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Scientific Article

Partial correlations between production traits and grain protein in wheat

Correlações parciais entre caracteres produtivos e proteína em grãos de trigo

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ABSTRACT - The objective of this study was to check whether there are linear relations between production traits and grain protein in early-, medium- and late-cycle wheat. Data from 204 competition trials of wheat genotypes conducted in the states of Rio Grande do Sul and Paraná were used, 78 trials with early-cycle, 34 with medium -cycle and 92 with late-cycle genotypes. The trials were conducted in a randomized block design, with 149 early-cycle, 95 medium-cycle and 193 late-cycle genotypes being evaluated from 2015 to 2019. Three production traits (grain yield, in kg ha^{-1}, thousand-grain weight, in g, and hectoliter weight, in kg hL^{-1}) and grain protein, in %, were evaluated. Scatter plots were created and the partial correlation coefficients between these four traits were calculated, based on 4330, 2497 and 4714 observations, referring to the early, medium and late cycles, respectively. There are linear relations between production traits and grain protein in early-, medium- and late-cycle wheat. Early- and late-cycle wheat genotypes show a negative correlation between grain yield and grain protein. Medium-cycle wheat genotypes show no correlation between grain yield and grain protein. Selection of wheat genotypes with higher grain yield and hectoliter weight can be carried out indirectly by means of thousand-grain weight.

Keywords: *Triticum aestivum* L. Linear relations. Grain yield.

RESUMO - O objetivo desse estudo foi verificar se há relações lineares entre caracteres produtivos e proteína em grãos de trigo de ciclos precoce, médio e tardio. Foram utilizados os dados de 204 ensaios de competição de genótipos de trigo conduzidos nos estados do Rio Grande do Sul e Paraná, sendo 78 ensaios com genótipos de ciclo precoce, 34 de ciclo médio e 92 de ciclo tardio. Os ensaios foram conduzidos no delineamento de blocos casualizados, sendo avaliados 149 genótipos de ciclo precoce, 95 de ciclo médio e 193 de ciclo tardio, nos anos de 2015 a 2019. Foram avaliados três caracteres produtivos (produtividade de grãos, em kg ha^{-1}, peso de mil grãos, em g e peso do hectolitro, em kg hL^{-1}) e a proteína dos grãos, em %. Foram confeccionados gráficos de dispersão e calcularam-se os coeficientes de correlação parcial entre esses quatro caracteres, a partir de 4330, 2497 e 4714 observações, dos ciclos precoce, médio e tardio, respectivamente. Há relações lineares entre caracteres produtivos e proteína em grãos de trigo de ciclos precoce, médio e tardio. Os genótipos de trigo de ciclos precoce e tardio apresentam correlação negativa entre a produtividade de grãos e a proteína nos grãos. Os genótipos de trigo de ciclo médio apresentam ausência de correlação entre produtividade de grãos e a proteína nos grãos. A seleção de genótipos de maior produtividade de grãos e peso do hectolitro pode ser realizada indiretamente por meio do peso de mil grãos.

Palavras-chave: *Triticum aestivum* L. Relações lineares. Produtividade de grãos.

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is widely used in human food and has important functional properties in its grains (LORO et al., 2023). Developing and selecting superior genotypes has been efficient in increasing the nutritional quality of grains (SZARESKI et al., 2019; SEGATTO et al., 2022; SEGATTO et al., 2023) and production performance (SILVA et al., 2015), in order to meet the demand for wheat grains. It is important that wheat grains have sufficient quality for use in the bakery industry.

The quality of wheat grains and flour for baking is directly related to the protein content (KAUR et al., 2016; LYU et al., 2022). Protein quality and quantity in wheat are one of the main aspects to be considered when improving wheat genotypes. Thus, it is necessary to develop genotypes that meet the agronomic ideotype characterized by high grain yield and quality (SILVA et al., 2015).

