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Research Article

Experimental Statistical for Genetic Breeding Study of Wheat Crop

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Abstract

The key purpose of this study was used experimental statistics methods to evaluate, characterize and conserve the genetic resources of the Active Wheat Germplasm Bank (AWGB) and promote pre-breeding the Rural Development of Paraná State (IDR Paraná), Brazil. For that purpose, 209 accessions from the IDR Paraná Active Germplasm Bank and 16 cultivars in a simple lattice design (15x15) were sown in the experimental area of IDR Paraná, in Londrina, Paraná State, and data from 16 morphological and agronomic characteristics were taken. The statistics methods used were the analysis of variance (ANOVA), grouping of averages, analysis of simple linear correlation and analysis of genetic diversity with subsequent grouping by the UPGMA and Tocher methods were performed. It was verified the average efficiency of the lattice was 1.21 % with IC5 %: [99.31 ~ 103.11 %], representing little efficiency in relation to the randomized block design. Fourteen variables showed significance by the F test, indicating that at least one genotype differs from the others for each variable. By the analysis of genetic diversity, 3 groups were obtained in which the genotypes T092125 (Group C) and IA 072118 with T062113 (Group B) were in two isolated groups and the third group gathering the remaining 223 genotypes. This fact does not directly represent a narrow genetic basis for Active Germplasm Bank of IDR Paraná, due than 99 % of the variation is actually contained in agronomic variables: days to maturation (MAT) and ear (ESP), plant height (AP) and ear size (TE). Taking as a basis the grouping of means by Scott-Knott for these variables and grain weight per ear (PG / ESP), the formation of 4 for AP and ESP, 3 TE and PG / ESP groups, 2 for DC and P100G, reflecting wide diversity within each variable and in the set of these variables. The correlation analyzes showed a positive value between TE with PG / ESP and DC and a negative value between ESP and PG / ESP, both significant. Thus, the direction of crossings, to increase productivity, between genotypes of this set, must be in the direction of obtaining plants with earlier earing and with larger ears size. It can be inferred that the set of accessions evaluated has a broad genetic basis for agronomic variables. The 225 characterized accessions represent 49 % of the total accessions of wheat in the Active Wheat Germplasm Bank (AWGB) that have been regenerated and multiplied, being able to be directed to crossings focusing on pre-improvement and / or improvement to obtain new cultivars.

Introduction

Among plant breeders, there is a fear of decreasing genetic variability, conceptualized as genetic erosion, which can be circumvented through the institution of germplasm banks. Another point concerns the narrowing of the genetic base of modern cultivars of different species, including wheat, since researchers have preferred to use elite strains as parents in breeding programs [1,2]. This strategy opens a gap between the activities of genetic resources and breeding. While researchers involved with genetic resources collect and conserve variability, breeders have not explored the diversity available. According to data from FAO [3], the enormous genetic variability of wheat stored in germplasm banks ex situ has not been used in the development of new cultivars.

A classic way for researchers to find new genes of interest is to identify potentially useful traits in a germplasm bank or to use plant pre-breeding resources, since the genes with potential use, once identified, can be incorporated into elite genotypes. In this context, the FAO (Food and Agriculture Organization of the United Nations) has been suggesting the expansion of the characterization and evaluation activities, as well as the increase in the number of nuclear collections and pre-breeding programs, in order to favor the genetic basis of cultivated species, increasing genetic gain [4].

Crop breeding can be characterized as the art and science of developing plants with higher productivity, added to other agronomic characteristics of interest (resistance to biotic and abiotic stresses), and which reflects a reduction in investments with agricultural inputs. Wheat is one of the main foods in the human diet. It is used by 35% of the world population, [5], in addition to being one of the most planted cereals in the world [6], and representing about 20% of the total calories currently consumed by humanity. The wheat grown in Brazil belongs to the species *Triticum aestivum L.* and has three genomes, A, B and D, each represented by seven pairs of chromosomes. The known species of wheat form a polyploid series, and their relationships within the *Triticeae* tribe are extensively examined. The subtribe *Triticinae* is formed by the genera Triticum, which includes the two cultivated wheat species *(T. aestivum & T. turgidum)*, Aegilops, Agropyron, Secale and Haynaldia. In addition to these there is the triticale *(X Triticosecale Wittmack)* which is a hybrid cereal originating from the crossing between wheat and rye.

