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Carine Meier

**MODELOS BIOMÉTRICOS APLICADOS NA SELEÇÃO DE
GERAÇÕES AVANÇADAS DE TRIGO**

Frederico Westphalen, RS
2019

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Dissertação apresentada ao Curso de Pós-Graduação em Agronomia – Agricultura e Ambiente, da Universidade Federal de Santa Maria (UFSM, RS), como requisito parcial para obtenção do título de **Mestre em Agronomia**.

Orientador: Prof. Dr. Volmir Sergio Marchioro

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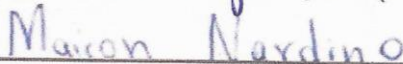
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A minha família, pelo amor, carinho e apoio incondicional.

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RESUMO

MODELOS BIOMÉTRICOS APLICADOS NA SELEÇÃO DE GERAÇÕES AVANÇADAS DE TRIGO

AUTOR: Carine Meier

ORIENTADOR: Volmir Sergio Marchioro

O trigo é um cereal que apresenta grande importância econômica no Brasil, o país produz 5,1 milhões de toneladas, essa situação faz com que o país seja um dos maiores importadores do cereal. Assim, o melhoramento genético tem grande importância na busca por aumento da produtividade e a qualidade do trigo produzido. Além disso, aumentar a eficiência dos programas de melhoramento é essencial para reduzir os custos e o tempo necessários para o lançamento de novas cultivares. O objetivo do estudo/pesquisa foi avaliar gerações avançadas de trigo por meio de modelos multivariados e biométricos, a fim de obter informações para seleção de genótipos superiores. A pesquisa foi conduzida na área experimental do Laboratório de Melhoramento Genético e Produção de Plantas, da Universidade Federal de Santa Maria, Campus de Frederico Westphalen/RS. Para tanto foram utilizadas inicialmente 420 progênies de trigo na geração F₅, conduzidos no delineamento experimental de famílias com testemunhas intercalares, no ano agrícola de 2017. A geração F₆ foi conduzida com quinze genótipos de trigo, dispostas em três repetições em 2018. Foram avaliados os seguintes caracteres: a) dias da emergência ao florescimento; b) altura de planta; c) comprimento da espiga; d) número de afilhos férteis; e) massa da espiga; f) massa de grãos da espiga; g) número de espiguetas; h) número de grãos por planta; i) massa total de grãos da planta. Posteriormente a geração F₇ foi conduzida a campo no delineamento experimental de blocos casualizados, sendo onze genótipos de trigo, dispostas em três repetições. Foram avaliados os seguintes caracteres: a) altura de planta; b) altura de inserção de espiga; c) número de afilhos férteis; d) largura de grão; e) massa hectolitrica; f) número de espiguetas e g) massa de grãos por planta. A partir das informações obtidas, os genótipos foram submetidos a análise de ganhos por seleção e índices de seleção, componentes de variância e parâmetros genéticos, diversidade genética, correlações fenotípicas, genéticas e ambientais, além de valores genotípicos preditos. A seleção de plantas com maior número de afilhos, resultou em genótipos mais produtivos. A formação de grupos distintos indicou a presença de variabilidade genética entre as populações avaliadas. O ciclo é variável e apresentou a maior contribuição para divergência genética entre os genótipos estudados. O uso dos índices de seleção é vantajoso em gerações avançadas de trigo, uma vez que estes proporcionam ganhos com a seleção, distribuídos entre todos os caracteres avaliados, situação mais adequada aos programas de melhoramento. O índice FAI-BLUP revelou a possibilidade de redução para altura de planta e aumento nos ganhos para número de afilhos e massa total de grãos por planta. O genótipo UFSM FW1 02 se mostrou superior a testemunha utilizada nos ensaios, estando apta a ser avaliada em ensaios de valor de cultivo e uso, pois reúne características mais próximas do ideal, apresentando elevado potencial produtivo.

Palavras-chave: Modelos Biométricos, Divergência genética, Parâmetros genéticos, *Triticum aestivum* L.

ABSTRACT

BIOMETRIC MODELS APPLIED IN SELECTING ADVANCED WHEAT GENERATIONS

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ADVISOR: Volmir Sergio Marchioro

Wheat is a cereal that has great economic importance in Brazil, the country produces 5,1 million tons, this situation makes the country one of the largest importers of this cereal. Thus, genetic improvement is of great importance in an attempt to increase yield, productivity and quality of the wheat produced. In addition, increasing the efficiency of breeding programs is essential to reducing the costs and time required to launch new cultivars. The objective of this study was to evaluate advanced wheat generations using multivariate and biometric models in order to obtain information for selecting superior genotypes. The research was conducted in the experimental area of the Laboratory of Genetic Improvement and Plant Production, Federal University of Santa Maria, Frederico Westphalen Campus / RS. For this purpose, 420 wheat genotypes were initially used in the F5 generation, conducted in the experimental design of families with interim controls in the 2017 agricultural year. The F6 generation was conducted with fifteen wheat genotypes, arranged in three replicates in 2018. The following characters were evaluated: a) days from emergence to flowering; b) plant height; c) spike length; d) number of fertile tillers; e) spike weight; f) kernel weight; g) number of spikelets; h) number of kernels per plant; (i) total plant kernel weight. Subsequently, the F7 generation was conducted in the field in a randomized complete block design. The following characters were evaluated: a) plant height; b) spikelets insertion height; c) number of fertile tillers; d) kernel width; e) hectolitic weight; f) number of spikelets and g) kernel weight per plant. From the information obtained, the genotypes were submitted to selection gain analysis and selection indices, variance components and genetic parameters, genetic diversity, phenotypic, genetic and environmental correlations, as well as predicted genotypic values. The selection of plants with higher tiller numbers increased in more productive genotypes. The formation of distinct groups indicated the presence of genetic variability among the evaluated populations. The cycle is the variable that presented the largest contribution to genetic divergence among the studied genotypes. The use of selection indices is advantageous in advanced wheat generations, since they provide selection gains, distributed among all evaluated characters, a situation that is better suited to breeding programs. The FAI-BLUP index revealed the possibility of reduction for plant height and increase in gains for tiller number and total grain mass per plant. The UFSM FW1 02 genotype provides to be superior to the control used in the assays, being able to be evaluated in cultivation and use value assays, since it gathers characteristics closer to the ideal, presenting high productive potential.

Key words: Biometric models, Genetic divergence, genetic parameters *Triticum aestivum* L.

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1 INTRODUÇÃO

O trigo (*Triticum aestivum* L.) é um cereal amplamente cultivado por se adaptar a diferentes ambientes, sendo uma das principais fontes energéticas, com grande importância na alimentação humana e animal, devido a sua qualidade e quantidade de proteínas e por sua variedade de produtos derivados. Ocupa mais de 25% da terra mundial agricultável, sendo uma alternativa para os sistemas de produção agrícola, além de sua utilização na rotação e sucessão de culturas (PUNIA et al., 2017).

Diversos programas de melhoramento de trigo trabalham com o objetivo de desenvolver cultivares que apresentem incremento no rendimento de grãos em condições naturais de lavoura, buscando aumentar a produção nacional, amenizando assim os problemas causados pela falta de trigo que existe no Brasil (METTE et al., 2015). Para garantir e atender a demanda por alimentos é necessário aumentar a produção por meio de melhorias nas práticas agronômicas e disponibilizar genótipos mais produtivos. Neste sentido, é essencial diminuir o tempo e os custos para o lançamento de novas cultivares. Assim, um dos métodos de condução de populações segregantes em plantas autógamas é o SSD (*Single Seed Descent*) que mantém a variabilidade total da população até gerações avançadas, permitindo o avanço de gerações fora do ambiente de cultivo e possibilitando o avanço de mais de uma geração por ano (CARVALHO et al., 2008)

Nos programas de melhoramento de trigo visando a seleção de genótipos com elevado rendimento de grãos, busca-se por táticas de seleção cada vez mais eficazes, desta forma, a genética quantitativa tem fundamental importância. O rendimento de grãos é um caráter de herança quantitativa de alta complexidade, determinado por vários genes, em decorrência da combinação entre seus diferentes componentes o que acaba tornando complexa e de difícil tarefa a seleção de genótipos superiores (GONDIM et al., 2008).

Para garantir a obtenção de constituições genéticas superiores com elevado potencial produtivo, a identificação de genótipos superiores pode ser facilitada pela utilização de modelos multivariados e biométricos.

Com o conhecimento das associações entre os caracteres é possível estabelecer a melhor estratégia de seleção e a partir das covariâncias estimar os índices de seleção (CRUZ et al., 2012). As associações entre os caracteres são estabelecidas através de coeficientes de análise de trilha, que permite entender as relações de causa e efeito, de forma direta e indireta sobre a variável principal (WRIGHT, 1921). Inúmeras pesquisas tem relatado a eficiência do uso destas estimativas em cereais de inverno, dentre as quais para a cultura do trigo (HARTWIG et al.,

2006), (VESOHOSKI et al., 2011), (KAVALCO et al., 2014), (CARVALHO et al., 2017), em aveia (MEIRA et al., 2017); (CARGNELUTTI FILHO et al., 2015); (UARROTA et al., 2017).

Entre as técnicas biométricas utilizadas destaca-se também a estimação dos parâmetros genéticos que permitem identificar a natureza de ação dos genes envolvidos, bem como avaliar a eficiência de diferentes métodos de seleção, seja de cruzamentos ou seleção (CRUZ et al., 2014), diversos relatos foram encontrados para a cultura do trigo (MOROJELE et al., 2013), (RAHMAN et al., 2014), (PIMENTEL et al., 2014b).

As medidas de dissimilaridade com base em variáveis quantitativas também se tornam relevantes na busca por genótipos superiores, uma vez que é possível constatar a diversidade genética e o padrão de dissimilaridade dos genótipos de trigo estudados (BERTAN et al., 2006; SILVA et al., 2007), por fim a estimação dos ganhos por seleção se tornaram uma ferramenta que possibilita prever o sucesso da resposta direta e a quantificação dos efeitos indiretos da seleção de um ou vários caracteres sobre outros secundários para orientar os programas de melhoramento genético, para simultaneamente, selecionar os atributos favoráveis (CRUZ et al., 2012), na cultura do trigo esta seleção é amplamente adotada (GUMMADOV et al., 2015), (KESER et al., 2017).

1.1 HIPÓTESES

Frente ao exposto, foram formuladas as seguintes hipóteses: (i) os ganhos de seleção nas gerações avançadas são satisfatórios para o trigo; (ii) compreender as associações entre características agronômicas pode ajudar a obtenção de genótipos que atendem às expectativas de produtividade do mercado; (iii) os desvios genéticos podem ser usados para seleção de genótipos superiores.

1.2 OBJETIVO GERAL

As hipóteses formuladas fundamentaram o seguinte objetivo geral: avaliar gerações avançadas de trigo por meio de modelos multivariados e biométricos, a fim de obter informações para seleção de genótipos superiores.

1.3 OBJETIVOS ESPECÍFICOS

Estimar os componentes de variância e parâmetros genéticos em gerações avançadas de trigo.

Verificar a melhor estratégia de seleção em gerações avançadas

Determinar as correlações fenotípicas, genéticas e de ambiente em genótipo de trigo.

Estudar as associações de causa e efeito e variáveis canônicas a fim de apontar caracteres importantes para a seleção indireta do trigo.

Determinar o potencial genético de gerações avançadas de trigo.

2 REVISÃO DA LITERATURA

2.1 IMPORTÂNCIA DA CULTURA

O trigo é um dos principais cereais de inverno cultivados na região Sul do Brasil, envolvido especialmente no fornecimento de matéria-prima base para elaborar produtos alimentícios para seres humanos e animais, com vasta aplicabilidade, na alimentação humana é empregado na fabricação de pães, massas, biscoitos, bolos (PELEGRIN et al., 2016; SCHEUER et al., 2011). É uma das principais fontes de proteína e carboidratos para os seres humanos (SINGH et al., 2015). O cereal também é utilizado em produtos de origem não alimentícia como na indústria de fármacos e cosméticos (BORÉM et al., 2015). O trigo tem sua importância para pequenas e grandes propriedades rurais, isto porque integra esquemas de rotação ou sucessão de culturas, junto ao cultivo da soja e do milho no sistema de semeadura direta, gerando oportunidades de emprego no setor primário de produção e na indústria de transformação (VALÉRIO et al., 2009).

O Brasil produz anualmente cerca de 5 milhões de toneladas de trigo, em uma área cultivada de aproximadamente 2 milhões de hectares, fato que demonstra o potencial da cultura e sua grande importância econômica, no entanto, a produção nacional não atende à demanda interna do país, se tornando assim, um dos maiores importadores deste cereal (Conab, 2019).

O cultivo do trigo no Brasil se dá em diferentes zonas agrícolas que apresentam solos com níveis diferenciados de fertilidade, acidez, textura e direcionados para diferentes aptidões, dessa forma, é fundamental conhecer as diferentes condições climáticas, edáficas e de manejo, pois estas podem influenciar diretamente o rendimento de grãos, a qualidade tecnológica para panificação, o manejo cultural a ser adotado e a utilização de cultivares mais adaptadas às diferentes regiões de cultivo (FRANCESCHI et al., 2009). Neste sentido, estudos que visam identificar cultivares mais adaptadas são importantes para melhorar o desempenho da cultura do trigo no Brasil.

2.2 DESCRIÇÃO BOTÂNICA

O trigo (*Triticum aestivum* L.) pertence à família Poaceae, tribo Triticeae, sub tribo Triticinea e gênero *Triticum* (AKABARI, 2018). Caracterizado por ser uma espécie alohexaplóide (AABBDD), o trigo comum ($2n \ 6x = 42$) apresenta um conjunto de três genomas diploides completos, desta forma, cada genoma é proveniente de uma espécie, o *Triticum urartu*

corresponde ao genoma AA, o *Aegilops speltoides* corresponde ao genoma BB e o *Aegilops tauschii* corresponde ao genoma DD (BRENCHLEY et al., 2012).

O trigo possui em sua morfologia flores hermafroditas, ocorrendo a cleistogamia, com a polinização e fecundação do estigma antes da abertura das flores. Nestas condições, o melhorista promove a variabilidade através de cruzamentos artificiais sendo necessário dois processos básicos a emasculação e polinização (ALLARD, 1971).

A inflorescência do trigo constitui um conjunto de espiguetas aderidas individualmente a ráquis sendo a inflorescência considerada uma espiga. O enchimento dos grãos de trigo começa nas espiguetas centrais e prospera para as basais e distais da inflorescência (SILVA et al., 2005).

2.3 MELHORAMENTO GENÉTICO

As espécies autógamias são caracterizadas por apresentarem alta taxa de autofecundação (CARVALHO et al., 2008). A utilização de cruzamentos artificiais nos programas de melhoramento de espécies autógamias, é um importante recurso visando a ampliação da variabilidade genética. Este processo de “hibridação” origina populações heterozigotas, as quais, a partir de sucessivas gerações de autofecundações resultam em genótipos com elevado grau de homozigose (BALDISSERA et al., 2014). Os programas de melhoramento de trigo em sua grande maioria são voltados para a identificação de variações naturais que auxiliam na agregação e no enriquecimento dos estoques genéticos (WANG et al., 2018). A geração de variabilidade genética é usada pelo melhorista de forma direcionada, buscando novos genes, para resistência a doenças, qualidade industrial dos grãos, aumento do potencial produtivo (DEPAUW et al., 2016), dentre outras características de interesse.

