

RESEARCH ARTICLE

# Akaike criteria and selection of physiological multi-character indexes for the production of black oat seeds

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## ABSTRACT

The selection of characters provides the identification of complex characteristics, the objective of the work was to use the Akaike criteria and multiple regressions to prove the multi character selection and the interrelationships based on the Phenotypic, Standardized, Willians, Multiplicative, Mulamba and Mock indexes for the selection of black oat genotypes with high physiological potential of seeds. The study was conducted in Fortaleza dos Valos - RS in an experimental design used in randomized blocks with three replications. The trends for the selection of various Step Wise variables and the Akaike criteria are similar for most selection indices. For selection indexes, the phenotypic index and the standardized index correlate with the morphological characteristics, being mainly for the number of tillers. The genetic and multiplicative indices correlate with the characteristics of the seed. The phenotypic selection index was the one that stood out the most, regardless of the criterion used. This index correlates positively with the number of tillers. To select plants that present superior quality seeds, individuals with characteristics such as smaller panicles and with less spikelet ramifications and less panicle mass are sought.

## Highlighted Conclusions

1. The phenotypic selection index was the one that stood out the most.
2. To obtain quality seeds, plants with smaller panicles, less spiky branching and less panicle mass are sought.

## INTRODUCTION

Black oats (*Avena strigosa*) is a crop widely used in comparison to other winter cereals, it stands out mainly for its rusticity and low demand on soil fertility. It can be used as a cover to reduce the incidence of invasive plants, erosion, contributing to the improvement of the physical and chemical quality of the soil, when added in crop rotation systems, making it a good economic alternative in winter crops, animal feed as pasture, combined with its low production cost (Nirmalakumari et al. 2013).

For the winter crop of 2020, the area sown with black oats for the state of Rio Grande do Sul (RS) was 248,566 ha<sup>-1</sup> (Emater 2020). Some aspects are important for the crop to present a good seed productivity, these being, based on the number of fertile tillers per unit area, number of seeds per panicle and seed mass, are considered the direct components of productivity, also considering germination and seed vigor (Hawerth et al. 2014).

Due to the little information related to the genetic improvement of black oats, for the development of new genotypes, and biometric strategies that facilitate the selection process (Silveira et al. 2010), the use of multi-character selection tools provides the identification of complex characteristics, being able to consider components the selection of characters of the components of yield of the oats, that present indirect improvement in the indicators of physiological quality of the seeds. These methods allow for more homogeneity, minimal losses, assignment of multiple selection strategies and rapid gains during breeding and seed production (Pelegrin et al. 2017; Sponchiado 2018; Szareski et al. 2018; Carvalho et al. 2019; Szareski et al. 2019; Corazza et al. 2020).

In addition to developing the application of indexes, it is necessary to understand the associations and linear trends between the analyzed characteristics that may or may not be included in the multifunctional approach, allowing the breeder to identify which correlations may result in genetic gain and less time and resource expenditure during selection strategies and methods.

Due to the lack of information directed to the productive chain of black oat seeds with high physiological potential, this work aimed to employ the Akaike criteria and multiple regressions to prove the multi-character selection and the interrelationships based on the phenotypic criteria, Standardized, Willians, Multiplicative, Mulamba and Mock indices for the selection of black oat genotypes with high physiological potential of the seeds.

## MATERIAL AND METHODS

The study was conducted in Fortaleza dos Valos - RS, Brazil, under the coordinates 28°47'50 "S and 53°13'22" W, with 406 meters of altitude, corresponding to the 2019 crop season, the soil of the place is classified as dark red Latosol (Oxisol). Fourteen elite black oat genotypes were evaluated, with the physiological parameters of the seed based on the rules of the Rules for Seed Testing (Brasil 2009).

The experimental design used was a randomized block with three replications, totaling 42 experimental units composed of 10 sowing lines with 5 meters in length, spaced by 0.17 meters. The sowing took place on June 17, 2019 at a density of 300 plants per square meter, the management of fertilization was proposed according to the soil analysis and the harvest occurred when the plants showed physiological maturation, selecting 10 representative random plants per experimental unit.

