



# Linear relations among phenological, morphological, productive and protein-nutritional traits in early maturing and super-early maturing maize genotypes



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## ABSTRACT

The objective of this study was to verify through canonical correlation analysis if there is linear dependence among phenological, morphological, and productive traits with protein-nutritional traits in maize genotypes. The experiments were carried out in a randomized block design with three repetitions. In one experiment, 36 early maturing maize genotypes were evaluated and in another experiment 22 super-early maturing maize genotypes. The canonical groups were determined and structural equation models were elaborated. The matrix of phenotypic correlation coefficients among 23 traits was determined. Thereafter, the multicollinearity diagnosis was conducted within each group of traits. The canonical correlation analysis was performed within the groups: phenological versus protein-nutritional, morphological versus protein-nutritional, and productive versus protein-nutritional. In early maturing maize genotypes, the canonical correlations were not significant among groups of traits showing that the traits cannot be used as indicative of protein-nutritional quality in the indirect selection of plants. Moreover, in super-early maturing maize genotypes, the significant canonical correlation among phenological versus protein-nutritional traits and among productive versus protein-nutritional indicate that the traits number of days from sowing to female flowering, number of ears, and grain yield can be used for indirect selection as indicative of protein nutritional quality in maize grains.

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## 1. Introduction

With increasing population, the demand for food increases significantly. To meet this demand, it becomes necessary to increase the production of fruits, vegetables, leguminous plants,

oilseed and cereals, such as maize, with an improvement in the nutritional quality to meet the human and animal demands, especially for protein and energy. Facing the demand for cereals, maize stands out in worldwide production volume, estimated at 1006.87 million tons for the crop of 2015/2016. Considering the global scene, the United States is the greatest producer, followed by China and Brazil, with production estimated for the 2015/2016 crop of 345.07, 226.04 and 84.31 million tons, respectively (Fao, 2015).

Maize breeding programs seek improvements mainly in genotype stability to environments and increasing growth in the grain yield because, until now, this is the most sustainable crop trait. With forecasts of increase in the demand of this cereal for human and animal feeding, improvements in the nutritional quality, mainly in the protein and amino acid composition of this cereal, are necessary. The maize genotypes must be developed according to their purpose. A study carried out by Krivanek et al. (2007), with QPM - quality protein maize, saw increases in the composition of amino acids such as lysine and tryptophan. Increases in the protein and amino acid quality of maize can bring about expressive results

**Abbreviations:** NIRS, near infrared reflectance spectroscopy; CN, condition number; CV, coefficient of variation; MF, number of days from sowing until male flowering; FF, number of days from sowing until female flowering; PH, plant height at harvest; in cm; EH, ear insertion height at harvest, in cm; EP, ear placement; NP, number of plants; NE, number of ears; EI, ear index; EW, ear weight; GY, grain yield; TGW, weight of one thousand grains; CP, crude protein; Lys, lysine; Met, methionine; Cys, cysteine; Thr, threonine; Trp, tryptophan; Val, valine; Ile, isoleucine; Leu, leucine; Phe, phenylalanine; His, histidine; Arg, arginine; VIF, variance inflation factor; Fc, F test; % RM, percentage of raw matter.

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in animal nutrition, with improvements in animal development, reduction of costs, with less increment of synthetic amino acids and human feeding, especially in the emerging countries, where maize is a protein source.

The quality and chemical composition of grains is important for human and animal diets. The average content of proteins, oil and starch in maize grains is 9%, 4% and 73%, respectively (Balconi et al., 2007). These contents can be determined by near infrared reflectance spectroscopy (NIRS) a non-destructive, accurate and easy-to-measure method, (Dale et al., 2010). However, this equipment is expensive and requires skilled labor, restricting its use (Rahman et al., 2015).

In plant breeding via indirect selection, the knowledge of the linear associations between agronomic traits, aiming at identifying the genotypes that show traits of interest, is important. When the trait to be improved has low heritability and is difficult to measure and identify, then simultaneous selection more than one trait becomes problematic (Cruz and Regazzi, 1997).

Genetic correlation, used in the orientation of selection programs, seeks to explain through genetic mechanisms the joint variation of two variables allowing for indirect selection of traits based on high heritability traits (Robinson et al., 1951). Phenotypic correlation is the association between two traits directly observed and is ruled by genetic and environmental components (Falconer and Mackay, 1996).

To identify linear combinations of two sets of traits that are correlated to each other canonical correlation analysis has been used (Witten and Tibshirani, 2009). Canonical correlation analysis is a multivariate statistical to be determined procedure that allows to the linear relations between two groups or sets of traits (X and Y). Through this method, it is possible to estimate the maximum correlation between two complexes of traits, especially when there is a great number of traits being studied, enabling the discovery of linear combinations of traits in each group, in order to study the interrelations between two complexes determined by an arbitrary number of traits (Cruz and Regazzi, 1997).

