Mean performance and stability in multi-environment trials II: Selection based on multiple traits

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ABSTRACT

Modeling the genotype-vs-environment interaction (GEI) and quantifying genotypic stability are crucial steps for selecting/recommending genotypes in multi-environment trials (MET). The efficiency in selection/recommendation could be greater if based on multiple traits, but identifying genotypes that combine high performance and stability across many traits has been a difficult task so far. In this study, we propose a multi-trait stability index (MTSI) for simultaneous selection considering mean performance and stability (MPE) in the analysis of MET using both fixed- and mixed-effect models. Data from a MET where 14 traits were assessed in 22 genotypes of *Avena sativa*, L. were used to illustrate the application of the method. The genotypic stability was quantified for each trait using the WAASB index (lower is better). A superiority index, WAASBY (higher is better) was calculated to consider the MPE. The selection differential (SD) for the WAASBY index ranged from 9.7 to 44.6%. Positive SDs ($1.75\% \leq SD \leq 17.8\%$) were observed for trait means that wanted to increase and negative (-11.7%) for one variable that wanted to reduce. The negative SDs observed for WAASB ($-63\% \leq SD \leq -12\%$) suggested that the selected genotypes were more stable. The MTSI should be useful for breeders and agronomists that looks for a selection for MPE based on multiple traits since it provides an undoubtedly and easy-to-handle selection process, accounting for the correlation structure of the traits. The application of the MTSI in future studies is facilitated by a step-by-step guide and an R package containing useful functions.

Abbreviations: AMMI, Additive Main effects and Multiplicative Interaction; BLUP, Best Linear Unbiased Prediction; GEI, genotype-by-environment interaction; IPCA, interaction principal component axis; LMM, linear mixed-effect model; MET, multi-environment trials; MTSI, multi-trait stability index; SVD, singular value decomposition; WAASB, weighted average of absolute

scores from the SVD of the matrix of BLUPs for the GEI effects generated by an LMM; WAASBY, weighted average of WAASB and response variable

Highlights

The genotypic stability was quantified in multi-environment trials (MET) using mixed models

A superiority index that allows weighting between mean performance and stability was used

A multi-trait stability index (MTSI) for identifying superior genotypes in MET was proposed

Using a real dataset from a MET, stable and high-performance genotypes were identified.

The MTSI should make easier and clearer the genotype selection in a multi-trait framework

INTRODUCTION

Multi-environment trials (MET) are experiment networks where a set of genotypes are evaluated in a series of environments, which may have a spatial separation (e.g., locations), a temporal separation (e.g., cultivation years) or a combination of these factors (e.g., combination of location and years), aiming at the recommendation of genotypes to specific environments or delineation of mega-environments. It is very common that a relatively large number of genotypes, say, more than 20, are conducted in each environment, usually in a complete randomized block design (RCBD) with 2−4 replicates (Piepho, 1994). In this context, MET allows identifying genotypes that exhibit a small temporal variability or that are consistent from location-to-location (Yan and Kang, 2003).

When more than one genotypes are conducted in more than one environment, in addition to the additive effect of genotype and environment, a third −multiplicative− effect arises from the interaction between these factors. This effect is called genotype-environment interaction (GEI). The desire to properly model the GEI has led to the development of procedures called stability analyzes, from which ideas precede even analysis of variance (Mooers, 1921). Yates and Cochran (1938) introduced the theoretical bases of the joint regression analysis, popularized years later by Eberhart

and Russell (1966) and Finlay and Wilkinson (1963). During many years, stability analyses were limited to the regression-based method. Because of the ease of access to personal computers from the late 1970s, more sophisticated methods, which had not been used in practice due to the complexity of matrix operations, were proposed (Gollob, 1968).

Nowadays, the Additive Main Effect and Multiplicative Interaction AMMI (Gauch, 2013) has been widely used in the MET analysis, since it provides more accurate estimates when compared to the traditional ANOVA, besides presenting nice graphical tools for an easy interpretation of the GEI. In the near future, however, methods for MET analysis will depend less on linear-bilinear models -such as AMMI- and more on linear mixed-effects model, LMM (van Eeuwijk et al., 2016). This is because the estimates of genotypic responses obtained by Best Linear Unbiased Prediction (BLUP) are generally more accurate than those obtained by fixed-effect models (Piepho, 1994).

It is very common that stability analysis in MET is performed for a single variable, often the grain yield (e.g., Nowosad et al., 2016, Bornhofen et al., 2018, Mohammadi et al., 2018). Reliability in recommending genotypes, however, could be increased if the mean performance and stability (MPE) of several traits were considered. Recent studies that assessed several variables in MET have been observed (eg, Adjebeng-Danquah et al., 2017; Nduwumuremyi et al., 2017; Shahriari et al., 2018; Bocianowski et al., 2019; Koundinya et al., 2019; Veenstra et al., 2019), and the simultaneous selection for stability and mean performance has met with some success when each variable was analyzed individually.

As far as is known, there is no method for MET analysis that combines the simultaneous selection for MPE of several traits into a single and easy-to-interpret index, especially in an LMM framework. Thus, our efforts in this study were focused on to: (i) introduce the theoretical foundations of an index for selecting high-performance and stable genotypes based on multi-trait; (ii) evaluate the applicability of this index in a real dataset from a MET with the white oats (*Avena*

sativa, L.) crop; (iii) introduce an R package that makes easier the application of the index by breeders and agronomists in future studies.

MATERIAL AND METHODS

Plant material, site description, and experimental design

Twenty-two white oat (*Avena sativa* L.) genotypes released by Brazilian breeding programs between 2001-2015 (Supplementary Table S1), and that are considered the most cultivated in Brazil, were evaluated in the experimental area of the Regional Institute of Rural Development, in Augusto Pestana, RS, Brazil (28˚26'30"S, 54˚00'58"W, at 250 masl) during three cultivation years (2015-2017).

For each year, a randomized complete block design with three replicates was used, totaling 198 plots. Each plot had five 5-m-long cropping rows spaced at 0.18 m. The sowing was carried out in the first week of June using tractor-seeder and a seeding rate of 300 seeds m^{-2}. 10 Kg ha^{-1} of N, 45 Kg ha^{-1} of P_2O_5, and 30 Kg ha^{-1} of K_2O were applied in basal fertilization. The remainder of the nitrogen was applied in topdressing at GS14 Zadoks' scale (Zadoks et al., 1974)], with a rate for an expected yield of 4 Mg ha^{-1}. Weed control was performed using the herbicide metsulfuron-methyl (2.4 g ha^{-1} AI). Three applications of propiconazole 250 g L^{-1} (0.75 L ha^{-1} commercial product) were performed at 60, 75 and 90 days after sowing to prevent foliar diseases.

Accessed traits

Biweekly evaluations were performed to monitor the progress of the necrotic leaf area in each plot. The first evaluation was performed at 60 days after sowing (DAS) and the last one at 105 DAS, totaling four measurements. Three plants of each plot were randomly collected and taken to the laboratory for analysis. The top three leaves of each plant were scanned and the leaf area necrotized (in percentage) obtained using the ImageJ software. The area under the disease progress

curve (AUDPC) was calculated to combine the multiple measurements into a single value, according to the formula described by Jeger and Viljanen-Rollinson (2001).

At the harvest, the average value of 10 panicles randomly selected in each plot was obtained for the following traits: panicle length (PL, cm), panicle mass (PM, g), number of spikelets per panicle (NEP, n); number of grains per panicle (NGP, n), grain weight per panicle (GWP, g); panicle mass (PM, g). By using the grains harvested in the three central cropping rows of each plot the following traits were assessed: grain yield (GY, kg ha^{-1}), estimated by adjusting the GY obtained in each plot to GY per hectare; thousand-grain weight (TGW, g), obtained by counting and weighing 250 grains in a precision scale and multiplying the result by four; hectoliter weight (HW, kg hL^{-1}): estimated by the weight ratio of grains in a volume of 250 cm^{-3}; number of grains greater than 2 mm (NG2, n), the number of grains of a sample of 100 grains remaining in a 2 mm sieve; grain weight (GW, g), weight of 50 grains greater than 2 mm; caryopses weight (CW, g), obtained by weighing the caryopses of the 50 hulled grains; hulling index (HI, g g^{-1}), obtained by the equation HI = WC / GW; industrial grain yield (IGY, kg ha^{-1}), obtained by the equation IGY = GY × NG2 × HI.