The characteristics analyzed were: first count (FC, percentage), germination (G, percentage), seedling dry mass (SDM, grams), shoot length (SL, centimeters), radicle length (RL, centimeters), plant height (PH, centimeters), panicle insertion height (IH, centimeters), flag leaf angle (LE, degrees), stem diameter (SD, millimeters), tiller diameter (TD, millimeters), panicle length (PL, centimeters), number of ramifications of the panicle (NR, units), panicle mass (PM, grams), number of seeds per panicle (NS, units), seed mass per panicle (SM, grams), seed length (SEL, millimeters) and seed width (SW, millimeters).

With the information obtained, different selection indexes were used in order to improve the characteristics of the genotypes, targeting the physiological aspects. The phenotypic index or classic selection index was developed by Smith (1936) and Hazel (1943), which is based on the linear combination of phenotypic values of the characters with equal economic importance to maximize the correlation between the phenotypic aggregate and the selection index, considers the value of each experimental unit weighted by its sample standard deviation of the character, the phenotypic index is calculated from the formula:

$$PI = \left[ \left( \left( \frac{FC_{ij}}{\sigma FC_{ij}} \right) \times \left( \frac{G_{ij}}{\sigma G_{ij}} \right) \times \left( \frac{SDM_{ij}}{\sigma SDM_{ij}} \right) \times \left( \frac{SL_{ij}}{\sigma SL_{ij}} \right) \times \left( \frac{RL_{ij}}{\sigma RL_{ij}} \right) \right) \right]$$

where:

*PI*: Phenotypic multi-character index.

*FC<sub>ij</sub>*: Values referring to the first germination count in the *i*-th experimental unit in the *j*-th repetition.

*σFC<sub>ij</sub>*: Sample standard deviation for the first germination count.

*G<sub>ij</sub>*: Values referring to the germination percentage in the *i*-th experimental unit in the *j*-th repetition.

*σG<sub>ij</sub>*: Sample standard deviation for germination percentage.

*SDM<sub>ij</sub>*: Values referring to seedling dry mass in the *i*-th experimental unit in the *j*-th repetition.

*σSDM<sub>ij</sub>*: Sample standard deviation for seedling dry mass.

*SL<sub>ij</sub>*: Values referring to the shoot length of the seedling in the *i*-th experimental unit in the *j*-th repetition.

*σSL<sub>ij</sub>*: Sample standard deviation for the shoot length of the seedling.

*RL<sub>ij</sub>*: Values regarding the seedling root length in the *i*-th experimental unit in the *j*-th repetition

*σRL<sub>ij</sub>*: Sample standard deviation for seedling root length.

The standardized selection index is obtained through the phenotypic effects standardized by subtracting the arithmetic mean and weighted by the effects of the sample standard deviations (Gesteira et al. 2018), according to the formula:

$$ZI = \left[ \left( \left( \frac{FC_{ij} - \bar{y}FC_{ij}}{\sigma FC_{ij}} \right) + \left( \frac{G_{ij} - \bar{y}G_{ij}}{\sigma G_{ij}} \right) + \left( \frac{SDM_{ij} - \bar{y}SDM_{ij}}{\sigma SDM_{ij}} \right) + \left( \frac{SL_{ij} - \bar{y}SL_{ij}}{\sigma SL_{ij}} \right) + \left( \frac{RL_{ij} - \bar{y}RL_{ij}}{\sigma RL_{ij}} \right) \right) \right]$$

where:

*ZI*: Standardized Multicharacter Selection Index

*FCij*: Values referring to the first germination count in the i-th experimental unit in the j-th repetition.

$\bar{y}FCij$ : General average for first germination count in the i-th experimental unit in the j-th repetition.

$\sigma FCij$ : Standard deviation for first germination count in the i-th experimental unit in the j-th repetition.

*PGij*: Values referring to the germination percentage in the i-th experimental unit in the j-th repetition.

$\bar{y}Gij$ : General average for the germination percentage in the i-th experimental unit in the j-th repetition.

$\sigma Gij$ : Standard deviation for the germination percentage in the i-th experimental unit in the j-th repetition.

*SDMij*: Values referring to seedling dry mass in the i-th experimental unit in the j-th repetition.

$\bar{y}SDMij$ : General average of the seedling dry mass in the i-th experimental unit in the j-th repetition.

$\sigma SDMij$ : Standard deviation for seedling dry mass in the i-th experimental unit in the j-th repetition.

