

Determination of Genotypic Stability and Adaptability in Wheat Genotypes Using Mixed Statistical Models

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ABSTRACT

The objective of this study was to evaluate the adaptability and stability of wheat genotypes simultaneously in unbalanced Multi-Environment Trials (MET) in four different regions of Brazil, using the method of harmonic means of the relative performance of genetic values. Mixed model was applied to the analysis of Genotype-Environment Interaction (GEI) in wheat. Grain yield data were obtained from a network of MET carried out at seven locations from 2008 to 2010. A joint of experiments in complete randomized blocks design with some common treatments was used in all 21 experiments. Adaptability and stability parameters were obtained by several different methodologies, based on prediction, Harmonic Mean, and of the Relative Performance of Genotypic Values (HMRPGV). These methodologies ranked in a very similar way the studied genotypes and indicated the genotypes CD0950, CD0857, CD0667, CD0915, CD0914, CD0669, CD0859, and CD0851 as the superior ones for grain yield, adaptability, and stability in all environments. Dourados-MS (2010) was the worst environment with lowest mean (1,560.26 kg ha⁻¹) and São Gotardo-MG (2008) was the best environment with highest mean (5,687.08 kg ha⁻¹). The genotype more stable by HMRPGV across 21 environments tested was CD085; in the best environment, it was ranked the sixth (6,319.30 kg ha⁻¹), but changed your values in the worst environment and was ranked the fifth (2,051.53 kg ha⁻¹). The HMRPGV proved to be a practical and useful statistical tool in the determination of the Value for Cultivation and Use (VCU), particularly in the selection of genotypes' reliability when genotypes are selected for the environments evaluated. This method has the advantage of providing results that are directly interpreted as breeding values for yield, stability, and adaptability.

Keywords: Genetic values, REML/BLUP, *Triticum aestivum* L. Interblock.

INTRODUCTION

Multi-Environment Trials (MET) are assays to assess variation in relative performance of genotypes in different environmental conditions and frequently show significant fluctuation in yield performance resulting from Genotype-by-Environment interaction (GE). The nature of GE can be assessed by partitioning the total GE variability into two components: (i)

Change in scale of a trait measured in different environments, that is, heterogeneity of variances, and (ii) Imperfect genetic correlation of the same trait across environments (or genotypes) (Yang and Baker, 1991).

The use of cultivars with wide adaptability and stability is an alternative to overcome some problems arising from the GE interaction in breeding programs. Adaptability is the ability of the material to

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be high-yielding with respect to a given environment or given conditions. Stability is related to the maintenance of performance and to the production predictability in different environments (Annicchiarico *et al.*, 2005; Ceccarelli, 1989; Khalili and Pour-Aboughadareh, 2016; Lin and Binns, 1988). There are various methods to analyze the genetic stability and adaptability, which differ in conceptual terms and biometric procedures (Khalili and Pour-Aboughadareh, 2016; Mohammadia *et al.*, 2015; Sayar *et al.*, 2013).

The number of genotypes included in MET for recommending superior cultivars in relation to stability and adaptability tends to be very large. Under these conditions, it may be difficult to ensure a correct distribution of genotypes in the experimental area, due to the effect of soil heterogeneity within the blocks, which increases the experimental error (Cochran and Cox, 1957). METs also are used in the process of crop cultivar registration for assessing the Value for Cultivation and Use (VCU). In MET, it is common that breeders add, remove, or replace certain genotypes over the years. This causes an unbalance of genotypes in the experimental network.

Estimation methodologies based on the least square method, as those applied in the analysis of variance, are not very recommendable when the experiments are unbalanced or in experiments with different number of treatments or replications (Piepho *et al.*, 2003; Piepho and Möhring, 2006).

The processing of experimental data by mixed models provides great flexibility in analysis and can usually overcome these difficulties by the estimation of variance components through the Restricted Maximum Likelihood (REML) method (Patterson and Thompson, 1971). They are able to handle complicated data structures and they possess the properties of consistency and asymptotic normality of the estimators desirable for hypothesis testing (Searle *et al.*, 1992).

New methodologies based on mixed models are being used for a better

understanding of the GE interaction. However, the use of methods based on mixed models (REML/BLUP - Best Linear Unbiased Prediction) in the study of adaptability and stability is still relatively rare (Piepho and Möhring, 2006; Viana *et al.*, 2011).

The use of HMRPGV proposed by Resende (2007a) is an alternative analysis based on mixed models for adaptability and stability studies. The HMRPGV method provides information on adaptability, stability, and yield in the same measured unit and on the same scale as the assessed trait. According to Resende (2007a), the lower the standard deviation of the genotypic behavior at the locations, the greater will be the harmonic mean of their genotypic values across locations. Thus, selection for the highest values of *HMGV* allows a simultaneous selection for yield and stability.

Studies using HMRPGV methodology have been carried out for grain yield with various species such as sorghum (Almeida-Filho *et al.*, 2014), corn (Mendes *et al.*, 2012; Rodovalho *et al.*, 2015), and upland rice (Colombari-Filho *et al.*, 2013).

The aim of this study was to apply mixed models in the analysis of groups of experiments in randomized blocks with common treatments at unbalanced multi-environment trials, in order to study the GE interaction with proper methodologies to analyze wheat adaptability and stability genotypic.

MATERIALS AND METHODS

Experiments

In this work, all the analysis were performed with the grain yield data obtained from the VCU experiments carried out by the wheat breeding program of Coodetec (Central Cooperative of Agricultural Research), Cascavel - Paraná, Brazil. Unbalanced Multi-Environment (MET)

Trials were performed between 2008 and 2010 at seven locations, thus adding up to 21 environments. Wheat map and geographic data of adaptation regions for the VCU trial and location and altitudes of the environments were evaluated (Supplementary Figure 1).

All the experiments were statistically designed in joint of experiments in complete randomized blocks with some common treatments (Pimentel Gomes and Guimarães, 1958), with three replications (Supplementary Figure 2). In 2008, three groups of experiments with 3 replications and 21 genotypes per test resulted in 63 regular genotypes, with

three cultivars in common in all experiments. In 2009, four experimental groups with 21 genotypes each were carried out, resulting in 84 regular genotypes and 3 cultivars present in all experiments. In 2010,

two groups of experiments with 22 genotypes each were carried out, with 44 regular genotypes and two cultivars in common per group.