Understanding the relations between the yield components and protein in grains allows the development of strategies for indirect selection of genotypes based on multi-traits. To this end, linear correlation analysis has been widely used to understand the direction and magnitude of relations among traits in wheat (CARVALHO et al., 2015; GIANCASPRO et al., 2019; BAYE et al., 2020; SOLOMON, 2021). However, the linear correlation coefficient between pairs of traits can be influenced by the effect of other trait(s). Partial correlation analysis can be used for that, since it is possible to remove the effect of the other traits (CRUZ; REGAZZI; CARNEIRO, 2012).

Studies have shown that thousand-grain weight (KAVALCO et al., 2014; JANMOHAMMADI et al., 2014; LIU et al., 2018) and hectoliter weight

(SOLOMON, 2021) correlate positively with grain yield in wheat. In addition, studies conducted by Carvalho et al. (2015) and Baye et al. (2020) indicate positive correlations between thousand-grain weight and hectoliter weight in wheat. These positive relations reveal the possibility of simultaneously maximizing the magnitude of these traits in wheat genotypes.

Negative relations have been found between wheat grain yield and protein content, i.e., the most productive genotypes express lower protein content in the grains (SILVA et al., 2015; THORWARTH et al., 2018; GIANCASPRO et al., 2019; NIGRO et al., 2019; THORWARTH et al., 2019). This negative relation has also been identified in barley (WIEGMANN et al., 2019) and white oats (MANTAI et al., 2020). This makes it difficult to simultaneously select the traits for the wheat ideotype with increased yield and protein. However, no studies were found in the literature on the linear correlation in wheat genotypes, classified according to their development cycle.

Thus, understanding the linear relations between wheat traits by development cycle allows maximizing efficiency in genotype selection. In this context, the objective of this study was to check whether there are linear relations between production traits and grain protein in early-, medium- and late-cycle wheat.

MATERIAL AND METHODS

Genetic material

The data used came from 204 competition trials with wheat genotypes over five years (2015, 2016, 2017, 2018 and 2019), conducted in the states of Rio Grande do Sul and Paraná (Figure 1). The trials were separated by cycle: 78 trials with early-cycle, 34 with medium-cycle and 92 with late-cycle genotypes. 149 early-cycle, 95 medium-cycle and 193 late-cycle genotypes were evaluated in the trials. The number of genotypes evaluated per trial ranged from 13 to 36 in the early-cycle trials, 27 to 44 in the medium-cycle trials and 14 to 44 in the late-cycle trials. Classification of the genotypes according to development cycle length, conduction of the trials and data collection were carried out by the company Biotrigo Genética.