*SLij*: Values referring to the seedling shoot length in the i-th experimental unit in the j-th repetition.

$\bar{y}SLij$ : General average for the seedling shoot length in the i-th experimental unit in the j-th repetition.

$\sigma SLij$ : Standard deviation for the seedling shoot length in the i-th experimental unit in the j-th repetition

*RLij*: Values referring to seedling root length in the i-th experimental unit in the j-th repetition.

$\bar{y}RLij$ : General average for seedling root length in the i-th experimental unit in the j-th repetition.

$\sigma RLij$ : Standard deviation for seedling root length in the i-th experimental unit in the j-th repetition.

The Willians index consists of the product between the economic weight of the character and the phenotypic value that will be compiled in a producer (Sponchiado 2018). The weight of each character was determined as follows: percentage of germination (50%), seedling dry mass (20%), seedling shoot length (12.5%), radicle length (12.5%) and first germination count (5%), according to the formula:

$$WI = [((P1\% \times \bar{y}FCij) + (P2\% \times \bar{y}Gij) + (P3\% \times \bar{y}SDMij) + (P4\% \times \bar{y}SLij) + (P5\% \times \bar{y}RLij))]$$

where:

*WI*: Willians Index.

*P1%*: Economic weight attributed to the variable.

$\bar{y}FCi$ : Phenotypic mean of the genotype for the first germination count in the i-th experimental unit in the j-th repetition.

*P2%*: Economic weight attributed to the variable.

$\bar{y}Gi$ : Phenotypic mean of the genotype for the germination percentage in the i-th experimental unit in the j-th repetition.

*P3%*: Economic weight attributed to the variable.

$\bar{y}SDMi$ : Phenotypic mean of the genotype for the dry mass in the i-th experimental unit in the j-th repetition.

*P4%*: Economic weight attributed to each variable.

$\bar{y}SLi$ : Phenotypic mean of the genotype for the shoot length in the i-th experimental unit in the j-th repetition.

*P5%*: Economic weight attributed to each variable.

$\bar{y}RLi$ : Phenotypic mean of the genotype for root length in the i-th experimental unit in the j-th repetition.

The multiplicative index was obtained by the producer of the predicted genetic values of each specific genotype per experimental unit, these estimates being obtained by the restricted maximum likelihood (REML) and the predictions extracted by the Best unbiased prediction (BLUP) (Silva et al. 2017), the multiplicative index was calculated using the formula:

$$MI = [(Vg FCij \times Vg Gij \times Vg SDMij \times Vg SLij \times Vg RLij)]$$

where:

*MI*: Multiplicative Index.

*VgFCij*: Genetic value for the first germination count in the i-th experimental unit in the j-th repetition.

*VgGij*: Genetic value for the germination percentage in the i-th experimental unit in the j-th repetition.

*VgSDMij*: Genetic value for seedling dry mass in the i-th experimental unit in the j-th repetition.

*VgSLij*: Genetic value for seedling shoot length in the i-th experimental unit in the j-th repetition.

*VgRLij*: Genetic value for seedling root length in the i-th experimental unit in the j-th repetition.

The Mulamba and Mock index is based on the sum of the predictive genetic ranks obtained by REML and BLUP for each genotype multiplied by (economic weights (percentage of germination (50%), seedling dry mass (20%), seedling shoot length (12.5%), root length (12.5%) and first germination count (5%) (Bizari et al., 2017), according to the formula:

$$MMI = [(P1\% FC_{ij} + P2\% G_{ij} + P3\% SDM_{ij} + P4\% SL_{ij} + P5\% RL_{ij})]$$

where:

**MMI:** Mulamba and Mock Index

**P1%:** Economic weight attributed to the variable.

**FC<sub>ij</sub>:** Value for the first germination count in the i-th experimental unit in the j-th repetition.

**P2%:** Economic weight attributed to the variable.

**G<sub>ij</sub>:** Value for the germination percentage in the i-th experimental unit in the j-th repetition.

**P3%:** Economic weight attributed to the variable.

**SDM<sub>ij</sub>:** Value for seedling dry mass in the i-th experimental unit in the j-th repetition.

**P4%:** Economic weight attributed to each variable.

**SL<sub>ij</sub>:** Value for the seedling shoot length in the i-th experimental unit in the j-th repetition.

**P5%:** Economic weight attributed to each variable.

**RL<sub>ij</sub>:** Value for the seedling root length in the i-th experimental unit in the j-th repetition.

The data were submitted to the assumptions, normality and homogeneity of the residual variances and additivity of the statistical model. Afterwards, analysis of variance at 5% probability was used to identify the attribution to the effects of the different genotypes. To identify the trend of association between the characters, linear correlation was applied to all variables and indices with significance based on the t test at 5% probability, as the main character was attributed to the selection indices, and the methods of multiple regression with the Stepwise algorithm and the selection of models by the Akaike criterion to identify the independent variables determining the indices and their respective contributions. Due to the various characters involved, multivariate tools were applied, such as canonical correlations to define the interrelations between group I (selection indexes) and the other measured components. Subsequently, the Mahalanobis algorithm was applied to obtain the matrix of distances weighted by the residual matrix that served as the basis for the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) grouping.

## RESULTS AND DISCUSSION

The predictor models presented similar trends for the multi-character indexes, both by the multiple regression methodology with selection of variables by Step Wise and by the Akaike criteria (Table 1). The use of the Stepwise multiple regression method, used mainly to select the variables that most influence the output set, in this way can decrease the number of variables that make up the regression equation (Alves et al. 2013). One of the most used selection criteria is the linear regression of the F test, which is used since it has a normal distribution (Silva Junior et al. 2017). The indexes of selection of variables by multiple Step Wise regression showed similarity between the phenotypic index (IF) and the multiplicative index (IM), since they consider the multiplication of the results between the variables. The first index considers the values obtained from the count of each variable divided by the standard deviation and the second considers the genetic value of each variable multiplied with each other.

**Table 1. Predictive models based on multiple Step Wise regression and Akaike criteria.**

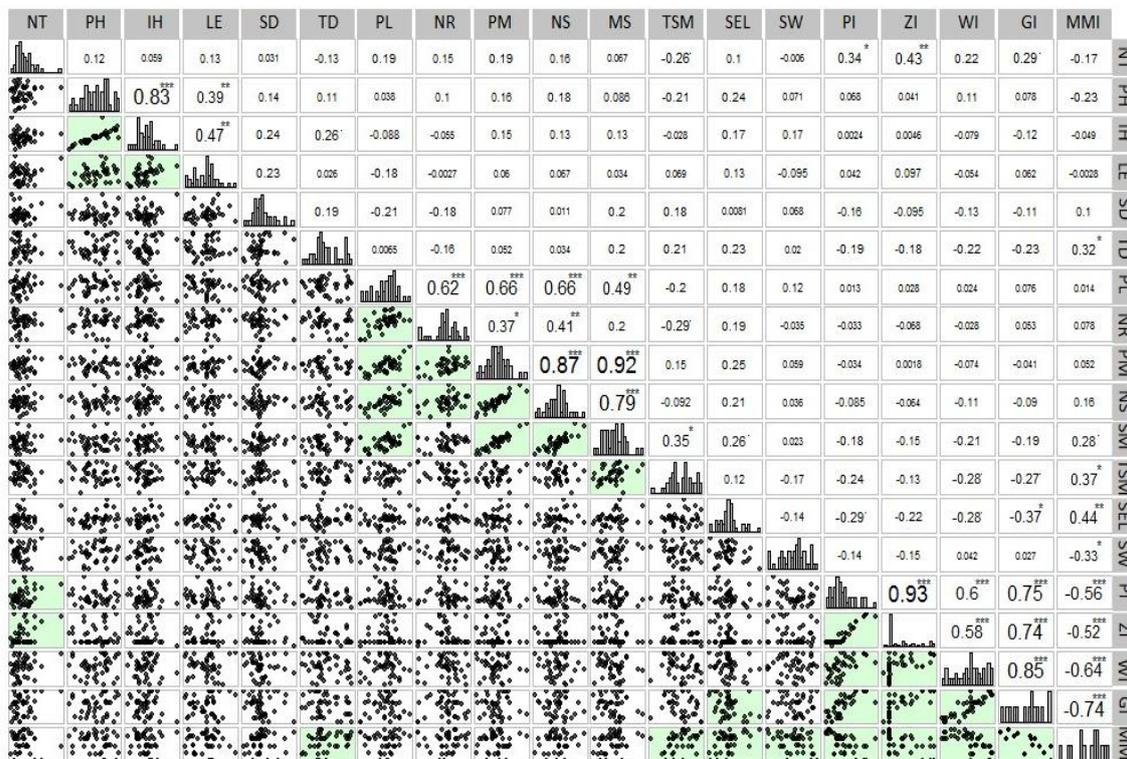
Multicharacter Index	Predictive model					
	Based on Multiple Regression (Step Wise)					
Y	Intercept	FC	G	SDM	SL	RL
PI*	-318833	509.45396	1412.48547	1322541	7757.86989	8179.13355
ZI	-32.50681	0.09624	0.08976	105.54398	0.73122	0.2979
WI	0.00111	5.00001	49.99999	19.97791	12.50003	12.5000
MI	-49754	222.51077	534.45155	129183	1559.87122	562.15814
MMI	121.01036	-	-0.64744	-327.72848	-	-101175
	Based on the Akaike Criteria					
PI	-318800	7758	8179	1412.0	1323000	509.5
ZI	-3.251 <sup>01</sup>	0.7309	0.2979	0.08987	105.6	0.09613
WI	5.122 <sup>-12</sup>	12.500	12.50	50.00	20.0	5.000
MI	-49750	1560.0	562.2	534.5	120200.0	222.5
MMI	121.00	-	-1.0120	-0.6474	-	-327.70