Statistical Procedures

The mathematical model for experimental groups in randomized blocks with common treatments in several environments in scheme 3 is given by Equation (1). Statistical procedures for the mixed modeling consisted of deviance analysis of data. The parameters b , g and ge were considered random, and the matrix form of the mathematical model was represented by:

$$y = X\alpha + Zg + Wb + Ti + \varepsilon \quad (1)$$

Where, y : Is the data vector; α : Vector of experiment λ at environment effects (assumed as fixed) plus the overall mean,

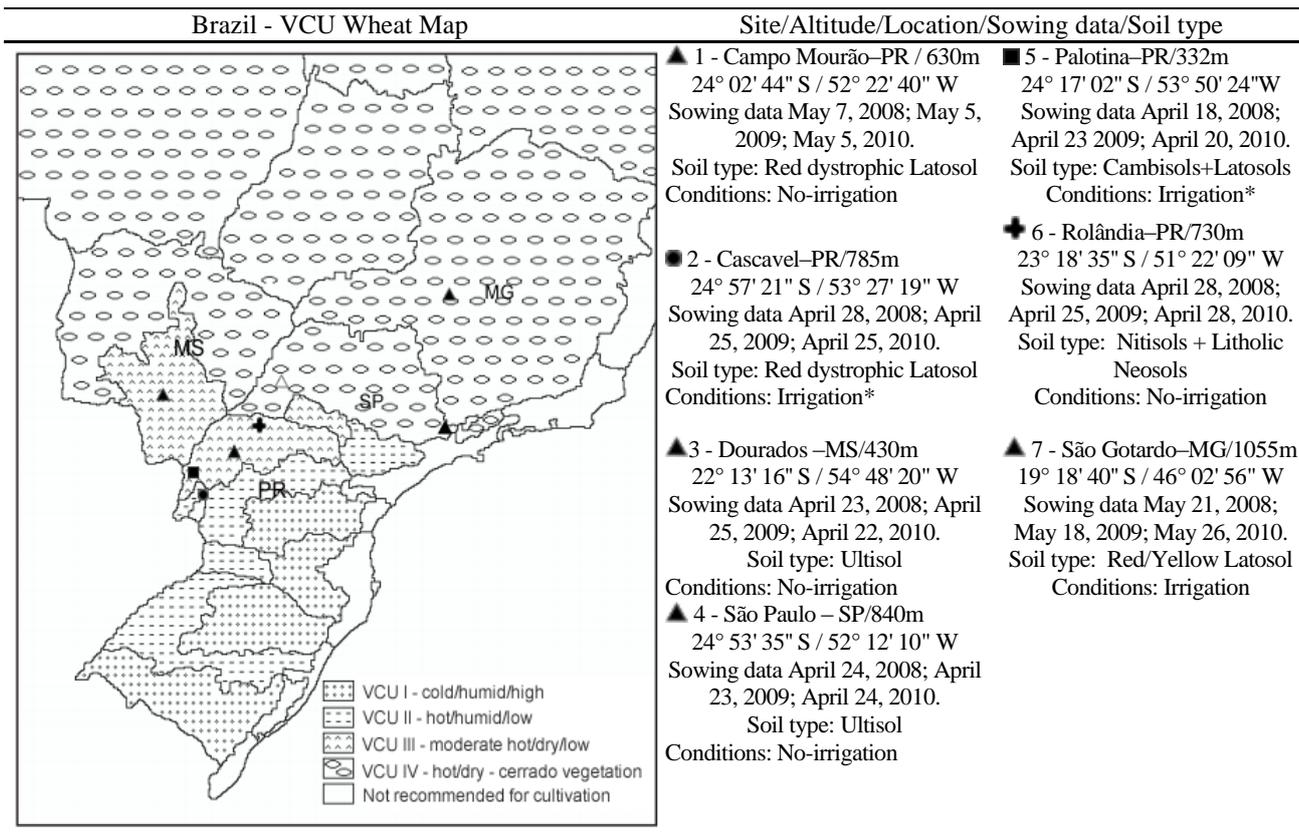


Figure 1. Adaptation regions for the Value for Cultivation and Use (VCU) trial and location and altitudes from environments evaluated. State Abbreviations: PR- Paraná, MG- Minas Gerais, MS- Mato Grosso do Sul, SP- São Paulo. (* Irrigated only until germination; Source: Cunha *et al.*, 2006).

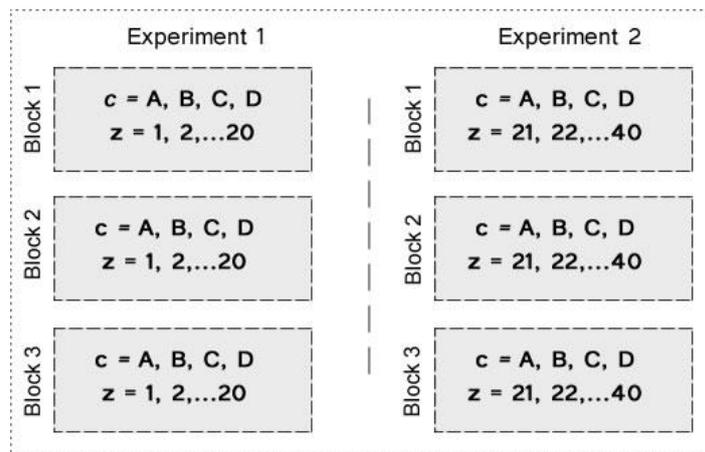


Figure 2. Resume diagram of an experiment group in randomized block design with common treatments with three replications. The letters represent the treatments in common given by (c) and the numbers represent the regular treatments (regular treatments are not repeated between experiments) given by (z), all assigned randomly within the blocks.

the vector α includes all experiments of all environments (fits experiments-environments combinations); g : Vector of genotypic effects (assumed as random); b : Vector of block within experiment within environment effects (assumed as random); i : Vector of genotype-environmental interaction effects ge (assumed as random), and e : The error or residue vector, random effect of experimental error, assuming $NID(0, \sigma^2)$.

