American Journal of Plant Sciences, 2017, 8, 3324-3337
http://www.scirp.org/journal/ajps
ISSN Online: 2158-2750
ISSN Print: 2158-2742

Adaptability, Stability and Multivariate Selection by Mixed Models

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How to cite this paper: de Pelegrin, A.J., Carvalho, I.R., Nunes, A.C.P., Demari, G.H., Szareski, V.J., Barbosa, M.H., da Rosa, T.C., Ferrari, M., Nardino, M., dos Santos, O.P., de Resende, M.D.V., de Souza, V.Q., de Oliveira, A.C. and da Maia, L.C. (2017) Adaptability, Stability and Multivariate Selection by Mixed Models. *American Journal of Plant Sciences*, **8**, 3324-3337.
https://doi.org/10.4236/ajps.2017.813224

Received: September 27, 2017
Accepted: December 11, 2017
Published: December 14, 2017

Abstract

The aim of this work was to estimate the adaptability and stability of grain yield per hectare and percentage of crude protein of maize grains combined in an index, and to establish a multicharacter selection through mixed models based on an objective character and 15 auxiliary traits. The trials were conducted in the 2013/2014 agricultural year in four growing environments of the Rio Grande do Sul, BR state. The experimental design was randomized blocks arranged in a factorial scheme, being four growing sites × 15 single cross maize hybrids, arranged in three repetitions. The genotypic index, composed by the grain yield and the crude protein percentage in the grains, is the best selection strategy to achieve maize superior genotypes. The multivariate genotypes selection, considering grain yield and crude protein, is efficient. The genotypes FORMULA TL®, AS1656PRO®, P30F53Hx®, LG6304YG® and 30F53 are more adapted and stable for grain yield and percentage of crude protein, in the conditions of this study. The mixed models were efficient to employ the multicharacter selection and to contribute for maize genetic breeding.

Keywords

Plant Breeding, *Zea mays* L., Phenotypic Index, Genetic Parameters, Multicharacter

1. Introduction

Maize (*Zea mays* L.) is one of the most produced cereals in the agribusiness scenario. Its importance is justified because of the wide utilization in animal nutrition, with 70% of the production in the form of silage or feed formulation, and even ethanol production in some countries such as USA [1]. The maize cultivation covers a wide range of growing environments. However, the genotypes may present differential behaviors as function of the environment modifications known as genotype environment interaction (G × E). The G × E interaction causes implications for breeding programs of any species, since the evaluation or recommendation of cultivars. Therefore, the study of this interaction is extremely important in order to find alternatives to minimize its effects, mainly by identifying genotypes highly responsive to environmental improvement, which are characterized by broad adaptability, predictable behavior and good stability [2].

Currently, breeding programs seek to identify high yielding genotypes, and posteriorly target their selection strategies in the quality of the grains, thus, the search for the ideal genotype that gathers productive and qualitative superiority demands elevated financial and labor resources of the breeding program, as well as suitable selecting strategies [3] [4] [5] [6]. An alternative to minimize this obstacle is the multivariate selection, which aims to select a set of simultaneous traits. In this way, the selection index proposed [7] [8] is used, which consists of a linear function of the predicted phenotypic or genotypic values of the characteristics pondered by estimated coefficients in order to maximize the correlation between the index and the true genetic values [9]. Therefore, genetic gain may be maximized when compared to direct selection, or selection individually performed for each trait [10]. The selection indexes have been successfully used in species of agronomic interest such as popcorn [11] [12], baby-corn and green corn [13]. However, there are few studies involving the selection of maize genotypes with high grain yield and protein content simultaneously.

Given the lack of information regarding multivariate selection in maize, this work aimed to estimate the adaptability and stability of grain yield per hectare and percentage of crude protein of maize grains combined in an index, and to establish a multicharacter selection through mixed models based on an objective character and 15 auxiliary traits.

2. Materials and Methods

The trials were conducted in the 2013/14 agricultural year, in four growing environments of the Rio Grande do Sul-BR state (**Table 1**). The climate for all growing environments is classified by Köppen as *Cfa* subtropical [16]. The experimental design was randomized blocks arranged in a factorial scheme, being four growing environments × 15 single cross maize hybrids, arranged in three repetitions. The genotypes used were: 1) 2A106, 2) 30F53, 3) P2530, 4) ADV9434PRO®, 5) AS1656PRO®, 6) DKB245PRO®, 7) LG6304YG®, 8) FORMULA TL®, 9) CELERON TL®, 10) P30F53Hx®, 11) P3646Hx®, 12) P1630Hx®,

Table 1. Description of growing environments regarding soil type, geographic coordinates, altitude, temperature and precipitation.