The relationships between species are studied by analyzing their respective genomes [7]. Each genome contains seven chromosomes; thus, there are diploid, tetraploid and hexaploid wheat: *Triticum urartu L.* (2n = 2X = 14, AA), *Triticum turgidum L.* (2n = 4X = 28, AABB) and *Triticum aestivum L.* in Thell (2n = 6X = 42 AABBDD) are examples of each ploidy group [7]. Common wheat *(T. aestivum)* combines the complete genomes of three distinct diploid species (AABBDD), but genetically related. Despite the similarity of chromosomes, pairing only occurs between pairs of counterparts. Thus, the behavior of wheat, in meiotic terms, is typically of a diploid species, however it was found that a large part of the wheat genome consists of transposable elements [8]. In addition, genes have polysomic inheritance, and part of the genes present in subgenome A must be repeated in subgenomes B and D, which makes Mendelian segregation patterns more complex. Despite these difficulties, natural polyploidy gives wheat certain peculiarities that facilitate the incorporation of genes from related species.

According to Allard [9] the concept, in the field of plant breeding, of germplasm is referred to as the total sum of the genotypes of each species, which may be in the form of pollen, anthers, plants, seeds, tissues, cells or simple structures. It is worth mentioning that until recently the use of germplasm was limited by the reproductive barriers of a species. Only those

genotypes that were able to transfer their genes through crosses were considered part of the germplasm, even if they were interspecific crosses. Currently, with the development of biotechnology techniques, it is possible to isolate genes of any species and transfer them to the plant to be improved, stressing the importance of conserving genetic resources. The characterization and conservation involve evaluations with local and temporal repetitions, specialized labor, being recommended the participation of professionals with different specializations, such as phytopathologists and breeders who, with extensive academic and scientific knowledge, will be able to verify and study the potential genotype of accessions [10,11].

The efficiency of a germplasm bank is directly proportional to the domain of information about the conserved accesses, and one of the greatest problems encountered is the cost of maintenance and the difficulty of making material available for research due to lack of knowledge. To minimize these limitations, the characterization and evaluation of the accesses allow the understanding of the variability existing in the collection, constituting priority activities, as they assist in:

a) documentation and cataloging of the accesses (or passport data)
b) identification of duplicates
c) conservation and storage in a controlled environment (cold room)
d) multiplication to meet the base collection and user demand
e) regeneration of accessions to maintain their genetic integrity
f) formation of a nuclear collection, among other aspects (Valois et al., 1996).

The term nuclear collection can be used when it is assigned to a restricted group of accessions, with the least possible repeatability, but maximum genetic diversity [12] of the cultivated species. For Brown & Spillane [13], a nuclear collection should under no circumstances exceed 2000 entries. Conservation carried out in research centers is called ex situ, while field conservation is identified as in situ [14]. There are many methodologies that have free access to help researchers in the formation of a nuclear collection. All are based on the information available from the accesses, such as passport data and morphological data. Several strategies have been developed for the development and formation of nuclear collections as mentioned by Shoen & Brown [15], Balfourier et al. [16], Hintum et al. [17], Hu et al. [18], Wang et al. [19], Vasconcelos et al. [20], Cordeiro & Abadie [21]. The considerable number of accessions in ex situ collections shows the wide genetic diversity of the species involved in this project. The largest one is found at the International Corn and Wheat Improvement Center, which gathers more than 100 thousand accesses [22]. In Brazil, the National Wheat Research Center (Embrapa Trigo, Passo Fundo-RS), coordinates the Active Germplasm Bank (AWGB) of wheat and related species, where more than 16,000 accessions of these cereals are preserved [23]. Pre-breeding can be defined as activities aimed at identifying desirable genes (alleles) found in non-adapted materials or that have not undergone any form of selection for breeding, with the purpose of promoting and stimulating the use of genetic resources conserved in collections germplasm, that is, it is a link between genetic resources and breeding programs [24].

