ARTICLE

Selection of high-yielding, adapted and stable wheat lines in preliminary trials

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Abstract: *Experimental design without replication, such as Federer's augmented block design, allows us to determine productivity, adaptability and stability in multi-environment trials. This work aimed to select productive wheat lines with high adaptability and stability in preliminary trials. The grain yield of 140 homozygous wheat lines was measured in 2015 at three locations. The cultivar TBIO Mestre was used as a check. Genetic parameters were evaluated by mixed models, and selection was based on the harmonic mean of the relative performance of the genetic values (HMRPGV) using models 74 (individual analysis) and 75 (joint analysis) of Selegen software. In the joint analysis, 33 wheat lines stood out in terms of productivity, adaptability and stability. These lines have the potential to be evaluated in Value for Cultivation and Use (VCU) trials for future release of new wheat cultivars.*

Keywords: *Triticum aestivum L., Federer's augmented block design, REML/BLUP, HMRPGV.*

INTRODUCTION

Breeding programs seek to obtain genotypes with high productivity, adaptability and stability. In autogamous plant breeding for species such as wheat (*Triticum aestivum* L.), the breeding process is initiated by the hybridization of contrasting parents with desirable traits; this may involve single or multiple crosses. After hybridization, many generations are evaluated and selected until a new cultivar is released. In early generations, when a low number of seeds are available that may be insufficient for conducting multi-environment trials (METs) with replication, breeders need accurate information about performance, adaptability and stability.

Even in homozygous generations, for predecessors to Value for Cultivation and Use (VCU) trials, called preliminary generations, the amount of seed may be low, leading to questions about the best design for how they are conducted and evaluated. Conducting trials with reduced seed availability may follow two ways: conducting trials in a single location with *n* replicates or conducting METs without replications. Conducting trials without replications requires relatively high accuracy in the selection, with the use of appropriate statistical models and experimental designs. In this sense, the use of Federer's augmented block design (Federer 1956, Federer and Raghavarao 1975) is an alternative.

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After choosing the experimental design for trials without replications, it is necessary to select adequate statistical models for the correct trial evaluation. In this sense, mixed models have been widely used. Analysis based on the restricted maximum likelihood and best linear unbiased prediction (REML/BLUP) allows the estimation of variance components as well as the prediction of genetic values, excluding environmental effects (Peixouto et al. 2016, Lopes et al. 2018).

Evaluating productivity, adaptability and stability is essential for the correct selection of superior genotypes. In this sense, productivity is the most important parameter to be considered for any crop. If they have desirable traits such as disease resistance genes, low-productive genotypes may be used in hybridization blocks, but they will rarely be a commercially released cultivar. However, stability involves the predictability of genotype performance at different locations, and the adaptability refers a genotype's ability to respond predictably to environmental stimuli (Matei et al. 2017). The use of REML/BLUP allows the harmonic mean of genotypic values (HMGV), relative performance of predicted genotypic values (RPGV) and harmonic mean of performance relative to the genotypic values (HMRPGV) (Borges et al. 2010) to be applied. Thus, with HMGV, it is possible to make inferences about stability, adaptability and productivity (RPGV) and an integrated evaluation of productivity, stability and adaptability (HMRPGV) (Spinelli et al. 2015, Costa et al. 2015). Estimating heritability is also important. Broad-sense heritability expresses genetic variance as a proportion of genetic variance in relation to the total variation (phenotypic variation). These parameters allow a breeding program to make advances and select superior lines. With respect to the importance of estimating these parameters in preliminary wheat lines, we used Federer's augmented block design in the evaluation of preliminary trials with reduced seed availability. Therefore, the objective of this work was to select productive, adapted and stable wheat lines.

MATERIAL AND METHODS

In the 2015 crop season, 140 homozygous wheat lines were evaluated. The experiments were performed at three locations of the Paraná state: Pato Branco (lat 26° 13' S, long 52° 40' W, alt 760 m asl, homogeneous region 2 of wheat cultivar adaptation), Renascença (lat 26° 09' S, long 52° 58' W, alt 698 m asl, homogeneous region 2), and Clevelândia (lat 26° 24' S, long 52° 21' W, alt 950 m asl, homogeneous region 1). Trials were conducted in accordance with Federer's augmented block design, with two blocks. The first block was composed of 70 plots containing 70 different wheat lines and 13 plots containing the check cultivar TBIO Mestre; i.e., this cultivar was randomly distributed in 13 plots within this block. The second block was composed of another 70 lines and 12 replicates of the check cultivar. This experimental design was applied in all evaluated environments. At each location, the new wheat lines did not have replications due the low seed availability.