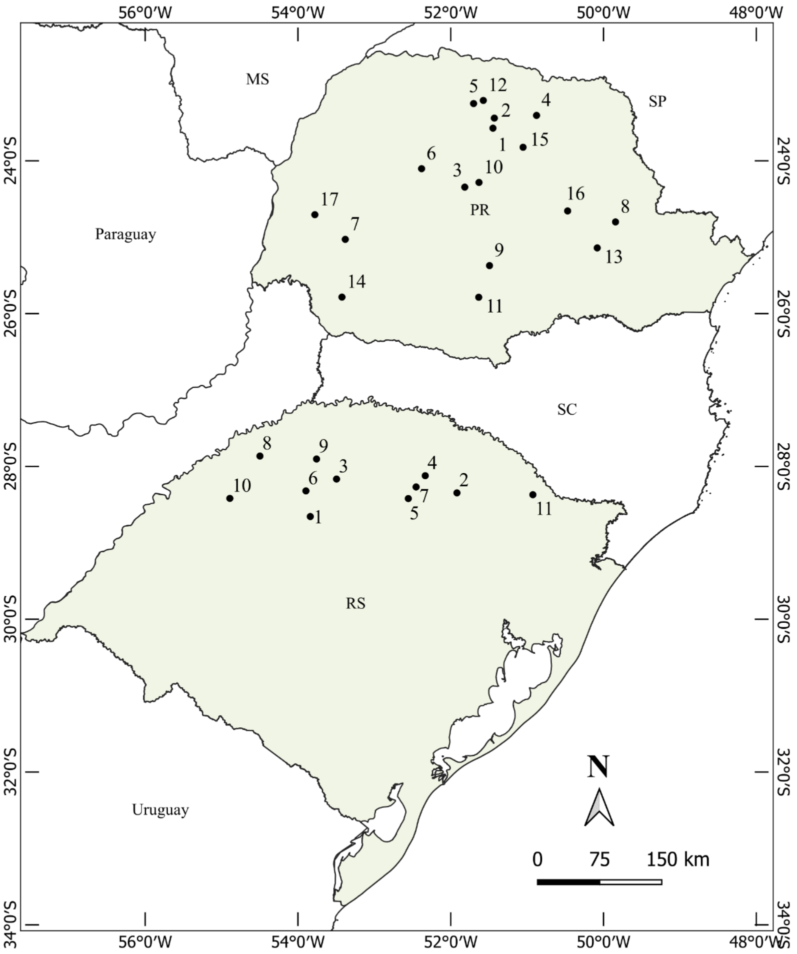

Figure 1. Geographic representation of the 28 sites where wheat genotype competition trials were conducted for five years in the states of Rio Grande do Sul (RS) and Paraná (PR), Brazil. Municipalities in the state of Rio Grande do Sul: 1 - Boa Vista do Cadeado, 2 - Ciríaco, 3 - Condor, 4 - Coxilha, 5 - Ernestina, 6 - Ijuí, 7 - Passo Fundo, 8 - Santa Rosa, 9 - Santo Augusto, 10 - São Luiz Gonzaga and 11 - Vacaria. Municipalities in the state of Paraná: 1 - Apucarana, 2 - Arapongas, 3 - Arapuã, 4 - Assaí, 5 - Astorga, 6 - Campo Mourão, 7 - Cascavel, 8 - Castro, 9 - Guarapuava, 10 - Ivaiporã, 11 - Pinhão, 12 - Pitangueiras, 13 - Ponta Grossa, 14 - Santa Izabel do Oeste, 15 - Tamarana, 16 - Tibagi and 17 - Toledo.

Field Experiments

The experiment was conducted in a randomized block design with four replicates. The plots consisted of seven rows of 5 m in length, spaced 0.17 m apart, totaling an area of 5.95 m^2. In each trial, sowing was carried out with a density of 350 seeds m^{-2} for all genotypes. Phytosanitary management was carried out to avoid the interference of biotic stress in the development of the crop.

Traits evaluated

At full physiological maturity, the plants of each plot were harvested to evaluate grain yield (GY, kg ha^{-1}), corrected to 13% moisture by drying the grains in a forced air dryer (65 ºC). Subsequently, thousand-grain weight (TGW, g) was determined using the Data Count S25 device. Hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) were determined using the NIR-Infratec 1241 grain analyzer. TGW, HW and PROT data were evaluated in two of the four blocks, obtaining a total of 4330, 2497 and 4714 observations for the early, medium and late cycles, respectively.

Statistical analysis and software

For the traits GY, TGW, HW and PROT, analysis of variance was performed in each trial, according to the mathematical model of the randomized block design (CRUZ; REGAZZI; CARNEIRO, 2012), and F test was performed for the genotype effect at 5% significance level.

From the GY, TGW, HW and PROT data, scatter plots were created and Pearson's correlation coefficients (r) and partial correlation coefficients (rp) between the pairs of traits were calculated for each development cycle of the wheat genotypes (early, medium and late).

A generalized way to obtain the partial correlation coefficient (rp) between two variables *i* and *j* is by means of the Pearson's correlation matrix (r) of dimension (m+2) × (m+2), which involves these two variables and *m* others, whose effect is to be removed from the association between *i* and *j*. With this technique, rp is estimated by means of the expression:

$$rp_{ij\,.m} = \frac{-a_{ij}}{\sqrt{a_{ii}\,a_{jj}}}$$

where a_{ij} is the element of order *ij* of the inverse of Pearson's correlation matrix (r) (CRUZ; REGAZZI; CARNEIRO, 2012). The significance of the r and rp coefficients was assessed using Student's t-test (CRUZ; REGAZZI; CARNEIRO, 2012). Statistical analyses were performed using the Microsoft Office Excel® application, Genes software (CRUZ, 2016) and the *ppcor* (KIM, 2015) and *ggplot2* (WICKHAM, 2016) packages of R software (R CORE TEAM, 2023).