Activities carried out in pre-breeding have been discussed and suggested to increase the efficiency of breeding programs or even to solve problems of genetic erosion. According to Goedert [25], management and conservation actions in Active Germplasm Banks should enrich the available genetic variability of the species of interest through collection, introduction and exchange actions, in addition to characterizing and evaluating germplasm in activities of pre-improvement and, finally, the dissemination of the results obtained by the researcher. According to Duvick [26], the primary function of pre-breeding is the identification of genes of interest in non-native germplasm or even in populations that have not been improved, in order to incorporate into elite genotypes, which can become a source of genetic variability. Pre-breeding is an alternative to make genetic resources directly available to the researcher [24]. Once performed, the use of germplasm is facilitated. An issue that must also be discussed concerns who should execute it. Frankel [27] argues that the curators should not have such responsibility, because, in addition to the multiple activities of the curators, they do not have training in the area of improvement to correctly identify the characteristics to be transferred. The situation may change, as breeders take on the curatorship of germplasm banks and lead research projects and subprojects on genetic resources.

Since the 1990s, the dynamics of the exchange of genetic resources worldwide has been marked by changes [28]. In Brazil, after the creation of the Law on the Protection of Cultivars [29], there was a greater restriction in the interchange between the various genetic improvement programs in the country, which reinforces the importance of characterizing and conserving accesses in databases. regional germplasm. Thus, the objective of the present work is to regenerate, multiply, characterize, conserve and promote the pre-improvement of the genetic resources of the Active Wheat Germplasm Bank (AWGB) of the IDR Paraná.

Material and Methods

Experiment

In order to characterize and assess accesses, a sample of 209 accessions from Active Wheat Germplasm Bank (AWGB) of IDR Paraná, were used 16 control cultivars (BRS 229, BRS 249, BRS Guamirim, BRS Pardela, BRS Tangará, Fundacep 51, Fundacep Horizonte, IPR 129, IPR 130, IPR 136, QUARTZO, Valente, BRS 264, Raízes, BRS 208, Embrapa 42), using a simple lattice design (15 x 15), with two repetitions. The plots consisted of three lines of two meters in length with a spacing of 0.17 m between rows, installed at the IDR Paraná experimental station in Londrina. The cultural treatments were recommended for the wheat crop and the cultivars used as witnesses were chosen because they show characteristics that help in the characterization of the referred accessions.

The data for characterizing the accessions were obtained only from the central line of each plot, evaluating all plants for quantitative characteristics and a sample of 10 plants for qualitative ones. The evaluations were carried out based on the minimum criteria required by Brazilian legislation [29] and also according to the wheat descriptors suggested by the International Board for Plant Genetic Resources [30].

Characteristics for evaluation

The sixteen characteristics measured for wheat crop in this study were: vegetative habit (HV); plant height (AP); spike and maturation of plants with value expressed in days (ESP and MAT, respectively); position of the main leaf (FB); auricle staining (AUR); stem diameter using values of 3 stems per strain (DC); the wheat ear shape (FE); ear length (CE); presence of awn (ARI); ear color (CES); grain color, texture and wax (CRG, TGR and CERG, respectively), weight of grains per ear (PGEsp) and weight of 100 grains (P100G).

Statistics Methods used in the experiment

For all characteristics evaluated, analyzes of variance (ANOVA), grouping of means, simple linear correlation analysis and analysis of genetic diversity were performed with subsequent grouping by the UPGMA and Tocher methods, as described by Cruz et al. [31]. For the qualitative variables HV, FB, AUR, FE, ARI, CES, CRG, TGR and CERG, the data were transformed for in order to maintain the assumptions of the analysis of variance as normality of errors, homogeneity of the variances of errors associated with levels of each given factor and additivity of the effects of the model, as Ramalho et al. [32] recommended.