The experimental plot consisted of six 5 m rows, with 0.2 m between rows, totaling 6 m^2. Seed density was standardized to 350 seeds m^{-2}. Sowing was performed in the first half of June 2015. Agronomic management followed technical indications for this crop species. Grain yield (GY, in kg ha^{-1}) was obtained from the harvest of the 6 m^2 area and weighted, and the grain moisture was corrected to 13%. Data analysis was performed using mixed models. The variance components were obtained by restricted maximum likelihood (REML), and the mean components were obtained by best linear unbiased prediction (BLUP), performed via Selegen-REML/BLUP software (Resende 2016). Models 74 (individual analysis) and 75 (joint analysis of locations) were used.

When the locations were analyzed individually (model 74), the model used was $y = X_f + Z_g + W_b + e$, where *y* is the vector of phenotypic data, *f* is the overall mean (fixed), *g* is of vector of the genotypic data (random), *b* is the vector of the environmental effects of blocks (random), and e is the vector of the error effects (random). *X*, *Z* and *W* are the incidence matrices of *f*, *g* and *b*, respectively (Resende 2007).

For the joint analysis of locations, model 75 was used: $y = X_f + Z_g + W_b + T_i + e$,where *y* is the vector of the phenotypic data, *f* is the overall location mean (fixed), *g* is the vector of the genotypic data (random), *b* is the vector of the environmental effects of blocks (random), *i* is the vector of the effects of the genotype x environment interaction (GEI) (random), and *e* is the vector of the error effects (random). *X*, *Z*, *W* and *T* are the incidence matrices of *f*, *g*, *b* and *i*, respectively

With these models, genetic effects (*g*), predicted genotypic values ($\mu + g$) genotype gain without the environmental effect, new genotype means and genotype ranking (Rank) were obtained. Furthermore, model 75 obtained the mean genotypic location values ($\mu + g + gem$), which capitalizes on a mean interaction inclusive of all evaluated locations (Resende 2007). Through this model, the genotypic stability parameters were obtained by the harmonic mean of the genotypic values (HMGV), and the relative performance of the genotypic values (RPGV) was used for the evaluation of adaptability; for stability, adaptability and productivity, the harmonic mean of RPGV (HMRPGV) was used, and these parameters were then multiplied by the overall mean of locations (RPGV*OM and HMRPGV*OM, respectively).

The Spearman correlation coefficient (r_s) (Steel and Torrie 1960) was used to verify the similarity in the lines' ranking between the locations and set of locations. For this, the new mean parameter was used (Resende 2007, 2016). The r_s was calculated using Microsoft Excel software.

RESULTS AND DISCUSSION

Estimation of the genetic parameters for the set of locations and for each location are presented in Table 1. Genotypic variance (V_g) for each location and for the set of locations was high, accounting for more than 50% of the variance in both cases. On the other hand, the residual variance (V_e) presented higher participation and values near V_g for Renascença. The coefficients of broad-sense heritability of individual plots (h^2_g) were high for the individual and joint analyses of locations. At individual locations, the h^2_g ranged from 0.82 ± 0.20 to 0.59 ± 0.17. In the joint analysis, the heritability was 0.77 (± 0.05). This indicates that a large part of the phenotypic variance (V_f) was due to the genotypic variance (V_g). GY is quantitative, polygenic trait and is strongly influenced by the environmental. As such, smaller values of h^2_g were expected in the joint analysis. The observed value ($h^2_g = 0.77 \pm 0.05$) occurred due to the low participation of the GEI variance (V_{int}) in relation to V_g and the total phenotypic variance (V_f). The values of standard deviation at each location were higher than those verified for the set of locations, ranging from 0.20 to 0.17. However, these values are within acceptable limits, indicating that the predictions are reliable for use in plant breeding (Resende 2004).