RESULTS AND DISCUSSION

Regarding GY, among the 78 trials with early-cycle, 34 with medium-cycle and 92 with late-cycle genotypes, the F -test of the analysis of variance showed significant effect (p£0.05) of genotype in 70 trials (89.74%), 27 trials (79.41%) and 76 trials (82.61%), respectively. For TGW, there was a significant effect of genotype in 93.59%, 97.06% and 96.74% of the early-, medium- and late-cycle trials, respectively. Regarding HW, the genotype effect was significant in 98.72%, 100.00% and 95.65% of the early-, medium- and late -cycle trials, respectively. For PROT, there was significant effect of genotype in 94.87%, 100.00% and 93.48% of the early-, medium- and late-cycle trials, respectively. These results show the possibility of identifying superior genotypes, due to the existence of genetic variability.

Scatter plots with the respective Pearson's correlation coefficients help to understand the relations between the pairs of traits and to check for linear association pattern (BUSSAB; MORETTIN, 2017). In early-, medium- and late-cycle genotypes, positive linear relations were observed among the three production traits (GY, TGW and HW) (Figures 2, 3 and 4). Similar results were obtained by Kavalco et al. (2014), Janmohammadi et al. (2014), Liu et al. (2018), and Solomon (2021). Negative linear relations of the production traits (GY, TGW and HW) with PROT were observed in the three development cycles. Therefore, it can be seen that the linearity pattern among the traits was similar between development cycles of the wheat genotypes.

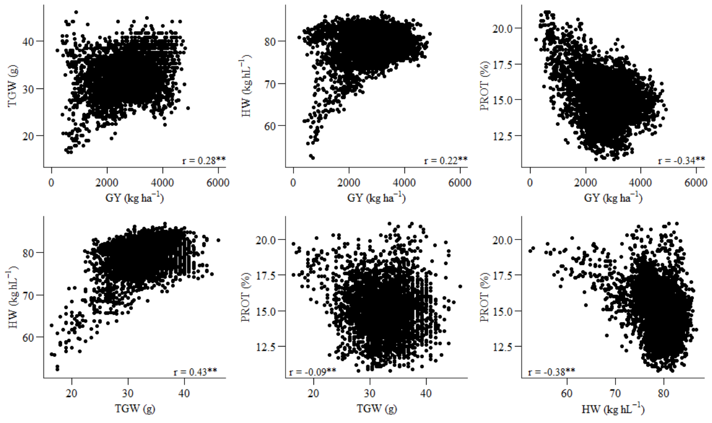

Figure 2. Scatter plots between grain yield (GY, kg ha^{-1}), thousand-grain weight (TGW, g), hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) in early-cycle wheat genotypes with the respective Pearson's correlation coefficients (n = 4330 observations). ** significant at 1% by Student's t-test.

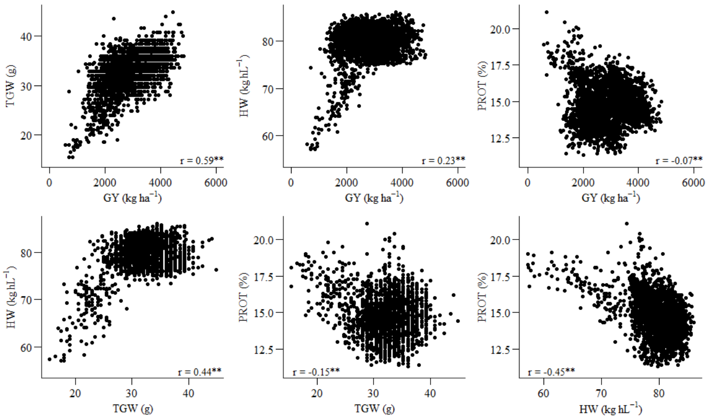

Figure 3. Scatter plots between grain yield (GY, kg ha^{-1}), thousand-grain weight (TGW, g), hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) in medium-cycle wheat genotypes with the respective Pearson's correlation coefficients (n = 2497 observations). ** significant at 1% by Student's t-test.