In the above model (2), the capital letters X , Z , W , and T represent the incidence matrices for the effects of α , g , b and i , respectively. We used model 52 Software Selegen REML/BLUP (Resende, 2007b) to represent this model, for the incomplete block design for groups of experiments, with GE interaction to study the stability and adaptability by the HMRPGV method.

The means and variances were structured and distributed as follows:

$$\begin{aligned}
 y/r, V &\sim N(X\alpha, V) \\
 g/\hat{\sigma}_g^2 &\sim N(0, I \hat{\sigma}_g^2) \\
 b/\hat{\sigma}_b^2 &\sim N(0, I \hat{\sigma}_b^2) \\
 i/\hat{\sigma}_i^2 &\sim N(0, I \hat{\sigma}_i^2) \\
 e/\hat{\sigma}_e^2 &\sim N(0, I \hat{\sigma}_e^2)
 \end{aligned}$$

The mixed model equations provided the genetic values:

$$\begin{bmatrix} X'X & X'Z & X'W & X'T \\ Z'X & Z'Z + I \frac{\hat{\sigma}_e^2}{\hat{\sigma}_g^2} & Z'W & Z'T \\ W'X & W'Z & W'W + I \frac{\hat{\sigma}_e^2}{\hat{\sigma}_b^2} & W'T \\ T'X & T'Z & T'W & T'T + I \frac{\hat{\sigma}_e^2}{\hat{\sigma}_{ge}^2} \end{bmatrix} \begin{bmatrix} \hat{\alpha} \\ \hat{g} \\ \hat{b} \\ \hat{i} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ T'y \end{bmatrix}$$

Solution Model

The model effects were estimated by analysis of deviance. The statistical significance of the model was tested by the Likelihood Ratio Test (LRT). The deviances were obtained by both analysis, with and without the effects of b , g , and ge . Each effect was subtracted from the deviance of the full model and compared with the chi-square value with one degree of freedom, at 1% probability by the *LRT*. Thus $\mu_{..}$ was obtained, which refers to the general mean in all environments; g : predicted genotypic values, $g+ge$: Genotypic effects with interaction; $\mu+g+ge$: Genotypic values with mean interaction, and $\mu+g+ge_m$: Genotypic

values capitalizing the mean environmental effect.

Genotypic Stability and Adaptability

The genotypic values of stability were obtained from the Harmonic Mean of Genotypic Values (HMGV), according to Equation (2). Adaptability was evaluated based on the Relative Performance of Genotypic Values (RPGV), by Equation (3). In the next step, Equation (4) was used for the simultaneous evaluation of stability, adaptability, and yield, by calculating the harmonic mean of the relative performance of genotypic values (HMRPGV) for all genotypes.

The Equations (2), (3), and (4) are:

$$HMGV = \frac{l}{\sum_{i=1}^l \frac{1}{GV_{ij}}} \quad (2)$$

$$RPGV = \frac{1}{l} \left(\frac{\sum GV_{ij}}{\mu_j} \right) \quad (3)$$

$$HMRPGV = \left(\frac{l}{\sum_{i=1}^l \frac{1}{RPGV_{ij}}} \right) \quad (4)$$

Where, μ_j is the general mean for each environment j ; l - Number of environments; GV_{ij} : $u_j + g_i + ge_{ij}$ - In which GV_{ij} genotypic value of genotype i in a specific environment j , u_j represents the mean of environment j , and g_i and ge_{ij} are the BLUP values of genotype i and the interaction between genotype i and or environment j , respectively.

Correlations

The degree of association between the estimated mean and the parameters of adaptability and stability from the different methods was checked by Spearman's rank correlation coefficient (r). The assumption of normality for each environment and data

analysis by mixed modeling were checked using software SAS (SAS Institute, 2003).

RESULTS

Genotype-Environment Interaction

The results of the combined analysis of deviance, coefficients of variation, and the general mean are shown in Table 1. The variance of genotype effect was highly significant ($P < 0.01$) by the Chi-square test for the Likelihood Ratio (LTR), indicating significant differences among the tested cultivars.

Similarly, as for the effect of genotypes, the variance of the GE interaction was also highly significant, showing a different behavior of genotypes in the tested environments. Thus, there were changes in the ranking of genotypes or changes in the magnitude of differences between them at the studied locations.

The values of genotype-environment correlation ($\hat{r}_{ge} = 0.25$) indicate the predominance of a complex correlation and that genotypic performance of genotypes was not exactly the same over the environments.

The estimated accuracy value was relatively high ($\hat{r}_{gg} = 0.87$), which maximizes selection of the best genotypes tested across many environments.

Genotypic Values Recommendation

The genotypes with highest predicted genotypic values ($\mu + g$) free from any interaction with environments and the mean genotypic value ($\mu + g + ge_m$) in different environments were CD0857, CD0667, CD0914, and CDI0809 and had high genotypic values, which exceeded the best check (Quartzo) (Table 2). The predicted genotypic value for the best line (CD0857) was $3843.0 \text{ kg ha}^{-1}$, with a gain of 372.2 kg



Table 1. Combined analysis of deviance in 21 environments involving 118 genotypes, which were tested for three years (2008-10).

Effects	21 Environments		Estimated parameters ^a			
	Deviance ^b	LRT (χ^2)	$\hat{\sigma}_B^2$:	17790.83**	\hat{r}_{gg} :	0.87
Blocks/Exp/environments (E)	59015.17	285.9**	$\hat{\sigma}_g^2$:	41752.21**	\hat{r}_{ge}	0.25
Genotypes (G)	60010.78	1281.51**	$\hat{\sigma}_{ge}^2$:	122519.52**	\hat{h}_g^2 :	0.1483 ± 0.0162
GE	59939.31	1210.04**	$\hat{\sigma}_e^2$:	99983.78	\hat{h}_{gm}^2 :	0.77
Complete model	58729.27		$\hat{\sigma}_f^2$:	282046.35	\hat{c}_{ge}^2 :	0.43
	CV _{gi%} : 5.88	CV _{e%} : 9.11		$\bar{\mu}_{..}$: 3470.88		

^a Components of variance, coefficients of determination and correlations. ^b Deviance from the adjusted model without the corresponding effects. * and **: Significant by the Chi-square test with 1 degree of freedom: At 5% (3,84) and 1% (6,63) respectively.