Environment	Soil*	Latitude	Longitude	Altitude (m)	Temperature °C**	Precipitation (mm)
Campos Borges—RS	Dark Red Latosol	28°55'36"S	53°01'40"O	513	18.42	134.52
Fortaleza dos Valos—RS	Dark Red Latosol	28°47'50"S	53°13'22"O	406	18.91	137.58
Santa Rosa—RS	Dystroferric Red Latosol	27°52'16"S	54°28'55"O	268	20.02	150.08
Tenente Portela—RS	Typical Red Ferric Aluminic Latossol	27°23'31"S	53°46'50"O	420	19.20	153.16

*Soil Classification [14]. **Historical averages of temperature and precipitation [15].

13) MAXIMUS VIP3®, 14) DEFENDER VIP® and 15) IMPACTP VIP3® (Table 2).

The experimental units were composed by four lines of five meters length, spaced 0.5 meters, totalizing 10 m^2 [17]. No-tillage system was used for all growing environments, with population of 80 thousand plants per hectare. It was used 300 kg·ha^{-1} of NPK in the formula (10-20-20) as base fertilization, and 135 kg·ha^{-1} of N in the amidic form as topdressing, applied at V_4 and V_6 vegetative stages. The management of weeds, pest and diseases were carried out preventively, in order to reduce interferences in the experiment's results.

The traits of interest were measured in the useful area of each experimental unit, which was composed by two central lines, discarding 0.5 m of each edge. The measured traits were: spike diameter (SD), results in millimeters (mm); spike length (SL), results in centimeters (cm); spike mass (SM), results in grams (g); cob diameter (CD), results in millimeters (mm); cob mass (CM), results in grams (g); spike insertion height (SH), results in meters; number of rows with grains in the spike (NRG), results in units; plan height (PH), results in meters (m); number of grains per row in the spike (NGR), results in units; prolificity (PRO), results in units; mass of a thousand grains (MTG), results in grams (g); grain yield (GY), results in kg·ha^{-1} [5] [17]; percentage of crude protein (CP) and mineral material (MM) in the grains [18].

The phenotypic index (PI) was generated by the product of grain yield per hectare and the percentage of crude protein of each genotype's grains [19].

$$\mathrm{PI}=\left(\frac{\mathrm{GY}}{S_{\mathrm{GY}}}\right)\times\left(\frac{\mathrm{CP}}{S_{\mathrm{CP}}}\right) \tag{1}$$

where: PI = phenotypic index combining grain yield per hectare and percentage of crude protein in the grains; GY = grain yield per hectare; CP: percentage of crude protein in the grains; S_{GY} = standard deviation of grain yield; S_{CP}: standard deviation of crude protein. Equal relative economic weights were attributed to both traits (GY and CP), *i.e.*, this phenotypic index was taken as objective character.

Table 2. Description of hybrids.

Hybrids	Type of Hybrid	Cycle	Company
2A106	Modified single cross	Super Early	Dow Agrosciences
30F53	Single cross	Early	Dupont do Brasil S.A
P2530	Single cross	Super Early	Dupont do Brasil S.A
P30F53Hx®	Single cross	Early	Dupont do Brasil S.A
P3646Hx®	Single cross	Early	Dupont do Brasil S.A
P1630Hx®	Single cross	Super Early	Dupont do Brasil S.A
ADV9434PRO®	Single cross	Early	Advanta
AS1656PRO®	Single cross	Early	Agroeste
DKB245PRO®	Single cross	Early	Dekalb
LG6304YG®	Modified single cross	Early	Limagrain/Guerra
FORMULA TL®	Single cross	Super Early	Syngenta Seeds Ltda
CELERON TL®	Single cross	Super Early	Syngenta Seeds Ltda
MAXIMUS VIP3®	Single cross	Early	Syngenta Seeds Ltda
DEFENDER VIP®	Three way cross	Early	Syngenta Seeds Ltda
IMPACTP VIP3®	Single cross	Early	Syngenta Seeds Ltda