Statistical analysis

BLUP-based genotypic stability

In this study, we used the singular value decomposition (SVD) of the matrix of BLUPs for the GEI effects generated by a linear mixed model (LMM) to quantify the genotypic stability. Briefly, each variable was analyzed using LMM where the genotype and genotype-vs-environment interaction (GEI) effects were assumed to be random and the effects of cultivation year (environment) and of block-within-environment were assumed to be fixed effects, so that.

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu} + \boldsymbol{\varepsilon} \qquad [1]$$

where $\mathbf{y}$ is an $n[=\sum_{j=1}^{e}(gb)]\times 1$ vector of observations in the kth block of the ith genotype in the jth year (i = 1, 2, ..., g; j = 1, 2, ..., e; k = 1, 2, ..., b); $\boldsymbol{\beta}$ is an $eb\times 1$ vector of fixed effects; $\mathbf{u}$ is an

$m[=g+ge]\times 1$ vector of random effects; $\mathbf{X}$ is an $n\times eb$ design matrix relating $\mathbf{y}$ to $\boldsymbol{\beta}$; $\mathbf{Z}$ is an $n\times m$ design matrix relating $\mathbf{y}$ to $\mathbf{u}$; and $\boldsymbol{\varepsilon}$ is an $n\times 1$ vector of within-group errors.

The vectors $\boldsymbol{\beta}$ and $\mathbf{u}$ were estimated using the well-known mixed model equation (Henderson, 1975).

$$\begin{bmatrix}\hat{\boldsymbol{\beta}}\\ \hat{\mathbf{u}}\end{bmatrix}=\begin{bmatrix}\mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z}\\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}+\mathbf{G}^{-1}\end{bmatrix}^{-}\begin{bmatrix}\mathbf{X}'\mathbf{R}^{-1}\mathbf{y}\\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y}\end{bmatrix} \quad [2]$$

The variance component estimates in $\mathbf{G}$ and $\mathbf{R}$ were obtained by REstricted Maximum Likelihood (REML) using the expectation-maximization algorithm (Dempster et al., 1977).

The matrix $\hat{\mathbf{u}}_{\mathbf{ge}}$, containing the shrunken effects for the GEI was decomposed as follows

$$\hat{\mathbf{u}}_{\mathbf{ge}}=\mathbf{U}_{\mathbf{gp}}\boldsymbol{\Lambda}_{\mathbf{pp}}\mathbf{V}_{\mathbf{pe}}^{\mathbf{T}} \quad [3]$$

where $\boldsymbol{\Lambda}_{\mathbf{pp}}$ is a diagonal matrix with p singular values, in decreasing order [$p \le \min(g-1; e-1)$]. The matrices $\mathbf{U}_{\mathbf{gp}}$ and $\mathbf{V}_{\mathbf{ep}}$ are orthonormal matrices with genotype singular vectors from $\hat{\mathbf{u}}\hat{\mathbf{u}}^{\mathbf{T}}$ and environment singular vectors from $\hat{\mathbf{u}}^{\mathbf{T}}\hat{\mathbf{u}}$, respectively. The genotypic stability of each genotype was quantified by the WAASB index, acronym for **W**eighted **A**verage of **A**bsolute **S**cores from the SDV of the matrix of **B**LUPs for the GEI effects, estimated as follows:

$$WAASB_i=\sum_{k=1}^{p}\left|IPCA_{ik}\times EP_k\right| \Big/ \sum_{k=1}^{p} EP_k \quad [4]$$

where $WAASB_i$ is the weighted average of absolute scores of the ith genotype; $IPCA_{ik}$ is the score of the ith genotype in the kth IPCA, and EP_k is the amount of the variance explained by the kth IPCA. The genotype with the lowest WAASB value is considered the most stable.

Simultaneous selection for performance and stability

The simultaneous selection for MPE was performed by using the WAASBY index, which allows weighting between mean performance (Y) and stability (WAASBY), as follows:

$$WAASBY_i=\frac{\left(rY_i\times\theta_Y\right)+\left(rW_i\times\theta_S\right)}{\theta_Y+\theta_S} \quad [5]$$

Where $WAASBY_i$ is the simultaneous selection index for the *i*th genotype that weights between MPE; θ_Y e θ_S are the weights for the response variable and the WAASB, assumed to be 65% e 35%, respectively; rY_i and rW_i are the rescaled values (0−100) for the response variable and WAASB, respectively, estimated as follows:

$$rY_i = rW_i = \frac{nma - nmi}{oma - omi} \times (o_i - oma) + nma \qquad [6]$$

where *nma* and *nmi* are the new maximum and minimum values after rescaling; *oma* and *omi* are the original maximum and minimum values, and o_i is the original value for the response variable or the WAASB index of the *i*th genotype. The values for *nma* and *nmi* were chosen according to the variable. Except for AUDPC, higher values are desired; thus *nma* = 100 and *nmi* = 0. In other words, the genotype with the higher mean had rY_i = 100 after rescaling. For AUDPC −and WAASB− where lower values are desired, we used *nma* = 0 e *nmi* = 100. Thus, a two-way table containing the WAASBY values for each genotype and trait was obtained. The codes for this procedure are in Supplementary material S1.2.

Multi-trait stability index based on factor analysis

The selection for MPE considering multi-trait was based on the genotype-ideotype distance (Euclidian) using the scores obtained in an exploratory factor analysis as follows:

$$\mathbf{X} = \boldsymbol{\mu} + \mathbf{Lf} + \boldsymbol{\varepsilon} \qquad [7]$$

where $\mathbf{X}$ is a $p\times1$ vector of observations; $\boldsymbol{\mu}$ is a $p\times1$ vector of means; $\mathbf{L}$ is a $p\times f$ matrix of factorial loadings; $\mathbf{f}$ is a $p\times1$ vector of common factors; and $\boldsymbol{\varepsilon}$ is a $p\times1$ vector of residuals, being p and f the number of traits and common factors retained, respectively. The eigenvalues and eigenvectors were obtained from the correlation matrix of the two-way table described above. The initial loadings were obtained considering only factors with eigenvalues higher than one. The *varimax* rotation criteria was used for the analytic rotation and estimation of final loadings. The scores for the genotypes were obtained according to the following equation.

$$\mathbf{F} = \mathbf{Z}(\mathbf{A}^{\mathbf{T}}\mathbf{R}^{-1})^{\mathbf{T}} \quad [8]$$

where **F** is a $g \times f$ matrix with the factorial scores being g the number of genotypes and f the number of factors; **Z** is a $g \times p$ matrix with the standardized means (WAASBY means); **A** is a $p \times f$ matrix of canonical loadings, and **R** is a $p \times p$ correlation matrix between the variables.

The second step was the ideotype planning. By definition (Eq. [5]), the ideotype has the highest WAASBY (100) for all analyzed variables. Thus, the ideotype was defined by a $1 \times p$ vector **I** such that **I** = [100, 100, ..., 100]. The scores of the ideotype were also estimated according to Eq. [8]. The third and last step was the estimation of the multi-trait stability index (MTSI), according to the following equation.

$$MTSI_i = \left[\sum_{j=1}^{f} \left(F_{ij} - F_j \right)^2 \right]^{0.5} \quad [9]$$

where the MTSI is the multi-trait stability index for the ith genotype; F_{ij} is the jth score of the ith genotype, and F_j is the jth score of ideotype. The genotype with the lowest MTSI is then closer to the ideotype and therefore presents high MPE for all analyzed variables.

The selection differential (SD) for mean performance and both WAASB and WAASBY index was calculated for each trait considering a selection intensity of 15%. To assist with an intuitive interpretation, graphics showing the mean and biplots for response variable vs WAASB were created for GY, AUDPC, and IGY. The codes in S1.3 may be used to reproduce the examples of this section.

RESULTS

Overall performance, likelihood ratio tests and variance components

According to the LR test, the genotype effect was significant for the TGW only (Supplementary Table S2). On the other hand, the GEI effect was significant for all traits except for TGW. The environment effect was highly significant for all variables except for HI. The overall mean of GY was 3349.29±113.4 Kg ha^{-1} whereas the grand mean for IGY was 1402±55.63 Kg

ha^{-1} (Supplementary Table S2). For all traits except for TGW, the GEI variance ($\hat{\sigma}^2_{ge}$) had a higher contribution to the phenotypic variance (Fig. 1).