Effects corresponding to:

$(\hat{\sigma}_B^2)$	Component of block variance	$(\hat{\sigma}_g^2)$	Genotypic variance	$(\hat{\sigma}_{ge}^2)$	Variance of the genotype - environment interaction
$(\hat{\sigma}_e^2)$	Error variance	$(\hat{\sigma}_f^2)$	Phenotypic variance	(\hat{r}_{gg})	Accuracy
(\hat{r}_{ge})	Correlation of genotypes with environment	(\hat{h}_g^2)	Genotypic heritability	(\hat{h}_{gm}^2)	Mean genotypic heritability
(\hat{c}_{ge}^2)	Coefficient of determination of the GEI	(CV _{gi%})	Coefficient of genotypic variation	(CV _{e%})	Coefficient or variation of the error
$(\bar{\mu}_{..})$	General mean.				

Table 2. Ranking of the genotypes in all environments evaluated for the genotypic prediction of wheat genotypes assessed in 21 environments at 7 locations (2008-10).^a

Or	Gen	<i>g</i>	$\mu+g$	Gain	<i>N</i> Mean	$\mu+g+ge_m$
1	CD0857	372.2	3843.0	372.2	3843.1	3895.1
2	CD0667	323.2	3794.0	347.7	3818.5	3839.2
3	CD0914	304.2	3775.1	333.2	3804.1	3817.6
4	CDI0809	296.4	3767.3	323.9	3794.9	3808.7
5	Quartzo	288.7	3759.5	316.9	3787.8	3799.9
6	CD0950	272.9	3743.8	309.6	3780.5	3781.9
7	CD0915	262.6	3733.5	302.9	3773.8	3770.2
8	CD0513	228.3	3699.1	293.5	3764.4	3731.0
9	CD0959	227.8	3698.7	286.3	3757.1	3730.5
10	CD0814	227.8	3698.6	280.4	3751.3	3730.5
11	CD0647	217.2	3688.0	274.7	3745.5	3718.4
12	CD0669	214.1	3684.9	269.6	3740.5	3714.9
13	CD154	213.7	3684.6	265.3	3736.2	3714.5
14	CDI0902	203.1	3673.9	260.9	3731.7	3702.3
15	CD0910	201.9	3672.8	256.9	3727.8	3701.0
⋮	⋮	⋮	⋮	⋮	⋮	⋮
118	CD0817	-512.7	2958.1	0	3470.8	2886.5
$\bar{\mu}_{..}$ ^b :	3470.88					

^a Or: Increasing Order; Gen: Genotype ranking. Genotypic effects, interaction free ($\mu+g$), prediction of genotypic values, capitalizing on the mean interaction ($\mu+g+ge_m$). ^b General mean of all environments; the parameters are expressed in grain yield (kg ha⁻¹).

ha⁻¹. The new mean was 3,843.1 kg ha⁻¹ and its mean genotypic value in all environments reached 3,895.1 kg ha⁻¹. The worst genotype was CD0817, whose predicted genotypic value was only 2,958.1 kg ha⁻¹ (u + g). The gain of this genotype was zero and its new mean reached 3,470.8 kg ha⁻¹, with a mean genotypic value for all environments of 2,886.5 kg ha⁻¹.

The cultivar Quartzo was the best check, with a mean genotypic value of 3,799.9 kg ha⁻¹ in all environments. As Quartzo occupied the fifth position, the results indicated a certain number of genotypes suitable for recommendation, since the new genotypes were able to perform better than the check cultivars. The genotypic values of these four genotypes were higher than those of the best control in all environments and their yield stability was considered high.

The patterns of stability and adaptability identified in the genotypic analysis using mixed models are shown in Figure 3. It should be noted that even those genotypes with a high phenotypic mean might have negative prediction estimates; the reason for which plant breeders should not use the phenotypic mean as the only criterion for recommending genotypes.

Genotype CD0857 and CD0914 were tested in 21 and 14 environments, respectively. Their genotypic values in relation to the mean effect of the environment ($\mu+g+ge_m$) exceeded the general mean of all genotypes in all environments (Figures 3a and b). Genotypes CD0857 and CD0914 were regarded as stable and adaptable, for their capacity to respond to

the environmental improvement and because they maintain stable yields under environmental alterations. The genotypes CD0911 and Onix had variations in the predicted genotypic values (g+ge), both in a positive and in a negative direction across environments. Thus, the genotypic mean values advantage of the environmental effect ($\mu+g+ge_m$) is offset by the general phenotypic mean $\bar{\mu}$ (Figures 3-c and -d). The standard values of $\mu+g+ge_m$ below the line of the general mean $\bar{\mu}$ are presented by genotypes CD0844 and CD0913 (Figures 3-e and -f), in which the values prediction (g+ge) were negative in most environments.

The method ($HMRPGV^*\bar{\mu}$) offers simultaneously genotypic stability and adaptability. The results of its application to experimental data were highly consistent in the ranking of genotypes, when compared to the results from the methods ($\mu+g+ge_m$), HMGV and $RPGV^*\bar{\mu}$ (Supplementary Table 3).

The estimated values of coefficients had a high positive and significant correlation (0.99*) with Spearman's correlation coefficients, at a probability level of 1%. The high Spearman's correlation coefficient for comparing $HMRPGV^*\bar{\mu}$ with HMGV (0.84*) shows the small difference in the ranking of these methods, due to the stricter ranking of HMGV, which penalizes instability of the genotypes.

Based on the results of the measure of stability and adaptability (HMRPGV) (Table 4), the top four genotypes that performed better than check Quartzo were CD0950,

Table 3. Spearman's correlation coefficients for the estimated parameters of adaptability and/or genotypic stability obtained by four methods for the trait grain yield tested in 21 environments.