A maior eficácia dos programas de melhoramento está relacionada com a escolha do método apropriado de condução das populações segregantes (PIMENTEL et al., 2013). Dentre os métodos de seleção e condução de plantas no melhoramento genético do trigo, se destacam a utilização do método de seleção massal, populacional, genealógico e descendente de apenas uma semente “Single Seed Descent” (SSD). Todos os métodos empregados nos programas de melhoramento são empregados a partir da geração F₂ de descendentes (BOREM et al., 2013).

O “Single Seed Descent”, SSD, é um método que permite, a obtenção rápida de linhagens, em função da possibilidade do avanço de mais de uma geração por ano, fora do ambiente de cultivo, sem a perda de alelos por seleção, pois a variabilidade original é mantida até que todos os indivíduos da população cheguem a homozigose (ALLARD, 1971), este

método vem sendo eficientemente utilizado principalmente para caracteres de baixa herdabilidade, desde que a população tenha uma base genética ampla e seja mantida durante o avanço de gerações.

A seleção em gerações avançadas é beneficiada pela maior variância genética aditiva presente na população e o elevado nível de homozigose, isso porque se não houver nenhum problema de germinação, a variabilidade genética de F_6 será similar à de F_2 (CARVALHO et al., 2008).

2.4 PARÂMETROS GENÉTICOS

Ao avaliar uma população de melhoramento, a existência de variabilidade genética é fundamental para eficiência da seleção. Os parâmetros genéticos da população, como os componentes de variância, a herdabilidade, os estimadores de precisão experimental (coeficientes de variação genética, experimental e a acurácia), e as correlações entre caracteres, são informações importantes para a seleção.

A variância fenotípica ($\hat{\sigma}_F^2$) ou total é composta pela variância genotípica ($\hat{\sigma}_G^2$) e pela variância de ambiente ($\hat{\sigma}_E^2$) (RAMALHO et al., 2012). A variância ambiental representa a variação devido a causas não genéticas, não herdável, a qual pode ser minimizada com o uso de delineamentos experimentais adequados, já a variância genética ou valor genético contém toda a porção que é herdável (FALCONER, 1987).

Os componentes de variância possibilitam estimar a herdabilidade (h^2) e prever o ganho esperado com a seleção. A herdabilidade no estudo genético do caráter tem seu papel preditivo, expressando a confiabilidade com que o valor fenotípico representa o valor genético, desta forma quanto maior for a herdabilidade, maior será o ganho por seleção (Gs) (SILVA et al., 2013).

No trigo a produtividade pode apresentar herdabilidade relativamente alta (NARDINO et al., 2016), ou mais baixa (PIMENTEL et al., 2014a), dependendo da população de estudo. Altas herdabilidades foram encontradas para altura de planta (PACHAURI et al., 2018; PIMENTEL et al., 2014a), enquanto que moderadas herdabilidades foram observadas para comprimento da espiga (ARYA et al., 2017). O número de perfilhos por planta apresentou baixa herdabilidade (NOORKA et al., 2018; ZERGA et al., 2016). Existem, portanto, divergências na literatura para os coeficientes de herdabilidade de alguns caracteres, o que exemplifica a propriedade de que as estimativas dos parâmetros genéticos são válidas para uma população específica, em determinadas condições ambientais a qual está inserida (ALLARD, 1971).

2.5 MODELOS MULTIVARIADOS

As análises multivariadas permitem o manuseio simultâneo de dezenas e até centenas de variáveis, de modo a extrair o conteúdo de informação (AGUIAR et al., 2007). Um dos métodos mais utilizados nestas análises são os de otimização e os métodos hierárquicos no qual os indivíduos são agrupados por um processo que se repete em vários níveis até que seja estabelecido o dendrograma (CRUZ et al., 2014).

Na análise de agrupamento, também denominada de “cluster analysis”, objetiva-se separar um grupo original de observações em vários subgrupos, de forma a existir homogeneidade dentro e heterogeneidade entre os subgrupos, dentre os métodos de agrupamento hierárquicos está o UPGMA (Unweighted Pair-Group Method using Arithmetic Averages) conhecido como “ligação média entre grupos”, utilizado por reduzir distorções quanto a representação das similaridades entre indivíduos de um dendrograma e tende a gerar valores mais elevados de coeficiente de correlação cofenética (CRUZ et al., 2014).

Esses agrupamentos dependem de uma medida de dissimilaridade que, para variáveis quantitativas, as mais empregadas são a distância Euclidiana ou a distância generalizada de Mahalanobis (BENIN et al., 2003). Estas medidas de dissimilaridade de acordo com CRUZ et al. (2014) são de grande importância em estudos de divergência genética em que se procura identificar genitores à serem utilizados em programas de hibridação, identificando combinações híbridas de maior efeito heterótico de forma que, em suas gerações segregantes, tenha maior possibilidade de recuperação de genótipos superiores, neste sentido trabalhos vem relatando o uso de medidas de dissimilaridade (SILVA et al., 2016; TORRES FILHO et al., 2018).

Dentre as várias técnicas multivariadas que podem ser aplicadas, também se encontra a análises por componentes principais (ACP) de modelagem da estrutura de covariância (CRUZ et al., 2012). De acordo com HONGYU et al. (2015) cada componente principal é uma combinação linear de todas as variáveis originais, são independentes entre si e estimados com o propósito de reter, em ordem de estimação, o máximo de informação, em termos da variação total contida nos dados. Este tipo de análise vem sendo utilizada na cultura da soja (TOBAR-TOSSE et al., 2015), no trigo (COSTA et al., 2013).

2.6 MODELOS BIOMÉTRICOS

O uso de modelos mistos vem sendo utilizado a muito tempo em programas de melhoramento animal e também de espécies vegetais perenes (RODRIGUES et al., 2013; SILVA et al., 2014). Neste sentido, os estudos envolvendo espécies anuais ainda estão em desenvolvimento (PEREIRA et al., 2016; PIMENTEL et al., 2014b). Os principais fatores que melhor explicam a adoção de modelos mistos, nos programas de melhoramento, são as situações de desbalanceamento causadas por limitações econômicas, redução do número de ambientes e recursos para avaliação de genótipos, perdas de indivíduos por parcela, diferenças nas quantidades de sementes utilizadas, número de repetições e os diversos tipos de delineamentos experimentais.

Desta forma as metodologias REML/BLUP (Restrict Maximum Likelihood / Best Linear Unbiased Prediction) vem sendo utilizadas, pois permitem maximizar a relação entre a predição do valor genético, com o verdadeiro valor genético, onde se busca minimizar o erro de predição (RESENDE et al., 2014).

A abordagem REML permite decompor a variância total obtida em um determinado ensaio experimental em componentes de variância, sendo estes não influenciados pelos efeitos fixos do modelo e ponderados pelos graus de liberdade, isto proporcionou obter estimadores não viciados e fidedignos (RESENDE et al., 2014). O método conhecido como BLUP foi proposto por HENDERSON (1975) como uma forma de predição dos efeitos aleatórios, ajustando os dados aos efeitos fixos e ao número desigual de informações por meio de modelos mistos. É uma alternativa com elevada acurácia para os trabalhos que envolvem conjuntos de dados desbalanceados, sendo, no entanto, aplicada também para dados em nível balanceado (PIMENTEL et al., 2014b).

O uso de REML/BLUP passa a apresentar vantagens para a melhor estimação e predição dos parâmetros genéticos e maior poder de discriminação entre genótipos, este método vem sendo empregado na análise de estabilidade e adaptabilidade, produtividade de grãos, sendo aplicado a diversas culturas como: algodão (CARVALHO et al., 2016), feijão (SOUZA et al., 2018), soja (FOLLMANN et al., 2019), milho (CREVELARI et al., 2019; NARDINO et al., 2016) e trigo (PIMENTEL et al., 2014b; SZARESKI et al., 2018).

Com base nos valores genéticos preditos ROCHA et al. (2018) desenvolveu um índice de múltiplas características o índice FAI-BLUP, que apresenta algumas vantagens sobre outros índices de seleção. Entre essas vantagens está o uso de efeitos genéticos previstos em comparação com o uso de efeitos fenotípicos. Os principais pontos desejáveis do FAI-BLUP são o mesmo peso para todas as características e os genótipos de seleção simultânea mais próximos do ideótipo usando uma abordagem de múltiplas características. Esta metodologia

desenvolvida recentemente com base em múltiplas características é uma questão fundamental no melhoramento de plantas e vem sendo utilizada na cultura do capim elefante (ROCHA et al., 2018), soja (WOYANN et al., 2019a) e feijão (ROCHA et al., 2019).

3 CAPÍTULO I - SELECTION GAIN AND INTERRELATIONS BETWEEN AGRONOMIC TRAITS IN WHEAT F5 GENOTYPES

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Selection gain and interrelations between agronomic traits in wheat F₅ genotypes

Ganho de seleção e interrelações entre caracteres agronômicos em genótipos F₅ de trigo

3.1 ABSTRACT

This work aimed to estimate the variance components and genetic parameters, the selection gain, and the cause and effect relationships among traits in order to identify important traits for direct and indirect selection of wheat (*Triticum aestivum* L.) lines. Three strategies were used to obtain selection gains: direct and indirect selection, an index based on “ranks,” and the Smith and Hazel index. In the 2017 crop season in Brazil, 420 wheat lines from the F₅ generation were conducted in families with intercalary controls. High heritability of spike weight, number of kernels, and total kernel weight resulted in the best direct selection gains. The selection of plants with a high number of tillers resulted in grain yield improvement. The use of selection indexes is important in advanced wheat lines; they promote genetic gains distributed among agronomic traits.

Keywords: correlation; genetic parameters; selection gains; *Triticum aestivum* L.

3.2 INTRODUCTION

Wheat breeding (*Triticum aestivum* L.) has evolved intensely over the last century. This is mainly because of the importance of wheat having a high grain yield and high quality of gluten proteins for use in the food industry in the production of breads, pastas, and cakes (Sun *et al.*, 2017). This evolution has been made possible by implementing precise experimental designs and sophisticated statistical methods and by understanding the concepts of quantitative and population genetics (Bassi *et al.*, 2016).

Selection indexes are among the most efficient statistical methods used for identifying the best crop lines and potential parents to be used for future crosses (Yao *et al.*, 2018). Among the indexes, Mulamba & Mock (1978), and Smith (1936) and Hazel (1943) are the most commonly used. The efficiency of using selection indexes for crop breeding has also been highlighted by Paula *et al.* (2002), Costa *et al.* (2004), Moreira *et al.* (2019) and Smiderle *et al.* (2019).

Among the analyses used to identify the association of traits, Pearson's linear correlation reveals the sense and degree of linear association between two traits (Pearson, 1920). However, to quantify and interpret trait associations based only on simple linear correlation may result in misunderstandings in the selection process; a third, or a group of traits may be acting in response to the selection of the main trait (Cruz *et al.*, 2014). Considering this, the path analysis developed by Wright (1921) has been an important tool in the evaluation of trait associations; it allows decomposition of the linear association of direct effects with the main trait and of indirect effects among other traits.

In order to select potentially high-yielding wheat lines in breeding programs, superior genotypes need to be selected for with greater accuracy. There is a large amount of information in the literature on selection in early generations, but knowledge of selection in advanced generations is lacking. Thus, the following hypotheses were formulated: (i) the selection gains in advanced generations are satisfactory for wheat and (ii) understanding the association among agronomic traits may help to obtain superior genotypes that meet market expectations for productivity. In this way, the aim of this work was to estimate the variance components, genetic parameters, selection gains, and the cause and effect relationships among traits in order to identify important traits for direct and indirect selection of wheat lines.

3.3 MATERIALS AND METHODS

3.3.1 Plant material

The study was performed in the 2017 crop season, in the city of Frederico Westphalen (27°23'26''S, 53°25'43''W; 481 m above sea level). The soil was classified as typical dystrophic Red Latosol (Santos *et al.*, 2013) and the climate as Cfa according to Köppen (Alvares *et al.*, 2013).

We evaluated 420 lines descending from a biparental cross between the cultivars Mirante and Abalone. The crosses were performed in a greenhouse during the 2013 crop season. The generation advance was performed using the Single Seed Descent (SSD) method until the F₄ generation was obtained. In generation F₅, the lines were studied in families with intercalary controls. Six replicates of six cultivars (BRS 327, Quartzo, Mirante, Pampeano, Abalone, and Supera) were used as the intercalary controls.

The base fertilization consisted of 200 kg ha⁻¹ of N-P₂O₅-K₂O (08-24-12). A supplementary fertilization with 90 kg ha⁻¹ of N (urea form; 45% N) was applied in two stages: one in the tillering stage and the other in the elongation stage (Zadoks *et al.*, 1974)(Reunião, 2016). Weeds, pests, and diseases were controlled according to the technical recommendations for wheat.

3.3.2 Traits studied

For lines and cultivars, the traits measured were a) days from emergence to flowering (DF); b) plant height (PH; cm), measured from the soil to the spike of the main tiller; c) number of tillers (NT), obtained by counting fertile tillers; d) spike weight (SW; g), obtained by weighing the spike of the main tiller; e) spike length (SL; cm), from the spike insertion point to start of the awn; f) number of spikelets (NS), obtained by counting the spikelets of the main

tiller spike;; g) kernel weight (KW; g), obtained by weighing the main tiller spike; h) total number of kernels per plant (TNK); and i) total kernel weight per plant (TKW; g).

3.3.3 Experimental design and genetic parameters

The variance analysis was performed according to families with intermediate witnesses controls experimental design (Cruz *et al.*, 2014). Thus, families were evaluated using the variance components of the controls as environmental effects.

The value of each observation for the controls was given by the regular treatment model evaluated with repetitions: $Y_{ij} = \mu + T_i + \varepsilon_{ij}$,

where Y_{ij} represents the value of the trait for i-th control in the j-th replicate; μ is the general controls average; T_i is the i-th controls effect ($i = 1, 2, \dots, t$); and ε_{ij} is the random error involving controls ($\varepsilon_{ij} \sim N(0, \sigma^2)$). For families submitted to non-regular treatments, without the use of repetitions: $y_i = \mu_f + F_i + \varepsilon_i$, where y_i represents the value of the trait for the i-th family; μ_f is the general genotypes average; F_i is the i-th genotype effect; and ε_i is the random error involving genotypes ($\varepsilon_{ij} \sim N(0, \sigma^2)$).

Variance-covariance phenotypic and genotypic matrix was estimated to be used in selection indexes.