Linear relationships

Pearson's correlation matrix for the WAASBY values is presented in Supplementary Fig. S1. High-magnitude correlations were observed among PL, PM, NEP, NGP, and GMP, suggesting that these traits may be grouped in a common factor. A positive association between GY and ADUPC was observed, which is explained due to *nma* and *nmi* value used for rescaling AUDPC. For this variable, genotypes with higher WAASBY present, in fact, lowest AUDPC and consequently higher GY.

Exploratory factor analysis

Loadings and factor delineation

Five principal components were retained, and the accumulated variance in these components was 83.1% (Table 1). After *varimax* rotation the average communality (h) was 0.83 (TGW $0.55 \leq h \leq 0.95$ GWP. The values of WAASBY in each one of the 14 traits were grouped in the five factors (FA) as follows: FA1, PM, NEP, NGP, and NGP; FA2, the traits related to grain density TGW, HW, and GW; FA3, the traits related to industrial yield NG2 and IGY; FA4, the traits CW and HI; and FA5, the traits PL and AUDPC (Table 1).

Multi-trait stability index and genotype selection

Figure 2 shows the genotype ranking for the MTSI. Considering the selection intensity of 15%, the three genotypes selected were G01, G15, and G16, with MTSI values of 3.99, 4.27, and 3.61, respectively). The contribution of each factor in the MTSI indicated that ~54% of the distance from G1 to the ideotype was related to FA2 (Supplementary tables S4 and S5). In other words, G1

had lower WAASBY for the traits TGW, HW, and GW. Regarding the G15 and G16, most of the MTSI was due to the FA4 (~35%) and FA1 (~52%), respectively.

The SD for the WAASBY index was positive for all traits, suggesting that the method was efficient in selecting the best performing and stable genotypes. The mean SD for the WAASBY index was 25.1%, being the lowest one (9.68%) for the GY and the highest one (44.6%) for the CW (Table 2).

Mean performance and stability of selected genotypes

The joint interpretation for MPE regarding the GY, AUDPC, and IGY is presented in Fig. 3. Unlike the well-known AMMI1 biplot, the ordinate (WAASB) quantify the stability considering all possible IPCA (Eq. [4]). Genotypes within quadrants I and II are assumed to be unstable. Genotypes within quadrant IV −for GY and IGY−, and within quadrant III −for AUDPC− are assumed to be desirable because they present desirable mean and lesser variation from environment-to-environment, which is explained by the WAASB values.

The IGY of the selected genotypes was 1652.1 kg ha^{-1} (17.8% higher than the grand mean). In addition, an SD of −11.7% for AUDPC and 1.8% for GY was observed (Fig. 4). The lower SD for GY is compensated by the higher IGY, which was resultant from the higher NG2 and HI of the selected genotypes (Supplementary Fig. S3). For most of the other analyzed traits, positive SDs ($1.75\% \leq SD \leq 17.8\%$) were observed. Regarding the WAASB, negative SDs were observed for all traits ($-63.9\% \leq SD \leq -12.3\%$), which indicates that the selected genotypes were considerably more stable (Supplementary Table S6).

DISCUSSION

Quantifying the stability using linear mixed-effect models

Quantifying stability is fundamental to the development of genotype selection/recommendation strategies. This has become an increasingly common practice in MET

analysis. In the context of models with multiplicative terms, AMMI stability value, ASV (Purchase et al., 2000) has been used for this purpose (Adjebeng-Danquah et al., 2017; Shahriari et al., 2018; Bocianowski et al., 2019, Koundinya et al., 2019). In this study, we have shown how genotypic stability can be quantified in the MET analysis using WAASB (Eq. [4]), which may be seen as a mixed model version of the ASV. In addition, different effects (environment as random or a random model) may be used for WAASB estimation as shown in Fig. 5.

In our study, two were the IPCA used for WAASB estimation; thus, the ranks for GY, AUDPC, and IGY obtained with the ASV and WAASB were highly and positively correlated (Supplementary Table S7). The extent to which the MET and the complexity of the GEI increase, the GEI pattern in AMMI analysis is retained in a larger number of IPCAs, tending to be captured in the last IPCAs. This results in a lower percentage of GEI explained in the first two IPCAs [(60-69% (Veenstra et al., 2019), 65.7% (Bocianowski et al., 2019) and 68% (Liang et al., 2015)], and may, for example, compromise the interpretation of the ASV. Thus, the WAASB index may be promising for quantifying genotypic stability in future studies.

Simultaneous selection for performance and stability

Successful selection of high-performance and stable varieties is fundamental to breeding programs. Non-parametric methods have been proposed (Kang, 1988; Lin and Binns, 1988) and used for this purpose, but no method developed so far in the context of mixed models has been universally adopted. More recently, the genotype stability index (GSI) proposed by Farshadfar, (2008) has been used in the simultaneous selection for MPE in AMMI analysis (Adjebeng-Danquah et al., 2017; Bocianowski et al., 2019). Due to the increasing use of this index, a brief comparison with the WAASBY index is presented.

Briefly, the GSI is computed by summation of the ranks for ASV (rASV) and response variable (rY), GSI = rASV + rY. Lower GSI values are desirable. Although it is an index of easy

interpretation, its ambiguity can lead to misunderstandings in genotype selection/recommendation. Let us consider two brief examples to make this concept a bit clearer.

The first example concerns the IGY of genotypes G4, G12, G19 and G22. The same value of GSI (36) was observed for these genotypes (Supplementary Table S8). These same genotypes were in quadrant I of Fig. 3c, characterizing them as poorly productive and highly unstable. Many researchers may not realize, but GSI = 36 may be the result of, for example, 36 = 14 + 22 or 36 = 22 + 14. In other words, genotypes with distinct patterns for MPE are assumed to be similar. Thus, we should keep in mind that the recommendation of a stable (but low-performance) genotype is completely different from the recommendation of a genotype that performs well in one environment but not in others. In the latter, the recommendation for specific environments should be explored. Considering the WAASBY index, the ranking of these genotypes ranged from 17º (G19) to 22º (G22), which is mainly explained by the difference in IGY of that genotypes (Fig 3c).

The second example still remains concerning the IGY, but now of the G16. According to the GSI, the G16 would be the ninth-ranked (Supplementary Table S8). This genotype showed the third largest value of WAASB (in other words, the third less stable) but ranked second for the WAASBY index. Why? There are two main reasons for this: The first is clearly the highest IGY of G16 (Fig. 3c). The second one is the highest weight assigned to the response variable (in our case 65%). It should be noted that this genotype was selected by the MTSI because it presented GY above the grand mean, AUDPC below the grand mean (Fig. 4) and performed well for important traits such as TWG, GW, CW and NG2 (Supplementary Fig. S3).

We have shown here how the simultaneous selection for MPE considering an LMM may be performed using the WAASBY index. Compared with already used indexes, the WAASBY is not ambiguous and weights can be used when the selection of genotypes should prioritize the mean performance over the stability or vice versa. In future studies, these weights should be chosen according to the purpose of the selection. In addition, there would seem to be value in an

investigation to compare the WAASBY index with already and widely used simultaneous selection indexes.

The theoretical basis and applicability of the MTSI index

Ideotyping procedure

It was shown that in the context of simultaneous selection for MPE considering several variables, the ideotype is assumed to have the maximum value of WAASBY (100) in all variables. In future studies, it will be up to the researcher to define the values of *nma* and *nmi* for rescaling the variables, as well as the weights for MPE. Let us, for the moment, consider a brief hypothetical example. Suppose that data on three traits, namely grain yield (GY), lodging (LOD) and crude protein content (CP) were evaluated in several oat genotypes (GEN) conducted in a set of environments (ENV) considering a randomized complete block design with three replicates (REP). The aim is selecting genotypes with high GY and CP content with good lodging resistance. It is assumed equal weights for MPE for the traits GY and CP. Due to the several problems caused by LOD, the researcher wants to prioritize those genotypes with lower LOD in detriment of the stable ones, say, assigning a weight of 70% to the mean response of this variable. Assuming that a data frame called "oat" containing the following columns ENV, GEN, REP, GY, CP, and LOD was properly loaded in R environment, the parameters to be used in the "WAASB ()" function assuming genotype as the random effect would be then:

```
model_oat = WAASB(data = oat,
                  resp = c(GY, CP,  LOD),
                  gen = GEN,
                  env = ENV,
                  rep = REP,
                  wresp = c(50, 50, 70),
                  mresp = c(100, 100, 0))
```

Accounting for the correlation structure

The hypothesis is that in a multi-trait framework, the WAASBY values may be related in some way due to an underlying correlation structure that is unknown beforehand. Thus, the EFA

was used to account for this correlation structure. Using the EFA, it was possible to determine how many factors exist −in other words, in how many latent variables the original set of variables could be reduced−, the relationship between the factors and how the variables were associated with these factors (Ullman, 2006). Finally, the estimation of final factor scores allowed dealing with the multicollinearity, a systemic issue in multivariate analyses (Olivoto et al., 2017), incorporating in the new first latent variables the original structure of the data, thus leading to dimensional reduction.