The method of grouping by optimization or Tocher method constitutes a method of simultaneous grouping, which performs the separation of genotypes into groups at once. This method uses a single grouping criterion and has the particularity of presenting the average distance within groups always less than the average distance between groups. For qualitative data, genetic diversity was assessed using the Tocher cluster method, based on the dissimilarity matrix obtained by the arithmetic complement (1-d) of the simple coincidence index (d), as described by Cruz & Carneiro [33]. The contribution of characteristics to genetic divergence was also measured using the methodology proposed by Singh [34]. To carry out the statistical analyzes, the software Genes [35], Sisvar [36], R [37] and Statistica 6 [38] were used. Pre-breeding activities were carried out at all stages of the project based on visual assessments. The genotypes that stood out for specific characteristics may be directed to more elaborate evaluations seeking to identify genes (alleles) of immediate or potential economic interest. Some strains that are part of the breeding block of the breeding program that showed difficulties in adapting and, or low potential for direct use as a source of desirable alleles, may, in the future, be directed to a specific program of backcrosses with superior cultivars.

A structural equation model was used to investigate relationships between morphological and morphometric characteristics of wheat plants. Such models allow considering the theoretical complexity of the variables under study by defining a system of linear equations that represent hypothetical effects, established by the researcher, of the independent variables along the causal chain of the outcome of interest. Two equations are used: measurement, referring to the definition of latent variables; and the structural, used to identify the effect of latent and/or observed variables on the outcome of interest [39]. Thus, a path diagram was created based on the data collected during the study. The ear characteristic latent variable (C_E) was constructed based on three observed variables: presence of awn, ear color and ear shape. Plant characteristics (C_P) resulted from two observed variables: vegetative habit and average plant height. The variables observed for earing in days (ESP) and days to maturity (MAT) composed the latent variable growth characteristics (C_C). Leaf characteristics (C_F) contains the variables: flag leaf position and atrium coloration. Finally, grain characteristics (C_G) are based on two observed variables: grain color and texture (CGR and TGR). In the structural model, the relationships between the endogenous latent variables C_E, C_P, C_C, C_F and C_G were considered. To adjust the model, the statistical package "Lavaan" was used. The goodness of fit of the model was verified using the Tucker-Lewis index (TLI) (good fit reference TLI > 0.90), the comparative fit index (CFI) (good fit reference > 0 .90), from the root mean square error of approximation (RMSEA) (good fit reference < 0.05) and the standardized root mean square residual error (SRMR) (good fit reference < 0.08). To perform the multivariate statistical analysis, the software Genes [35], Sisvar [36], R [37,40], Statistica 6 [38] were used.

Results and Discussion

From the analysis of variance according to the 15 × 15 lattice model, it was found that the average efficiency of the design was 101.21% (Table 1), where the real average was comprised in the confidence interval of 99.31 to 103.11%. This represents a low lattice efficiency and, in this case, it is possible to analyze the data as if they were in a randomized block design.

Table 1: Latency design efficiency averages for sixteen variables in 225 Wheat genotypes form the Active Germplasm Bank.

Vegetative Habit	**100.14**
Presence of awn	102.57
Color of the outer ear	100.02
Position of the main leaf	102.1
Form of the ear	99.71
Color of the ear	100
Size of the ear	98.66
Waxiness of the grain	103.84
Texture of the grain	102.79
Color of the grain	103.16
Time to ear (days)	96.73
Maturation (days)	100.2
Size of the Plants	113.35
Average diameter of the culm	96.4
Weight grain per ear	98.97
Weight of the 100 grains	100.7
Average Lattice Efficiency	**101.21**
Greater Efficiency - Height Plants	113.35
Lowest Efficiency – culm diam	96.4
Standard deviation	3.88
Sample Size	16
Alfa	0.05
Confidence margin	1.9
Maximum limit	103.11
Minimum limit	99.31

Table 2: ANOVA in randomized blocks, for sixteen variables in 225 accesses of Wheat.