Methods ^a	21 Environments		
	HMGV	$RPGV^*\bar{\mu}$	$HMRPGV^*\bar{\mu}$
$\mu+g+ge_m$	0.82*	0.99*	0.99*
HMGV		0.83*	0.84*
$RPGV^*\bar{\mu}$			0.99*

⁽¹⁾ $\mu+g+ge_m$: Prediction of the genotypic values capitalizing on the mean interaction; HMGV: Stability of Genotypic Values; $HMRPGV^*\bar{\mu}$: Harmonic Mean of the Relative Performance of the Predicted Genotypic Values (adaptability and stability), and $RPGV^*\bar{\mu}$: Adaptability of Genotypic Values. * Values different from zero at 1% probability

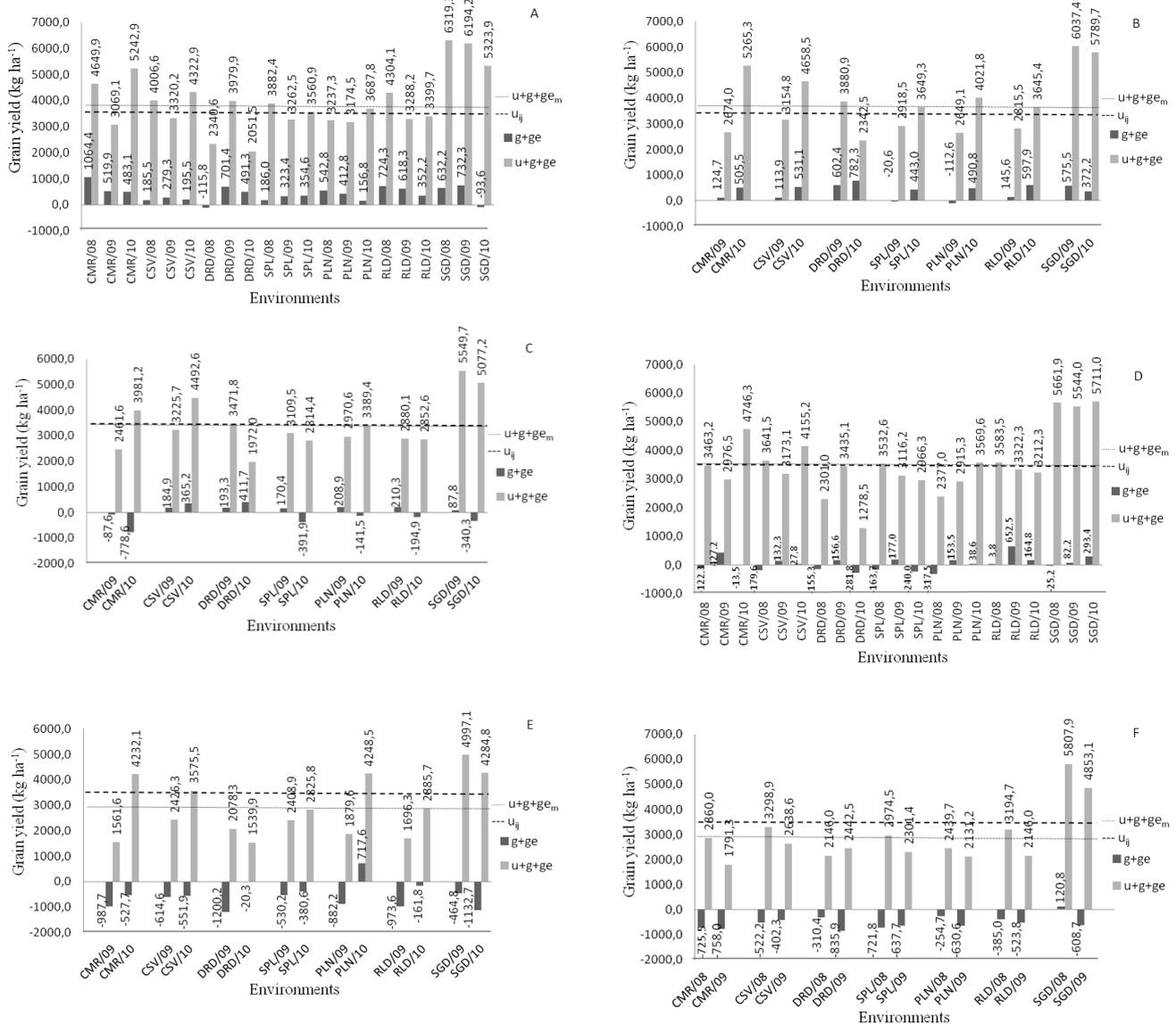


Figure 3. Genotypic values of grain yield at seven locations, genotypes that have positive BLUP values, high stability and adaptability: (A) Genotype CD0857 (2008, 2009 and 2010); (B) Genotype CD0914 (2009 and 2010). Genotypes that have intermediate ranking with positive, negative and null BLUP values: (C) Genotype CD0911 (2009 and 2010); (D) Genotype Onix (2008, 2009 and 2010); genotypes without stability with negative BLUP values; (E) Genotype CD0913 (2009 and 2010), (F) Genotype CD0844 (2008 and 2009). $\bar{\mu}_{..}$, $g+ge$, $\mu+g+ge$, and $\mu+g+ge_m$ are defined in the text.

CD0857, CD0915, and CD0914. The products of *HMRPGV* and the general mean ($HMRPGV * \bar{\mu}_{..}$) of these four genotypes were 3905.47, 3,902.42, 3,869.54 and 3,841.64 kg ha⁻¹, respectively. Assuming the selection of the four best-ranked genotypes for grain yield, an increase of 11.78% over the general mean

should be expected for this trait (in this case 3,470.88 kg ha⁻¹). It is important to measure *HMRPGV* because it expresses both stability and adaptability, indicating the capacity of a positive genotypic response to environmental improvements and the stability of genotypes over the tested environments.

Genetic Value Recommendation in Contrasting Environments

The adjusted means of the 21 environments with the ranking of the 10 best genotypes in contrasting environments are shown in Table 5. São Gotardo-MG was considered the best environment in 2008, with the highest mean (5,687.08 kg ha⁻¹). It should be noted that wheat is produced at high technological level in that location, growing under irrigation and in a no-tillage system.

Dourados-MS was the worst environment in 2010, with the lowest mean (1,560.26 kg ha⁻¹) considered. In 2008, the environment was below the general mean again. In fact, Dourados is a location where wheat is produced under low technical level and dry spells commonly occur during the crop cycle. However, Dourados was regarded as the second best environment in 2009.