The genotype-ideotype distance as a selection criterion

The MTSI (Fig. 2) allowed a unique and easy-to-interpret selection process. In addition, the MTSI was found to have many practical applications by breeders and agronomists who aims the simultaneous selection for MPE when data of several traits are available. For example, it could have been useful for already published studies that evaluated the stability and mean performance of genotypes considering several traits [e.g., Koundinya et al., (2019), six traits evaluated in *Solanum melongena* genotypes; Nduwumuremyi et al. (2017), nine traits evaluated in *Manihot esculenta* genotypes; and Bocianowski et al. (2019), five traits evaluated in *Brassica* spp. lines].

A step-by-step guide for future studies

In the near future, methods for GEI analysis in MET will rely less on linear-bilinear models and more on mixed-effect models (van Eeuwijk et al., 2016). This is mainly due to the higher predictive ability of BLUP, which often outperforms known models such as AMMI (Piepho, 1994), and the rapid dissemination of statistical packages that include specialized routines for mixed-effect model procedures. In this context, the use of MTSI should become broad. To assist with easy and correct implementation of the MTSI in future studies we provide a workflow (Fig. 5) suggesting the steps to be followed in the context of both mixed- and fixed-effect models. The thicker line represents the steps we followed in this study. Note that depending upon the nature of the model the

first step is to choose the proper function. If more than one trait is assessed in the experiment, the MTSI may be computed, considering the stability only, or the selection based on mean performance and stability. The R codes provided in the supplementary material S1 may be used and adapted for specific cases.

CONCLUSIONS

In this study, we introduced the theoretical foundations of a multi-trait stability index (MTSI) for selecting high-performance and stable genotypes in multi-environment trials (MET) based on multiple traits considering both a fixed- or mixed-effect model framework. The MTSI is based on the genotype-ideotype distance estimated with scores of factor analysis. The application of the MTSI was demonstrated using real data from 14 traits assessed in a MET with 22 oat genotypes. The MTSI allowed the selection of stable genotypes, with positive selection differentials for traits that wanted to increase and negative selection differential for one trait that wanted to decrease. This suggests that the MTSI should be useful for breeders and agronomists who aim at the simultaneous selection for mean performance and stability considering several traits since it provides a unique selection process that is easy-to-interpret and considers the correlation structure among the traits. Finally, the application of the MTSI in future studies is facilitated by a step-by-step guide (Fig. 5) and the introduction of an R package containing all the required functions.

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Figure captions

Note: Please, ensure that all figures have one-column fit.

Fig.1. Proportion of the phenotypic variance for fourteen oat traits evaluated during three cultivation years.

Fig.2. Genotype ranking and selected genotypes for the multi-trait stability index considering a selection intensity of 15%.

Fig. 3. Joint interpretation for mean performance and stability for grain yield (a), area under the disease progress curve (b) and industrial grain yield (c). In the online version of the manuscript, environments are depicted by dark green squares and selected genotypes by blue circles.

Fig. 4. Observed values for grain yield, area under the disease progress curve, and industrial grain yield of 22 oat cultivars evaluated during three cultivation years. Horizontal solid lines represent the grand mean whereas dashed lines represent the mean of the selected genotypes. Bars represents means$\pm$SE with $n = 9$.

Fig. 5. Suggested workflow for simultaneous selection for mean performance and stability in the analysis of multi-environment trials. The thicker line represents the steps that were followed in this article. The first option is choosing between fixed- and mixed-effect models. If more than one variable is available, the multi-trait stability index (MTSI) may be estimated. Shaded areas represent the functions/arguments that should be set to achieve the outputs, which are depicted by olive green rectangles in the online version of the manuscript.

Table 1. Eigenvalues, explained variance, factorial loadings after varimax rotation and communalities obtained in the factor analysis.

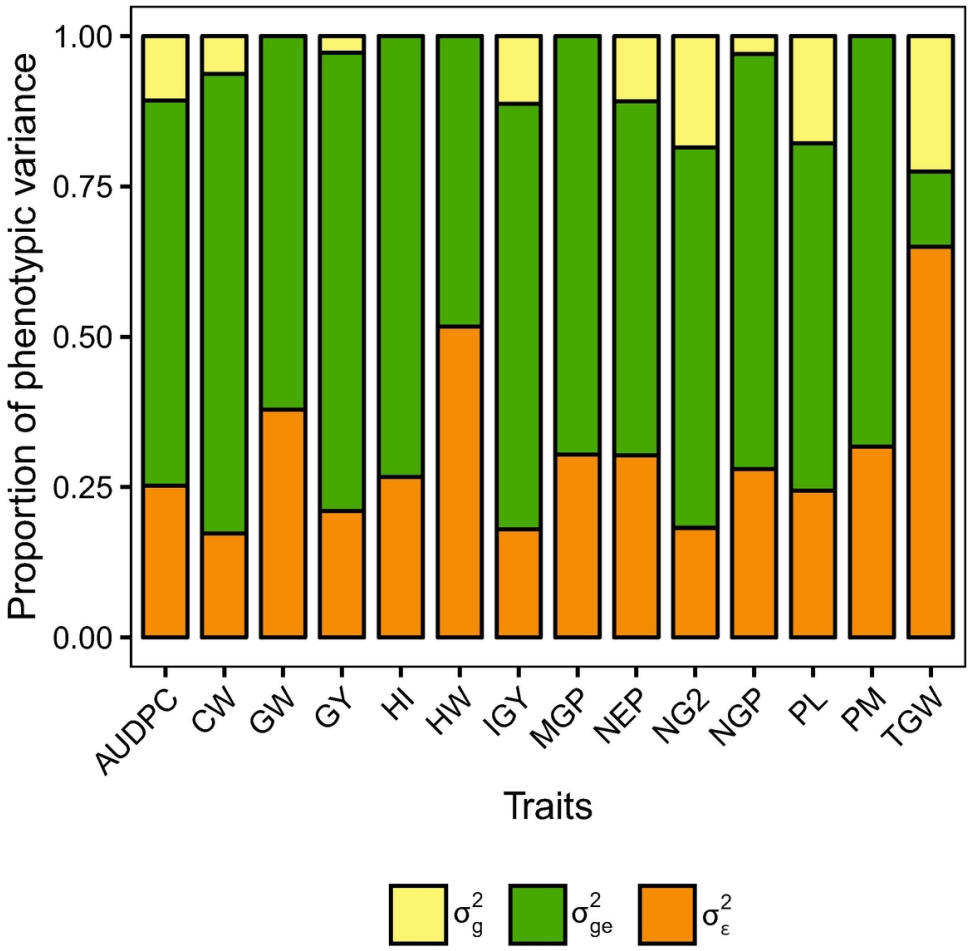
Trait†	FA1‡	FA2	FA3	FA4	FA5	*h*§
GY	−0.162	−0.332	−0.009	−0.138	**0.878**	0.926
TGW	−0.212	**−0.630**	−0.270	−0.010	0.194	0.553
HW	0.091	**−0.777**	0.247	0.145	0.207	0.736
PL	0.453	−0.124	0.197	−0.096	**−0.595**	0.623
PM	**0.948**¶	−0.039	0.000	0.177	−0.069	0.936
NEP	**0.901**	0.128	0.145	0.021	−0.260	0.918
NGP	**0.936**	0.139	0.107	0.064	−0.082	0.917
GWP	**0.945**	−0.019	0.021	0.203	−0.130	0.952
AUDPC	−0.132	0.145	−0.332	−0.489	**0.522**	0.660
NG2	−0.029	−0.110	**−0.955**	0.084	−0.021	0.933
GW	−0.027	**−0.835**	−0.165	−0.209	−0.164	0.796
CW	−0.077	−0.592	−0.123	**−0.745**	−0.104	0.938
HI	−0.212	0.024	0.015	**−0.868**	0.126	0.815
IGY	−0.180	−0.065	**−0.839**	−0.292	0.321	0.929
Eigenvalues††	5.03	2.37	1.73	1.34	1.16	−
Variance††	35.95	16.90	12.35	9.56	8.32	−
Accumulated (%)††	35.95	52.85	65.20	74.77	83.09	−

† See in material and methods section the complete description of the traits.
‡ FA, Factor retained
§ *h*, Communality
¶ Bold values indicate the variables grouped within each factor.
†† The values for all factors are in Supplementary table S3.