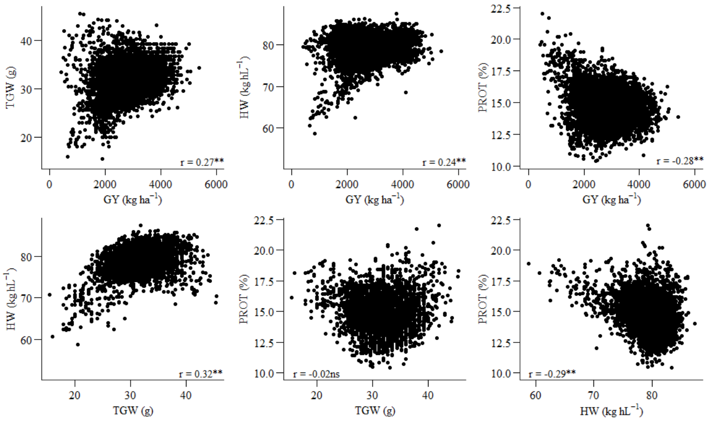

Figure 4. Scatter plots between grain yield (GY, kg ha^{-1}), thousand-grain weight (TGW, g), hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) in late-cycle wheat genotypes with the respective Pearson's correlation coefficients (n = 4714 observations). ** significant at 1% by Student's t-test. ns = not significant.

The partial correlation coefficients (rp) ranged from -0.43 (HW *vs* PROT) to 0.56 (GY *vs* TGW) among the early-, medium- and late-cycle genotypes (Figures 5, 6 and 7). GY was positively correlated with TGW, regardless of wheat genotype cycle. This indicates that the cycle of wheat genotypes does not alter the direction of the correlation between the traits. The magnitude of the correlation between the two traits decreased according to the cycles in the following order: medium (rp = 0.56), early (rp = 0.25) and late (rp = 0.24). Therefore, it can be inferred that the medium-cycle genotypes showed a higher magnitude of correlation between GY and TGW. Thousand-grain weight has a direct effect on grain yield in wheat (KAVALCO et al., 2014). Similar values for the relation between GY and TGW were observed by Janmohammadi et al. (2014). Liu et al. (2018) observed that increasing the thousand-grain weight promoted an increase in grain yield in wheat. This indicates that high-yield-performance wheat genotypes can be selected indirectly by means of thousand-grain weight, regardless of the cycle. However, indirect selection for GY based on TGW should be viewed with caution, since GY is easy and inexpensive to measure and can be selected directly.

The correlation coefficients between GY and HW were of low magnitude in the early-cycle (rp = -0.01), medium-cycle (rp = -0.04) and late-cycle (rp = 0.09) genotypes. Although these coefficients were statistically significant in the medium- and late-cycle genotypes, they do not have practical significance, since the statistical significance is due to the high number of degrees of freedom included in the Student's t-test (BUSSAB; MORETTIN, 2017). This indicates the absence of partial correlation between GY and HW, making it possible to select promising genotypes for both traits. In a study conducted by Solomon (2021), the author observed a positive relation between hectoliter weight and grain yield.

Negative partial correlation coefficients were observed between GY and PROT in the early-cycle (rp = -0.31) and late-cycle (rp = -0.25) wheat genotypes (Figures 5 and 7). There was no linear relation between GY and PROT traits in the medium-cycle genotypes (Figure 6). Therefore, it can be inferred that with the increase in the GY of early- and late-cycle wheat genotypes, there is a reduction in PROT contents. These results corroborate those reported by Silva et al. (2015), Thorwarth et al. (2018), Giancaspro et al. (2019), Nigro et al. (2019) and Thorwarth et al. (2019), who observed a reduction in the protein content of wheat grains with the increase in grain yield. The negative relation between these traits has also been identified in barley (WIEGMANN et al., 2019) and white oats (MANTAI et al., 2020).