The statistical model for analysis of the several environments in the experimental net, considering the plot mean value, is given by:

$$y = Xb + Zg + Wge + e$$

where: y, b, g, ge, and e are the data vectors. The model fixed effects are given by the average of the blocks through the sites, aleatory genotypic effects, aleatory G × E interaction effects, respectively. X, Z and W are matrices of incidence for b, g and ge, respectively [20]. The joint selection by PI, and the genotype's stability and adaptability were based on the statistic called harmonic mean of the relative performance of predicted genotypic values (HMRPGV) [20]. In this model, the interaction free predicted genotypic values consider all growing environments, are given by $u + g$, where u refers to the average of all environments. The predicted values for each trait in the univariate form were used in the genotypic selection index exemplified below. In addition, the genotypic correlation was obtained between the analyzed traits to elaborate the selection index. All the analyses were performed through Selegen software (Reml/Blup) [21]. The predicted genotypic values were used for estimating the pair to pair joint correlation between growing environments.

The predicted genetic values for each trait from the univariate analysis may be used to compose the selection indexes considering one objective character and the others as auxiliaries [22], being PI (GY × CP) the objective trait, and the other 15 traits, GY, CP, CD, NRG, MTG, CM, PH, SD, SL, SH, NGR, PRO, SM, SGM and MM, considered auxiliaries, a selection index may be derived using this 16 information simultaneously:

$$GI = b_1 g_o + b_2 g_{a1} + b_3 g_{a2} + \cdots + b_{16} g_{a15} \tag{2}$$

where g_o is the standardized genotypic value of the objective character, and g_{ai} is the standardized genotypic values of the auxiliary traits. The index's weighting coefficients (b_i) are given by [22]:

$$b = P^{-1}C$$

where:

$$P = \begin{bmatrix} r_{\hat{g}o}^2 & r_{\hat{g}o}^2 r_{\hat{g}a1}^2 r_{\hat{g}o\hat{g}a1} & r_{\hat{g}o}^2 r_{\hat{g}a2}^2 r_{\hat{g}o\hat{g}a2} & \cdots & r_{\hat{g}o}^2 r_{\hat{g}a15}^2 r_{\hat{g}o\hat{g}a15} \\ & r_{\hat{g}a1}^2 & r_{\hat{g}a1}^2 r_{\hat{g}a2}^2 r_{\hat{g}a1\hat{g}a2} & \cdots & r_{\hat{g}a1}^2 r_{\hat{g}a15}^2 r_{\hat{g}a1\hat{g}a15} \\ & & r_{\hat{g}a2}^2 & \cdots & r_{\hat{g}a2}^2 r_{\hat{g}a15}^2 r_{\hat{g}a2a15} \\ & Sim & & \ddots & \vdots \\ & & & & r_{\hat{g}a15}^2 \end{bmatrix}$$

$$C = \begin{bmatrix} r_{\hat{g}o}^2 \\ r_{\hat{g}a1}^2 r_{\hat{g}o\hat{g}a1} \\ r_{\hat{g}a2}^2 r_{\hat{g}o\hat{g}a2} \\ \vdots \\ r_{\hat{g}a15}^2 r_{\hat{g}o\hat{g}a15} \end{bmatrix}$$

Vector of genetic covariance between the predicted genetic value of the objective character and the 16 sources of information (standardized predicted genetic value for the auxiliary traits), where $r_{\hat{g}o}^2$ is the reliability of selection based on the objective character; $r_{\hat{g}a1}^2$ is the reliability of selection based on the auxiliary trait 1; $r_{\hat{g}a2}^2$ is the reliability of selection based on the auxiliary trait 2; $r_{\hat{g}o\hat{g}a1}$ is the genetic correlation between the objective character and the auxiliary trait 1; $r_{\hat{g}o\hat{g}a2}$ is the genetic correlation between the objective character and the auxiliary trait 2, and $r_{\hat{g}a1\hat{g}a2}$ is the genetic correlation between the two auxiliary traits.

The index's reliability is obtained by the ratio between the index's variance and the genotypic variance of the biological aggregate or objective character:

$$r_{gg}^2 = Var(\text{Indice})/\sigma_g^2 \tag{3}$$

With the predicted genetic values standardization, it gives $\sigma_g^2 = 1$ and $r_{gg}^2 = Var(\text{Indice})$.

Thus, the variance of the index is given by:

$$Var(\text{Indice}) = b'Pb \tag{4}$$

Consequently, the accuracy of GI is given by the root of reliability.