Table 2. Selection differential of the WAASBY index for fourteen oat traits.

Factor	Trait†	Xo‡	Xs§	SD¶	SD (%)
FA1	PM	59.46	74.89	15.44	25.96
	NEP	55.10	65.61	10.51	19.08
	NGP	64.46	77.48	13.02	20.20
	GWP	59.88	74.00	14.12	23.58
FA2	TGW	56.93	70.18	13.25	23.27
	HW	55.03	61.12	6.08	11.05
	GW	57.49	72.87	15.38	26.75
FA3	NG2	58.66	77.14	18.48	31.50
	IGY	47.80	64.30	16.49	34.50
FA4	CW	44.54	64.43	19.89	44.66
	HI	51.64	68.15	16.51	31.97
FA5	GY	49.53	54.33	4.80	9.68
	PL	51.22	59.69	8.47	16.53
	AUDPC	57.45	76.28	18.83	32.77
Mean	-	54.94	68.61	13.66	25.11

† See in material and methods section the complete description of the traits.
‡ Xo, Mean for WAASBY index of the original population
§ Xs, Mean for WAASBY index of the selected genotypes (G01, G15 and G16).
¶ SD, selection differential



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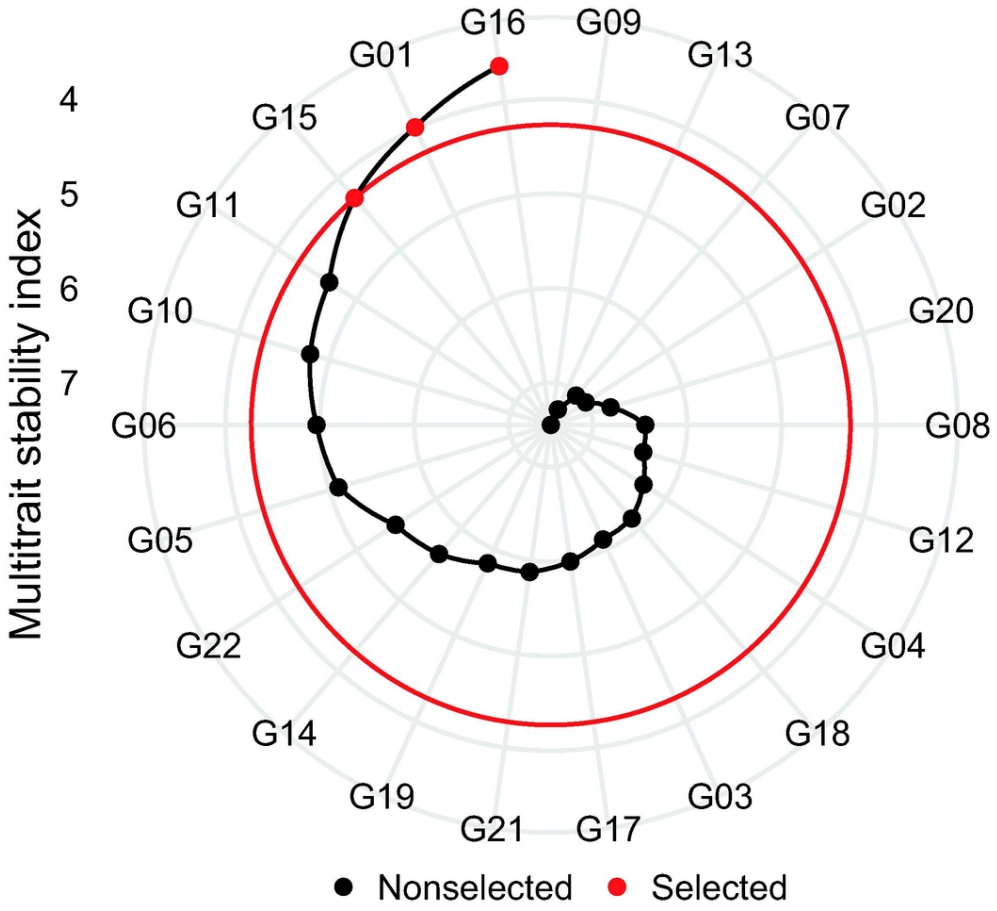

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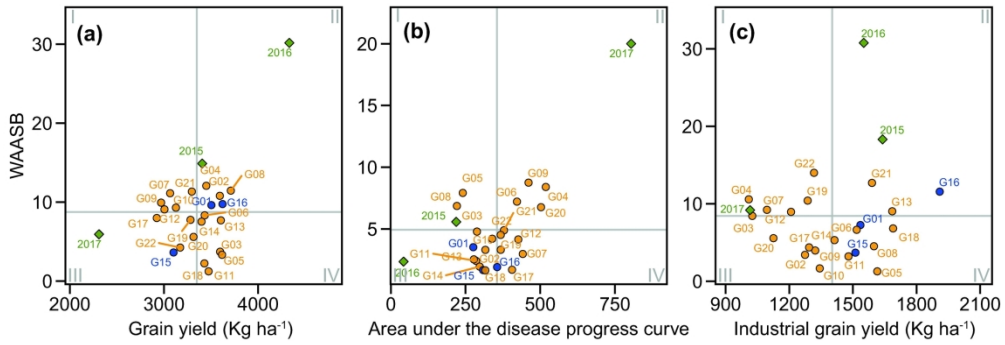