For the sub-region (Dourados-MS in year

2010), the best genotypes recommended were CD0914, CD0647, CD0854, CD0803 and CD0857 by exploitation of specific adaptation in rainfed condition. Moreover, these genotypes were stable in all environments tested (Table 4).

Genotypes CD0647, CD0857, and CD0854 had high genotypic means ($\mu+g+ge$), and ranked among the top 10 genotypes in both the best and in the worst environment (São Gotardo in 2008 and Dourados in 2010, respectively). This result allows indicating them as highly stable and adaptable genotypes.

The genotype tested in the best and worst environments and considered stable by *HMRPGV* across 21 environments tested was CD0857, which, in the best environment, was ranked the sixth (6,319.30 kg ha⁻¹) and changed your values in worst environment that was ranked the fifth (2,051.53 kg ha⁻¹).

The stability of genotype CD0803 was

Table 4. Ranking of the genotypes in all environments evaluated for adaptability parameters of genotypic values for the trait grain yield of wheat genotypes evaluated in 21 environments.^a

Or	Gen	HMGV	Gen	RPGV	RPGV* $\bar{\mu}$..	Gen	HMRPGV	HMRPGV* $\bar{\mu}$..
1	CD0669	3758.22	CD0857	1.1318	3928.46	CD0950	1.1252	3905.47
2	CD0667	3748.57	CD0950	1.1294	3919.96	CD0857	1.1243	3902.42
3	CD0857	3656.09	CD0914	1.1186	3882.57	CD0915	1.1149	3869.54
4	CD0859	3633.16	CD0915	1.1182	3881.21	CD0914	1.1068	3841.64
5	CD0851	3594.05	CD0667	1.1131	3863.45	QUARTZO	1.1045	3833.42
6	CD0668	3563.97	QUARTZO	1.1092	3849.74	CD0667	1.1012	3822.11
7	CD0810	3552.61	CD0959	1.1025	3826.77	CD0959	1.1006	3820.11
8	CD0807	3541.09	CDI0809	1.1020	3824.88	CDI0809	1.0898	3782.62
9	CD0814	3514.22	CD0669	1.0929	3793.43	CD0669	1.0887	3778.50
10	CD0914	3508.12	CD0910	1.0880	3776.40	CD0910	1.0847	3764.86
11	CDI0809	3507.95	CDI0902	1.0878	3775.76	CDI0902	1.0840	3762.20
12	QUARTZO	3506.78	CD0814	1.0850	3765.85	CD0814	1.0827	3758.08
13	CD0655	3493.81	CD0513	1.0836	3761.12	CD0513	1.0758	3734.11
14	CD0846	3469.27	CD0952	1.0804	3750.06	CD0952	1.0728	3723.53
15	CD0853	3467.88	CD0647	1.0751	3731.44	CD0961	1.0634	3690.94
∴	∴	∴	∴	∴	∴	∴	∴	∴
20	CD0860	3426.78	BRSQUAMIRIM	1.0623	3687.07	CD0803	1.0565	3666.91
∴	∴	∴	∴	∴	∴	∴	∴	∴
118	CD0913	2497.76	CD0918	0.8302	2881.36	CD0913	0.8047	2792.96
$\bar{\mu}$.. ^b :	3470.88							

^a Or: Increasing Order; Gen: Genotype ranking. Performance Genetic Value (RPGV); RPGV* $\bar{\mu}$..¹: Stability of Genotypic Values (HMGV), Adaptability and stability of Genotypic Values (HMRPGV); (HMRPGV* $\bar{\mu}$..)

^b General mean of all environments; the parameters are expressed in kg ha⁻¹, except for *RPGV* and *HMRPGV*.



Table 5. General means of the genotypes evaluated in each environment and rank of the 10 best genotypes with high genotypic values in contrasting environments.

Adjusted means of the environments- $\bar{\mu}_j$ - kg ha ⁻¹ /- Year-Mean rainfall (mm) (RCy/RHFM) ^a							
Location		2008		2009		2010	
1 - Campo Mourão-PR		3585.44 (687 /317)		2549.25 (933 /300)		4759.82 (422 /150)	
2 - Cascavel - PR		3821.07 (665 /224)		3040.87 (747 /240)		4127.40 (840 /158)	
3 - Dourados –MS		2456.35 (340 /26)		3278.47 (509 /210)		1560.26 (245 /57)	
4 - São Paulo-SP		3696.31 (377 /80)		2939.13 (644 /282)		3206.31 (401 /95)	
5 - Palotina-PR		2694.42 (403 /133)		2761.75 (512 /128)		3530.95 (551 /234)	
6 - Rolândia-PR		3579.70 (550 /209)		2669.85 (776 /340)		3047.48 (446 /120)	
7 - São Gotardo-MG^b		5687.08 (750 /250)		5461.85 (750 /250)		5417.51 (750 /250)	
Best environment (São Gotardo-MG 2008)				Worst environment (Dourados –MS 2010)			
Condition: Irrigated				Condition: Rainfed			
Ord	Gen	<i>g+ge</i>	$\mu+g+ge$	Ord	Gen	<i>g+ge</i>	$\mu+g+ge$
1	CD0667	1498.04	7185.13	1	CD0914	782.27	2342.54
2	CD151	961.18	6648.27	2	CD0647	776.89	2337.16
3	CD0647	897.82	6584.91	3	CD0854	631.91	2192.18
4	CDI0809	725.96	6413.05	4	CD0803	603.46	2163.73
5	CD0668	708.04	6395.13	5	CD0857	491.26	2051.53
6	CD0857	632.21	6319.30	6	CD0911	411.68	1971.90
7	CDI0809	612.25	6299.34	7	CD0961	321.59	1881.86
8	CD0854	578.03	6265.12	8	CD0953	307.87	1868.13
9	CD0845	549.45	6236.54	9	CD0908	199.50	1759.77
10	CD0858	549.41	6236.50	10	CD0960	198.05	1758.32
:	:	:	:	:	:	:	:
31	CD0803	61.29	5748.38	31	IPR85	-158.49	1401.77
:	:	:	:	:	:	:	:
118	CD0644	-1652.17	4034.92	118	CD0614	-619.72	940.54

^a Adjusted by the recovery of inter-block information-kg ha⁻¹. RCy: Rainfall total Cycle; RHFM= Rainfall wheat stage Heading, Flowering and Milk. ^b Condition: Irrigated.

considered to be high in all 21 environments (Table 3), with a *HMRPGV* of 1.0565, showing a 5.6% increase in grain yield over the general mean, and ranked 20th among the 118 genotypes. CD0803 had a high genotypic value in the most unfavorable environment (Dourados-MS 2010), where it ranked fourth. However, this genotype did not show a high grain yield in response to the best environment (São Gotardo-MG 2008), where it ranked 31st. Our results

suggest that a continuous evaluation of genotypes for several years at the same locations should be appropriate.