The accuracy of genotype selection (A_{cgen}) ranged from 0.90 in Pato Branco to 0.77 in Renascença. This parameter reflects the correlation between the true genotypic value of the genotype and the genotypic value estimated or predicted from the trial information. These values may be classified as belonging to the very high ($A_{cgen} \geq 0.90$) or high ($A_{cgen} \geq 0.70$) accuracy classes (Resende and Duarte 2007). The genotypic correlation between performance at the locations (rg_{loc}) was 0.89. This parameter indicates the similarity in the ranking of genotypes at the tested locations (Carvalho et al. 2016). The value obtained indicates no complex interaction between genotypes and locations; i.e., there were 89% and 11% simple and complex interactions, respectively. This may be the result of similar environments and/or lines having productive stability or broad adaptability. Thus, there were no significant changes in the genotype ranking at the different test locations. However, relatively large numbers of significant changes in ranking between locations, i.e., lower values of rg_{loc}, were expected since Pato Branco and Renascença belong to homogeneous region 2 of wheat adaptation in Brazil and since Clevelândia belongs to the homogeneous region 1. The homogenous region of wheat adaptation is determined according to the altitude (meters above sea level) and the average air temperature and humidity. Thus, homogeneous region 1 is characterized by cold, wet and high altitudes. In contrast, the homogeneous region 2 is moderately warm and wet, with low altitudes (Cunha et al. 2006).

Table 1. Estimates of variance and genetic parameters for grain yield of homozygous wheat lines tested at three locations via individual and joint analyses in the 2015 cropping season

Parameters	Pato Branco	Clevelândia	Renascença	Parameters	Locations mean
V_g	453070	457154	361816	V_g	487622
V_{bloc}	8748	57739	19677	V_{bloc}	27554
V_e	91549	186599	227288	V_{int}	35593
V_f	553367	701492	608781	V_e	85252
h^2_g	0.82(±0.20)	0.65(±0.18)	0.59(±0.17)	V_f	636021
c^2_{bloc}	0.02	0.08	0.03	h^2_g	0.77 (±0.05)
h^2_{mgen}	0.82	0.65	0.59	c^2_{bloc}	0.04
h^2_{mgenaj}	0.83	0.71	0.61	c^2_{int}	0.05
A_{cgen}	0.90	0.81	0.77	rg_{loc}	0.89
Mean (kg ha^{-1})	3823	2777	2954	Overall Mean (kg ha^{-1})	3183

V_g:genotypic variance; V_{bloc}: environmental variance between blocks; V_e: residual variance; V_f: individual phenotypic variance; h^2g: coefficient of broad-sense heritability of individual plots; c^2_{bloc}: coefficient of determination of the block effects; h^2_{mgen}: adjusted heritability of the genotypic mean; A_{cgen}: accuracy of the genotype selection; V_{int}: variance of genotype x environment interactions; c^2_{int}: coefficient of determination of the effects of genotype x environment interactions; rg_{loc}: genotypic correlation between performance at all locations; Mean of trial/Overall mean of trials.

Table 2. Spearman's correlation coefficients (r_s) for the ranking of 140 homozygous wheat lines and the check TBIO Mestre for the locations Pato Branco, Clevelândia, and Renascença, in Paraná state, and the set of locations

	Pato Branco	Clevelândia	Renascença	Set of locations
Pato Branco	1.00			
Clevelândia	0.61**	1.00		
Renascença	0.88**	0.80**	1.00	
Set of locations	0.86**	0.90**	0.95**	1.00

** significant at the 1% level according to *t* tests.

Possible explanations for these results are related to the wheat lines tested and their high stability, which resulted in no complex interactions with the environments. Another relevant point is the adverse climatic conditions in the 2015 wheat crop season in Clevelândia. Excess rainfall and above-average temperatures are cited as the main adverse conditions. These conditions favored disease development. This condition resulted in a reduction in the photothermal quotient due to many cloudy days (Silva et al. 2014). Clevelândia had the lowest productivity among the three evaluated locations (2777 kg ha^{-1}), even though it was in homogeneous region 1, which is considered ideal for wheat cultivation. As such, this location did not present favorable characteristics to wheat crops in this season.

The Spearman correlation coefficient (r_s) indicated an association between lines rankings at different locations and the set of locations. In this sense, the r_s for the set of locations was relatively high at Renascença (r_s = 0.95) (Table 2). Moreover, the lowest r_s was obtained between the set of locations and Pato Branco. The greatest differences in genotype rankings were obtained between Pato Branco and Clevelândia (r_s = 0.61). In general, the results of the line rankings between each location and the joint analysis were similar, which justifies a high genotypic correlation (rg_{loc}).