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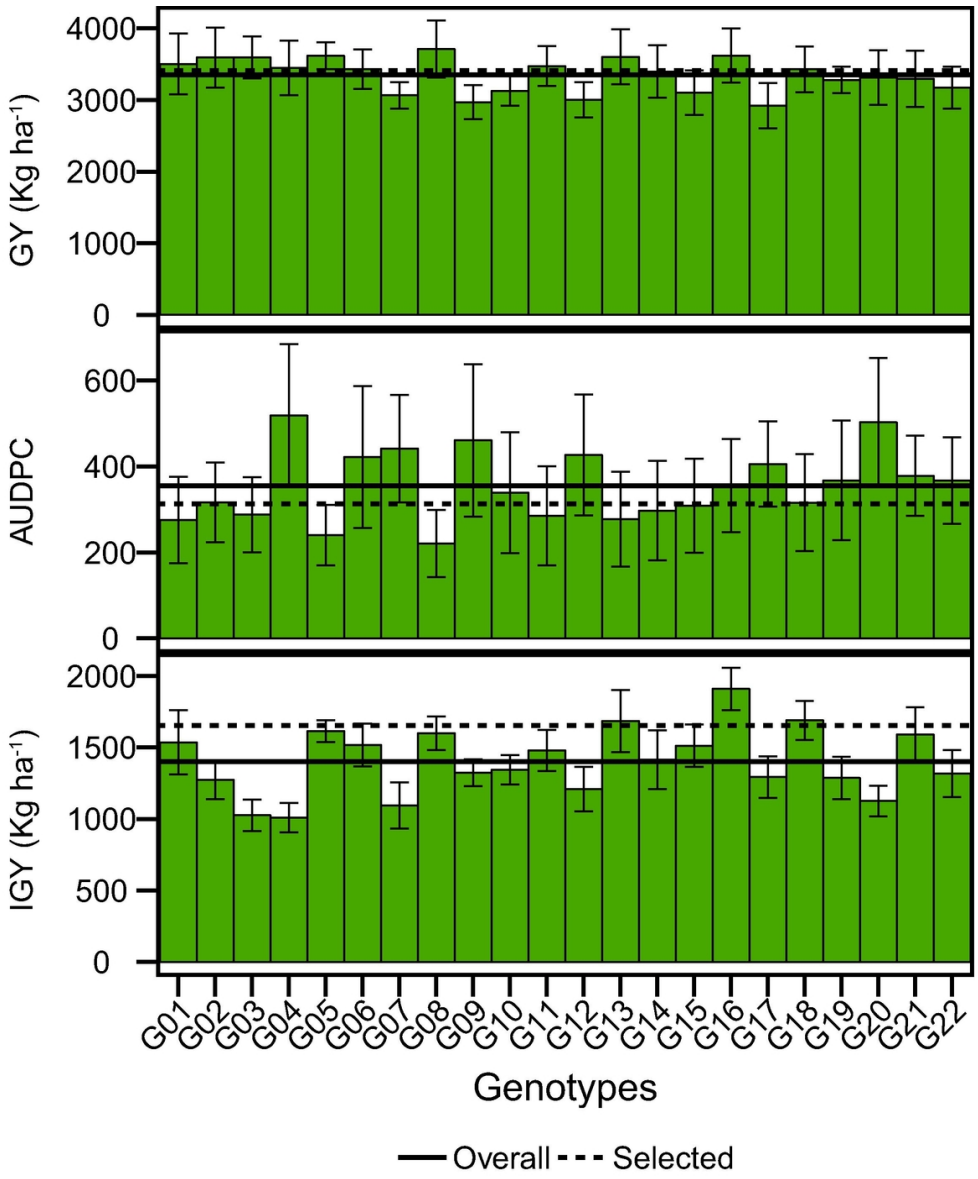
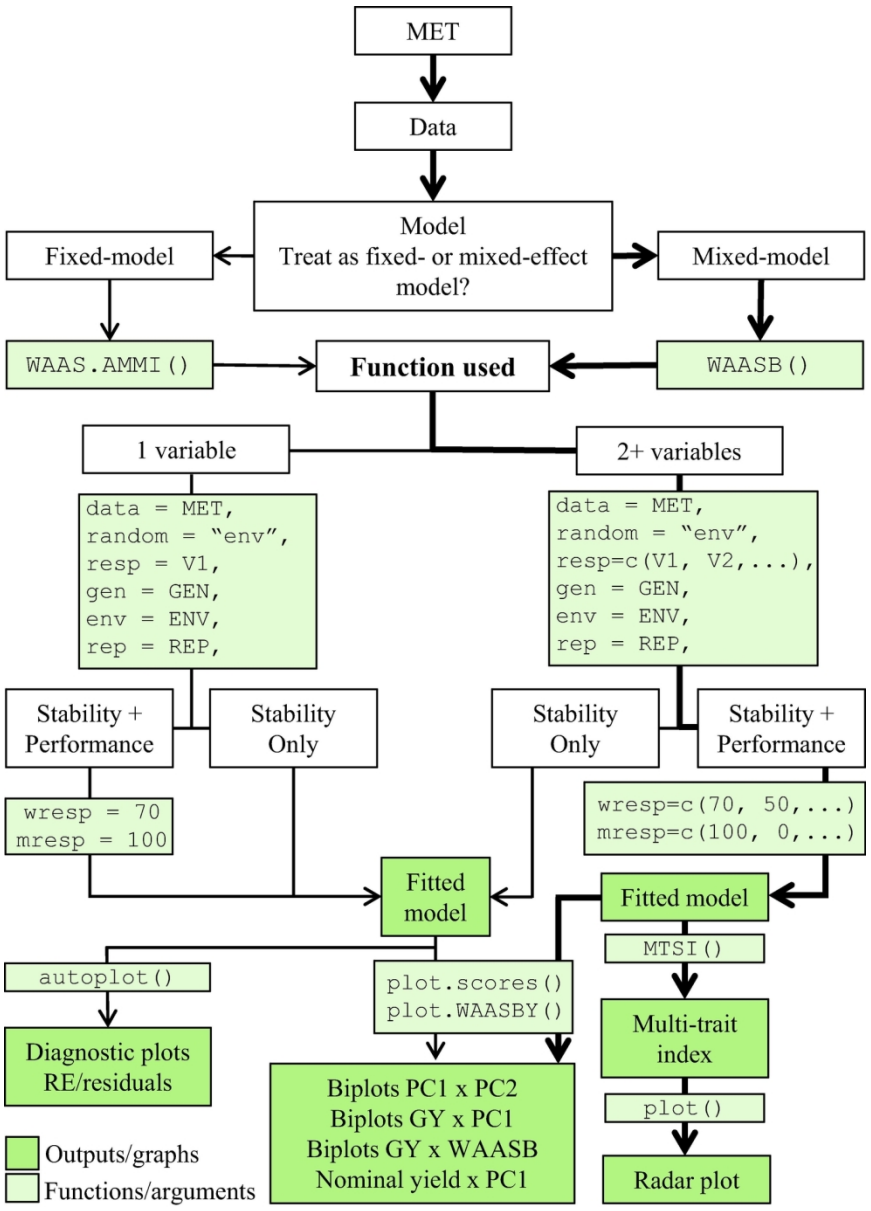


99x121mm (300 x 300 DPI)



132x183mm (300 x 300 DPI)

Mean performance and stability in multi-environment trials II:

Selection based on multiple traits

Contents

This is the supplemental material for the article **Mean performance and stability in multi-environment trials II: Selection based on multiple traits**. In this material, we will present some functions from the `METAAB` (**M**ulti-Environment **T**rials **A**nalysis using **A**MMI and **B**LUP) R package that were used to compute the **M**ul**T**i-trait **S**tability **I**ndex (MTSI)

1 Supplemental R codes

1.1 Loading/installing the METAAB R package

All the functions used in the current paper are available in the `METAAB` R package. The leatest development version may be obtained from the GitHub Repository by running the following code. For a complete descrition of the `METAAB` package, please, visit its site

```
if (!require("devtools")) install.packages("devtools")
devtools::install_github("TiagoOlivoto/METAAB")
library(METAAB)
```

For reasons of confidentiality, the dataset was not made available. Only the structure of such data is shown.

```
str(mtsi_data)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    198 obs. of  18 variables:
##  $ YR   : Factor w/ 3 levels "2015","2016",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ GEN  : Factor w/ 22 levels "G01","G02","G03",..: 1 1 1 2 2 2 3 3 3 4 ...
##  $ NAME : Factor w/ 22 levels "Barbarasul","Brisasul",..: 1 1 1 2 2 2 3 3 3 4 ...
##  $ REP  : Factor w/ 3 levels "1","2","3": 1 2 3 1 2 3 1 2 3 1 ...
##  $ GY   : num  3572 3824 3820 3768 3692 ...
##  $ TGW  : num  32.7 30 34 30.3 32 33 29 33 33 30 ...
##  $ HW   : num  54 52 53 53 55 ...
##  $ PL   : num  22.9 23.9 21.9 16.2 16.8 ...
##  $ PM   : num  3.28 3.48 3.08 1.7 2.26 ...
##  $ NEP  : num  53.2 55.9 50.5 28.4 35 ...
##  $ NGP  : num  98.4 104.4 92.4 62 75.1 ...
##  $ GWP  : num  2.98 3.14 2.82 1.52 2.06 ...
##  $ AUDPC: num  111 144 108 197 142 ...
##  $ NG2  : num  64 55 75 64 55 65 44 57 50 52 ...
##  $ GW   : num  2.05 2.28 1.82 1.67 1.9 ...
##  $ CW   : num  1.67 1.96 1.38 1.23 1.52 ...
##  $ HI   : num  0.813 0.858 0.756 0.74 0.803 ...
##  $ IGY  : num  1859 1805 2167 1785 1631 ...
```

1.2 Estimating the WAASBY index

The stability in this paper was quantified by the *WAASB* index, acronym for **W**eighted **A**verage of **A**bsolute **S**cores from the singular value decomposition of the matrix of **B**LUPs for the genotype-vs-environment interaction (*gei*) effects generated by an linear mixed-effect model (LMM). The `WAASB()` function provide options for computing the *WAASB* considering an LMM with random effects for (i) genotype (g) effects; (ii) environment (e) effects; or (iii) a completly random-effect model. The *WAASB* is computed as follows:

$$WAASB_i = \sum_{k=1}^{p} |IPCA_{ik} \times EP_k| / \sum_{k=1}^{p} EP_k$$

where $WAASB_i$ is the weighted average of absolute scores of the ith genotype; $IPCA_{ik}$ is the scores of the ith genotype in the kth IPCA; and EP_k is the explained variance of the kth PCA for $k = 1, 2, .., p$, $p = min(g - 1; e - 1)$.

