	-0.279	-0.287	-0.178	-0.135	0.165	-0.152	5.331					
Genotypic correlation (r_g)	-0.359	-0.706	-0.684	-0.785	-0.849	-0.852	-0.870	-0.861	-0.878	-0.841	-0.682	-0.152	-0.377	0.008	-0.141						
Direct of GY on	-0.027	-0.399	-0.239	-0.216	-0.316	-0.222	-0.320	-0.264	-0.348	-0.281	-0.289	-0.180	-0.136	0.166	-0.153	6.556					
Indirect of GY via MF on	-0.217	-0.077	0.020	-0.156	-0.208	-0.267	-0.073	-0.092	-0.150	-0.162	-0.098	0.198	-0.011	-0.053	0.198	1.061					
Indirect of GY via FF on	-0.241	-0.048	-0.313	-0.291	-0.178	0.046	-0.170	-0.225	-0.082	-0.132	-0.205	-0.383	-0.377	0.127	-0.231	2.615					
Indirect of GY via PH on	0.044	0.020	0.002	0.025	0.012	0.051	-0.002	-0.008	0.006	0.015	0.022	0.001	0.028	-0.083	0.018	0.052					
Indirect of GY via EH on	0.220	0.094	-0.033	0.146	0.220	0.095	0.123	0.210	0.219	0.169	0.031	-0.350	-0.242	0.112	-0.307	0.844					
Indirect of GY via EW on	-0.137	-0.273	-0.123	-0.279	-0.354	-0.505	-0.395	-0.446	-0.480	-0.416	-0.140	0.495	0.309	-0.232	0.295	4.902					
Genotypic correlation (r_g)	-0.361	-0.722	-0.709	-0.793	-0.857	-0.870	-0.852	-0.869	-0.835	-0.708	-0.238	-0.442	-0.533	-0.196							
Determination coefficient	0.313	0.519	0.565	0.727	0.816	0.811	0.761	0.776	0.806	0.746	0.539	0.489	0.586	0.151	0.223						
Residual variable	0.829	0.693	0.660	0.522	0.429	0.435	0.489	0.473	0.441	0.504	0.679	0.715	0.643	0.922	0.881						

¹VIF = variance inflation factor. Number of days from sowing until male flowering (MF), number of days from sowing until female flowering (FF), plant height (PH), ear insertion height (EH), ear weight (EW), and grain yield (GY) on the main variables: crude protein (CP), lysine (Lys), methionine (Met), cysteine (Cys), threonine (Thr), tryptophan (Trp), valine (Val), isoleucine (Ile), leucine (Leu), phenylalanine (Phe), and arginine (Arg), apparent metabolizable energy corrected for nitrogen (AMEn), ether extract (EE), crude fiber (CF), and amylose (AML).

The MF, FF, and PH traits showed the greatest indirect effects via EH on AMEn and AML. MF showed an indirect effect via FF on EE (indirect effect = 0.444). EH showed an indirect effect via MF on Trp (indirect effect = 0.419). EW showed an indirect effect via GY on Lys (indirect effect = -0.396). GY showed an indirect negative effect via EW on Trp, Val, Ile, Leu, and Phe (-0.505 ≤ indirect effect ≤ -0.395) and positive indirect effect on AMEn (indirect effect = 0.495) (Table 6).

There was a difference between early maturing genotypes and super-early maturing genotypes in the linear relationships and the magnitudes of the estimates of direct and indirect effects of explanatory variables on principal variables. In early maturing genotypes, FF, PH, EH, and GY can be used in indirect selection, and in super-early maturing genotypes, this is

true for MF, FF, PH, EH, EW, and GY. Therefore, breeders can consider indirect selection in early maturing genotypes based on higher EH and lower FF, PH, and GY, since these traits contribute to increasing levels of CP, Lys, Cys, Thr, Trp, Val, Ile, Leu, Phe, Arg, AMEn, CF, and AML in maize grains. In super-early maturing genotypes, selection should be based on higher MF, FF, PH, and EH, and lower EW and GY, since these traits indicate increased levels of Lys, Trp, Val, Ile, Leu, Phe, AMEn, EE, CF, and AML.

CONCLUSIONS

The number of days from sowing to male flowering, the number of days from sowing to female flowering, plant height, ear insertion height, ear weight, and grain yield can be used in indirect selection as indicators of grain nutritional quality.

Conflicts of interest

The authors declare no conflict of interest.

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