3. Results and Discussion

The Deviance analysis revealed significance at 5% of probability by the chi-square test for the phenotypic index (PI), grain yield per hectare (GY), percentage of crude protein in the grains (CP), cob diameter (CD), number of rows with grains per spike (NRG), mass of a thousand grains (MTG), cob mass (CM), plant height (PH), spike diameter (SD), spike length (SL), spike insertion height (SH), number of grains per row in the spike (NGR), prolificity (PRO), spike mass (SGM), spike grains mass (GM), and percentage of mineral material in the grains (MM). As consequence, it is inferred that the estimates of variance components and genetic parameters (heritabilities) for the traits evaluated in the 15 maize hybrids are significantly different from zero.

The variance components obtained through the restricted maximum likelihood (REML) revealed, for the traits CD, NRG, MTG and CM, the highest contribution of the genetic fraction ($\sigma^2 G$) for the studied traits' phenotypic expression ($\sigma^2 P$). The highest effects of environment ($\sigma^2 E$) were evidenced for the traits NGR, PRO, SM and SGM. However, the genotype × environment interaction ($\sigma^2 INT$) evidenced higher effects through the traits PI, GY, CP and MM, which is justified because these traits are highly influenced by the variation imposed by the G × A interaction and their genetic nature, being controlled by a large number of genes and differentially interacting with the environment, modifying the trait's phenotypic expression.

The heritability of a trait is as an important property for genetic breeding, as it expresses the proportion of the total phenotypic variation that comes from the genetic variation, which is determined by the average effect of genes and the degree of similarity between genotypes [23], *i.e.*, it regards the total variation heritable fraction. In breeding programs, components and estimates of heritability are of fundamental importance to the breeder, since they assist in the decision-making process about which trait should be preconized in the selection, directing the financial resources, labor and the time spent to achieve greater genetic gain for the trait of interest.

The genetic parameters estimated for the traits of interest (**Table 3**) revealed broad sense heritability ($\hat{h}^2 g$) of low (from 0.01 to 0.15) and mean (from 0.15 to 0.37) magnitudes, according to classification [20]. These low magnitudes are probably linked to the great effect of environment on the phenotype. In study with nine landrace varieties and four commercial hybrids, the authors [24] verified $\hat{h}^2 g$ for grain yield (0.85), number of grains per row (0.45), number of rows with grains (0.80), and mass of a hundred grains (0.84). Research [25] with maize hybrids presented broad sense heritability for spike length (0.70), spike mass (0.65), spike grains mass (0.62), cob mass (0.70) and grain yield (0.23). Similarly, studies [26] have revealed broad sense heritability for plant height (0.59), spike insertion height (0.39), mass of a hundred grains (0.42), protein (0.96) and grain yield (0.56). The magnitude of heritability can be influenced by the estimation method, inbreeding level, genetic variability, sample size, number of environments, evaluated traits, size of the experimental unit, precision in conducting the experiment and data collection.

Regarding the broad sense heritability of the mean ($\hat{h}^2 mg$), the traits CD (0.84), NRG (0.81), MTG (0.78), CM (0.71), PH (0.62), SD (0.56) and SL (0.56) presented intermediate to high magnitudes. These results agree with those found by Nardino *et al.* [27], where the pre-commercial hybrids presented $\hat{h}^2 mg$ for plant height (0.72), spike diameter (0.74), number of rows with grains (0.75),

Table 3. Estimates of variance components and genetic parameters (individual REML) for the objective character of selection or phenotype index (PI) and the 15 auxiliary traits in maize hybrids evaluated in the joint analysis between environments.

REML$^+$	Traits^{++}							
	PI	GY	CP	CD	NRG	MTG	CM	PH
$\sigma^2 G$	0.21	719,035.75	0.19	2.36	0.7	341.97	7.28	41.60
$\sigma^2 E$	0.63	195324	0.42	3.3	1.55	917.12	16.41	225.18
$\sigma^2 INT$	8.55	4,228,051.9	3.37	0.66	0.12	72.09	6.56	27.14
$\sigma^2 P$	9.40	5,172,411.7	3.98	6.32	2.38	1331.19	30.26	293.93
$\hat{h}^2 g$	0.02	0.14	0.05	0.37	0.29	0.26	0.24	0.14
$\hat{h}^2 mg$	0.09	0.41	0.18	0.84	0.81	0.78	0.71	0.62
Acgen	0.30	0.64	0.42	0.92	0.90	0.89	0.84	0.79
C^{2}INT	0.91	0.82	0.85	0.10	0.05	0.05	0.22	0.09
Řğloc	0.02	0.15	0.05	0.78	0.85	0.83	0.53	0.61
CVgi (%)	6.49	10.00	6.71	5.82	5.29	6.70	12.91	3.41
CVe (%)	11.19	5.11	9.97	6.88	7.89	10.97	19.38	7.94
CVr	0.58	1.96	0.67	0.85	0.67	0.61	0.67	0.43
Mean	7.11	8655.9	6.50	26.43	15.81	276.03	20.91	188.97