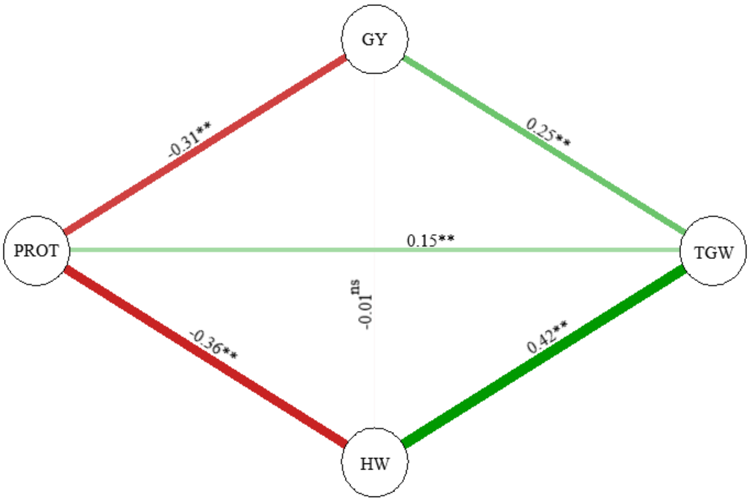

Figure 5. Partial correlation diagram between grain yield (GY, kg ha^{-1}), thousand-grain weight (TGW, g), hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) in early-cycle wheat genotypes (n = 4330 observations). ** significant at 1% by Student's t-test. ns = not significant.

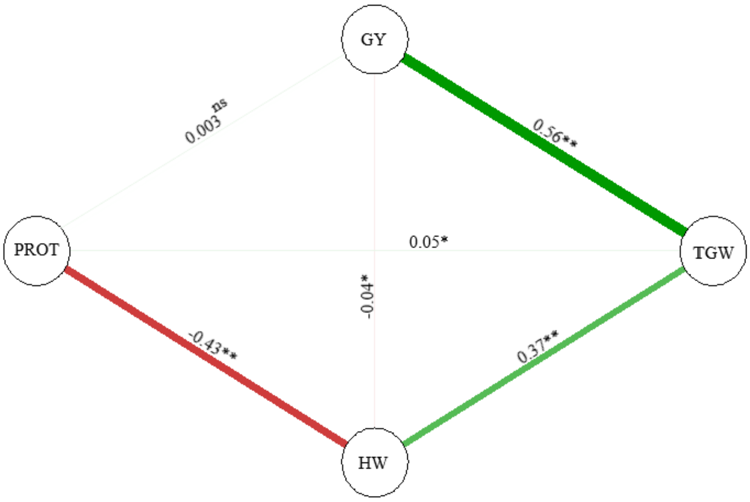

Figure 6. Partial correlation diagram between grain yield (GY, kg ha^{-1}), thousand-grain weight (TGW, g), hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) in medium-cycle wheat genotypes (n = 2497 observations). *, ** significant at 5% and 1%, respectively, by Student's t -test. ns = not significant.

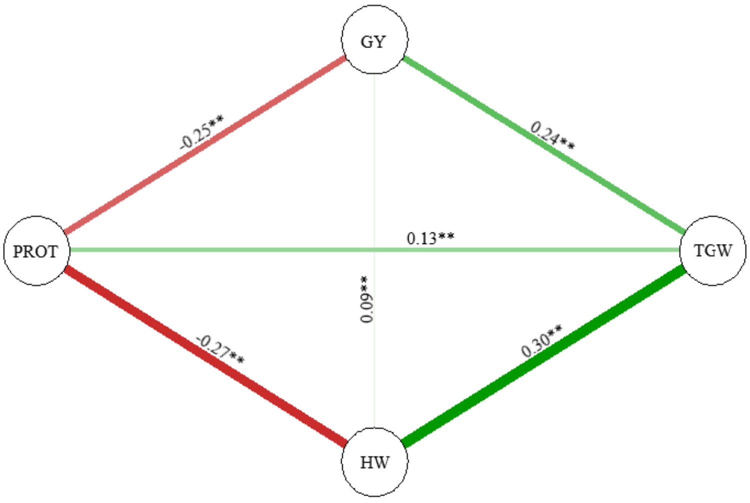

Figure 7. Partial correlation diagram between grain yield (GY, kg ha^{-1}), thousand-grain weight (TGW, g), hectoliter weight (HW, kg hL^{-1}) and grain protein (PROT, %) in late-cycle wheat genotypes (n = 4714 observations). ** significant at 1% by Student's t-test.