\* PI: Phenotypic Index; ZI: Standardized Selection Index; WI: Classic William Index; MI: Multiplicative Index; MMI: Mulamba and Mock index, first count (FC, percentage), germination (G, percentage), seedling dry mass (SDM, grams), shoot length (SL, centimeters), radicle length (RL, centimeters).

For the Akaike criterion it is estimated by using the formula  $AIC = -2 \log L + 2 p$ , where  $p$  is  $p$  number of estimated parameters, so the lower the index values, it refers to a better fit of the model (Resende et al. 2014). According to the same author, this criterion penalizes verisimilitude by the number of adjusted independent parameters, the lowest values show a better global adjustment, that is, it shows the best model. This methodology can be used to compare any type of model: linear, non-linear, nested and non-nested (Floriano et al. 2006). The indices that are similar for the first count variable were the classic Willians index (IW) and the multiplicative index (IM). The first index considers the evaluation of the economic weights of each variable, multiplied by the average of each variable, and the second index considers the genetic value of each variable multiplied with each other. For the variable length of aerial part, similar indices were the phenotypic index (IF) and the multiplicative index (IM). For most indexes, the selection criteria show positive trends. The Mulamba and Mock index is the one that presents the greatest difference from the others, due to the fact that they consider the ranking of each variable.

The Akaike criteria show that the indexes express variables with a positive effect, in contrast to the Mulamba and Mock index (MMI), which has an opposite effect to the other indexes. The highlight variable for this index was germination percentage (G). For the phenotypic index (PI), the variable that presented the greatest magnitude was the seedling shoot length (SL). For the Standardized Selection Index (ZI) the best answers were found for the variables seedling root length (RL) and seedling dry mass (SDM). For the Willians index (WI) the variables that stood out were the first germination count (FC) and radicle length (RL). Analyzing the multiplicative index (MI), the response variable that stood out positively was the seedling shoot length (SL).

The linear correlations (Figure 1) between the components of the panicle and the phenotypic indices, for the selection aiming at increasing the Number of Tillers (NT), the indices that contribute to the increase of the expression of this characteristic are the Phenotypic Index (PI) and the Willians Index (WI). For the height increase of (PH), the characteristics that tend to increase are the panicle insertion height (IH) and the flag leaf angulation (LE). The same occurs for the increase in IH, as there is an increase in LE, since they are related morphological characteristics. For the characteristic tiller diameter (TD), the index that presents the greatest contribution to the expression of this characteristic is the MI.