REML$^+$	Traits^{++}							
	SD	SL	SH	NGR	PRO	SM	SGM	MM
σ^2G	0.97	0.29	25.28	0.98	0.004	21.98	43.59	0.007
σ^2E	5.53	2.52	117.5	13.76	0.066	835.77	5858.99	0.12
σ^2INT	1.21	0.10	59.29	0.28	0.0002	106.78	856.78	1.24
σ^2P	7.73	2.91	202.07	15.05	0.071	964.53	6759.35	1.37
$\hat{\mathrm{h}}^2$g	0.13	0.10	0.13	0.07	0.06	0.02	0.01	0.01
$\hat{\mathrm{h}}^2$mg	0.56	0.56	0.51	0.45	0.41	0.19	0.06	0.02
Acgen	0.75	0.75	0.71	0.67	0.64	0.43	0.24	0.15
C^{2}INT	0.16	0.03	0.29	0.02	0.01	0.11	0.13	0.90
řğloc	0.45	0.75	0.30	0.78	0.83	0.17	0.05	0.01
CVgi (%)	2.15	3.29	4.95	3.22	6.07	3.15	1.73	3.70
CVe (%)	5.12	9.67	10.67	12.04	24.78	19.43	20.06	15.55
CVr	0.42	0.34	0.46	0.27	0.24	0.16	0.09	0.24
Mean	45.98	16.43	101.58	30.81	1.04	148.76	381.66	2.27

$^+\sigma^2 G$: genotypic variance; $\sigma^2 E$: Residual variance; $\sigma^2 INT$: genotype × environment interaction variance; $\sigma^2 P$: phenotypic variance; $\hat{h}^2 g$: individual broad sense heritability coefficient, interaction-free; $\hat{h}^2 mg$: heritability of the genotype's means; *Acgen*: genetic accuracy; $C^2 INT$: coefficient of determination of the genotype x environment interaction; *řğloc*: genotypic correlation between environments; *CVgi* (%): coefficient of genotypic variation; *CVe* (%): coefficient of experimental variation; *CVr*: coefficient of relative variation; and *Mean*: Overall mean of the traits for the different environments. $^{++}$GY: grain yield per hectare (kg·ha^{-1}); CP: percentage of crude protein in the grains (%); CD: cob diameter (mm); NRG: number of rows with grains in the spike (unit); MTG: mass of a thousand grains (g); CM: cob mass (g); PH: plant height (cm); SD: spike diameter (cm); SL: spike length (cm); SH: spike insertion height (cm); NGR: number of grains per row in the spike (unit); PRO: prolificity (unit); SM: spike mass (g); SGM: spike grains mass (g) and MM: mineral material of the grains (%).

spike length (0.58), and mass of a hundred grains (0.52). Research [24] demonstrated $\hat{h}^2mg$ for mass of a hundred grains (0.97), and number of grains per row (0.83). Considering it, researches define that traits presenting this parameter elevated, are likely to be selected [28].

Regarding the genetic accuracy ($Acgen$), it is observed except for PI (0.30), CP (0.42), SM (0.43), SGM (0.24) and MM (0.15), moderated to high magnitudes (from 0.64 to 0.92) for the other traits. The high selective accuracy is indicative of precision, being the ration between predicted and real values [29]. It culminates in greater breeding success due to the selection of superior genotypes.

The genotypic correlation among the performance in the growing environments ($\check{r}\breve{g}loc$) revealed higher magnitudes for the traits CD (0.78), NRG (0.85), MTG (0.83), PH (0.61), SL (0.75), NGR (0.78) and PRO (0.83). This fact indicates that the G × E interaction for these traits expressed simple effects, in other words, although there was differentiated behavior, the genotypes classification was not substantially altered in function of the different tested environments [30]. The coefficient of genotypic variation ($CVgi$) ranged from 2.15% to 12.91%, indicating the presence of genetic variation for the evaluated traits. Researches define that the higher magnitude of coefficient of genotypic variation allows genetic gains in the genotypes selection [20]. Regarding the coefficient of experimental variation (CVe), low magnitudes were observed, which reflects the suitable experimental conditions and reliable estimates. The coefficient of relative variation (CVr) ranged from 0.09 (SGM) to 1.96 (GY), with higher contribution of the genotypic value for the trait's total variation, indicating they may be less influenced by environment effects [31].