DISCUSSION

Genotype-Environment Interaction

Genotype×Environment Interaction (GEI) is very important for plant breeding

programs (Yang and Baker, 1991; Mortazavian *et al.*, 2014; Sayar and Han, 2015). GEI stemmed from changing of ranking of genotypes because of changing environmental conditions (Kendal, 2015). The assessment of genotypes in many locations and years could increase the reliability of plant breeding programs (Sayar *et al.*, 2013; Sayar and Han, 2016; Kendal and Sayar, 2016). The GE interaction often causes some concern because it contributes to some mistakes during the selection of superior genotypes, especially when breeders work with pure lines, since the inbred lines do not behave in a similar way in different environments (Yang and Baker, 1991; Viana *et al.*, 2011; Kendal, 2015). The low correlations can occur when a type performance of genotypes in a certain environment cannot be seen in other conditions, preventing a reliable recommendation (Yang and Baker, 1991; Mortazavian *et al.*, 2014). The low value found in this study for correlation was considered complex and indicated some changes in rank order of genotypes.

Genotype-environment correlations are commonly reported in the literature. Rodovalho *et al.* (2015) found a GE correlation of $r_{ge} = 0.47$ when studying genotypic stability and adaptability for selecting corn hybrids. Working with grain yield corn, Mendes *et al.* (2012) found a correlation of 45%, which was reported as a result of a complex interaction, confirming the different genotypic behavior over the environments.

The assessment of genotypes in potential strategic environments across randomly occurring cycles of normal and extreme conditions and the analysis of stability parameters allows the identification of promising materials from the experimental network where they are evaluated. Genotypes identified to be stable in dynamic sense can have wide adaptation if they show simultaneously high yield potential (high mean yield across environments), or they do not show this agronomic attribute if they do

not have high yield potential (Khalili and Pour-Aboughadareh, 2016).

Accuracy in the Genotype Ranking

The accuracy indicates the precision of the inferences concerning genotypic means because the higher it is, the more accurate will be the ranking of cultivars for selection purposes (Piepho *et al.*, 2008; Resende, 2002; Viana *et al.*, 2011). Thus, accuracy measures the correlation between the predicted value and the true genotypic value.

According to Piepho *et al.* (2008), the lower the value of the Predicted Error Variance (PEV), the greater will be the accuracy and precision. Therefore, in the class of unbiased estimators/predictors, the strategy of minimizing PEV also results in maximized accuracy. In general, the reduction of the residual mean square is important since the residues quantify the differences between the genetic parametric values and the predicted values used in plant breeding. The high accuracy value that was found in this study indicates an excellent experimental quality and a high reliability in the selection of genotypes with more stability and adaptability (Thomason and Phillips, 2006).

The BLUP is a predictor with maximum correlation with the true genotypic value (g), fulfilling the assumption that there are no departures from trait normality, while μ is the major criterion of selection, for its role in the ranking of the genotypes that maximize the genotypic population mean (Duarte *et al.*, 2001; Searle *et al.*, 1992). For Resende (2007a), the use of predicted genotypic values ($\mu+g$) for the evaluated genotypes allows their recommendation even in not-yet-evaluated environments, i.e., out of the network and maybe with a different GE interaction pattern. The predicted genotypic values are also useful in case of environmental heterogeneity, since genotypes are ranked based on genotypic values free of GE interaction. These aspects



show the great advantage of using the proposed methodology.

For balanced tests in randomized complete blocks, in which means are not adjusted by the recovery of inter-block information, the genotypic values obtained by BLUP can differ from those of phenotypic means due to the shrinkage effect. However, the ranking of treatments will be the same as the one based on BLUP or on phenotypic means (Duarte and Vencovsky, 2001). If the heritability is taken as a regression function, the predictions of random effects start to be targeted towards the general average, by the effect of shrinkage, and this compromises the predictions made from small samples.

Genotypic Stability and Adaptability Recommendation

The breeder can select a genotype for the higher ranking of genotypic values, without comparing means. With the acceptance of the treatment effects as random and/or use of shrinkage estimators, multiple-comparison tests between treatment means are not recommended because such tests are designed under the assumption of fixed treatment effects (Resende, 2007a).

The importance of adaptability in plant breeding justifies the effort of breeders to identify this desirable behavior in the new developing cultivar (Ceccarelli, 1989). According to Resende (2007a), the HMRPGV method is similar to that of Lin and Binns (1988). However, unlike the method of Lin and Binns, which is based on phenotypic results, the HMRPGV method processes simultaneously grain yield, adaptability, and stability data, in a genotypic context. Stability is important to allow the identification of those genotypes less affected by the environmental variation, which may be recommended for a wide range of environments (Ceccarelli, 1989; Thomason and Phillips, 2006; Sayar *et al.*, 2013).

According to Smith *et al.* (2001) and Resende (2007a), as the genotypic values of

cultivars cannot be observed, they are unknown random variables. On the other hand, the future performance of these random variables can be predicted when the genotypic effects are regarded as random. Thus, the results of this conception are more consistent during the growing seasons.

The observation from Table 4 assumes that stability is associated with higher grain yield and a greater tolerance to environmental changes (Annicchiarico *et al.*, 2005). However, plant breeders may eventually eliminate stable genotypes when such materials have a homogeneous performance in different environments, but fail to express a high grain yield in response to environmental improvements.