Source	**DOF**	**Mean Squares**							
		HV(1)	ARI(1)	AUR(1)	FB(1)	FE(1)	CES(1)	TE	CERG(1)
Repetitions	1	0,00	0,04	0,27	0,53	0,09	0,01	142,24	0,04
Genotypes	224	0,11**	0,02	0,11**	0,16**	0,13*	0,02	169,97**	0,10**
Error	224	0,03	0,02	0,05	0,07	0,10	0,02	53,34	0,04
Average		3	5	1	3	3	1	92	1
CV (%)		9,89	6,57	15,36	14,77	16,2	9,85	7,98	18,78
Source	**DOF**	**TGR(1)**	**CGR(1)**	**ESP**	**MAT**	**AP**	**DC**	**PG/ESP**	**P100G**
Repetitions	1	0,03	0,01	62,72	81,07	346,72	0,40	0,40	0,14
Genotypes	224	0,11**	0,04**	80,31**	48,51**	117,35**	0,46**	0,20**	0,64**
error	224	0,04	0,01	9,41	27,35	37,01	0,30	0,06	0,27
Average		4	3	64	108	90	3,94	1,45	3,41
CV%		8,78	6,34	4,83	4,82	6,76	13,83	17,57	15,18

*,** 5% and 1%, by F Test, respectively

Variables: Vegetative habit of the plant (HV); presence of the awn (ARI); color of the outer ear (AUR); position of the main leaf (FB); form of the ear (FE); color of the ear (CES); size of the ear (TE) in cm; waxiness of the grain (CERG), texture and color of the grain (TGR e CGR); days for ear (ESP); days for maturation (MAT); size of the plant (AP), in cm; diameter of the culm (DC) in cm; weight of the grains per ear (PG/ESP) weight of 100 g (P100G).

(1): Original averages presented, and analyzes performed with transformed averages for $\sqrt{x+0,5}$

Through the analysis in randomized blocks (Table 2) it was verified that only for ARI and CESP variables, no significant difference was detected by the F test ($p > 0.05$), which suggests a low variability of these two characteristics for the set of evaluated genotypes. For the variable FE, significance was found at 5 % probability and for the other variables, significance at 1 % probability, indicating that there is genetic variability and that, at least, 1 genotype differs significantly from the others within each trait. The variation coefficients ranged from 4.82 to 18.78% and can be classified as low to medium, indicating good experimental precision.

Through the analysis of genetic diversity, the average data of the 16 variables were standardized and used in a multivariate scheme for calculations of genetic distance and grouping of genotypes. It was found that the grouping by the Tocher method (Table 3) allocated the genotype T092125 (access 128) in an isolated group, the genotypes IA 072118 (access 121) and T062113 (access 127) in a second group and the remaining 222 genotypes, including the witnesses, were allocated to a third group. Through the dendrogram (Figure 1) it is possible to confirm that T092150 again belongs to an isolated group, however the genotypes IA 072118 and T062113 were allocated close to IA 9718 (access 122) and IA082115 (access 32) which allows it to be considered a second group. The other genotypes were allocated to a third isolated group as in the Tocher method.

Table 3: Grouping of 225 -Wheat genotypes by Tocher method of optimization.

Tocher	
Group A	222 genotypes
Group B	IA 072118 e T062113
Group C	T 092125
UPGMA	
Group A	222 genotypes
Group B	IA 072118, T062113, IA 9718 e IA 082115
Group C	T 092125

Considering that the efficiency of a given grouping method, that is, the ability to present the contrasts between genotypes that may differ, depends on the type of data analyzed (qualitative or quantitative and on the distribution) and on the genetic variability between the tested genotypes, it can be inferred that the Tocher and UPGMA techniques were efficient. Results, these, also found by Bertan et al. [41], evaluating 19 wheat genotypes for seventeen quantitative characters.

The results in the present study do not directly represent a narrow genetic base in the set of genotypes evaluated from Active Wheat Germplasm Bank (AWGB) since more than 99% of the contribution to genetic divergence was due to the quantitative variables MAT, ESP, AP, TE, in addition to 0.31% for DC, PG / ESP and P100G.