The genetic correlations for growing environments obtained pair to pair, and referent to the PI objective character, were all low [29], revealing elevated dissimilarity among environments and indicating the absence of breeding zones, therefore, the selection strategies must be exclusively proceeded in each one (**Table 4**). Studies [32] with maize open pollinated varieties grown in 15 environments in the Goiás state-BR, evidenced formation of two groups of stable environments over the agricultural years studied, and a reduction of 16% of the environments currently used. Research [33] stratified the environments regarding maize lodging and breaking, thus, when considering these traits, the experimental net can be reduced because the genotypes do not present differential responses as function of environmental variations.

Table 4. Pair to pair genetic correlation among the studied environments regarding PI index.

	CB*	FV	SR	TP
CB	-	0.019	0.0035	0.007
FV		-	0.086	0.017
SR			-	0.38
TP				-

*CB: Campos Borges, RS; FV: Fortaleza dos Valos, RS; SR: Santa Rosa, RS and TP: Tenente Portela, RS.

The genotype ordering by the interaction free predicted genotypic values (u + g) among growing environments (**Table 5**) is useful for recommending maize hybrids to any other environment which was not considered in the experimental net. From the reckoning of the gains with selection for PI (objective character or phenotype index), a relatively small gain of 4.46% is verified for selecting the best maize hybrid (FORMULA TL®) considering simultaneously grain yield per hectare and percentage of crude protein in the grains. This result is explained by the low heritability of these traits. Thus, selection indexes that consider information of the auxiliary traits should be elaborated, aiming to increase the objective character's genetic variance and selective accuracy.

Besides the best genotypes recommendation through the interaction free genotypic values ($u + g$), a general recommendation for all environments of the experimental net can be realized by the capitalization of the mean interaction ($u + g$ + gem) among environments (**Table 5**). This ordering is greatly relevant for plant breeding because it considers the mean genotypes performance in the experimental net environments. The gains with selection through $u + g$ + gem were superior to gains achieved through $u + g$ (**Table 5**) due to the average performance increment of each genotype in the four environments. Therefore, the use of mixed models methodology and the REML/BLUP procedure allows to access important effects to guide genetic selection by the breeder.

Table 5. Ordering of maize hybrids through genotypic values free from genotypes × environments interaction effects ($u + g$), genotypic values plus one mean effect of interaction ($u + g$ + gem) and predicted gains for the objective character or phenotype index (PI), in the joint analysis among environments.

Ranking	Genotype	g	$u + g$	cumulative gain in relation to the overall mean	Individual gain in relation to the general mean	$u + g$ + gem	Cumulative gain u + g + gem in relation to the overall mean (%)	Individual gain u + g + gem in relation to the overall mean (%)
1	FORMULA TL®	0.32	7.42	4.46%	4.46%	10.61	49.36	49.36
2	P30F53Hx®	0.15	7.25	3.26%	2.06%	8.73	36.09	22.82
3	AS1656PRO®	0.12	7.23	2.75%	1.72%	8.46	30.41	19.06
4	LG6304YG®	0.08	7.18	2.34%	1.10%	7.97	25.85	12.17
5	30F53	0.06	7.17	2.04%	0.84%	7.77	22.54	9.31
6	IMPACTP VIP3®	0.02	7.13	1.75%	0.30%	7.34	19.33	3.27
7	ADV9434PRO®	−0.01	7.10	1.48%	−0.10%	7.03	16.41	−1.13
8	CELERON TL®	−0.01	7.09	1.28%	−0.17%	6.97	14.11	−1.93
9	DKB245PRO®	−0.02	7.09	1.11%	−0.21%	6.94	12.29	−2.33
10	P2530	−0.03	7.08	0.96%	−0.37%	6.81	10.65	−4.10
11	P3646Hx®	−0.07	7.04	0.79%	−0.99%	6.33	8.69	−10.90
12	P1630Hx®	−0.08	7.03	0.63%	−1.10%	6.24	6.95	−12.15
13	2A106	−0.11	6.99	0.46%	−1.61%	5.84	5.05	−17.81
14	MAXIMUS VIP3®	−0.19	6.91	0.23%	−2.74%	4.95	2.52	−30.32
15	DEFENDER VIP®	−0.23	6.88	0.00%	−3.19%	4.60	0.00	−35.31