3.3.4 Linear correlation and path analysis

The linear correlation matrix containing nine explanatory traits (DF, PH, SL, NT, SW, TNK, KW, NS, and TKW) was evaluated for the level of multicollinearity. This was determined using the condition number, which is given by the ratio between the major and minor eigenvalues of the correlation matrix. Traits that caused multicollinearity problems were excluded from the analysis, as recommended by Olivoto *et al.* (2017). Subsequently, path

analysis was performed using the matrix of genotypic correlations, considering TKW as a dependent trait and the other traits as explanatory.

A *t* test was used to evaluate whether the phenotypic correlation coefficient (*r*) was equal to zero, by means of the expression, $t = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2}$, where *t* is associated with *n*-2 degrees of freedom and 1% probability, *n* is the number of pairs of observations (*n* = 420), and *r* is correlation coefficient (Stell & Torrie, 1980). The magnitudes of the correlation estimates were classified according to Carvalho et al. (2004).

3.3.5 Selection gain

The direct selection gains for traits were estimated using the equation, $GS = (X_{si} - X_{oi}) = DS_i h^2$, where X_{si} is the mean value of individuals selected for trait *i*; X_{oi} is the original population mean; DS_i is the differential selection performed in the population; and h^2 is heritability of trait *i*. The indirect gain in trait *j*, by selection in trait *i*, is given by $GS_j(i) = DS_j(i) h^2$, where $DS_j(i)$ is the indirect selection differential obtained as a function of the trait mean of superior individuals on which direct selection was performed (Cruz, 2006).

Superior individuals were indicated according to the genotypic values obtained from the selection index proposed by Smith (1936) and Hazel (1943), and on the sum of ranks index of Mulamba & Mock (1978). The classic index (Smith, 1936; Hazel, 1943) consists of the linear combination of several traits of economic importance, whose weighting coefficients were estimated by the genetic coefficient of variation of the experiment, in order to maximize the correlation between the index and the aggregate genotype. According to Cruz (2006), the economic weight may be estimated from the experimental data. In the index based on the sum of ranks, the genotypes were classified by the selection index, described as $I = r_1 + r_2 + \dots + r_n$, where *I* is the index value for a given genotype or family; r_j is the rank of a progeny in relation

to the j th trait; and n is the number of traits considered for performing the index described by Mulamba e Mock (1978).

The selection was aimed at increasing SL, NT, SW, KW, NS, TNK, and TKW, and reducing DF and PH. Selection was applied in order to select the 10 best genotypes. All statistical analyses were performed using the Genes software (Cruz, 2016).

3.4 RESULTS

3.4.1 Variance components and genetic parameters

There was genetic variability in the wheat lines and cultivar controls evaluated. This variability was affirmed by finding significant differences between DF, SW, SL, NS, KW, TNK, and TKW in different lines. For the controls, the observations were meaningful for PH, SW, SL, NS and TKW (Table 1). The wheat lines displayed a high potential for improving these agronomic traits via selection.

The wheat lines presented higher phenotypic variance for the PH, NT, and TNK traits, which was mostly attributed to the lower environmental variation (Table 2). It may be highlighted that the PH revealed higher values of variance for controls, suggesting that they were more influenced by the environmental variation than advanced generation wheat lines. The heritability, coefficient of genetic variation (CV_g), and ratio between the coefficients of genetic and experimental variation (CV_g/CV_e), as a function of the environmental influence, revealed higher heritability values for SW, KW, and TKW, of more than 70%.

Table 1: Summary of variance analysis, means, and heritability for wheat lines and controls studied in Frederico Westphalen, Brazil.

Source of variation	GL	MS								
		DF	PH	NT	SW	SL	NS	KW	TNK	TKW
Lines	419	40.44*	77.04 ^{ns}	66.35 ^{ns}	0.31**	2.26*	4.30*	0.21**	924.99*	53.51**
Control	5	30.51 ^{ns}	655.21**	65.88 ^{ns}	0.20**	6.37**	9.43**	0.11 ^{ns}	999.71 ^{ns}	25.83**
Residue	24	20.13	50.39	39.22	0.05	1.19	2.16	0.05	465.91	4.70
General mean		80.45	61.75	22.55	1.69	10.29	15.87	1.17	727.10	13.03
Lines mean		80.38	60.28	22.65	1.69	10.28	15.85	1.18	729.90	13.26
Controls mean		81.44	68.25	18.17	1.63	10.48	16.20	1.08	687.79	9.83
CV (%)		5.58	11.50	27.77	12.82	10.58	9.25	19.25	29.66	16.64
CV (%) Line		5.58	11.58	27.65	12.79	10.59	9.27	19.15	29.55	16.35
CV (%) Control		5.51	10.40	29.58	13.27	10.39	9.06	20.87	31.36	22.06
Heritability (%)		50.20	34.60	40.89	84.37	47.50	49.91	74.17	49.67	91.21

* and ** represent significance at $p < 0.05$ and $p < 0.01$, respectively, as determined by t test, ^{ns} not significant,. GL, degrees of freedom, MS, mean square; CV, coefficient of variation; DF, days from emergence to flowering; PH, plant height; SL, spike length; NT, number of tillers. TNK: total number of kernels per plant. SW: spike weight. KW: kernel weight; NS, number of spikelets; TKW, total kernel weight per plant.

Table 2: Variance components and genetic parameters estimated for wheat lines and controls studied in Frederico Westphalen, Brazil.

Line									
Parameter	DF	PH	NT	SW	SL	NS	KW	TNK	TKW
Phenotypic variance	40.44	77.05	66.35	0.30	2.26	4.30	0.20	92.99	53.51
Environmental variance	20.14	50.39	39.22	0.05	1.19	2.16	0.05	46.91	4.70
Genotypic variance	20.30	26.66	27.13	0.25	1.07	2.15	0.15	45.08	48.81
Heritability (%)	50.20	34.60	40.89	84.37	47.50	49.91	74.17	49.67	91.21
CVg (%)	5.61	8.42	23.00	29.71	10.08	9.25	32.44	29.35	52.68
Ratio CVg CVe ⁻¹	1.04	0.73	0.83	2.32	0.95	0.98	1.69	0.99	3.22
Control									
Parameter	DF	PH	NT	SW	SL	NS	KW	TNK	TKW
Phenotypic variance	6.10	131.04	13.18	0.04	1.28	1.89	0.02	95.54	5.17
Environmental variance	4.03	10.08	7.84	0.01	0.24	0.43	0.01	93.98	0.94
Genotypic variance	2.07	120.97	5.33	0.03	1.04	1.45	0.01	10691.56	4.23
CVgt (%)	1.77	16.11	10.91	10.78	9.72	7.45	10.06	15.03	20.91
Ratio CVg CVe ⁻¹	0.32	1.55	0.37	0.81	0.94	0.82	0.48	0.48	0.95

DF, days from emergence to flowering; PH, plant height; SL, spike length; NT, number of tillers; TNK, total number of kernels per plant; SW, spike weight; KW, kernel weight; NS, number of spikelets; TKW, total kernel weight per plant. CVg, coefficient of genetic variation; CVe, coefficient of experimental variation; CVgt, coefficient of the controls' genetic variation.

3.4.2 Linear associations

Evaluating the linear associations among the traits studied (Figure 1), DF showed a moderate negative association with PH, SW, KW, and TKW. This demonstrated that precocity in wheat is promising for breeding programs owing to the positive association with total kernel weight.

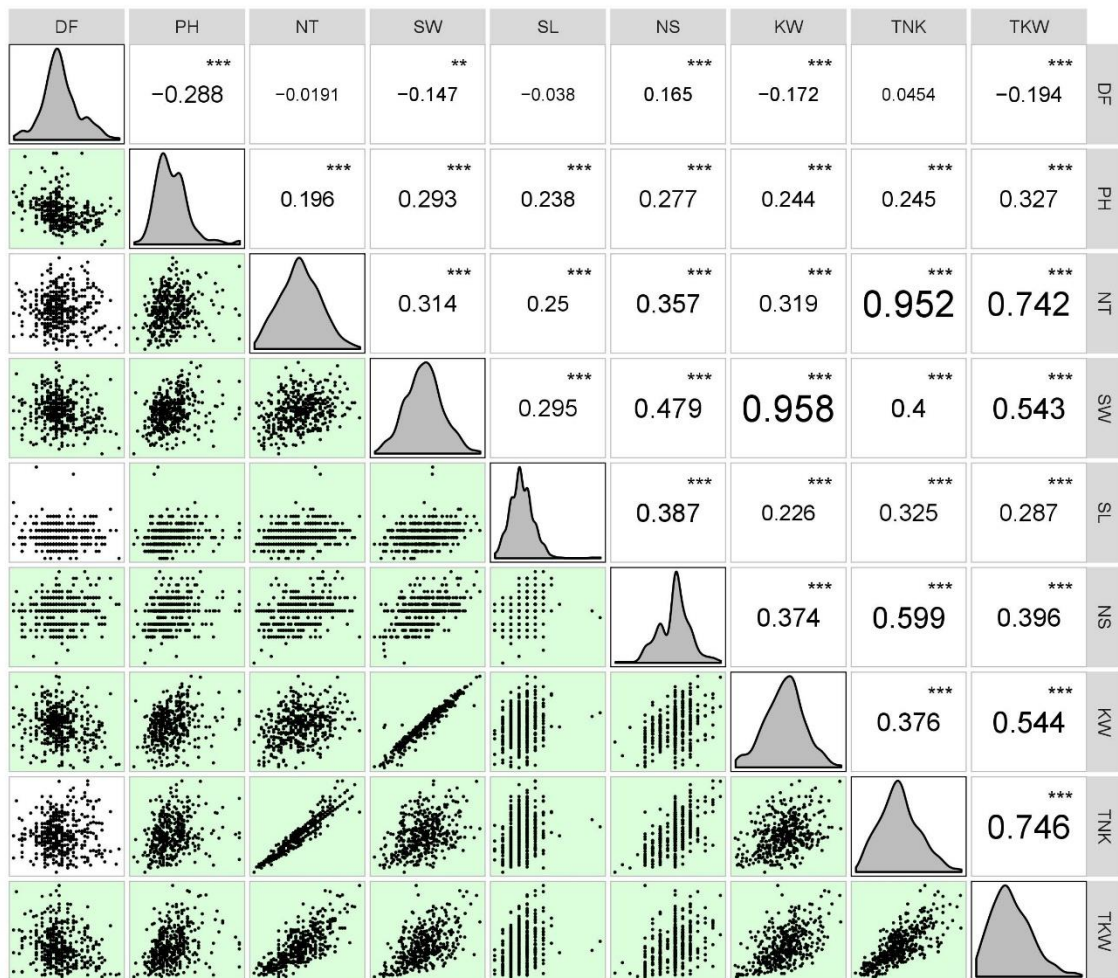


Figure 1: Pearson's linear correlation among agronomic traits of 420 wheat lines. *, **, and ***, which represent Pearson linear correlation coefficient ($n = 420$) significance levels at $p < 0.05$, 0.01, and 0.001, respectively, are highlighted in green. DF, days from emergence to flowering; PH, plant height; NT, number of tillers; SW, spike weight; SL, spike length; TNK, total number of kernels per plant; NS, number of spikelets; KW, kernel weight; TKW, total kernel weight per plant.

The number of tillers showed a positive and strong association with TNK (0.952) and TKW (0.742) and a moderate association with other variables. The NT was directly associated with grain yield increase; considering this, the NT is an efficient trait to use for indirect selection for increasing grain yield.

The SW displayed a positive and strong correlation with KW (0.958) and a moderate correlation with TKW (0.543) and NS (0.479). Important associations were found between NG and TKW (0.746) on that the increase in the number of kernels maximizes grain yield.

3.4.3 Direct and indirect effects

According to the coefficient of determination, the analyzed traits may explain 78% of the total grain weight per plant (Table 3). The NT displayed a linear correlation of positive and moderate magnitude with TKW ($r = 0.606$). The DF had a direct negative effect on TKW, indicating that selecting for plants with a long flowering cycle is not advantageous for potentially increasing the grain yield. The KW had a positive direct effect on TKW and an indirect effect on NT. These associations may have been observed owing to the plant spacing implemented in the experiment.

Table 3: Estimates of direct (main diagonal) and indirect effects of eight agronomic traits on total kernel weight per plant (TKW) evaluated in 420 wheat lines, Frederico Westphalen, Brazil.

	Explanatory traits					
	DF	PH	NT	SL	NS	KW
DF	-0.120	0.034	0.002	0.005	-0.020	0.021
PH	-0.024	0.082	0.016	0.019	0.023	0.02
NT	-0.012	0.119	0.606	0.151	0.216	0.193
SL	-0.001	0.006	0.006	0.025	0.010	0.006
NS	0.01	0.017	0.022	0.024	0.062	0.023
KW	-0.048	0.069	0.090	0.064	0.105	0.282
Linear	-0.194	0.327	0.742	0.287	0.544	0.396
Determination coefficient						0.784
Residual effect of variable						0.561
Number Condition						5.111
Determining variable						0.424

DF, days from emergence to flowering; PH, plant height; SL, spike length; NT, number of tillers; NS, number of spikelets; KW, kernel weight; TKW, total kernel weight per plant; bold values correspond to direct effects

3.4.4 Selection gains

The selection gain results revealed variation in gains for evaluated traits and methods used (Table 4). Direct and indirect selection showed gains from -23.82% for DF to 301.85% for TKW. The gains recorded for TKW, TNK, KW, and SW were overall positive. However, higher DF and PH values resulted in negative gains. Although direct selection resulted in high gains, indirect selection gains were also significant, in particular for NT and TNK. Selection

for NT resulted in indirect gains of 45.38% and 100% for TNK and TKW, respectively, and a direct gain of 35.83% (Table 4). Selection for TNK resulted in direct gains of 53.34% and indirect gains in TKW of 96.12%.

Table 4: Selection gains in wheat lines (GS%) determined using three methods: direct and indirect selection, and Mulamba & Mock and Smith and Hazel selection indexes.

Traits	X0	XS	GS%									
			DF	PH	SL	NT	TNK	SW	KW	NS	TKW	Total
DF	80.37	65.70	-9.17	2.78	2.41	-1.18	-2.99	-8.17	-7.42	-1.09	1.01	-23.82
PH	61.28	45.60	1.76	-8.85	-4.98	-10.57	-17.06	-20.89	-18.67	-7.39	-45.84	-132.49
SL	10.27	14.80	-1.23	4.3	20.89	1.71	6.36	23.25	17.28	4.58	18.06	95.2
NT	22.65	42.50	1.51	4.24	2.41	35.83	45.38	11.53	14.71	2.06	100.62	218.29
TNK	729.91	1513.89	2.33	2.15	3.8	30.78	53.34	33.82	33.69	10.57	96.12	266.6
SW	1.69	3.03	-0.23	5.26	7.03	6.4	17.81	66.78	61.72	8.99	79.72	253.48
KW	1.18	2.21	-1.05	5.15	5.64	8.03	17.19	63.29	65.24	6.79	87.78	258.06
NS	15.84	21.10	4.39	2.38	7.49	12.72	35.93	38.7	32.56	16.55	43.1	193.82
TKW	13.26	34.03	-1.55	4.24	5.64	27.16	38.21	39.5	41.23	4.58	142.84	301.85
Smith & Hazel			-0.61	3.34	23.37	41.05	6.16	35.67	40.23	137.77	6.57	293.55
Mulamba & Mock			1.39	3.96	22.65	51.22	11.51	43.72	51.29	106.73	8.42	300.89

Bold values correspond to direct gains. DF, days from emergence to flowering; PH, plant height; SL, spike length; NT, number of tillers; TNK, total number of kernels per plant; SW, spike weight; KW, kernel weight; NS, number of spikelets; TKW, total kernel weight per plant.