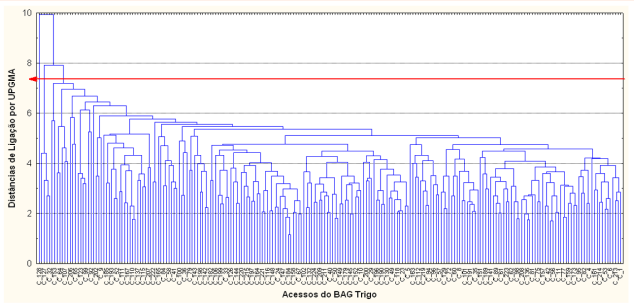

Figure 1: Dendrogram obtained from average Euclidean distances with standardized data between 225 genotypes and grouped by the UPGMA method.

By the method of Singh [34] it can be considered that the relative importance of the characters helps in the disposal of variables, enabling a choice of variables that will reflect more significantly in the direct and indirect selection gains. Thus, as mentioned by Cruz et al. [31], knowing the degree of importance of the analyzed variables, it is possible to characterize a collection with good precision (approximately 90 %), but with a lower number of descriptors, reducing the labor, time and costs employed.

In order to better detail the behavior of this variation, genotypes were grouped using their means by the Scott-Knott method [42] at the level of 5% probability, where the grouping of accessions, for each variable, uses the ratio verisimilitude to test the significance that accesses can be divided into groups that maximize the sum of squares between groups. The results for each access within each variable can be seen in Attachments1 to 4. For agronomic variables, formation of 4 for AP and ESP, 3 groups TE and PG / ESP, 2 for DC and P100G and one for MAT was found, which reflects the wide diversity within each agronomic variable and when considering the set of these variables for grouping genotypes. One point that should be highlighted concerns the distribution of genotypes in a single group of MAT, even though ANOVA has high significance, whereas for the variables ARI and CES there was the formation of 2 groups by the Scott-Knott test even though ANOVA did not. detecting significance at the tested levels. What should be emphasized is that the analyzes are not complementary to each other, that is, there may be differences in responses for the same set of genotypes and variables. Borges & Ferreira [43] performed simulations to evaluate the power and type I error rates of different tests of means. They found that the Scott-Knott test controlled the error rates per experiment for all distributions considered. However, they concluded that the test was powerful (Type I error rates almost always according to nominal levels) and robust in relation to the violation of normality. These facts reflect the high reliability of the test with regard to the grouping of means in relation to univariate ANOVA [44].

For qualitative variables, the test perfectly separated the pre-established classification groups for each variable, again indicating the high power of the Scott-Knott test and that it should be preferred during the genotype selection processes for both qualitative and quantitative variables. It can be considered that due to the different groupings in the qualitative and quantitative variables in the present study, the wide variability within variables is explicit and considering the behavior of a given genotype in the set of these variables. Through simple correlation analyzes (Table 4), it is possible to measure the degree of association between two variables, in order to direct the selection of promising genotypes to one or more variables together. A positive value was found between TE and PG / ESP and TE and DC, where a selection for larger ears may affect both grain weight per ear and stem diameter in the same direction. For P100G, negative correlations were found for both MAT and ESP as well as ESP and PG / ESP, that is, the selection of earlier individuals, both in flowering and

maturation, can reflect gains in weight of 100 grains and productivity. For the HV variable, positive and significant correlations were found with MAT and ESP.

Thus, the selection for genotypes with a more upright size can lead to genotypes with a longer cycle. The high positive correlation between MAT and ESP was already expected, which confirms the good experimental precision in the data collection. Structural equation model correlating morphological and agronomic characteristics from variables observed during the growth of wheat plants of 225 evaluated genotypes.

Table 4: Estimates of phenotypic correlations between sixteen variables from 225 AWGB Wheat genotypes.