Mixed model analysis makes it possible to determine the performance of each line for the set of locations and for each location (Tables 3 and 4) without environmental effects, considering only the genotypic value of each line. For the joint analysis of locations, the highest genetic effects (*g*) were observed for lines UTFT 1110, UTFT 1608, UTFT 1620, UTFT 1025, UTFT 1691, UTFT 1043, UTFT 1003, UTFT 1037, and UTFT 1463. These lines also presented the highest predicted genotypic values (μ + *g*). The random effect of locations allows these results to be extrapolated to other locations of the target region because the locations are considered representative. When wheat lines are evaluated in two groups, selected and nonselected, it is possible to infer that the selected group showed meaningful superiority, with a minimum significant difference (data not shown).

These top 33 lines (Table 3) can be selected to compose the selections of the first year of VCU trials because these lines were superior to TBIO Mestre, which presented the 34th highest genotypic effects. Thirty-three is a suitable number of lines to be conducted according to VCU standards, which are established by the Ministry of Agriculture, Livestock and Food Supply (MAPA). In addition to presenting the highest *g* and μ + *g*, these lines also presented the highest values of HMGV, RPGV*OM and HMRPGV*OM. The genotypic stability analysis, which was based on the HMGV method, is related to the dynamic concept of stability because it is associated with GY (Resende 2004). Thus, lines with high HMGV values are productive and stable in different environments. The selection via RPGV*OM takes into account the productive mean and the adaptive capacity of the genotypes. In this sense, productive genotypes with the capacity to positively respond to environmental conditions are selected. The integrated selection (HMRPGV*OM) allows selection considering the HMGV and RPGV*OM methods, i.e., considering the stability, adaptability and productivity means together (Matei et al. 2017). Carvalho et al. (2016) and Santos et al. (2018) reported the efficiency of the HMRPGV method in the simultaneous selection for productivity, stability and adaptability of cotton and bean genotypes, respectively. Thus, selected lines based on this method are essentially productive, are stable in different environments and have the ability to positively respond to environmental stimuli.

Methods involving the adaptability, stability and productive means are very useful in breeding programs. These methods use mixed models to obtain the information, and they have the main advantage of estimating genetic values without environmental effects. In addition, this type of method allows us to obtain these results from trials without replications. Mixed models differ from traditional methods for stability and adaptability estimation since GY has a greater weight in the analysis than adaptability and stability, which do not occur in traditional methods such as the Wricke ecovalence method (Gomez et al. 2014). Studying sugarcane, Paula et al. (2014) observed that the HMRPGV method is similar to Lin and Binns'and Annicchiarico's methods and that the Wricke and AMMI methods tend to select more stable genotypes that are less productive. Santos et al. (2016) reported similarity in the identification of improved cowpea genotypes in terms of productivity, adaptability and stability using GGE biplot and REML/BLUP methods. Similarly, Milioli et al. (2018) indicated that the HMGV and the genotype main effect + GEI effect by ideal genotype (GGE IG) methods present consistent results and strong associations with GY; they are the most adequate methods to select productive and stable genotypes.

Table 3. Genetic effects (*g*), predicted genotypic values (μ + *g*), predicted mean gain (Gain), new mean of the genotype (New mean), genotype ranking by the new mean (Rank) and genotypic mean value of locations (μ + *g* + *gem*). The genotypic stability and adaptability were determined by the harmonic mean of the genotypic values for the grain yield of wheat lines through joint analyses