Selection gains obtained by the Smith (1936) and Hazel (1943) selection index, for the main trait, were similar among the methods studied (Table 4). The higher gains were observed for TKW, KW, NK, SW, and NT. The wheat lines rank for the Mulamba & Mock (1978) index had a 90% coincidence with the direct selection (Table 5), while the coincidence of the Smith (1936) and Hazel (1943) index was lower. The superior lines selected from the selection indexes (145, 183, 189, 193, and 299) are promising lines, mainly for improving grain yield.

Table 5: Wheat lines selected by direct and indirect selection, Mulamba & Mock and Smith and Hazel selection indexes, Frederico Westphalen, Brazil.

Selection Index	Lines
Direct selection	145, 183, 189, 193, 242, 299, 303, 310, 404, 413
Smith & Hazel	81, 145, 183, 189, 193, 299, 372, 396, 408, 412
Mulamba & Mock	145, 183, 189, 193, 242, 299, 303, 310, 385, 404

3.5 DISCUSSION

The phenotypic variance is related to the genotypic and environmental variance. In this study, the lines that presented higher plant heights were highly influenced by the environment. This trend was also observed by Keser *et al.* (2017), who found that the mean plant height decreased from 140.7 cm to 79.5 cm, from the oldest to the most current wheat cultivar. This reduction was associated with the introduction of the *Rht1* gene. Reducing plant height is an important factor to be considered in breeding programs as it is an essential and desirable trait (Yao *et al.*, 2018).

The heritability of DF found in the experiment was similar to that found in the studies conducted by Bind *et al.* (2016). These authors showed that the white oat cycle had a low heritability. Cargnelutti *et al.* (2009) observed that high heritability is linked to greater genetic variability, and therefore, greater accuracy in selection.

In relation to the association of traits, most (91%) of the coefficients revealed significance even with low magnitudes (Figure 1). This may be explained by the high degrees of freedom ($n = 418$) included in the *t* test (Stell & Torrie, 1980). The association of NT with TNK and TKW is an important consideration for wheat breeding, since the NT can be easily measured.

In this study, the NS was associated with TNK. Thus, a higher sowing density provides an increase in the number of kernels per spikelet. In accordance with the results of this study, Board & Maricherla (2008) found a high ratio between the number of kernels and kernel weight per area. Spike size is an important agronomic trait for breeding, especially as it is positively associated with grain yield. Results from a previous study have shown that a larger spike resulted in a greater number of spikelets (Silva *et al.*, 2010).

Agronomic traits with high magnitudes of correlation must be considered in selection strategies (Vale *et al.*, 2014). Thus, based on our results for the experimental design used, the strategy adopted could be positive indirect selection. The traits suggested by the analysis for selection are the number of kernels and tillers, in front of the correlations among traits. However, it is important to highlight that a greater spacing of plants leads to a greater number of tillers per plant; this diverges from commercial sowing conditions, which involve high planting densities.

In order to improve our knowledge of the association of traits, path analysis is an important technique as it provides information on the direct and indirect effects on the main trait. Studies carried out by Entringer *et al.* (2014) and Carvalho *et al.* (2017) found satisfactory gains using both direct and indirect selection, since the traits showed favorable correlation. Falconer (1987) highlighted that indirect selection may promote greater gains; the same was evidenced by Pereira *et al.* (2017), who studied the genus *Paspalum*.

The selection gains obtained infer that all methods may be used for wheat line selection. The direct and indirect selection showed the best selection gains. The Mulamba & Mock sum of ranks index presented higher gains when compared to the Smith and Hazel index. The efficiency of using selection indexes has also been observed in silage maize (Crevelari *et al.*, 2019), soybean (Teixeira *et al.*, 2017), and wheat (Fellahi *et al.*, 2018). Almeida *et al.* (2019)

showed concordance between indexes with regards to the ranking of the best genotypes; the magnitude of the expected gain must be considered.

3.6 CONCLUSIONS

The heritability of the spike weight, total number of kernels, and total kernel weight per plant reveals that selection of these traits may result in greater direct selection gains.

Selection of plants with a higher number of tillers resulted in more productive lines. Selection indexes are advantageous for breeding advanced generations of wheat, since they provide the gains, distributed among all the evaluated traits. The selection index based on the sum of ranks (Mulamba & Mock) was more efficient in the selection of productive wheat lines.

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4 CAPÍTULO II - CORRELATION AND SELECTION GAINS IN F6 WHEAT GENOTYPES ESTIMATED USING MULTIVARIATE ANALYSIS

Submetido para o periódico: *Bragantia*

Situação: Aguardando revisão

Correlation and selection gains in F₆ wheat genotypes estimated using multivariate analysis

4.1 ABSTRACT

The objective of this work was to estimate the phenotypic (rP), genotypic (rG) and environmental (rE) correlation coefficients and the genetic parameters, as well as to estimate the selection gains between agronomic traits in wheat using multivariate analysis. F₆ generation was carried out in a randomized block experimental design, with fifteen wheat genotypes arranged in three replications in 2018. Agronomic traits were evaluated at the physiological maturity stage. Correlation coefficients, variance components, genetic parameters, selection gain, Euclidian's distance, relative contribution of traits and canonical variables were estimated. Selection in advanced wheat generations using number of tiller per plant and grain mass can result in greater selection gains. The higher genotypic correlations were verified between thousand kernel weight associated to plant height, number of tillers and number of spikelets. The crop cycle presented greater contribution to genetic divergence among the studied genotypes. In front of distinct groups, it can be stated that there is genetic variability among the evaluated populations.

Key words: advanced generation, genetic divergence, *Triticum aestivum* L.

Correlação e ganhos de seleção em genótipos F₆ de trigo estimados por meio de análise multivariada

4.2 RESUMO

O objetivo do trabalho foi estimar os coeficientes de correlação fenotípica (rP), genotípica (rG) e ambiental (rE), e parâmetros genéticos, assim como estimar os ganhos de seleção entre caracteres de interesse agrônomo em trigo usando análise multivariada. A geração F₆ foi conduzida a campo em delineamento experimental de blocos casualizados, sendo quinze genótipos de trigo, dispostas em três repetições em 2018. Os caracteres agrônômicos foram avaliados no estágio de maturação fisiológica. Foram estimados os coeficientes de correlação, componentes de variância, parâmetros genéticos, ganho de seleção, distância Euclidian, contribuição relativa dos caracteres, e variáveis canônicas. A seleção em gerações avançadas

de trigo a partir de número de afilhos por planta, massa de grãos pode resultar em maiores ganhos de seleção. Os maiores valores de correlação genotípica foram verificados entre peso de mil grãos associado com altura de planta, número de afilho e número de espiguetas. O ciclo apresentou maior contribuição para divergência genética entre os genótipos estudados. Frente aos grupos distintos, pode-se afirmar presença de variabilidade genética entre as populações avaliadas.

Palavras chave: divergência genética, geração avançada, *Triticum aestivum* L.

4.3 INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal in the world, being a major commodity in the international grain market. It is used as a source of human and animal food (SINGH et al., 2016). Crop has been extensively searched in recent decades, with breeders' main focus on increasing productivity. But as the agronomic traits have complex quantitative inheritance, thus, wheat breeding has a highly cost and time expending to achieve advanced lines, and new cultivars (NI et al., 2017).

The increase in wheat productivity is the result of two elements: improvement of the growing environment and the genetic gain (XIAO et al., 2014). Environmental improvement through agronomic practices is to provide the crop with an environment more favorable to the best development, providing adequate water supply, adequate fertility and elimination of other biotic and abiotic stresses (LAIDIG et al., 2016). Genetic gain refers to the increase in performance that is achieved through plant breeding, in this context, a new breeding program should increase grain yield. Several authors have been reporting the genetic gain in wheat worldwide, in Brazil (WOYANN et al., 2019b), Argentina (LO VALVO et al., 2018) and China (YAO et al., 2019).

In plant breeding programs, the study of linear relationships among traits may provide important results, especially in identifying traits to be used in indirect selection (FALCONER et al., 1996) The correlation coefficient (r) is used to measure the intensity and sense of linear association between two random variables (OLIVOTO et al., 2017). Knowledge of the phenotypic, genetic and environmental correlation among traits is essential for simultaneous selection of several traits, also it's important when target trait reveals low heritability or is difficult to measure (FALCONER&MACKAY, 1996).

Selection of superior genotypes is easily proceeded when there are large differences in phenotypic expression, thus grouping analysis aims to gather classification criteria, so that there

is high homogeneity within the group and heterogeneity between groups, according to criteria of similarity or dissimilarity (CRUZ et al., 2014). In order to select potentially high-yielding wheat lines in breeding programs, superior genotypes need to be selected for with greater accuracy.

The following hypotheses were formulated: (i) understanding the correlation among agronomic traits may help to obtain superior genotypes to attend market expectations for productivity, (ii) the selection gains in advanced generations are satisfactory for wheat and (iii) genetic deviations can be used to select superior genotypes. In this way, the objective of this work was to estimate the phenotypic (r_P), genotypic (r_G) and environment (r_E) correlation coefficients and genetic parameters; as well as to estimate the selection gains between agronomic traits in wheat using multivariate statistics.

4.4 MATERIAL AND METHODS

4.4.1 Plant material

The study was performed in 2018 crop season, in Frederico Westphalen (27°23'26"S, 53°25'43"W, 481 m above the sea level). The soil was classified as ferric aluminum Hapludox type and the climate as Cfa according to Köppen (ALVARES et al., 2013).

Wheat genotypes F₇ from crosses were used: Mirante x Quartzo (UFSMFW1 01), Mirante x Horizonte (UFSMFW1 02), TBIO Toruk, Supera x Quartzo (UFSMFW1 03), Supera x Quartzo (UFSMFW1 04), BRS 327 x Horizonte (UFSMFW1 05), Supera x Abalone (UFSMFW1 06), BRS 327 x Horizonte (UFSMFW1 07), Supera x Abalone (UFSMFW1 08), BRS 327 x Horizonte (UFSMFW1 09), Mirante, Supera, Supera x Horizonte (UFSMFW1 10), Pampeano e Quartzo. To obtain these lines, the crosses were realized in greenhouse and generation advance was performed using Single Seed Descent method (SSD). The experimental design was randomized complete blocks, with three replicates. The plots were composed by four rows that were 4 m long, and separated by 0.17 m, in a density of 350 plants m⁻². The sowing was performed on Jun 12^{sd} 2018, in the no-tillage system; and pest, disease and weed control was done preventively.

4.4.2 Traits studied

The traits measured were: a) days of emergence to flowering (DF); b) plant height (PH, cm), measured from the soil to spike of main tiller; c) number of tillers (NT), obtained by count of fertile tillers; d) spike length (SL, cm), considering spike insertion point to start of awns; e)

number of spikelets (NS), obtained by counting of spikelets of main tiller spike; f) kernel weight (KW, g) obtained by weight of main tiller spike; g) thousand kernel weight (TKW, g).

4.4.3 Meteorological data

The meteorological data were obtained from the Instituto Nacional de Meteorologia (INMET), referring to automatic weather station of Frederico Westphalen - RS (A854), located about 350 m from experiment, for cultivation period of Jun 12th 2018 to Oct 31st 2018. For that, instantaneous, maximum and minimum air temperature recorded every hour was used, obtaining average for instantaneous, maximum and minimum temperature recorded for day. And for daily precipitation was carried out accumulation on a day.

4.4.4 Statistical analysis

Data were submitted to analysis of variance carried out at 5% significance level of test using the statistical model (Eq. 1):

$$Y_{ij} = \mu + g_i + b_j + \varepsilon_{ij}, \quad (1)$$

Where μ is the mean, g_i is the effect of i^{th} genotype, b_j is the effect of j^{th} block, ε_{ij} is random error. Assuming treatments effects as random, the accuracy was estimated according to Eq. 2 (RESENDE et al., 2007):

$$\hat{r} = \left[\frac{1}{1 + (\sigma_b^2/b)/\sigma_g^2} \right]^{1/2} \quad (2)$$

where: b is number of replicates or blocks.

For genotypic, phenotypic and environmental correlations between two traits (x and y) were estimated by analysis of variance. For it, the mean square associated with treatments (PMT) and residual (PMR) according the formulas: $\text{PMT}_{xy} = \frac{\text{MST}_{x+y} - \text{MST}_x - \text{MST}_y}{2}$ and $\text{PMR}_{xy} = \frac{\text{MSR}_{x+y} - \text{MSR}_x - \text{MSR}_y}{2}$, phenotypic correlation: $r_f = \frac{\text{PMT}_{xy}}{\sqrt{\text{MST}_x \text{MST}_y}}$, environmental correlation: $r_a = \frac{\text{PMR}_{xy}}{\sqrt{\text{MSR}_x \text{MSR}_y}}$ and genotypic correlation: $r_g = \frac{\hat{\sigma}_{gxy}}{\sqrt{\hat{\sigma}_{gx}^2 \hat{\sigma}_{gy}^2}}$, being $\hat{\sigma}_{gxy} = \frac{\text{PMT}_{xy} - \text{PMR}_{xy}}{r}$, where MQT is mean square of treatment, MSR is mean square of residue, $\hat{\sigma}_{gxy}$ is genotypic covariance estimator, $\hat{\sigma}_{gx}^2$ and $\hat{\sigma}_{gy}^2$ are the genotypic variance of X and Y, respectively.

The significance test of the phenotypic and environmental correlations, the t test was used as described by STEEL et al. (1980) according to the Eq. 3:

$$t = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2} \quad (3)$$

Genotypic correlations were submitted to *bootstrap* analysis with five thousand (5000) simulations to identify correlations with significance.

Selection gains were estimated through heritability and the proportion of the additive variance explored (Cruz, 2014), and it was estimated by (Eq. 4):

$$GS = i p \hat{\sigma}_g h \quad (4)$$

Where i is the selection intensity; p parental control; $\hat{\sigma}_g$ genetic standard deviation; h square of heritability, for the selection unit considered.

The relative contribution of each trait was estimated by SINGH (1981) methodology. After, for canonical variables analysis, only traits with relative contribution up to 10% were used. Statistical software Genes (CRUZ, 2016) and R (R Development Core Team, 2016) was used to perform the analysis.

In order to study genetic diversity of populations genetic distance matrix was estimated by Euclidian's distance, and clustering analysis was done using the UPGMA (Unweighted Pair Group Method with Arithmetic Averages), and it was represented on a dendrogram. The cut level in the dendrogram, which separates populations into distinct groups, was determined by the Mojena's method (1977), and adjusted by cophenetic correlation. The clusters analysis were performed using "HDMD" (McFerrin, 2013) and "cluster" (Maechler et al., 2018) package in R (R Development Core Team, 2016).