**Figure 1. Estimates of Pearson's linear correlation for seed quality, agronomic characteristics and multicharacter indexes for black oats.**

\* Pearson's linear correlation coefficients, significant at 5% probability of error. NT: Number of tillers; PH: Plant height; IH: Panicle insertion height; LE: Flag leaf angulation; SD: Stem diameter; TD: Tiller diameter; PL: Panicle length; NR: Number of ramification; PM: Panicle mass; NS: Number of Seeds; SM: Seed Mass; TSM: thousand seed mass; SEL: Seed Length; SW: Seed Width; PI: Phenotypic Index; ZI: Standardized Selection Index; WI: Classic William Index; MI: Multiplicative Index; MMI: Mulamba and Mock Index.

For the panicle length (PL) at the moment it seeks to increase it, there is an increase in the number of ramifications (NR), panicle mass (PM), number of seeds (NS) and seed mass (SM). According to studies by Meira et al. (2017) reports that the size and weight of seeds are related to vigor and seedling germination. Thus, it can be said that larger panicles tend to have a higher grain yield. To increase the number of ramifications (NR), there is an increase in panicle mass (PM) and number of seeds (NS), that is, more branched panicles tend to have a number of seeds and panicle mass, and with the increase of panicle mass (PM), there is an increase in the number of seeds (NS) and seed mass (SM). With the increase in the number of seeds (NS), there is an increase in the seed mass (SM). Studies by Meira et al. (2019a), report that the increase in productivity is highly correlated with the increase in the number of grains per plant and grain weight. By increasing the seed mass (SM), there are increases in TSM.

For the TSM variable, the index that contributes to the expression of this characteristic is the MI. For SEL, the indexes that best present this characteristic are GI and MI, and for SW the index that contributes to its expression is MI. Therefore, one must choose these indexes to carry out the indirect selection for this characteristic. Linear correlation helps as a tool that helps to demonstrate which characteristics increase a given variable.

The canonical correlations were stratified into two distinct groups of characteristics, group 1 is related to the selection indexes of the maximum physiological potential of oat seed and group 2 considers the morphological components of oat panicle, namely: Panicle length (PL), Number of ramifications (NR), Panicle Mass (PM). And physical characteristics of the seed, which are: Number of Seeds (NS), Seed Mass (SM), Seed Length (SEL) and Seed Width (SW). There was significance for the maximum likelihood between the groups of characters, stating that there is a linear dependence between these characteristics, confirmed by the high interclass correlation of 0.85 (Table 2).

**Table 2. Estimates of correlations between selection indexes (group 1) and morphological characters (group 2) in black oat genotypes.**

Character	Canonical pair
Group 1	
PI	-0.3664
ZI	-0.3840
WI	-0.404
MI	-0.4177
MMI	0.7919
Group 2	
PL	0.0611
NR	0.1775
PM	0.0342
NS	0.1596
SM	0.2674
SEL	0.3465
SW	-0.3734
<b>r*</b>	<b>0.858659</b>
<b>p**</b>	<b>&lt; 0.0033</b>

r\* = canonical correlation

p\*\* = significance.

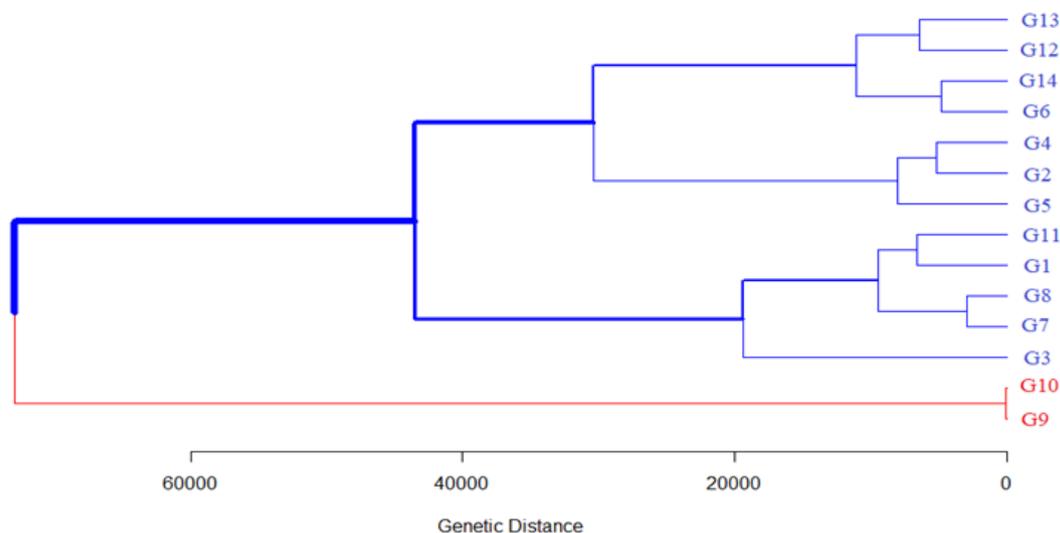
PI = phenotypic index, ZI = standardized selection index, WI = Willians Classic Index, MI = Multiplicative index.