Therefore, it is possible to understand the difficulty in selecting and developing wheat genotypes with high yield associated with high protein content in the grains. This is because resource allocation within the plant is limited, and directing more nutrients to protein production may reduce the amount of grains produced (TAIZ et al., 2017). Protein content is a complex trait, i.e., of low heritability, influenced by environmental variations (GIANCASPRO et al., 2019), which hinders the selection of protein-rich genotypes. However, some wheat genotypes deviate from this negative relation (MONAGHAN et al., 2001), showing high values of GY and PROT. This suggests the possibility of selecting genotypes with simultaneous increment of GY and PROT. Selection indices can also be used as an efficient strategy to identify genotypes that have the best balance between GY and PROT, allowing simultaneous selection (MICHEL et al., 2019).

The absence of a linear relation between GY and PROT in medium-cycle wheat genotypes may indicate the possibility of selecting genotypes for simultaneous increment of these traits. Therefore, the study of the linear relations between grain yield and protein content stratified development cycle represents an important strategy to isolate the phenological effects on the relations between wheat traits.

TGW and HW were positively correlated, regardless of wheat genotype cycle ($rp \geq 0.30$), indicating that the higher the TGW, the higher the HW. In dual-purpose wheat and bread wheat, Carvalho et al. (2015) and Baye et al. (2020), respectively, also observed a positive correlation between TGW and HW.

TGW was positively correlated with PROT, regardless of wheat genotype cycle. The correlation coefficients between TGW and PROT were significant, but of low magnitude, with a decrease observed in the following order: early ($rp = 0.15$), late ($rp = 0.13$) and medium ($rp = 0.05$). Giancaspro et al. (2019) reported that the relation between TGW and PROT varies according to the conditions of the growing year. This may explain the smaller magnitudes of linear relation.

HW was negatively correlated with PROT, regardless of wheat genotype cycle. The magnitude of the coefficients between HW and PROT decreased according to the cycles in the following order: medium ($rp = -0.43$), early ($rp = -0.36$) and late ($rp = -0.27$). Thus, it can be inferred that wheat genotypes with high HW have low PROT content. The negative relation of GY and HW with PROT hinders the development and selection of wheat genotypes that fulfill an agronomic ideotype of high yield performance, which meets the requirements of industries ($HW \geq 78$), associated with high protein contents in the grains.

The relation between TGW and PROT was negative according to the scatter plots (Figures 2, 3 and 4), while the partial correlation revealed a positive relation. This can be explained by the fact that the partial correlation isolates the effects of the other traits on the correlation between a pair of traits (CRUZ; REGAZZI; CARNEIRO, 2012). Therefore, the negative trend observed in the scatter plot was due to the effect of the GY and HW traits on the correlation between TGW and PROT. This highlights the importance of using partial correlation for the study of linear relations between pairs of traits.

Strategies such as the use of genotypes that deviate from the relation between traits (MONAGHAN et al., 2001) and selection indices (MICHEL et al., 2019) can be adopted to simultaneously improve the traits of wheat genotypes. In addition, studies of the relations between traits, stratified by development cycle, make it possible to isolate phenological effects. These strategies contribute to identifying genotypes with a better balance between traits and developing more productive and nutritious wheat genotypes.

CONCLUSIONS

There are linear relations between production traits and grain protein in early-, medium- and late-cycle wheat.

Early- and late-cycle wheat genotypes show a negative correlation between grain yield and grain protein.

Medium-cycle wheat genotypes show no correlation between grain yield and grain protein.

Selection of wheat genotypes with higher grain yield and hectoliter weight can be carried out indirectly by means of thousand-grain weight.

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