4.5 RESULTS AND DISCUSSION

The average air temperature during the crop cycle was 17.8°C, with a minimum temperature of 0.7°C and maximum of 33.7 °C (Fig. 1). The air temperature above 30°C in the pre and post-anthesis stages for long periods may reduce grain filling rate and, therefore, decreases grain yield and quality (ASSENG et al., 2015). Wheat is a winter cereal that develops over a wide temperature range, and the base air temperature may vary from 3.1°C to 18.4°C (SALAZAR-GUTIERREZA et al., 2013). Thus, it can be highlighted that 2018 provided ideal meteorological conditions for wheat growth and development. The accumulated precipitation was 720.8 mm during the crop development (Fig. 1).

The analysis of variance (Table 1) showed significant difference for DF, PH, NS and KW by t test ($p < 0.01$ and $p < 0.05$) genotypes. The data presented low accuracy (SL), moderate (NT) and high magnitudes (DF, PH, NS, KW, TKW) (RESENDE&DUARTE, 2007). The genotypes studied presented greater phenotypic variance for the PH and DF, and it's important

to highlight that the environment had large influence (Table 2). It stands out the PH traits, which revealed higher values of variance being the most influenced by environment.

Regarding the heritability, the higher estimates were observed for DF (0.99), PH (0.91), NS (0.71) and KW (0.73). The results reveal a favorable condition for genetic gains with selection through these traits. Thus, these high heritability estimates indicated genetic control over evaluated traits. Therefore, it is possible to infer that traits studied in this set of genotypes may be used to evaluate genetic variability and they are efficient for prediction of selection.

The highest selection gains of wheat genotypes were evidenced for TKW (40.56), PH (15.84), NT (13.25), KW (13.64), followed by DF (4.91), SL (1.91) and NS (5.50) that had low estimates of selection gain among the genotypes. Therefore, selection for NT and TKW may increase selection gains, since these traits response to more easily to selection due to high heritability coefficients. According to MEIRA et al. (2019), in the study of black oat populations the selection strategy is to reduce variability within families and to increase variability among families. This is to combine selection between and within populations to achieve high efficiency in the selection gain.

Around 90% of the correlations showed higher genotypic coefficient than phenotypic (Table 3). These results favor the selection strategy for breeding programs, since phenotypic correlations have genetic and environmental interactions, but only associations of a genetic nature are inheritable.

The results indicated that at the genotypic level there was a positive correlation between NS and KW ($r=0.63$) (Table 3). The increase number of spikelets per spike is an efficient strategy to improve grain yield of wheat, since this trait is associated to the increase in the number of grains per spike, considered an important wheat yield component (FIOREZE et al., 2012).

The negative correlation coefficients were observed between DF and NT ($r= -0.55$). Compensatory potential of wheat tillering is modified according to development cycle and determine the number of spikes per plant (CARVALHO et al., 2015). In this way, photosynthetically active tillers tend to increase grain yield (FIOREZE&RODRIGUES, 2012).

The correlation coefficients observed to DF and KW showed tendencies to positive associations with grain mass. The PH showed a strong correlation with KW ($r=0.60$), this association suggests that tall plants had greater accumulation of photosynthates for the grains, with a longer reproductive period resulting in higher grain weight (KHAN et al., 2013; RIGATTI et al., 2019).

The number of fertile tiller per plant showed a significant and positive intermediate association with KW ($r=0.52$) and positive correlation with NS ($r=0.46$) for genotypic correlation indicating that this trait may be used in indirect selection aiming for to increment grain yield in wheat.

Spike length (SL) showed a significant negative genotypic association with TKW ($r=-0.442$), indicating that larger spikes tend to increase yield. In this way, these traits are important to be considered in the cereals breeding, due to being closely related to the yield components and define wheat productivity (SILVA et al., 2010).

For canonical variables, two variables explained more than 90% of the genetic variation among the genotypes (Table 4). In this way, a two-dimensional graph was used to represent canonical variables (Fig. 2). There is large distance among the wheat genotypes, emphasizing the genotypes Pampeano, UFSMFW1 14, UFSMFW1 03 and UFSMFW1 07 (Fig. 2). Based on the graphic dispersion of the populations it's possible to direct he crosses between divergent parents to the desired traits, in order to promote genetic recombination. In this case, hybridizations could be programmed, for example, between genotypes Pampeano with UFSMFW1 06, TBIO Toruk with Pampeano, UFSMFW1 01 with UFSMFW1 08.

Regarding the relative contribution of traits (SINGH, 1981), DF expressed the largest contribution (81%) to genetic divergence among genotypes (Table 5). The traits KW, NS and NT contributed with 5%, 2% and 2%, respectively, such results are in agreement with GURJAR et al. (2018).

The cluster analysis verified two distinct groups, expressing genetic differences, according to evaluated traits (Fig. 3). Group I: composed by genotype Pampeano; Group II: genotypes UFSMFW1 01 to UFSMFW1 10, Mirante, Quartzo, Supera, in exception of PAMPEANO, the other genotypes have similarity among agronomic traits, being plant height and days of emergence to flowering the traits that more contribution to the divergence. The highest plant height for the genotype Pampeano, corroborated to results obtained by BORNHOFEN et al. (2013) studying the best genotypes for general combining ability.

4.6 CONCLUSIONS

Selection based on number of tillers, kernel weight and thousand kernel weight may result in expressive selection gains. The higher significative positive genotypic correlations were verified between number of fertile tillers associated to kernel weight and thousand kernel weight. The increase number of spikelets per spike is an efficient strategy to improve grain

yield of wheat. The cycle showed greater contribution to the genetic divergence among genotypes studied. Distinct groups highlighted the genetic variability among genotypes.

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Table 1. Summary of variance analysis, mean (\bar{x}) and selective accuracy (\hat{r}_{gg}) for wheat genotypes.

SV	MS							
	DOF	DF	PH	SL	NT	NS	KW	TKW
Block	2	3.75	62.15	1.75	0.28	1.68	0.05	0.90
Genotypes	14	34.92**	364.03**	1.80	2.4	2.56**	0.09**	1.32
Residue	28	0.08	33.67	1.46	1.5	0.73	0.03	0.48
Total	44							
\bar{x}		75.57	68.77	8.15	2.75	13.04	1.03	33,02
\hat{r}_{gg}		0,98	0.95	0.40	0.64	0.88	0.87	0.66

**, *Significative to t test ($p < 0.01$ and $p < 0.05$). SV: source variation; DOF: degree of freedom; MS: mean square; CV: coefficient of variation; DF: days of emergence to flowering; PH: plant height; SL: spike length; NT: number of tillers; NS: number of spikelets; KW: kernel weight; TKW: thousand kernel weight.

Table 2. Estimates of phenotypic variance ($\hat{\sigma}_f^2$), genetic variance ($\hat{\sigma}_g^2$), environmental variance ($\hat{\sigma}_e^2$), heritability (h^2), gentic gain (G_s) for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TKW) for wheat genotypes.

Estimates	DF	PH	SL	NT	NS	KW	TKW
$\hat{\sigma}_f^2$	11.64	121.34	0.60	0.80	0.85	0.03	0.44
$\hat{\sigma}_g^2$	11.61	110.11	0.11	0.30	0.60	0.02	0.17
$\hat{\sigma}_e^2$	0.03	11.23	0.49	0.50	0.25	0.01	0.26
h^2 (%)	99.74	90.74	18.48	37.45	71.28	73.15	40.56
G_s (%)	4.91	15.84	1.91	13.25	5.50	13.64	40.56

Table 3. Estimates of phenotypic (r_f), genotypic (r_g) and environmental (r_e) correlation between agronomic traits for wheat genotypes.

Trait		PH	SL	NT	NS	KW	TKW
DF	r_f	0.31*	0.08	-0.55*	-0.07	0.35	0.28
	r_g	0.46	0.45	-0.59 ⁺⁺	-0.42	0.51	0.46
	r_e	-0.23	-0.24	0.18	0.34*	-0.26	0.15
PH	r_f	-	0.34	-0.30	0.32	0.48	0.47
	r_g	-	0.55	-0.49 ⁺⁺	0.49	0.60	0.57
	r_e	-	0.37*	-0.16	-0.24	-0.19	-0.01
SL	r_f		-	0.04	0.03	0.04	-0.24
	r_g		-	0.43 ⁺⁺	0.46	0.49	-0.44 ⁺⁺
	r_e		-	-0.28	-0.22	-0.29	0.04
NT	r_f			-	0.18	0.35	0.13
	r_g			-	0.46	0.52 ⁺⁺	0.39 ⁺⁺
	r_e			-	0.20	0.45*	-0.19
NS	r_f				-	0.57*	-0.11
	r_g				-	0.63	-0.48
	r_e				-	0.14	-0.01
KW	r_f					-	0.17
	r_g					-	0.48
	r_e					-	-0.37

Note. Genotypic correlation index “+” and “++” significant to t test ($p < 0.05$ and $p < 0.01$). Phenotypic and environmental correlation index, “*” and “**” significant to t test ($p < 0.05$ and $p < 0.01$). DF: days of emergence to flowering; PH: plant height; SL: spike length; NT: number of tillers; NS: number of spikelets; KW: kernel weight; TKW: thousand kernel weight.

Table 4. Variance (eigenvalues), percentage variance and accumulated variance of canonical variance, aiming to estimate the dissimilarity between ten wheat genotypes.

Trait	Variance (eigenvalues)	Percentage variance (%)	Accumulated variances (%)
DF	63.16	89.06	89.06
PH	4.98	7.02	96.08
SL	1.27	1.79	97.87
NT	0.70	0.99	98.86
NS	0.43	0.61	99.47
KW	0.26	0.36	99.84
TKW	0.12	0.16	100.00

Note: DF: days of emergence to flowering; PH: plant height; SL: spike length; NT: number of tillers; NS: number of spikelets; KW: kernel weight; TKW: thousand kernel weight.

Table 5. Relative contribution of traits to divergence to Singh method for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TKW) for wheat genotypes.

Trait	S.j	Value (%)
DF	12089.94	81.18
PH	1089.92	7.32
SL	105.72	0.71
NT	306.31	2.06
NS	302.60	2.03
KW	856.88	5.75
TKW	141.48	0.95

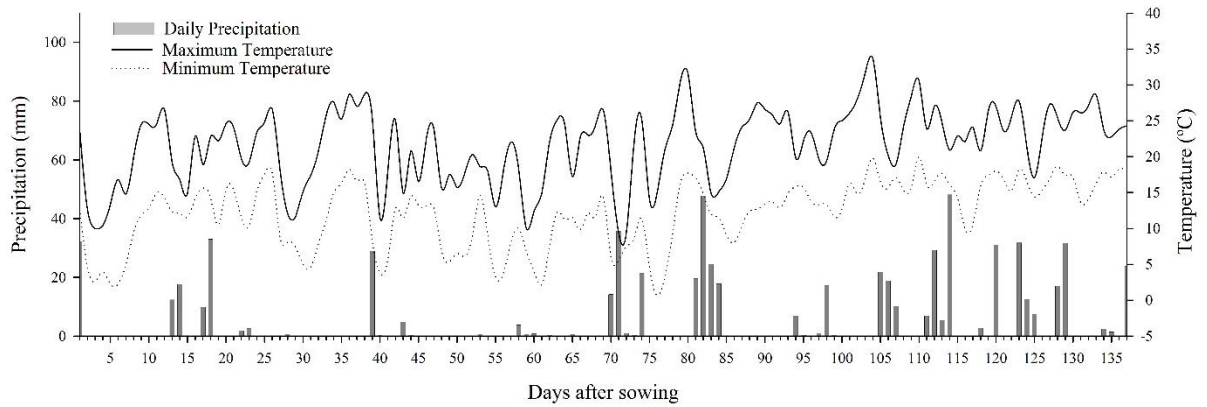


Figure 1. Meteorological data of daily precipitation, maximum and minimum air temperature during the wheat development in 2018 crop season. Source: INMET, (Frederico Westphalen - A854) Frederico Westphalen automatic weather station – RS.

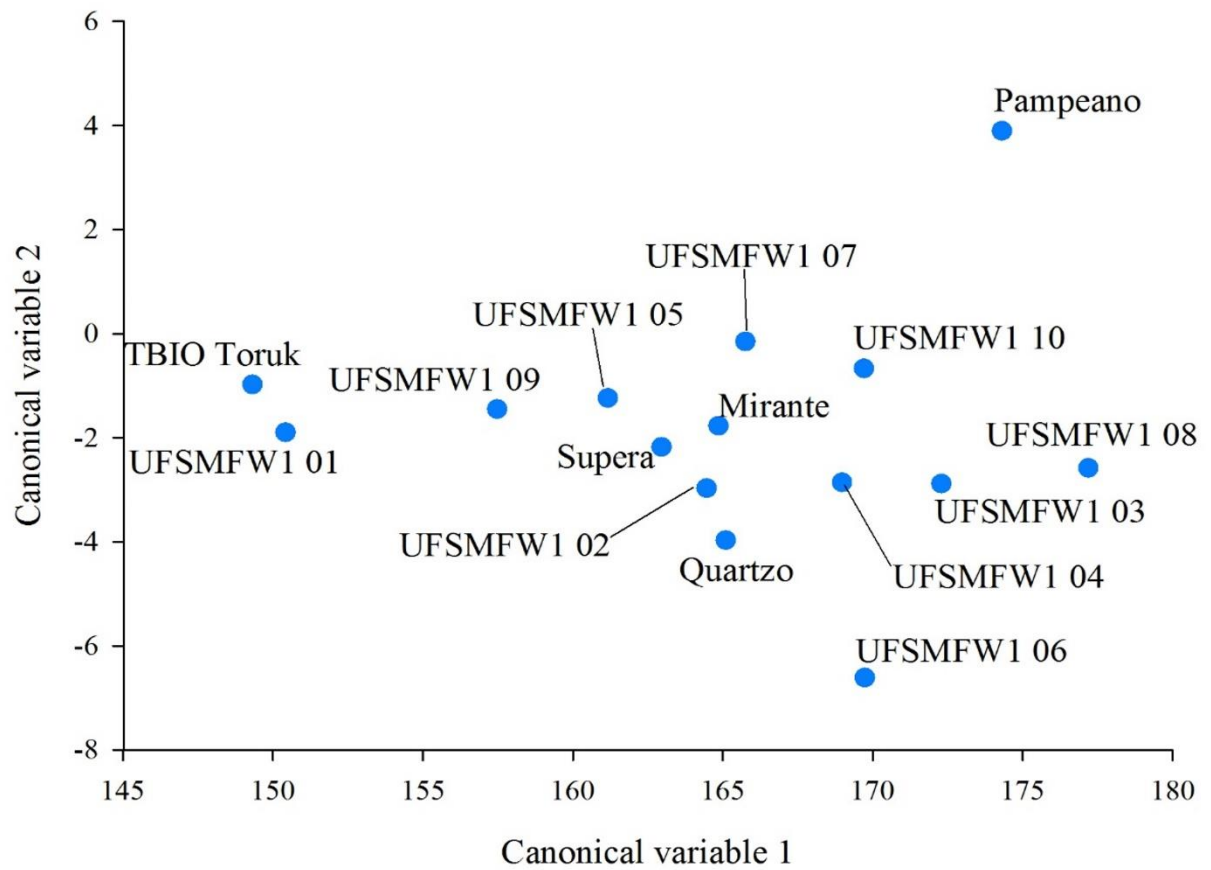


Figure 2. Graphic dispersion of first score (canonical variable 1) and second score (canonical variable 2) for wheat genotypes.