	ARI[1]	CESP[1]	FE[1]	CE	MAT	HV[1]	AP	ESP
ARI[1]	1							
CESP[1]	-0.14*	1						
FE[1]	0.06	-0.14*	1					
CE	0.07	0.001	-0.06	1				
MAT	0.12	-0.18**	0.06	0.08	1			
HV[1]	0.08	0.1	0.07	0.08	0.30**	1		
AP	-0.23**	0.13*	-0.07	0.12	-0.002	-0.04	1	
ESP	0.21**	-0.25**	0.09	0.12	0.65**	0.43**	-0.14*	1
FB[1]	-0.06	0.07	0.03	-0.11	-0.12	-0.18**	-0.02	-0.22**
AUR[1]	-0.11	0.04	-0.11	0.09	-0.09	-0.08	0.09	-0.19**
CERG[1]	-0.01	0.03	0.08	0.15*	0.21**	0.23**	0.04	0.25**
TGR[1]	-0.13	0.09	0.04	-0.1	-0.17*	-0.08	0.09	-0.17*
CGR[1]	-0.13	0.09	0.05	-0.09	-0.17*	-0.08	0.09	-0.16*
DC	-0.01	-0.05	0.13	0.39**	0.16*	0.19**	0.05	0.11
PGEsp	-0.01	0.03	0.09	0.35**	-0.08	-0.02	-0.06	-0.17*
P100G	-0.1	0.09	-0.02	0.05	-0.34**	-0.18**	-0.02	-0.46**
	FB[1]	AUR[1]	CERG[1]	TGR[1]	CGR[1]	DC	PGEsp	P100G
FB[1]	1							
AUR[1]	-0.08	1						
CERG[1]	0.1	-0.17*	1					
TGR[1]	0.02	0.1	-0.06	1				
CGR[1]	0.01	0.1	-0.06	0.99**	1			
DC	-0.11	-0.01	0.26**	-0.06	-0.05	1		
PGEsp	0.15*	-0.06	0.18**	-0.27**	-0.26**	0.34**	1	
P100G	0.08	0.03	-0.08	-0.05	-0.05	0.08	0.64**	1

*,** significance for 5 and 1% by F Test.
Variables: Vegetative habito of the plant (HV); presence of the awn (ARI); color of the outer ear (AUR); position of the main leaf (FB); formo f the ear (FE); color of the ear (CES); size of the ear (TE) em cm; waxiness of the grain (CERG), texture and color of the grain (TGR e CGR); days for ear (ESP); days for maturation (MAT); size of the plant (AP), in cm; diamenter of the culm (DC) in cm; weigth of the grains per ear (PG/ESP) weigth of 100 g (P100G).

[1]: Original averages presented, and analyzes performed with transformed averages for figure 2. Structural equation model correlating morphological and agronomic characteristics from variables observed during the growth of wheat plants from 225 evaluated genotypes.

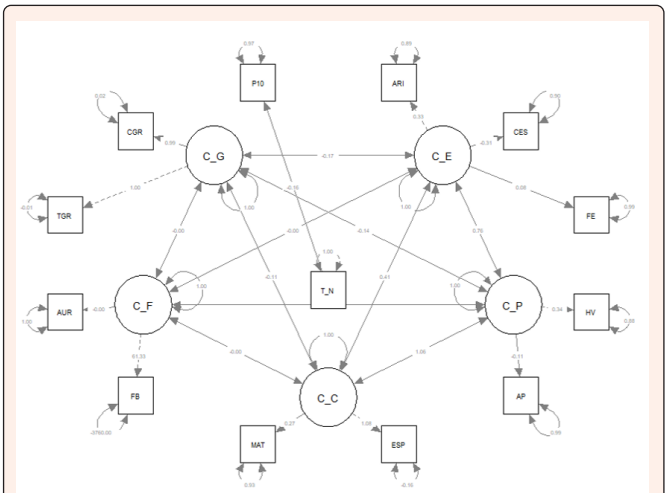

Figure 2: Structural equation model correlating morphological and agronomic characteristics from variables observed during the growth of wheat plants from 225 evaluated genotypes.

Conclusion

The selection of parents or the advancement of segregating generations must be in the sense of obtaining individuals with larger ears, who are more precocious and with a habit of intermediate to prostrate growth for marked production gains. The set of accessions evaluated for wide genetic variability for the different agronomic variables. The 225 characterized accessions represent 49% of the accessions of Germplasm Bank that have been regenerated and multiplied, and can be directed to intersections focusing on pre-breeding and / or breeding to obtain new cultivars.

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