The simultaneous selection for performance and stability was performed using the *WAASBY*. This index considers both stability (*WAASB*) and performance (dependent variable, Y) for genotype ranking considering the following model:

$$WAASBY_i = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S}$$

where $WAASBY_i$ is the simultaneous selection index for the i-th genotype that weights between performance and stability; rY_i and rW_i are the rescaled values (0-100) for dependent variable and WAASB, respectively; θ_Y and θ_S are the weights for dependent variable and WAASB, respectively. Rescaled values are used to make *WAASB* and Y directly comparable. The maximum and minimum values for rescaling the dependent variable will depend upon the goal of the selection. For example, assuming that the highest value for the dependent variable is better, say, for grain yield, the genotype with the highest mean will have $rY_i = 100$ after rescaling. On the other hand, if the lowest value is better, say, for lodging, the genotype with the lowest mean will have $rY_i = 100$ after rescaling. The genotype with the lowest *WAASB* will then have $rW_i = 100$

The codes in 1.3.1 and 1.3.2 compute the *WAASBY* index and return the values into an object of class *WAASB*, which is a list. The first argument of the function is the data. The argument `random` is used to indicate the random effect in the model. In our example, `random = "gen"`, means that genotype effects and genotype-vs-environment effects, are assumed to be random. The argument `resp` is the response(s) variable(s) that will be analyzed. Several variables may be analyzed in a single running by using `c(var1, var2, ...)`. The arguments `gen`, `env`, and `rep` are the columns of the dataset that contains the levels for genotype, environment and block effects, respectively. The argument `wresp` is a vector with the same length of `resp` that contains the weight for the response variable. In our example, we attributed the weight of 65 for response variable. Internally, the weight for *WAASB* is computed as `100 - wresp`. The argument `mresp` is a vector with the same length of `resp` that contains the values for rescaling the response variable. Allowed values are 100 or 0. In our example, all traits except AUDPC have $rY_i = 100$. This means that the genotype with the highest mean will have 100 after rescaling and the genotype with the lowest mean will have 0 after rescaling.

```
model = WAASB(mtsi_data,
                  random = "gen",
                  resp = c(GY,   TGW,    HW, PL, PM, NEP,    NGP,
                           GWP,  AUDPC,  NG2,    GW, CW, HI, IGY),
                  gen = GEN,
                  env = YR,
                  rep = REP,
                  wresp = rep(65, 14),
                  mresp = c(100, 100, 100, 100, 100, 100, 100,
                            100, 0, 100, 100, 100, 100, 100))
```

```
## Evaluating variable GY 7.1 %
## Evaluating variable TGW 14.3 %
## Evaluating variable HW 21.4 %
## Evaluating variable PL 28.6 %
## Evaluating variable PM 35.7 %
## Evaluating variable NEP 42.9 %
## Evaluating variable NGP 50 %
## Evaluating variable GWP 57.1 %
```

```
## Evaluating variable AUDPC 64.3 %
## Evaluating variable NG2 71.4 %
## Evaluating variable GW 78.6 %
## Evaluating variable CW 85.7 %
## Evaluating variable HI 92.9 %
## Evaluating variable IGY 100 %
## ------------------------------------------------------------
## Variables with nonsignificant GxE interaction
## TGW
## ------------------------------------------------------------
## Done!
```

After fitting, the models may be summarized using the function `summary()`

1.3 Multi-trait index based on factor analysis

The function `MTSI()` is used to compute the multi-trait stability index (*MTSI*). The first argument is a model of the class `WAASB` or `WAAS.AMMI`. It is possible to compute the *MTSI* for both *WAASB* -stability only- and *WAASBY* -simultaneous selection for stability and performance. If `show = T`, some results are shown in the console. The argument `SI` is the selection intensity, in percentage. The last argument is the minimum value so that an eigenvalue is retained.

```
options(digits = 3)
index = MTSI(model, index = "WAASBY", show = T, SI = 15, mineval = 1)
```

```
##
## ------------------------------------------------------------------------------
## Principal Component Analysis
## ------------------------------------------------------------------------------
##      Eigenvalues Variance (%) Cum. variance (%)
## PC1      5.03316      35.9511              36.0
## PC2      2.36564      16.8974              52.8
## PC3      1.72958      12.3542              65.2
## PC4      1.33880       9.5629              74.8
## PC5      1.16482       8.3201              83.1
## PC6      0.82364       5.8831              89.0
## PC7      0.65619       4.6870              93.7
## PC8      0.44715       3.1939              96.8
## PC9      0.18142       1.2958              98.1
## PC10     0.15757       1.1255              99.3
## PC11     0.05527       0.3948              99.7
## PC12     0.02365       0.1689              99.8
## PC13     0.02037       0.1455             100.0
```

```
## PC14     0.00276       0.0197             100.0
##
## ---------------------------------------------------------------------------
## Factor Analysis - factorial loadings after rotation-
## ---------------------------------------------------------------------------
##           FA1     FA2       FA3     FA4     FA5 Communality Uniquenesses
## GY    -0.1616 -0.3319 -0.008579 -0.1377  0.8778       0.926       0.0741
## TGW   -0.2124 -0.6299 -0.270223 -0.0102  0.1941       0.553       0.4473
## HW     0.0914 -0.7766  0.247366  0.1445  0.2068       0.736       0.2637
## PL     0.4528 -0.1240  0.196844 -0.0958 -0.5953       0.623       0.3772
## PM     0.9478 -0.0387  0.000431  0.1769 -0.0686       0.936       0.0641
## NEP    0.9012  0.1283  0.144668  0.0206 -0.2603       0.918       0.0823
## NGP    0.9357  0.1395  0.107345  0.0636 -0.0818       0.917       0.0827
## GWP    0.9450 -0.0188  0.021219  0.2031 -0.1298       0.952       0.0480
## AUDPC -0.1323  0.1449 -0.331935 -0.4889  0.5222       0.660       0.3396
## NG2   -0.0292 -0.1101 -0.955433  0.0844 -0.0210       0.933       0.0666
## GW    -0.0275 -0.8350 -0.165392 -0.2093 -0.1640       0.796       0.2040
## CW    -0.0767 -0.5925 -0.122973 -0.7452 -0.1036       0.938       0.0619
## HI    -0.2124  0.0240  0.015306 -0.8676  0.1258       0.814       0.1855
## IGY   -0.1796 -0.0651 -0.839223 -0.2923  0.3208       0.929       0.0709
##
## ---------------------------------------------------------------------------
## Comunalit Mean: 0.831
##
## ---------------------------------------------------------------------------
## Multitrait stability index
## ---------------------------------------------------------------------------
##  G16  G01  G15  G11  G10  G06  G05  G22  G14  G19  G21  G17  G03  G18  G04
## 3.61 3.99 4.27 4.66 4.79 4.96 5.10 5.49 5.64 5.84 5.87 5.99 6.11 6.13 6.28
##  G12  G08  G20  G02  G07  G13  G09
## 6.42 6.44 6.79 7.00 7.04 7.27 7.44
##
## ---------------------------------------------------------------------------
## Selection differential for WAASBY index
## ---------------------------------------------------------------------------
##       Factor   Xo   Xs    SD SDperc
## PM       FA1 59.5 74.9 15.44  25.96
## NEP      FA1 55.1 65.6 10.51  19.08
## NGP      FA1 64.5 77.5 13.02  20.20
## GWP      FA1 59.9 74.0 14.12  23.58
## TGW      FA2 56.9 70.2 13.25  23.27
## HW       FA2 55.0 61.1  6.08  11.05
## GW       FA2 57.5 72.9 15.38  26.75
## NG2      FA3 58.7 77.1 18.48  31.50
## IGY      FA3 47.8 64.3 16.49  34.50
```

```
## CW       FA4 44.5 64.4 19.89  44.66
## HI       FA4 51.6 68.1 16.51  31.97
## GY       FA5 49.5 54.3  4.79   9.68
## PL       FA5 51.2 59.7  8.47  16.53
## AUDPC    FA5 57.5 76.3 18.83  32.77
##
## ---------------------------------------------------------------------------
## Mean of selection differential
## ---------------------------------------------------------------------------
##     Xo     Xs     SD SDperc
##   54.9   68.6   13.7   25.1
##
## ---------------------------------------------------------------------------
## Selected genotypes
## G16 G01 G15
## ---------------------------------------------------------------------------
```