The Dourados-MS environment had high contrast of means between years, forming a sub-region across years: considered as favorable in 2010 and unfavorable in 2008 and 2009. Ceccarelli (1989) defined an environment “favorable” when characterized by low stress and high mean yield and “unfavorable” with high stress and low yield. This difference is explained by the variation of the weather conditions during the evaluation time. According to Fietz *et al.* (2005), the water stress is a major cause of crop losses in Dourados (MS), where droughts are frequent due to the irregular rainfall distribution. Sub-regions may be defined for genotype recommendation, in which each sub-region coincides with a recommendation domain, grouping those environment with the same best-performing genotypes (Gauch and Zobel, 1997). The definition of sub-regions is not just geographical, but may also encompass farming practices (e.g. irrigated or rainfed cropping).

The predicted genotypic value for the mean of the 21 environments is useful not only to take advantage of the mean effect of the ($\mu+g+ge$) interaction, but also to indicate genotypes in other environments, provided that they have the same pattern of GE interaction verified on the test network (Resende, 2004). The indication based on the general phenotypic mean (Figure 3)

usually favors those genotypes with high behavior in the best environments, but does not discriminate genotypes particularly adapted to a better or worse environmental condition. Knowledge about the behavior or adaptability of genotypes to certain environments is essential for the agronomic evaluation of cultivars (Ceccarelli, 1989; Lins and Binns, 1988).

According to Piepho and Möhring, (2006), the values of BLUP obtained from all environments are more accurate than those from the individual analysis of each environment, due to the quality of information generated from the entire experimental network.

The methods adopted in this study had a high correlation in the ranking of genotypes across environments. The use of one or more stability parameters obtained by different methodologies for the study of the effect of environmental variations on genotypic performance requires a level of association between such estimates (Duarte and Zimmermann 1995).

The predicted genotypic values can be used in relation to the environments with the same pattern of GE interaction observed in the experimental network, otherwise the superior genotypes should be selected based on their genotypic means (u+g), a safer procedure for being free of the GE-interaction.

CONCLUSIONS

The mixed models proved to be adequate to analyze GE-interaction and genotypic adaptability and stability study. Wheat genotypes CD0950, CD0857, CD0667, CD0915, CD0914, CD0669, CD0859 and CD0851 had the best grain yield performance, adaptability, and stability. The HMRPGV method has the advantage of providing results that are directly interpreted as breeding values for yield, stability, and adaptability. The high value of accuracy ($\hat{r}_{\hat{g}g}$), over 87%, revealed a satisfactory

experimental quality and a higher reliability when genotypes were selected for each environment.

The grain yield obtained in this study was determined at which intervals among all of the 21 environments tested the most stable by HMRPGV was CD0857 (3,902.42 kg ha⁻¹), in the best environment, was ranked the sixth (6,319.30 kg ha⁻¹) and changed your values in the worst environment that was ranked the fifth (2,051.53 kg ha⁻¹). Dourados-MS (2010) was the worst environment with lowest mean yield (1,560.26 kg ha⁻¹) and São Gotardo-MG (2008) was the best environment with highest mean yield (5,687.08 kg ha⁻¹). The classification of genotypes resulting from the application of the methods (u+g+ge_m), HMGV, RPGV, and HMRPGV was very similar in all the evaluated environments. The predicted genotypic values based on genotypic means (u+g), can be used in relation to the environments with the same pattern of GE interaction observed in the experimental network, for being free of the GE-interaction.

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Appendix A. Supplementary data
Supplementary data related to this article can be found at...[LINK FROM JAST](#)

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تعیین پایداری و سازگاری ژنوتیپی در ژنوتیپ های گندم با استفاده از مدل های آماری مخلوط

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چکیده

هدف این پژوهش ارزیابی همزمان سازگاری و پایداری ژنوتیپ های گندم در آزمون های نامتعادل چند محیطی (MET) در چهار منطقه متفاوت برزیل بود. برای این منظور، از روش میانگین های هارمونیک عملکرد نسبی (harmonic means of the relative performance) ارزش های ژنتیکی استفاده شد. در تحلیل برهمکنش و تعامل ژنوتیپ – محیط (GEI) گندم، مدل مخلوط به کار



گرفته شد. داده های عملکرد دانه از شبکه ای از MET که در هفت محل در سال های ۲۰۰۸ تا ۲۰۱۰ اجرا شده بود به دست آمد. در تمامی ۲۱ آزمایش، از آزمایش های به هم پیوسته (joint of experiments) با طرح بلوک های کاملاً تصادفی و برخی تیمارهای مشترک استفاده شد. پارامترهای سازگاری و پایداری با چند روش متفاوت مبتنی بر پیش بینی، میانگین هارمونیک، و عملکرد نسبی ارزش ژنوتیپی (HMRPGV) به دست آمد. با این روش ها، ژنوتیپ های آزمون شده به طور مشابهی رده بندی شد و از نظر عملکرد، سازگاری، و پایداری، برتری ژنوتیپ های CD0950، CD0857، CD0667، CD0915، CD0914، CD0669، CD0859 و CD0851 در تمام محیط ها آشکار شد. منطقه (Dourados- MS (2010) بدترین محیط بود و کمترین میانگین عملکرد ($1560.26 \text{ kg ha}^{-1}$) را داشت درحالیکه São Gotardo – MG (2008) بهترین محیط بود با بیشترین میانگین عملکرد ($5687.08 \text{ kg ha}^{-1}$). ژنوتیپ CD0857 با روش HMRPGV دارای پایداری بیشتر در ۲۱ محیط مطالعه شده بود و در بهترین محیط، این ژنوتیپ از نظر عملکرد ($6319.30 \text{ kg ha}^{-1}$) رده ششم را داشت و در بدترین محیط، با تغییر ارزش ها به رده پنجم عملکرد ($2051.53 \text{ kg ha}^{-1}$) رسید. بر پایه نتایج، ثابت شد که روش HMRPGV روشی عملی و ابزار آماری مفیدی است در تعیین ارزش کاشت و مصرف (value for cultivation and use)، به ویژه برای انتخاب اطمینان ژنوتیپ ها در مواردی که ژنوتیپ ها برای محیط های ارزیابی شده انتخاب می شوند. مزیت این روش در آن است که نتایجی را به دست می دهد که از نظر ارزش بهنگزادگری مستقیماً برای عملکرد، پایداری، و سازگاری قابل تفسیر اند.