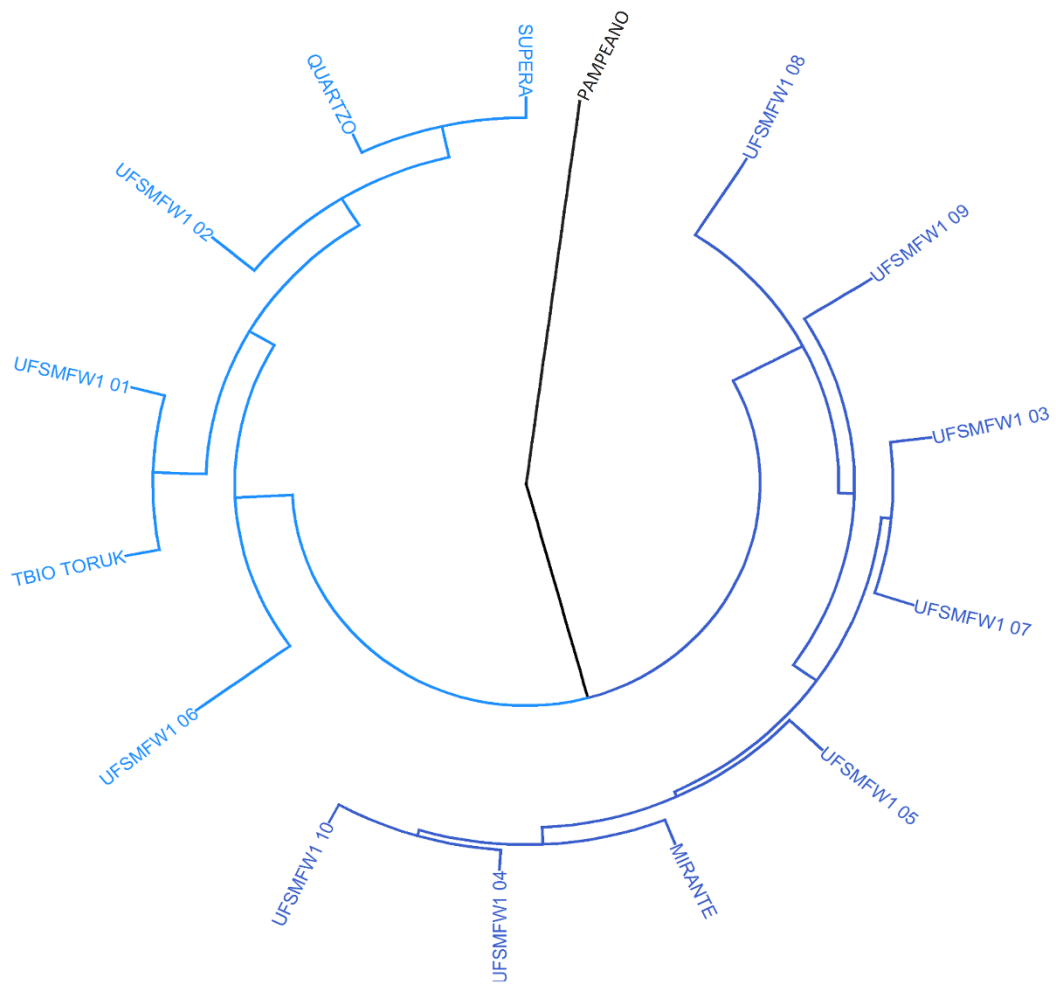


Figure 3. Dendrogram using unweighted pair group method with arithmetic mean (UPGMA) from Euclidian's distance matrix for wheat genotypes. Cophenetic correlation coefficient (r): 0.73.

**5 CAPÍTULO III - GENETIC PARAMETERS AND MULTIPLE-TRAIT
SELECTION IN WHEAT GENOTYPES**

Submetido para o periódico: Anais da Academia Brasileira de Ciências

Situação: Aguardando revisão

FRONT PAGE**Genetic parameters and multiple-trait selection in wheat genotypes**

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Key words: ideotype-design index, mixed model, REML/BLUP, *Triticum aestivum* L.

Running Title: Multiple-trait selection in wheat genotypes

Academy Section: Agrarian Sciences

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5.1 ABSTRACT

Mixed models and multivariate analysis are powerful tools for genotype selection in plant breeding programs. The best linear unbiased prediction method (BLUP) has been used to predict genetic values without environmental effects. Furthermore, the FAI-BLUP (ideotype-design index) procedure is especially valuable for plant breeding because of the multiple-trait selection. Thus, this study aimed to determine the genetic potential of advanced wheat generations using REML/BLUP in combination with multivariate techniques for superior genotype selection. 11 wheat genotypes were performed in randomized block design, and evaluated for plant height, spikelet insertion height, number of tillers, number of spikelets, kernel width, hectoliter weight and kernel weight per plant. Genetic parameters were estimated using the REML/BLUP methodology, and FAI-BLUP index was calculated using predicted genetic values. Genotypes UFSMFW1 02, UFSMFW1 05, and UFSMFW1 04 showed potential to increase grain yield. The selection gains of tiller number and grain yield per plant (14.63 and 22.35%, respectively) indicated the potential of superior genotypes. Therefore, the present study demonstrates that the FAI-BLUP index is a valuable tool for genotype selection.

Key words: ideotype-design index, mixed model, REML/BLUP, *Triticum aestivum* L.

5.2 INTRODUCTION

Wheat is staple food wide world and, as such, is an important part of the daily diet and carbohydrate source of millions of people (Litoriya et al. 2018). Furthermore, the cereal is widely used in Brazil, owing to the development of high-yielding cultivars and market consumption in foods of better industrial quality and high nutritional content (Battenfield et al. 2016).

The selection of superior genotypes is usually based on phenotypic expression, which involves genetic and environmental effects. However, the use of mixed models facilitates the prediction of genotypic values and improves selection efficiency (Pimentel et al. 2014). In this context, one of the most appropriate selection procedures involves the estimation of variance components (i.e., restricted maximum likelihood method, REML) and the prediction of genotypic values (i.e., best linear unbiased prediction, BLUP) (Resende 2007). Accordingly, these methods are being used in plant breeding studies, such as white oat (Olivoto et al. 2019), soybean (Follmann et al. 2019), bean (Santos et al. 2019), and corn (Olivoto et al. 2017), as well as in early-segregating generations of wheat (Pimentel et al. 2014, Woyann et al. 2019b).

The use of mixed models improves selection efficiency for the improvement of autogamous plants since progenies or lines with higher genotypic merit are identified (Ramalho and Araújo 2011). To obtain cultivars with desirable agronomic characteristics, large numbers of characters are evaluated. However, at selection time is difficult to identify individuals with the interested traits. Thus, multivariate techniques have been used to discriminate lines of soybean (Tobar-Tosse et al. 2015) and wheat (Costa et al. 2013). One of the most commonly used techniques is principal component analysis (PC), which condenses numerous variables into a limited number of new variables (PCs), and each PC is a linear combination of original, independent, and uncorrelated variables, where the former is most important because it retains most of the total variation contained in the original data (Cruz et al. 2014).

In order to select potentially high-yielding wheat lines in breeding programs, superior genotypes must be selected with greater accuracy. Thus, among the recently released selection indexes, Rocha et al. (2018) proposed a selection index based on factor analysis and genotype-ideotype distance (FAI-BLUP index). The performance of such a multi-trait index, predicted genetic effects with mixed models, and genetic values using REML/BLUP (Resende et al. 2014) presents a good strategy for selecting genotypes. The efficiency of this selection index for crop breeding has also been highlighted by Rocha et al. (2019), Oliveira et al. (2019), Woyann et al. (2019a), and Silva et al. (2018).

The aim of this study was to determine the genetic potential of advanced wheat genotypes using REML/BLUP combined with multivariate techniques to superior genotype selection.

5.3 MATERIALS AND METHODS

5.3.1 Plant material

The study was performed in the 2018 crop season at Frederico Westphalen (27°23'26"S, 53°25'43"W; 481 m above sea level). The soil was classified as a typical Dystrophic Red Latosol (Santos et al. 2013) or Typic Hapludox (USDA 2014). The climate was classified as Cfa, according to Köppen (Alvares et al. 2013).

Wheat genotypes in generation F₇ were used. The genotypes were derived from single crosses: Mirante × Quartzo (UFSMFW1 01), Mirante × Horizonte (UFSMFW1 02), Supera × Quartzo (UFSMFW1 03), Supera × Quartzo (UFSMFW1 04), BRS 327 × Horizonte (UFSMFW1 05), Supera × Abalone (UFSMFW1 06), BRS 327 × Horizonte (UFSMFW1 07), Supera × Abalone (UFSMFW1 08), BRS 327 × Horizonte (UFSMFW1 09); the cultivars TBIO Toruk and Quartzo were used as check.

5.3.2 Experimental design

The trials were conducted using a randomized block design, with 11 genotypes of wheat, with six replicates. The plots were composed by four rows that were 4 m long, with row spacing of 0.17 m and a plant density of 350 plants m⁻². Sowing was conducted on May 26, 2018, with a base fertilization rate of 200 kg ha⁻¹ N-P₂O₅-K₂O (08-24-12). Supplementary fertilization of 90 kg ha⁻¹ N (urea form; 45% N) was applied twice, once during the tillering and elongation stage. Weeds, pests, and diseases were controlled according to the technical recommendations for wheat.

5.3.3 Evaluated traits

The agronomic traits evaluated were plant height (PH, cm), measured by distance from the soil to the spike of the main tiller; number of fertile tillers (NT), obtained by count of fertile tillers; spikelet insertion height (SHI, cm), limited by plant measurement from ground level to an spike insertion; number of spikelets (NS, cm), hectoliter weight (HW, kg hL⁻¹), measure of the volume of grain per unit; kernel width (KW, mm); and kernel weight per plant (KWP, g).

5.3.4 Statistical analysis

Each trait was analyzed using a mixed-effect model based on the following equation:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where \mathbf{y} represents an $n[= \sum_{j=1}^r (gr)] \times 1$ vector of response variable, i.e., the response of the i th genotype in the j th block ($i = 1, 2, \dots, g; j = 1, 2, \dots, r; \mathbf{y} = [y_{11}, y_{12}, \dots, y_{gr}]'$); \mathbf{b} represents an $1 \times r$ vector of unknown and unobservable block fixed effects $\mathbf{b} = [\gamma_1, \gamma_2, \dots, \gamma_r]'$; \mathbf{u} represents an $m[= 1 \times g]$ vector of unknown and unobservable genotype random effects

$\mathbf{u} = [\alpha_1, \alpha_2, \dots, \alpha_g]'$; \mathbf{X} represents an $n \times r$ design matrix of 0s and 1s relating \mathbf{y} to \mathbf{b} ; \mathbf{Z} represents an $n \times m$ design matrix of 0s and 1s relating \mathbf{y} to \mathbf{u} ; \mathbf{e} represents an $n \times 1$ vector of random errors $\mathbf{e} = [y_{11}, y_{12}, \dots, y_{gr}]'$; and the prime symbol ($'$) represents vector transposition. The random vectors \mathbf{u} and \mathbf{e} are assumed to be normal and independently distributed with zero mean and variance-covariance matrices \mathbf{G} and \mathbf{R} , respectively, such that

$$\begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} \sim N \left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{G} & \mathbf{0} \\ \mathbf{0} & \mathbf{R} \end{bmatrix} \right)$$

Here the simplest forms of \mathbf{G} and \mathbf{R} , namely $\mathbf{G} = \hat{\sigma}_\alpha^2 \mathbf{I}_g$ and $\mathbf{R} = \hat{\sigma}_e^2 \mathbf{I}_n$, will be used, where $\hat{\sigma}_\alpha^2$ and $\hat{\sigma}_e^2$ represent variances for genotypes and random errors, respectively, and \mathbf{I}_g and \mathbf{I}_n represent the identity matrices of order g and n , respectively. The vectors \mathbf{b} and \mathbf{u} were then estimated using the well-known mixed model equation (Henderson 1975):

$$\begin{bmatrix} \hat{\mathbf{e}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$

where the superscripts “ -1 ” and “ $-$ ” represent the inverse and generalized inverse of the matrices, respectively. Variance components $\hat{\mathbf{G}}$ and $\hat{\mathbf{R}}$ were obtained by REstricted Maximum Likelihood (REML) using the expectation-maximization algorithm (Dempster et al. 1977). The significance of the random effects was evaluated using a likelihood ratio (LR) test, and the probability was then obtained using a two-tailed chi-square test with one degree of freedom (χ_1^2). Since the data was balanced, the effect the i th genotype (\hat{g}_i) within \mathbf{u} was given in standard ANOVA notation, as follows:

$$\hat{g}_i = h_g^2 (\bar{y}_i - \bar{y}_{..})$$

where $h_g^2 = (r\hat{\sigma}_\alpha^2) / (\hat{\sigma}_e^2 + r\hat{\sigma}_\alpha^2)$ represents the shrinkage effect for the genotype effect. The BLUP of the i th genotype was given by $BLUP_i = \mu + \hat{g}_i$ where $\bar{\mu}$ represents the overall mean. The confidence intervals for the BLUPs were estimated according to the following equation (Resende 2002):

$$CI = Gv \pm t[(1-r^2\hat{\sigma}_\alpha^2) \sigma_g^2]^{0.5}$$

where CI represents the confidence interval, Gv represents the genotypic value, t represents the Student's t distribution value associated with a given significance level in a two-tailed test ($t = 2.57$, considering $\alpha = 0.05$), $r^2_{\hat{\sigma}_\alpha}$ represents the selective accuracy, and σ_g^2 represents the genotypic variance.

Principal component (PC) analysis of the agronomic traits of the wheat genotypes was performed using the *stats* and *factoextra* packages (Kassambara and Mundt, 2017) in R (version 3.5.3; R CORE TEAM, 2019).

Genetic values were used to calculate a multi-trait index based on the FAI-BLUP index (Rocha et al. 2018). The factor analysis and ideotype-design (FAI-BLUP) index (Rocha et al. 2018) was computed aiming at ranking the genotypes based on multitrait, free from multicollinearity. It was considered a selection intensity of ~18% (two genotypes selected). The maximum values for KW, NS, HW, and KWP, mean values for NT, and minimum values for PH and SHI were used to identify ideal traits. To compute the index, the FAI-BLUP function of the *metan* package (Olivoto et al. 2019) was used. A radar chart was generated using the *radarchart* function of the *fmsb* package (Nakazawa, 2018).