MMI = Mulamb and Mock Index, PL = panicle length, NR = number of ramifications, PM = panicle mass, NS = number of seeds, SM = seed mass, SEL = seed length, SW = seed width.

It was then sought to evidence which characteristics relevant to group 2 that determine group 1, focus of selection in the indirect field, it was based then that the canonical loads of the characteristics of group 2 positively influence for: PL, NR, PM, NS, SM, SEL and negative for SW. For group 1, the canonical characteristics positively influenced the MI index, and negatively the PI, ZI, WI, MI. For this purpose, from a biological point of view, the focus of indirect selection is to increase the physiological potential of seed in the field based on multicharacteristic indices. Among the indices that stand out in the same direction, were the PI, ZI, WI, MI which sought to select plants that express smaller panicle lengths, followed by fewer spikelet branches per panicle and less panicle mass because they are morphological characteristics, such as a drain of photoassimilates and partition of assimilates to the plant. In this way, these characteristics will reduce the number and mass of panicle seeds followed by their length, however this will increase the width of the seed. With this parameter, it is possible to identify that from the width of the seed, it is possible to focus on the indirect selection in two ways, one based on the dimensions of the panicle and the other based on the dimensions of the seed, an agronomic ideotype for seed production. with greater vigor, they would be larger, shorter seeds, formed in smaller panicles, with less seeds and fewer branches, so that the objective of selection in an breeding program was achieved.

For MMI, it presents the following relation for indirect selection, where the characteristics that stand out are plants with greater panicle length, greater number of panicle branches, greater panicle mass, greater number of seeds, greater seed mass, greater length of the seed and shorter seed width. Selection based on panicle length, panicle weight, number of panicle grains and grain weight can result in greater selection gain, due to heritability values greater than 80% for these characters (Meira et al. 2019b, 2019c).

The dendrogram (Figure 2) shows that the studied genotypes have similarity for two large groups, with the group in blue standing out for a greater number of genotypes with similar characteristics.



**Figure 2. Dissimilarity expressed by the dendrogram obtained by the Mahalanobis algorithm and the method of medium connections (UPGMA), based on the information of the characters first count (FC, percentage), germination (G, percentage), seedling dry mass (SDM, grams), shoot length (SL, centimeters), radicle length (RL, centimeters), plant height (PH, centimeters), panicle insertion height (IH, centimeters), flag leaf angle (LE, degrees), stem diameter (SD, millimeters), tiller diameter (TD, millimeters), panicle length (PL, centimeters), number of ramifications (NR, units), panicle mass (PM, grams), number of seeds per panicle (NS, units), seed mass per panicle (SM, grams), seed length (SEL, millimeters) and seed width (SW, millimeters).**

The trends for the selection of multiple Step Wise variables and the Akaike criteria are similar for most selection indexes. The Phenotypic Index (PI) and the Multiplicative Index (MI), were similar for the multiple selection of Step Wise and for the Akaike criteria the indices that were similar were the Classic Willians Index (WI) and the Multiplicative Index (MI), for the variable first count and the phenotypic index (PI) and multiplicative (MI) for the variable shoot. For selection indexes, the phenotypic index (PI) and the standardized index (ZI) correlate with morphological characteristics, being mainly for the number of tillers. The GI and the multiplicative (MI) indices correlate mainly with seed characteristics, such as width, length. Similar indices, based on the multiple selection of Step wise, are the phenotypic index and the multiplicative index, for the Akaike criteria, the indices that show similarity were the classic Willians index and the multiplicative index for the first count and the phenotypic index and the multiplicative for the shoot length.

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