By comparing the ordering for PI through the predicted genotypic value ($u + g$), genotypic value plus the mean interaction ($u + g +$ gem), stability (HMGV), adaptability (RPGV) and stability, adaptability and grain yield simultaneously (HMRPGV*GY) (**Table 6**), it is verified an alternation in the ranking of genotypes. This fact reveals that the use of new selection attributes or criteria in the study of maize hybrids performance in different environments provides greater efficiency in the selection of superior genotypes. Thereby, a gain of 62% was obtained in the selection of the five best maize hybrids (FORMULA TL®, AS1656PRO®, P30F53Hx®, LG6304YG® and 30F53) in relation to the best hybrid for the criterion HMRPGV*GY.

The ranking of genotypes through HMRPGV*GY was ideal and should be considered for the final recommendation of the best genotypes. This criterion of selection simultaneously considers stability, adaptability and grain yield of the genotypes grown in the experimental net environments.

The index (GI) with an objective character (PI) and 15 auxiliary traits was elaborated according to methodology of global optimization and multivariate BLUP initially derived by Viana and Resende [22], for utilization with three characters. In this study, the approach was expanded for genotypes selection using 16 characters, being a pioneering work in this sense (**Table 7**). The GI is

Table 6. Ranking of the genetic value stability (HMGV), genetic values adaptability (RPGV), stability and adaptability simultaneously (HMRPGV) for IP (objective character of selection).

	Stability		Adaptability			Stability and Adaptability		
Ranking	Genotype	HMGV	Genotype	RPGV	RPGV*GY	Genotype	HMRPGV	HMRPGV*GY
1	FORMULA TL®	8.77	FORMULA TL®	1.47	10.43	FORMULA TL®	1.38	9.82
2	AS1656PRO®	7.47	P30F53Hx®	1.23	8.73	AS1656PRO®	1.14	8.12
3	P30F53Hx®	7.32	AS1656PRO®	1.19	8.45	P30F53Hx®	1.11	7.91
4	30F53	7.18	30F53	1.18	8.37	LG6304YG®	1.01	7.19
5	LG6304YG®	6.19	LG6304YG®	1.08	7.66	30F53	1.00	7.08
6	DKB245PRO®	5.79	CELERON TL®	1.01	7.19	IMPACTP VIP3®	0.87	6.15
7	2A106	5.67	DKB245PRO®	0.99	7.01	CELERON TL®	0.86	6.08
8	IMPACTP VIP3®	5.24	IMPACTP VIP3®	0.97	6.87	P2530	0.82	5.80
9	CELERON TL®	5.12	ADV9434PRO®	0.96	6.79	P1630Hx®	0.80	5.70
10	P2530	5.00	P2530	0.93	6.62	2A106	0.78	5.52
11	ADV9434PRO®	4.96	2A106	0.91	6.50	ADV9434PRO®	0.76	5.37
12	P1630Hx®	4.95	P3646Hx®	0.84	5.97	CELERON TL®	0.74	5.26
13	P3646Hx®	4.36	P1630Hx®	0.84	5.97	P3646Hx®	0.69	4.90
14	DEFENDER VIP®	3.36	MAXIMUS VIP3®	0.73	5.16	DEFENDER VIP®	0.45	3.23
15	MAXIMUS VIP3®	2.72	DEFENDER VIP®	0.69	4.87	MAXIMUS VIP3®	0.39	2.77
	Gain related to the overall mean through HMRPGV*GY (best hybrid): 62%							

Note: the underlined hybrids are the best five according to the ordering of mean genotypic effects ($u + g +$ gem) in the selection among environments, also present in the selection ordering for stability, adaptability and stability and adaptability (15 in 15, 100%).

Table 7. Weighting coefficients (bi) of GI and ranking of maize hybrids and their genotypic values free from G × A interaction ($u + g$), and by the genotypic index (GI) scores composed by the PI objective character, which combines grain yield per hectare and the percentage of crude protein of the grains, jointly with the 15 auxiliary traits.