5.4 RESULTS AND DISCUSSION

5.4.1 Variance components and genotypic performance

Higher phenotypic variance was observed for KWP than for other traits, due to environmental variation (Table I), and the highest individual heritability were observed for PH (0.73) and NT (0.51). These results reveal a favorable condition for genetic gains with selection mainly for the number of tiller, which is directly related to increases in grain quantity, consequently, increasing the yield.

Heritability estimates based on genotype average (h^2_{ml}) were high for all traits, ranged of 0.43 to 0.94 for NS and PH, respectively. These values were generally greater than heritability estimates at the individual level (h^2_g), which suggests that the evaluated traits can be used to evaluate genetic variation and prediction to the set of genotypes.

The selective accuracy (Ac_{clinh}) used to predict genetic values reflects the results quality. This parameter is associated with selection accuracy, and refers to the correlation between predicted genetic values and genetic values of individuals (Pimentel et al. 2014). The selective precision was 0.66 for spikelet number, and 0.97 for PH, which are considered high values.

The coefficient of genetic variance (CV_{gi}) values for KWP and NT were 16.61 and 10.37, respectively. High values are desirable in the search for higher genetic constitutions since the variable quantifies the magnitude of genetic variation available for selection.

Table I

Positive genotypic effects were observed for the PH in genotypes UFSMFW1 01, UFSMFW1 05, UFSMFW1 06, TBIO Toruk, UFSMFW1 04, and UFSMFW1 03 (Figure 1a). On the other hand, negative genotypic effects were observed for the PH in genotypes UFSMFW1 08, UFSMFW1 07, Quartzo, UFSMFW1 02, and UFSMFW1 09. It should be emphasized that genotypic effect is the difference between each point and the horizontal dashed line, which represents the overall mean of the trait. The UFSMFW1 01 genotype presented the

greatest predicted mean PH (77.55 cm) but was not statistically distinct from that of the UFSMFW1 05 genotype (75.39 cm), owing to overlapping confidence intervals. The genotypes UFSMFW1 09, UFSMFW1 02, Quartzo, and UFSMFW1 07, represented minimum predicted mean indicating that there is no difference between these genotypes for the evaluated trait. Such height reduction is important for breeding programs and is an essential and desirable trait associated with the *Rht1* gene (Yao et al. 2018, Keser et al. 2017).

Negative genotypic effects were observed for the SHI of genotypes UFSMFW1 08, Toruk, UFSMFW1 07, Quartzo, UFSMFW1 02, and UFSMFW1 09 (Figure 1b). These genotypes exhibit desirable traits for plant breeding since greater SHI is not always desired in cultivars with low stem resistance. According to Souza et al. (2013), greater SHI exerts a greater force for tipping, providing the lodging, crop losses, and productivity.

When considering confidence intervals, the mean NT values of genotypes UFSMFW1 02 (NT= 4.04), TBIO Toruk (NT=3.84), and UFSMFW1 05 (NT=3.58) were statistically similar (Figure 1c), which indicated that NT can be used for the indirect selection of grain yield. In wheat, the number of fertile tillers is positively correlated with KWP (Meier et al. 2019). Thus, genotypes with mean NT values superior to 3.44 exhibit additive genetic effects and may be positively correlated with grain yield.

However, there were no significant differences in NS values of the genotypes included in the present study (Figure 1d), and the mean NS of the present study (14.60) was similar to that reported by Silva et al. (2015). Inflorescence yield components may contribute to productivity since increases in NS can increase the number of grains per spike, which is considered an important component of wheat yield.

Figure 1

The genotypes with the most favorable BLUPs for HW (Figure 2a) were those included between UFSMFW1 03 (79.25 kg hL⁻¹) and UFSMFW1 09 (79.05 kg hL⁻¹). The predicted

values were lower than those observed by Martin et al. (2017), who studied genotypes with the same genetic basis, although this difference can be attributed to environmental conditions, especially rainfall (Tavares et al. 2014). Therefore, the decrease in HW can be associated to successive changes in grain moisture, owing to the sequence of rain before harvest.

For KW (Figure 2b), positive genotypic effects were observed for genotypes UFSMFW1 01, UFSMFW1 06, UFSMFW1 02, UFSMFW1 03, and UFSMFW1 04. However, no statistical differences were observed in the mean KW to UFSMFW1 01 and UFSMFW1 09. KW is an important agronomic trait, since seed size is positively correlated with seed quality, and larger seeds corresponding to higher quality seedlings (Meira et al. 2017).

The KWP is the main trait associated with agronomic performance. The BLUPs for KWP (Figure 2c) revealed that genotypes UFSMFW1 02, TORUK, UFSMFW1 05, and UFSMFW1 04 showed positive genotypic effects, whereas genotypes UFSMFW1 03, UFSMFW1 08, UFSMFW1 01, UFSMFW1 07, UFSMFW1 06, UFSMFW1 09, and QUARTZO exhibited negative genotypic effects. Based on confidence intervals, there were no significant differences in the mean KWP values of genotypes UFSMFW1 02 to UFSMFW1 08, likely owing to the high contribution of phenotypic and environmental variation. Greater residual variation is associated with greater retraction effects on predicted means. Because of the random effects components are considered in the prediction of response variable, these findings indicate that individuals with these genotypes could possess concentrated favorable alleles for grain yield.

Genotypes UFSMFW1 02, UFSMFW1 04, and UFSMFW1 05 presented high genetic potential, since the BLUP method relies on the estimation of genotypic values, without environmental effects. The genetic values are more important for breeders, because of they present the true values to predict and represent the genetic potential of individuals (Cortes et al. 2019).

Figure 2

5.4.2 Principal components

Principal component analysis aims to understand genetic diversity among genotypes for evaluated agronomic traits. The seven traits analyzed in the present study were reduced in two main components, which, together, accounted for 72% of the phenotypic variation (Figure 3). Similar results were reported by Gonzalez-Navarro et al. (2016), who investigated the variation in developmental patterns among 27 elite wheat lines and their relationships with yield, and observed that 60% of the total variance was explained by two PCs.

Figure 3

In the present study, the associated traits with grain yield are to the left of PC1 (Figure 3). The association between set of traits and wheat genotypes revealed that Toruk and UFSMFW1 02 were likely in greater KWP, NT, and NS values. However, the UFSMFW1 01 showed greater association to SHI and PH.

5.4.3 FAI-BLUP index and predicted genetic gains

To determine ideotype, the FAI-BLUP index calculated the genetic correlation of each factor, thereby identifying three factors. Factor 1 exhibited a high genetic correlation with NT and KWP, whereas Factor 2 was correlated with PH, SHI, and HW, and Factor 3 was correlated with NS and WK (Table II). The genetic gain observed for the evaluated traits revealed the possibility of reduction for PH (-1.19%) and SHI (-1.69%) (Table II). In addition, the NT and KWP gains were 14.63 and 22.35%, respectively. The evaluated genotypes included genetic constitutions with desirable characteristics, in regards to grain yield. The mean communality

(i.e., common variance) accounted for 86% of all genetic variability present in the dataset (Table II).

Table II

The FAI-BLUP index has the potential to improve multiple traits simultaneously since it considers the use of predicted genetic effects (Rocha et al. 2018). This multiple trait index identifies the genotypes with traits closest to the ideotype (Figure 4). The FAI-BLUP index indicated the UFSMFW1 02 and TORUK genotypes with the greatest potential for wheat breeding programs, because of the traits closer to the ideotype, with relatively low PH and relatively high NT and KWP.

Figure 4

5.5 CONCLUSION

The number of fertile tiller and kernel weight per plant are important traits for wheat genotypes characterization. Also, these traits showed the highest predicted genetic gains. FAI-BLUP index identify the UFSMFW1 02 and TORUK genotypes to be used in future wheat breeding programs.

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5.7 DECLARATION OF CONFLICTING INTERESTS

We have no conflict of interest to declare.

5.8 AUTHORS' CONTRIBUTIONS

CM and DM, performed the experiments and wrote the manuscript; TO and MN, performed data analysis; LAK, LRA and GNPR, development of the project and organization; VSM and VQS, supervised the study and revised manuscript.

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Table I. Estimates of variance components and genetic parameters for the plant height (PH), number of fertile tillers (NT), spikelets height insertion (SHI), number of spikelets (NS), kernel weight per plant (KWP), hectoliter weight (HW) and kernel width (KW) for 11 wheat genotypes. Frederico Westphalen, 2019.

Parameters	Traits						
	PH	NT	SHI	NS	KWP	HW	KW
Vg	6.95	0.13	3.66	0.05	63.83	0.01	0.02
Ve	2.56	0.12	7.95	0.42	150.58	0.03	0.06
Vf	9.51	0.25	11.60	0.48	214.42	0.03	0.08
h2g	0.73	0.51	0.32	0.11	0.30	0.27	0.27
h2ml	0.94	0.86	0.73	0.43	0.72	0.69	0.69
Aclinh	0.97	0.93	0.86	0.66	0.85	0.83	0.83
VCgi%	3.63	10.37	2.98	1.58	16.61	0.14	5.34
Vce%	2.20	10.10	4.39	4.46	25.51	0.24	8.76
Mean	72.69	3.44	64.26	14.58	9.61	79.21	2.76
LRT	40.71**	23.24**	9.47**	1.48 ^{ns}	8.55**	7.06*	7.2*

Vg: genotypic variance; Ve: environmental variance; Vf: phenotypic variance; h2g =h2: heritability of individual plots in the broad sense; h2ml: heritability of genotype average, assuming complete survival; Acgen: selective accuracy assuming no loss of plots; VCgi%: genotypic coefficient of variation; Vce%: residual coefficient of variation; Mean: Overall Experiment Average; LRT: Likelihood-Ratio Test

Table II - Factorial loadings, communalities and predicted genetic gain based on FAI-BLUP index.

Trait	Factor			Communality	Predicted genetic gain (%)
	Factor 1	Factor2	Factor3		
PH	0.00	-0.95	0.03	0.90	-1.19
SHI	0.09	-0.97	-0.04	0.95	-1.68
NT	-0.98	0.12	-0.01	0.98	14.63
NS	-0.51	0.15	0.78	0.90	1.86
HW	-0.05	-0.58	0.18	0.37	-0.01
WK	-0.01	0.26	-0.93	0.94	-3.19
KWP	-0.93	-0.14	0.27	0.96	22.35
Communality Mean				0.86	-

PH: plant height, NT: number of fertile tillers, SHI: spikelets height insertion, NS: number of spikellets, KWP: kernel weight per plant, HW: hectoliter weight and KW: kernel width.

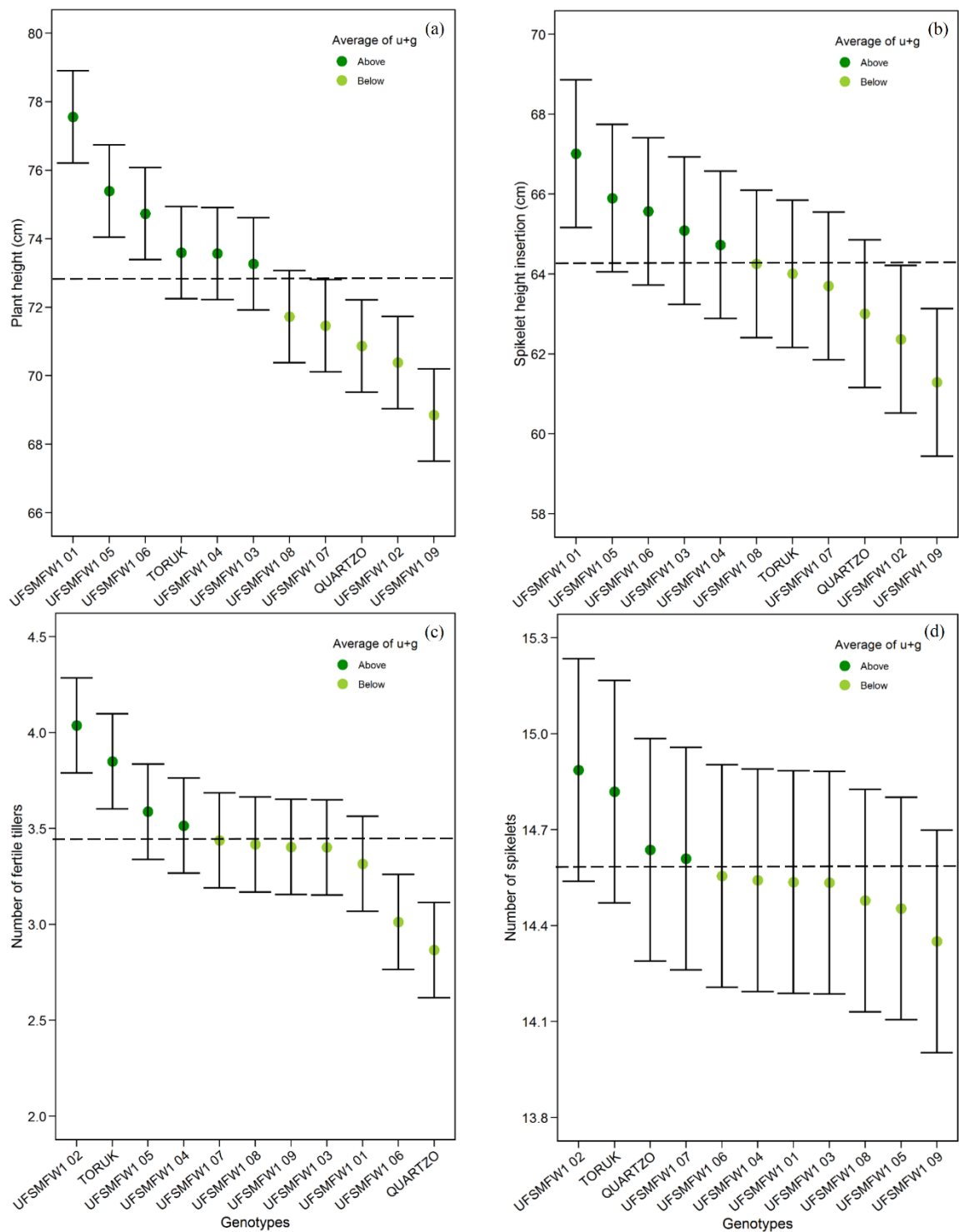


Figure 1. Predicted genetic values to (a) plant height, (b) spikelets height insertion, (c) number of fertile tillers and (d) number of spikelets for 11 wheat genotypes.