The canonical correlation analysis has been an important tool for crop breeding, since it allows to verify the existing associations among groups of traits. Moreover, it allows to identify the promising traits that can be used in indirect selection to maximize genetic gain.

Structural equation models are another multivariate analysis technique used in plant breeding studies. These models allow explaining a causal relation model, estimate and test simultaneously the direct, indirect, and total effects among one or more explanatory variables and among one or more response variables (Hair et al., 2009).

Studies to characterize maize genotypes and genetic divergence through grouping analysis in early maturing and super-early maturing genotypes have been done by Alves et al. (2015). However, studies about the association between groups of phenological, morphological and productive traits versus protein-nutritional traits through canonical correlations in maize were not found in the literature. Thus, the objective of this study was to verify through canonical correlation analysis if there is linear dependence among phenological, morphological, and productive traits with protein-nutritional traits in early maturing and super-early maturing maize genotypes.

## 2. Material and methods

### 2.1. Field experiments

The experiments with maize (*Zea mays* L.) were carried out during the agricultural year of 2009/2010 in the experimental area

of the Plant Science Department at the Federal University of Santa Maria, Southern Brazil, at 29°42'S, 53°49'W and 95 m altitude. Thirty-six early maturing genotypes of maize (experiment 1) and 22 super-early maturing maize genotypes (experiment 2) were evaluated. The genotypes were from belonging to the Network of Evaluation of Maize Genotypes in Rio Grande do Sul, coordinated by the Agriculture Research State Foundation (Fundação Estadual de Pesquisa Agropecuária - FEPAGRO). The complete description of the genotypes evaluated has already been presented by Alves et al. (2015).

The experimental design was a randomized block with three replications. The experimental units were composed of two rows 5 m length, with 0.80 m space between rows and 0.20 m between the plants in the row. The sowing procedure was carried out manually on 26/10/2009, with base fertilization of 37.5 kg ha<sup>-1</sup> of nitrogen (N), 150 kg ha<sup>-1</sup> of phosphorus (P<sub>2</sub>O<sub>5</sub>) and 150 kg ha<sup>-1</sup> of potassium (K<sub>2</sub>O). The emergence of plants occurred between 01/11/2009 and 03/11/2009, and the population was adjusted by thinning to 62,500 plants ha<sup>-1</sup>. In the topdressing fertilization, 200 kg ha<sup>-1</sup> of nitrogen were applied, divided in three applications, when the plants were at the three, five and ten leaf stage. The harvest of maize ears was done manually on 15/03/2010.

### 2.2. Measurement of the variables and lab procedures

In every experimental entry the following phenological traits were measured: number of days from sowing until male flowering (MF) and number of days from sowing until female flowering (FF); and morphological traits: plant height at harvest (PH, in cm), ear insertion height at harvest (EH, in cm) and ear placement (EP = EH/PH) was calculated. On March 15, 2010, the maize ears were harvested. At that point, data was collected on productive traits: number of plants (NP, plants ha<sup>-1</sup>), number of ears (NE, ears ha<sup>-1</sup>), ear index (EI = NE/NP), ear weight (EW, in t ha<sup>-1</sup>), grain yield at 13% humidity (GY, in t ha<sup>-1</sup>) and one thousand grain weight (TGW, in grams). A sample of 500 g was separated, stored in a paper bag, and placed in a forced circulation oven until it reached 10% humidity. After drying, the grains were ground in a micro mill (MA-630, Marconi) to obtain a sample with granulometry between 0.30 and 0.50 mm. Each ground sample was stored in a hermetically closed package until grain nutritional analyses. For each sample the following protein-nutritional traits were determined: crude protein (CP); lysine (Lys), methionine (Met), cysteine (Cys), threonine (Thr), tryptophan (Trp), valine (Val), isoleucine (Ile), leucine (Leu), phenylalanine (Phe), histidine (His), arginine (Arg), all of them in raw matter percentage (%RM). The evaluations were done through NIRS - Near Infrared Reflectance Spectroscopy using a calibration adjustment through the analytical procedure CEAN 010 of Adisseo Brasil AS.

### 2.3. Variance analysis and frequency histograms

For the phenological, morphological, productive, and protein-nutritional traits, in each experiment (early and super-early maturing) assumptions of the mathematical model were tested: normality of errors and homogeneity of residual variances. The normality of the errors was checked through the Kolmogorov-Smirnov test and the residual variance homogeneity by the Chi-square test of Bartlett (Steel et al., 1997). A variance analysis was carried out at a 5% significance level noting the estimated values of the F test for genotype (Fc) and coefficient of variation (CV). The frequency histograms were developed based on the means of each genotype, for each measured trait in each of the experiments.

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