Rank	Genotype	*g*	μ + *g*	Gain	New mean	μ + *g* + *gem*	HMGV	RPGV *OM	HMRPGV *OM
1	UTFT 1110	1193	4376	1193	4376	4379	4335	4402	4396
2	UTFT 1608	1172	4355	1182	4365	4357	4314	4381	4374
3	UTFT 1620	1148	4331	1171	4354	4334	4290	4356	4350
4	UTFT 1025	1039	4222	1138	4321	4224	4178	4244	4239
5	UTFT 1691	942	4125	1099	4282	4127	4081	4146	4142
6	UTFT 1043	904	4087	1066	4249	4090	4042	4107	4103
7	UTFT 922	873	4056	1039	4222	4058	4011	4075	4071
8	UTFT 559	863	4046	1017	4200	4048	4000	4064	4061
9	UTFT 1765	847	4030	998	4181	4032	3985	4048	4045
10	UTFT 1602	843	4026	982	4165	4028	3980	4044	4041
11	UTFT 1001	822	4005	968	4151	4007	3959	4023	4020
12	UTFT 1504	803	3986	954	4137	3988	3942	4005	4001
13	UTFT 706	773	3956	940	4123	3958	3909	3973	3970
14	UTFT 1405	730	3913	925	4108	3915	3867	3930	3927
15	UTFT 1634	730	3913	912	4095	3915	3866	3929	3926
16	UTFT 900	727	3910	901	4084	3911	3865	3927	3924
17	UTFT 1047	705	3888	889	4072	3889	3840	3903	3900
18	UTFT 1761	696	3879	878	4061	3880	3832	3894	3892
19	UTFT 891	683	3866	868	4051	3868	3819	3881	3879
20	UTFT 1438	676	3859	858	4041	3861	3812	3874	3872
21	UTFT 1173	642	3825	848	4031	3827	3776	3839	3837
22	UTFT 209	623	3806	838	4021	3807	3758	3820	3818
23	UTFT 1651	603	3786	828	4011	3787	3738	3799	3797
24	UTFT 1609	599	3782	818	4001	3784	3733	3795	3793
25	UTFT 421	596	3779	809	3992	3780	3732	3793	3791
26	UTFT 1220	581	3764	801	3983	3766	3716	3777	3775
27	UTFT 1506	580	3763	792	3975	3765	3715	3777	3775
28	UTFT 657	570	3753	784	3967	3754	3704	3765	3764
29	UTFT 877	563	3746	777	3960	3748	3696	3758	3757
30	UTFT 1210	533	3716	769	3952	3718	3668	3729	3727
31	UTFT 1003	510	3693	760	3943	3694	3643	3704	3703
32	UTFT 1037	504	3687	752	3935	3688	3636	3698	3697
33	UTFT 1463	502	3685	745	3928	3686	3635	3696	3695
34	TBIO Mestre	497	3680	737	3920	3681	3634	3693	3691
35	UTFT 1694	476	3659	730	3913	3660	3610	3670	3669
36	UTFT 1628	457	3640	722	3905	3641	3589	3650	3649
37	UTFT 1280	438	3621	715	3898	3622	3570	3631	3630
38	UTFT 542	418	3601	707	3890	3602	3548	3610	3609
39	UTFT 435	397	3580	699	3882	3581	3528	3589	3588
40	UTFT 1716	387	3570	691	3874	3571	3516	3577	3576

HMGV, genotypic adaptability by relative performance of the genotypic values multiplied by the overall mean RPGV*OM, stability and adaptability by harmonic mean of RPGV multiplied by the overall mean of locations HMRPGV*OM, productivity, stability and adaptability multiplied by the overall mean of locations.

When the analysis was performed by location, few but significant changes occurred in the line rankings (Table 4). This indicates that locations were relatively homogeneous in the crop season. However, some lines had superior performance in single-location trials. For example, in Pato Branco, the lines UTFT 69, UTFT 877, UTFT 1158, UTFT 1173, UTFT 1633 and UTFT 1716 were among the selected lines, which were not selected in Clevelândia or Renascença. In Clevelândia, the lines UTFT 6, UTFT 1506 and UTFT 1634 were among the top 20 lines. In Renascença, the lines UTFT 657, UTFT 1003 and UTFT 1405 were among the top 20, which was not the case in Pato Branco or Clevelândia. As such, lines with specific adaptation may be identified in METs without replications, which would not occur if the single trial was conducted in one location with replications.

In the table of means (Table 3), the lines UTFT 69, UTFT 877, UTFT 1158, UTFT 1173 and UTFT 1716, which were only in the set of the improved lines in Pato Branco, were not classified among the top 20 lines in the set of locations.

Table 4. Genetic effects (*g*), predicted genotypic values (μ + *g*), predicted mean gain (Gain), new mean of the genotype (New mean), genotype ranking by new mean (Rank) for grain yield of homozygous wheat lines growing in Pato Branco (PR), Clevelândia (PR) and Renascença, Paraná state, in the 2015 cropping season