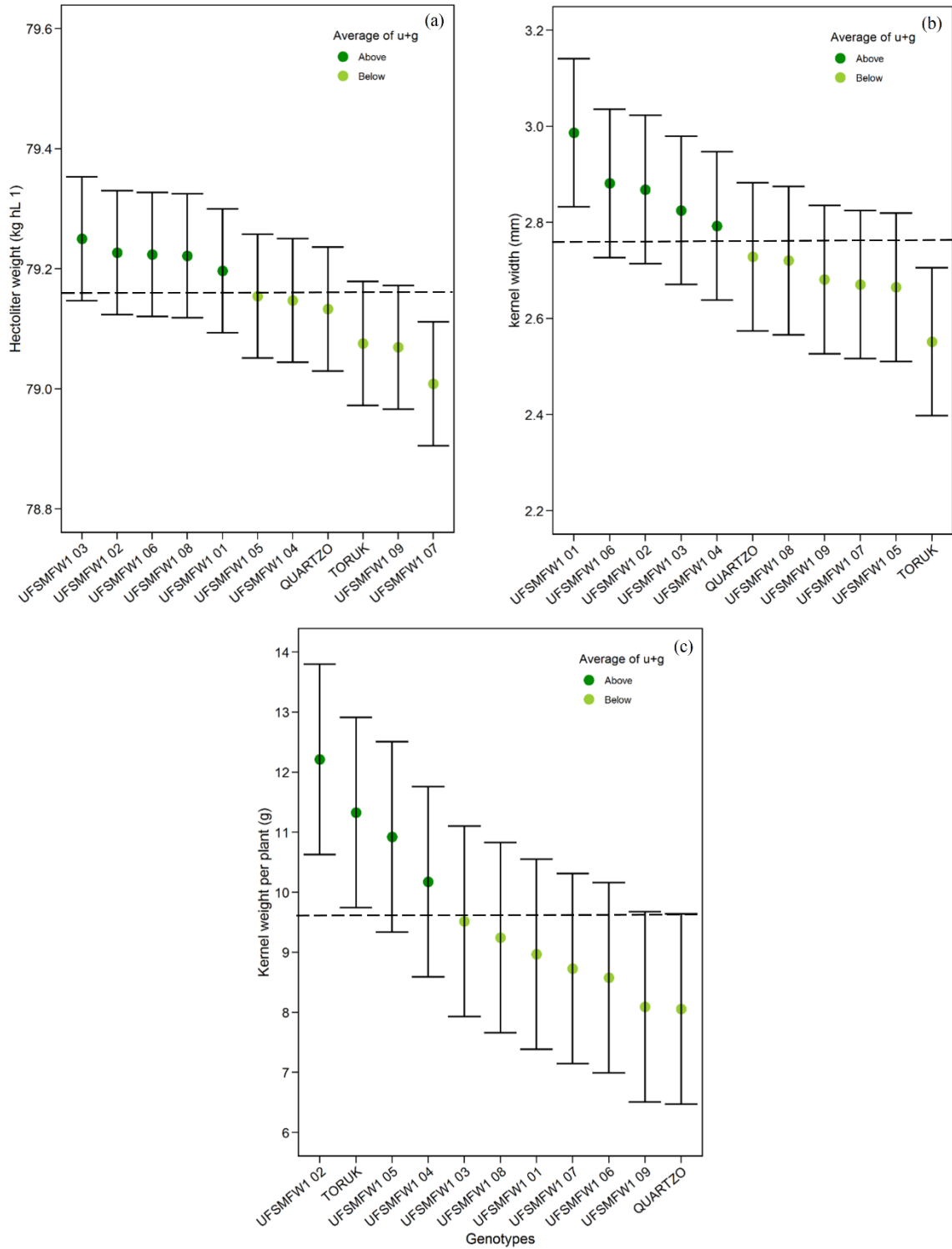


Figure 2. Predicted genetic values to (a) hectoliter weight, (b) kernel width and (c) kernel weight per plant for 11 wheat genotypes.

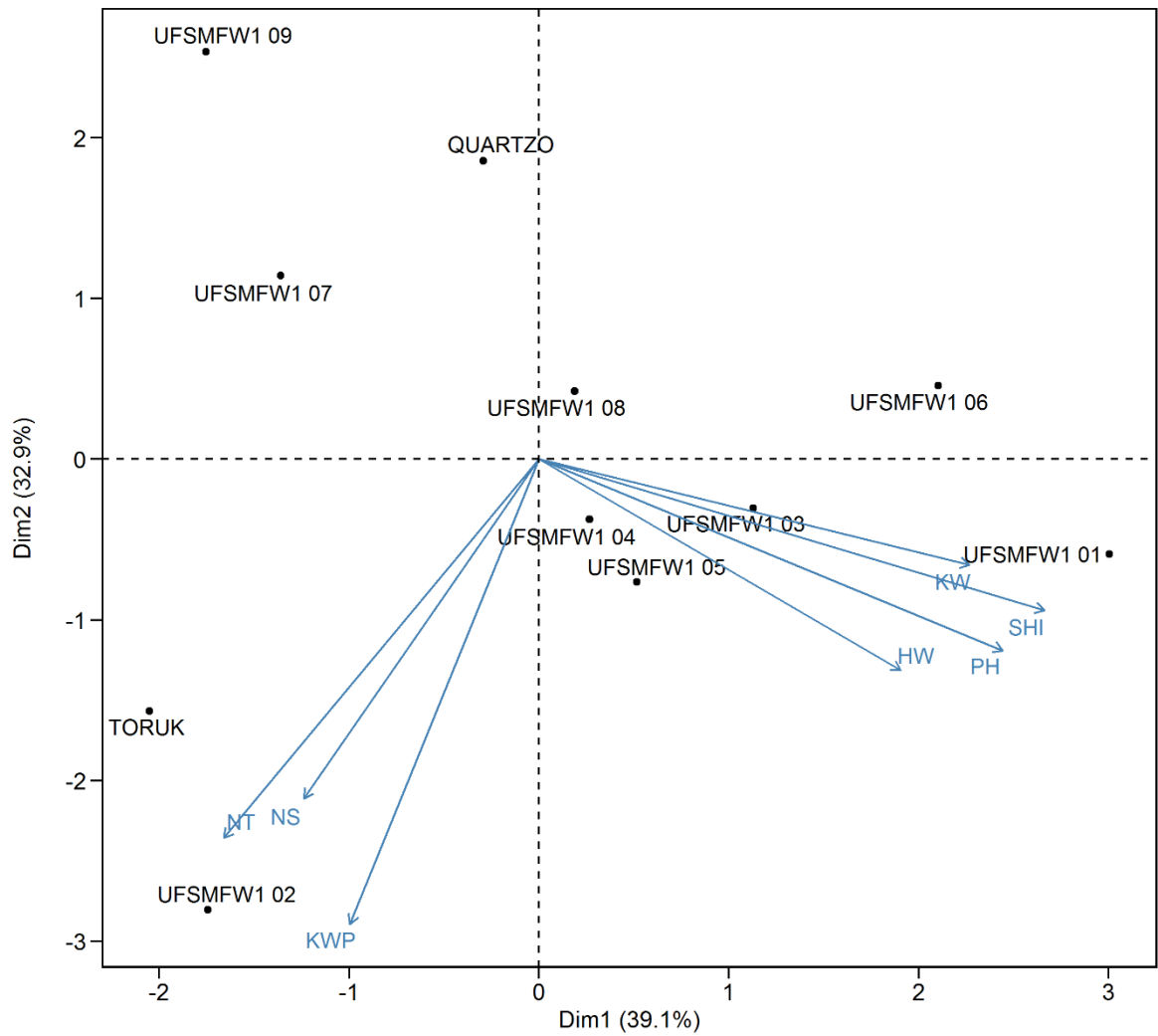


Figure 3. Plot of scores of the principal components, the association of wheat genotypes with agronomic traits. PH: plant height, NT: number of fertile tillers, SHI: spikelets height insertion, NS: number of spikellets, KWP: kernel weight per plant, HW: hectoliter weight and KW: kernel width.

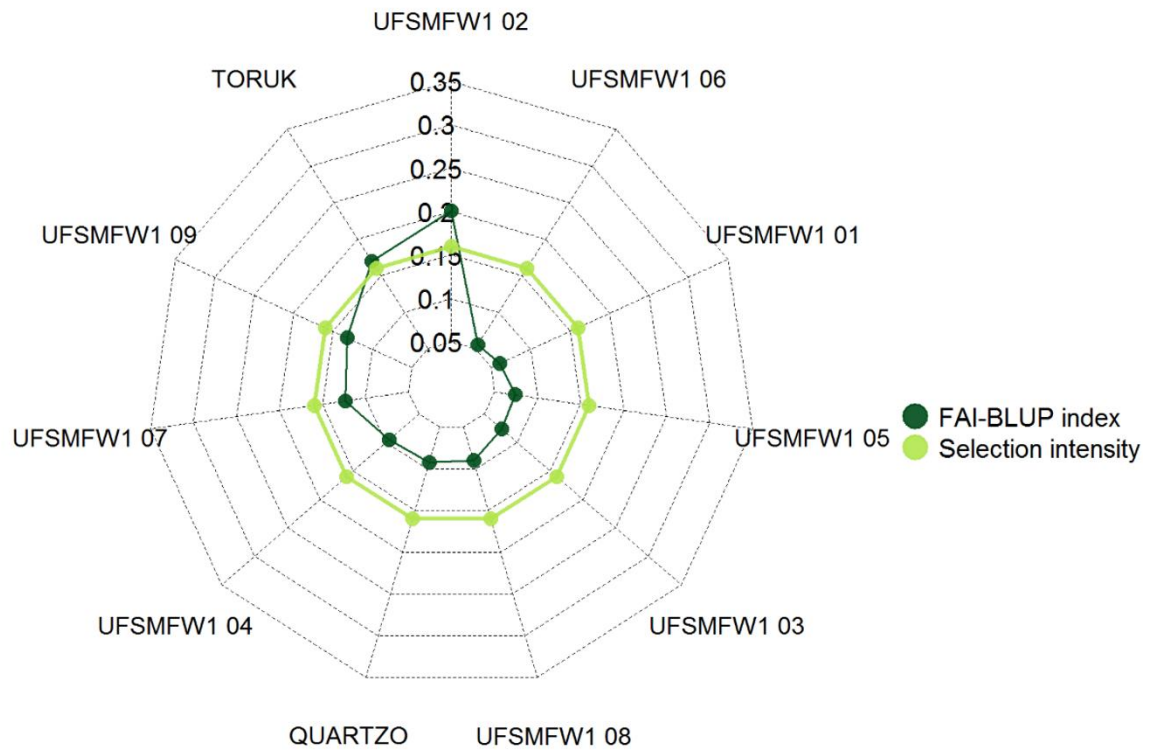


Figure 4. Wheat genotypes ranking and selected genotypes using the FAI-BLUP index.

6 CONSIDERAÇÕES FINAIS

O melhoramento genético da cultura do trigo tem grande importância para o cenário mundial, pois tem como principais funções incrementar o potencial de rendimento e a composição nutricional dos grãos. Desta forma, busca-se constituições genéticas superiores em relação as existentes no mercado, sendo estas, adaptadas às condições específicas dos ambientes de cultivo. O sucesso na seleção de genótipos superiores no melhoramento genético do trigo depende da variabilidade genética existente na população; método de melhoramento empregado; influência do ambiente; interação genótipo x ambiente; correlações fenotípicas e genotípicas e da interrelação entre esses fatores (ALLARD, 1971; PATERNIANI; VIÉGAS, 1987).

A geração de variabilidade genética através de cruzamentos artificiais possibilitou selecionar indivíduos superiores capazes de se adaptar a micro regiões específicas, resultando em maiores ganhos em rendimento de grãos. A seleção em gerações avançadas de trigo pelo método de condução SSD proporcionou elevados ganhos com a seleção, uma vez que toda a variabilidade genética foi levada de geração para geração. A seleção de plantas com maior número de afilhos, resultou em genótipos mais produtivos. O uso dos índices de seleção foi vantajoso em gerações avançadas, uma vez que estes proporcionam ganhos com a seleção, distribuídos entre todos os caracteres avaliados, situação mais adequada aos programas de melhoramento.

O estudo da dissimilaridade genética dos genótipos de trigo revelou a formação de grupos distintos, confirmando a presença de variabilidade entre os genótipos. Foi possível observar que o caractere que mais contribuiu para à divergência genética entre os genótipos foi dias da emergência ao florescimento. Os dados demonstraram que dois componentes principais (CPs) foram responsáveis pela maior variância fenotípica associada à caracterização agrônômica do conjunto de genótipos de trigo. O CP1 teve relação com o rendimento de grãos e o CP2 associado diretamente à estatura de plantas.

A metodologia REML-BLUP identificou que as variáveis número de afilhos e massa de grãos por planta são importantes na caracterização de genótipos de trigo e apresentaram os maiores ganhos genéticos preditos. Com base nos valores genéticos preditos foi possível verificar através do índice de múltiplas características (índice FAI-BLUP) a possibilidade de redução para altura de planta e altura de inserção da espiga e de ganhos para número de afilhos e massa de grãos por planta.

Esse trabalho é de grande importância, pois os resultados afirmam que a variabilidade genética é indispensável na busca de constituições genéticas superiores, estas constituições podem ser utilizadas como genitores em cruzamentos artificiais de programas de melhoramento genético e ou serem lançados como novas cultivares mais adaptadas e produtivas. A geração de variabilidade visando a ampliação da base genética é fator importante em caso de epidemia de uma determinada doença ou evento ambiental, reduzindo a probabilidade de perdas de produtividade em larga escala. Neste sentido foram identificados no programa de melhoramento genético da UFSM, linhagens melhoradas de trigo com adaptação agrônômica, elevado potencial para o rendimento de grãos, evidenciando potencial para novas cultivares adaptadas a região noroeste do Rio Grande do Sul.

7 CONCLUSÃO GERAL

Visando aumentar a eficiência dos programas de melhoramento, a avaliação em gerações avançadas de trigo F₅, F₆ e F₇ permitiu a identificação dos genitores que podem contribuir para elevar o ganho de seleção em diversos caracteres de importância agrônômica em trigo. Desta forma, genitores podem ser priorizados ou eliminados dos blocos de cruzamento de acordo com os efeitos que estes apresentam.

Com base em 420 genótipos de trigo na geração F₅ foi verificado que os ganhos de seleção em gerações avançadas são satisfatórios para o trigo. A seleção de plantas para número de filhos resultou em ganhos indiretos de 45,38% e 100% para número total de grãos por planta e peso total de grãos por planta, respectivamente, e ganho direto de 35,83%.

As maiores correlações genóticas positivas significativas evidenciadas na geração F₆ foram verificadas entre o número de filhos férteis associados ao peso do grão e o peso de mil grãos. De acordo com os desvios genéticos o ciclo foi o caractere que mostrou maior contribuição para a divergência genética entre os genótipos estudados, destacado a formação de grupos distintos e a presença de variabilidade genética entre os genótipos.

Dentre os genótipos avaliados na geração F₇ existem constituições genéticas que reúnem características desejáveis para aumento no rendimento de grãos. As variáveis número de filhos e massa de grãos por planta são importantes na caracterização de genótipos de trigo e apresentaram os maiores ganhos genéticos preditos. O ganho genético observado pelo índice FAI-BLUP revelou a possibilidade de redução para altura de planta e aumento nos ganhos para número de filhos e massa total de grãos por planta. O genótipo UFSM FW1 02 se mostrou superior a testemunha utilizada nos ensaios, estando apta a ser avaliada em ensaios de valor de cultivo e uso, pois reúne características mais próximas do ideal apresentando elevado potencial produtivo.

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