Weighting coefficients of GI		Ranking	Genotype	PI ($u + g$)	Genotype	GI (scores)	Cumulative gain in relation to GI overall mean (%)	Individual gain in relation to GI overall mean (%)
b1	0.65	1	FORMULA TL*	7.42	FORMULA TL*	62.07	6.79	6.79
b2	0.44	2	P30F53Hx*	7.25	AS1656PRO*	60.18	5.16	3.54
b3	0.63	3	AS1656PRO*	7.23	P30F53Hx*	59.92	4.47	3.08
b4	0.13	4	LG6304YG*	7.18	30F53	59.07	3.76	1.63
b5	−0.03	5	30F53	7.17	DKB245PRO*	58.95	3.29	1.43
b6	−0.18	6	IMPACTP VIP3*.	7.13	IMPACTP VIP3*	58.69	2.90	0.97
b7	−0.12	7	ADV9434PRO*	7.10	LG6304YG*	58.54	2.59	0.71
b8	−0.09	8	CELERON TL*	7.09	ADV9434PRO*	57.98	2.24	−0.25
b9	0.05	9	DKB245PRO*	7.09	CELERON TL*	57.91	1.95	−0.37
b10	0.19	10	P2530	7.08	P2530	57.62	1.67	−0.86
b11	−0.24	11	P3646Hx*	7.04	P3646Hx*	57.30	1.39	−1.42
b12	0.32	12	P1630Hx*	7.03	P1630Hx*	57.04	1.11	−1.87
b13	−0.04	13	2A106	6.99	2A106	56.76	0.85	−2.34
b14	0.07	14	MAXIMUS VIP3*	6.91	DEFENDER VIP*	55.05	0.41	−5.29
b15	0.11	15	DEFENDER VIP*	6.88	MAXIMUS VIP3*	54.78	0.00	−5.75
b16	−0.26	-	-	-	-	-	-	-

GI overall mean: 58,12

Coincidence (five best genotypes) between PI and GI: 80%

$^+$GY: grain yield per hectare (kg·ha^{-1}); CP: percentage of crude protein in the grains (%); CD: cob diameter (mm); NRG: number of rows with grains in the spike (unit); MTG: mass of a thousand grains (g); CM: cob mass (g); PH: plant height (cm); SD: spike diameter (cm); SL: spike length (cm); SH: spike insertion height (cm); NGR: number of grains per row in the spike (unit); PRO: prolificity (unit); SM: spike mass (g); SGM: spike grains mass (g) and MM: mineral material of the grains (%).

composed by the PI objective character which combines grain yield per hectare and percentage of crude protein in the grains, jointly to the 15 auxiliary traits optimally weighted by their accuracies, heritabilities and genetic correlations.

All these factors are adequately considered in the weighting coefficients (**Table 7**), which will be higher as higher the correlations of auxiliary traits with the objective character are [22]. The GI selective accuracy was 0.63, being 210% higher than the PI objective character individually considered (accuracy of 0.30). Selective accuracy refers to the correlation between true genotypic value and predicted value through experimental information [29]. This parameter's utilization is considered ideal for choosing the best selection method, mainly because the genetic gain is directly proportional to the accuracy, *i.e.*, as higher the accuracy is, better is the precision of selection [34].

It was verified a change of position between the genotypes selected by PI and

GI, with coincidence of 80% among the five best maize hybrids. Therefore, the ordering generated by GI should be used for the final recommendation of the genotypes, since it is a more accurate index than the PI, as it aggregates information of the auxiliary traits, their genotypic correlations with the objective character, genotypic values and selection reliability. In addition to accuracy increment, the GI character provided higher genetic gains than PI, where the use of GI increased genetic gain by 2.33% due to the selection of the best genotype, and 1.72% by the selection of the three best ones. In genetic breeding programs, there is an imminent difficulty for selecting superior genotypes of traits with low genetic control, due to the great effect that the environment exerts on the genotype's phenotypic variation. Therefore, the use of auxiliary traits becomes a viable practice to improve the selecting process efficiency of superior maize genotypes.

4. Conclusions

1) The genotypic index, composed by the grain yield and the crude protein percentage in the grains, is the best selection strategy to achieve maize superior genotypes.

2) The multivariate genotypes selection, considering grain yield and crude protein, is efficient.

3) The genotypes FORMULA TL®, AS1656PRO®, P30F53Hx®, LG6304YG® and 30F53 are more adapted and stable for grain yield and percentage of crude protein, in the conditions of this study.

4) The mixed models were efficient to employ the multicharacter selection and to contribute for maize genetic breeding.

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