Rank	Pato Branco					Clevelândia					Renascença				
	Genotype	g	μ + g	Gain	New mean	Genotype	g	μ + g	Gain	New mean	Genotype	g	μ + g	Gain	New mean
1	UTFT 1025	1027	4850	1027	4850	UTFT 1608	1028	3805	1028	3805	UTFT 1608	775	3729	775	3729
2	UTFT 559	959	4782	993	4816	UTFT 1110	997	3774	1012	3789	UTFT 1110	768	3722	771	3726
3	UTFT 1620	932	4754	973	4796	UTFT 1620	989	3766	1005	3782	UTFT 1620	664	3618	735	3690
4	UTFT 1110	902	4725	955	4778	UTFT 1025	867	3644	970	3747	UTFT 1504	645	3599	713	3667
5	UTFT 1043	895	4718	943	4766	UTFT 6	859	3636	948	3725	UTFT 1025	641	3595	698	3653
6	UTFT 1001	851	4674	928	4751	UTFT 922	842	3619	930	3707	UTFT 922	638	3592	688	3643
7	UTFT 69	844	4667	916	4739	UTFT 900	839	3616	917	3694	UTFT 900	631	3586	680	3634
8	UTFT 1608	800	4623	901	4724	UTFT 1043	819	3596	905	3682	UTFT 1405	596	3550	670	3624
9	UTFT 1691	761	4584	886	4709	UTFT 1691	779	3556	891	3668	UTFT 1001	587	3541	660	3615
10	UTFT 706	756	4579	873	4696	UTFT 1602	766	3543	879	3656	UTFT 1691	560	3515	650	3605
11	UTFT 1633	737	4560	861	4683	UTFT 1634	734	3511	865	3642	UTFT 1003	547	3501	641	3595
12	UTFT 1158	734	4556	850	4673	UTFT 559	726	3503	854	3631	UTFT 421	530	3484	632	3586
13	UTFT 1047	724	4547	840	4663	UTFT 1506	696	3473	842	3619	UTFT 209	523	3478	623	3578
14	UTFT 1602	720	4543	832	4655	UTFT 1504	689	3466	831	3608	UTFT 1765	513	3467	616	3570
15	UTFT 1765	694	4517	822	4645	UTFT 1765	673	3450	820	3597	UTFT 1043	511	3465	609	3563
16	UTFT 1716	641	4464	811	4634	UTFT 421	667	3444	811	3588	UTFT 1047	511	3465	602	3557
17	UTFT 877	625	4448	800	4623	UTFT 891	656	3433	802	3579	UTFT 706	496	3450	596	3550
18	UTFT 1173	617	4440	790	4613	UTFT 706	652	3429	793	3570	UTFT 657	491	3445	590	3545
19	UTFT 922	610	4433	781	4603	UTFT 1761	623	3400	784	3561	UTFT 559	461	3415	584	3538
20	UTFT 891	581	4404	771	4593	UTFT 209	620	3397	776	3553	UTFT 891	443	3397	577	3531
21	UTFT 1615	576	4399	761	4584	UTFT 1438	618	3395	769	3546	UTFT 1173	438	3392	570	3524
22	UTFT 151	565	4388	752	4575	UTFT 1210	608	3385	761	3538	TBIO Mestre	434	3388	564	3518
23	UTFT 1634	554	4377	744	4567	TBIO Mestre	599	3376	754	3531	UTFT 1037	429	3384	558	3512
24	UTFT 1761	509	4332	734	4557	UTFT 1001	579	3356	747	3524	UTFT 1651	419	3373	552	3506
25	UTFT 1609	499	4322	725	4548	UTFT 1694	579	3356	740	3517	UTFT 1602	404	3358	546	3500
26	UTFT 1645	475	4298	715	4538	UTFT 1502	515	3292	732	3509	UTFT 1716	404	3358	541	3495
27	UTFT 1405	474	4297	706	4529	UTFT 1220	509	3286	723	3500	UTFT 1609	397	3351	535	3490
28	UTFT 1438	474	4297	698	4521	UTFT 1047	505	3282	716	3493	UTFT 1761	390	3345	530	3484
29	UTFT 1032	467	4290	690	4513	UTFT 1116	501	3278	708	3485	UTFT 877	388	3342	525	3480
30	TBIO Mestre	442	4265	682	4504	UTFT 1463	496	3273	701	3478	UTFT 1438	382	3336	521	3475
31	UTFT 542	439	4262	674	4497	UTFT 1651	496	3273	694	3471	UTFT 542	357	3311	515	3469
32	UTFT 435	432	4255	666	4489	UTFT 1405	495	3272	688	3465	UTFT 1506	350	3305	510	3464
33	UTFT 1037	427	4250	659	4482	UTFT 1749	488	3265	682	3459	UTFT 606	343	3297	505	3459
34	UTFT 657	425	4247	652	4475	UTFT 1619	473	3250	676	3453	UTFT 496	341	3295	500	3454
35	UTFT 1220	407	4230	645	4468	UTFT 657	473	3250	670	3447	UTFT 1628	338	3292	496	3450
36	UTFT 963	381	4204	638	4461	UTFT 1280	465	3242	665	3441	UTFT 1220	336	3290	491	3445
37	UTFT 1504	378	4201	631	4454	UTFT 1003	436	3213	658	3435	UTFT 1463	336	3290	487	3441
38	UTFT 1651	369	4192	624	4447	UTFT 1069	413	3190	652	3429	UTFT 1694	335	3289	483	3437
39	UTFT 209	351	4174	617	4440	UTFT 877	405	3182	646	3423	UTFT 1210	333	3287	479	3433
40	UTFT 496	341	4164	610	4433	UTFT 1609	401	3178	639	3416	UTFT 1634	329	3283	475	3430

Likewise, the UTFT 6 and UTFT 1506 (Clevelândia) and the UTFT 657 and UTFT 1001 (Renascença) lines were not among the top 20 lines in the joint analysis. Two exceptions were observed: UTFT 1634 was selected only in Clevelândia, and UTFT 1405 was selected exclusively in Renascença. However, both lines were among the top 20 lines in the joint analysis. As they were selected in one location, these cultivars could not have been selected if the trials had been carried out in a single location. This shows that, possibly, these two lines have specific adaptations, with UTFT 1634 adapted to homogeneous region 1 and UTFT 1405 adapted to Homogeneous region 2. Homogeneous region 1 is characterized as a relatively cold region with relatively high relative humidity and altitudes, while Region 2 is moderately hot and humid and has relatively low altitudes (Franco and Evangelista 2018).

UTFT 1405 was among the top 20 only in Renascença. However, this line was also among the top 20 when the overall mean was considered. This result may be related to the good performance of UTFT 1405 in Renascença, which was ranked 8th. If the selection has been performed only in Pato Branco with replications, this line could have performed more poorly, and it would not have been chosen among the top 20 lines for inclusion into VCU 1 trials (27th in Pato Branco). This case shows how multi-environment selection, even without replications, is very important in plant breeding. However, selection intensity must be low when only one replication is considered. Trials conducted with three or more replications in multi-environments are recommended (Yan et al. 2015). Thus, it is possible to obtain precise and accurate data about adaptability and stability.

The GEI has a pronounced influence on genotype performance. Thus, the evaluation of METs is essential for a relatively accurate assessment of this interaction and for improving genotype evaluations (Yan 2016). Trials without replications for lines but with replications for the check are a viable and effective alternative for autogamous breeding programs when seed availability is limited (Wu et al. 2013). This system is effective because it allows the identification of the best lines more accurately in relation to selection in single-location trial with replications when adequate statistical models are used (Bondalapati et al. 2014). Thus, the use of the mixed-model methodology with the REML and BLUP parameters allows the selection of superior lines in trials without replications where genetic differences among lines may be observed, excluding environmental effects. However, although the use of only one replicate is a good alternative for breeding programs, the use of more than one check cultivar is essential. Furthermore, it is important to note that for the subsequent generations, when there is greater seed availability, trials should be performed with replications.

FINAL CONSIDERATIONS

In total, 33 wheat lines evaluated in preliminary trials can be selected in terms of their productivity, adaptability and stability by HMGV, RPGV and HMRPGV methods. When a large number of lines need to be evaluated or when seed availability is limited, trials without replications can be an alternative for plant breeders. However, reduced selection intensity should be applied to avoid eliminating promising lines.

REFERENCES

Bondalapati, KD, Wu J and Glover KD (2014) An augmented additive-dominance (AD) model for analysis of multi-parental spring wheat F2 hybrids. **Australian Journal of Crop Science 8**: 1441-1447.

Borges V, Soares AA, Reis MS, Resende MD, Cornélio VMO, Leite NA and Vieira AR (2010) Desempenho genotípico de linhagens de arroz de terras altas utilizando metodologia de modelos mistos. **Bragantia 69**: 833-841.

Carvalho LP, Farias FJC, Morelo CL and Teodoro PE (2016) Uso da metodologia REML/BLUP para seleção de genótipos de algodoeiro com maior adaptabilidade e estabilidade produtiva. **Bragantia 75**: 314-321.

Costa AF, Leal NR, Ventura JA, Gonçalves LSA, Amaral Júnior AT and Costa H (2015) Adaptability and stability of strawberry cultivars using a mixed model. **Acta Scientiarum. Agronomy 37**: 435-440.

Cunha GR, Scheeren PL, Pires JLF, Maluf JRT, Pasinato A, Caierão E, Silva MS, Dotto SR, Campos LAC, Felício JC, Castro RL, Marchioro VS, Riede CR, Rosa Filho O, Tonon VD and Svoboda LH (2006) Regiões de adaptação para trigo no Brasil. Embrapa Trigo, Passo Fundo, 35p. **(Circular Técnica Online, 20).**

Federer WT (1956) Augmented (or Hoonuiaku) designs. **Hawaiian Planters Record 55**: 191-208

Federer WT and Raghavarao D (1975) On augmented designs. **Biometrics 31**: 29-35.

Franco FA and Evangelista A (2018) **Informações técnicas para trigo e triticale – safra 2018**. In Franco FA and Evangelista A (eds) XI reunião da comissão brasileira de pesquisa de trigo e triticale. Comissão de Pesquisa de Trigo e Triticale, Editores Técnicos - Cascavel, 258p.

Gomez GM, Unêda-Trevisoli SH, Pinheiro JEB and Di Mauro AO (2014) Adaptive and agronomic performances of soybean genotypes derived from different genealogies through the use of several analytical strategies. **African Journal of Agricultural Research 9:** 2146-2157.

Lopes RR, Franke LB, Souza CHLD, Bertoncelli P, Graminho LA and Pereira EA (2018) Genetic parameters and predicted gains with selection of interspecific hybrids of *Paspalum* for seed production. **Crop Breeding and Applied Biotechnology 18**: 284-291.

Matei G, Benin G, Woyann, LG, Dalló SC, Milioli AS and Zdziarski AD (2017) Agronomic performance of modern soybean cultivars in multi-environment trials. **Pesquisa Agropecuária Brasileira 52**: 500-511.

Milioli AS, Zdziarski AD, Woyann LG, Santos R, Rosa AC, Madureira A and Benin G (2018) Yield stability and relationships among stability parameters in soybean genotypes across years. **Chilean Journal of Agricultural Research 78**: 299-309.

Paula TM, Marinho CD, Souza V, Barbosa MHP, Peternelli LA, Kimbeng CA and Zhou MM (2014) Relationships between methods of variety adaptability and stability in sugarcane. **Genetics and Molecular Research 13**: 4216-4225.

Peixouto LS, Nunes JAR and Furtado DF (2016) Factor analysis applied to the G + GE matrix via REML/BLUP for multi-environment data. **Crop Breeding and Applied Biotechnology 16**: 1-6.

Resende MDV (2004) **Métodos estatísticos ótimos na análise de experimentos de campo**. Embrapa Florestas, Colombo, 57p.

Resende MDV (2007) **SELEGEN-REML/BLUP: sistema estatístico e seleção genética computadorizada via modelos lineares mistos**. Embrapa Florestas, Colombo, 360p.

Resende MDV and Duarte JB (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical 37**: 182-194.

Resende MDVD (2016) Software Selegen-REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology 16**: 330-339.

Santos AD, Ceccon G, Teodoro PE, Correa AM, Alvarez RDCF, Silva JFD and Alves VB (2016) Adaptability and stability of erect cowpea genotypes via REML/BLUP and GGE Biplot. **Bragantia 75**: 299-306.

Santos PRD, Costa KDDS, Nascimento MR, Lima TV, Souza YPD, Costa AFD and Silva JWD (2018) Simultaneous selection for yield, stability, and adaptability of carioca and black beans. **Pesquisa Agropecuária Brasileira 53**: 736-745.

Silva RR, Benin G, Marchese JA, Silva ÉDB and Marchioro VS (2014) The use of photothermal quotient and frost risk to identify suitable sowing dates for wheat. **Acta Scientiarum Agronomy 36**: 99-110.

Spinelli VM, Dias LAS, Rocha RB and Resende MDV (2015) Estimates of genetic parameters with selection within and between half-sib families of *Jatropha curcas* L. **Industrial Crops and Products 69**: 355-361.

Steel RGD and Torrie JH (1960) **Principles and procedures of statistics**. McGraw-Hill Book Company Inc, New York, 481p.

Wu J, Bondalapati K, Glover K, Berzonsky W, Jenkins JN and McCarty JC (2013) Genetic analysis without replications: model evaluation and application in spring wheat. **Euphytica 190**: 447-458.

Yan W (2016) Analysis and handling of G × E in a practical breeding program. **Crop Science 56**: 2106-2118.

Yan W, Frégeau-Reid J, Martin R, Pageau D, Mitchell-Fetch J (2015) How many test locations and replications are needed in crop variety trials for a target region? **Euphytica 202**: 361-372.