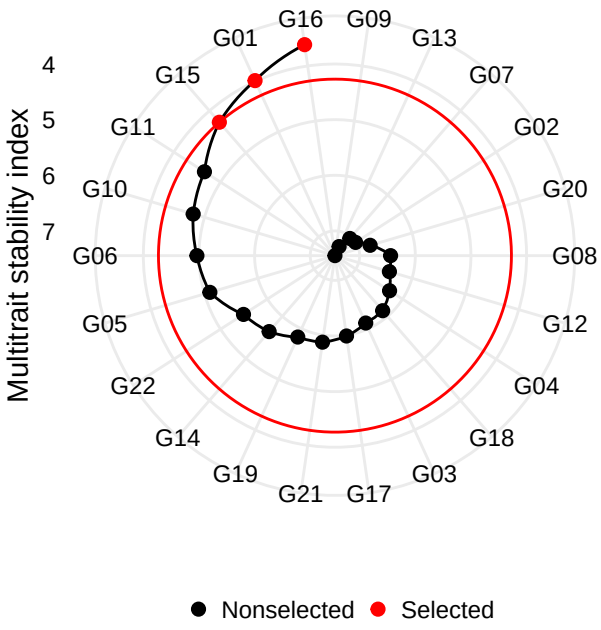
1.4 Plotting the MTSI index

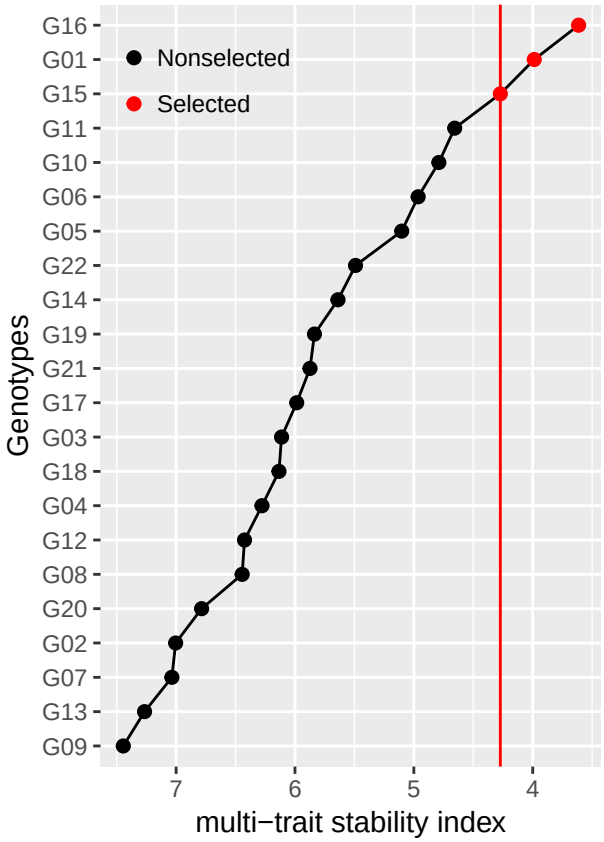
It is possible to use `plot(model)` to obtain ggplot-based plots for the *MTSI* index. Some examples are given below, and due to the "grammar" of the ggplot2 graphics, completely personalized plots may be obtained.

```
p1 = plot(index, SI = 15)
p2 = plot(index, SI = 15, radar = FALSE) +
  coord_flip() +
  theme_gray() +
  labs(x = "Genotypes", y = "multi-trait stability index") +
  theme(legend.position = c(0.2, 0.9),
        legend.background =  element_blank(),
        legend.key = element_blank(),
        legend.title = element_blank())

plot_grid(p1, p2, ncol = 2)
```

2 Supplemental tables





2 Supplemental tables

Table S 1: Code, commercial names, pedigree and release year of the oat cultivars used in the study.

Code	Commercial name	Pedigree	Release year	Reference
G01	Barbarasul	UPF 18 / CFT5	2007	NA
G02	Brisasul	OR 2 / UPF 18	2007	(Oliveira et al., 2011)
G03	FAEM 006	NA	NA	NA
G04	FAEM 007	NA	NA	NA
G05	FAEM Carlasul	UFRGS 10 / 90 SAT -285	2011	(Oliveira et al., 2012a)
G06	FAEM Chiarasul	UFRGS 17 / UFRGS 10 // 90 SAT -28	2011	(Oliveira et al., 2012b)
G07	IPR Afrodite	CFT 2 / ER 88144-1	2012	(Riede et al., 2015)
G08	UPFA Gaudéria	UPF 16 / CTC 5	2012	NA
G09	UPFA Ouro	UPF 16 / UFP 18	2012	NA
G10	UPFPS Farroupilha	UPF 18 / OR2	2015	NA
G11	URS 21	UFRGS 10 x CTC 84B993	2001	NA
G12	URS Altiva	UFRGS 995090-2 / URS 21	2015	(Nava et al., 2016)
G13	URS Brava	UFRGS 995078-2 / URS 21	2014	(Federizzi et al., 2015)
G14	URS Charrua	UFRGS 984126-1 / UFRGS 984109-7	2010	NA
G15	URS Corona	UFRGS 987016-1 / UFRGS 970497-1	2012	NA
G16	URS Estampa	UFRGS 995088-3 / UFRGS 006049	2012	NA
G17	URS Fapa Slava	UFRGS 984111-4 / UFRGS 988109-1	2011	NA
G18	URS Guará	UFRGS 987016-1 / UFRGS 970497-1	2012	NA
G19	URS Guria	UFRGS 987015-2 / UFRGS 960195-2	2010	NA
G20	URS Tarimba	UFRGS 987016-1 / UFRGS 19	2009	NA
G21	URS Taura	UFRGS 970216-2 / UFRGS 970461	2009	NA
G22	URS Torena	UFRGS 984111-4 / UFRGS 988109-1	2012	NA

Table S 2: Summary of the results for random- and fixed-effects of the 14 oat traits evaluated in the study.

Trait	LRTg†	LRTge	Vg‡	Vge	Vr	E-MS§	E/B-MS	Mean¶
GY	0.07ns	116.84***	5233.2238	142897.7308	39365.752	106.93***	16.51***	3349.29+-113.4
TGW	9.01**	3.51ns	1.0986	0.6082	3.162	41.7***	4.71***	30.82+-0.32
HW	0ns	39.02***	0.0000	2.4471	2.619	63.85***	2.21*	51.11+-0.45
PL	2.6ns	83.67***	0.8789	2.8507	1.204	4.56*	10.23***	20.65+-0.26
PM	0ns	78.01***	0.0000	0.3292	0.153	11.92***	8.67***	3.03+-0.09
NEP	1.09ns	70.41***	12.6405	68.4688	35.207	4.25*	8.23***	42.38+-1.23
NGP	0.08ns	86.42***	13.1860	303.0365	123.097	4.72*	8.02***	84.36+-2.47
MGP	0ns	82.5***	0.0000	0.2817	0.123	11.96***	8.35***	2.69+-0.08
AUDPC	0.98ns	88.5***	2074.5951	12394.1130	4892.520	194.49***	0.8ns	355.22+-43.2
NG2	2.56ns	113.02***	20.9537	71.4438	20.600	23.09***	86.67***	59.41+-1.5
GW	0ns	62.34***	0.0000	0.0295	0.018	3.82*	39.13***	1.86+-0.03
CW	0.31ns	134.09***	0.0025	0.0308	0.007	3.53*	156.98***	1.35+-0.03
HI	0ns	95.88***	0.0000	0.0050	0.002	0.06ns	28.34***	0.72+-0.01
IGY	0.97ns	123.67***	16822.5776	105242.2893	26769.302	15.28***	16.65***	1402+-55.63

Note:
* Significant at $P < 0.05$.
** Significant at $P < 0.01$.
*** Significant at $P < 0.001$.
ns, nonsignificant.

† LRTg and LRTge, Likelihood ratio tests for genotype and interaction gxe.
‡ Vg, Vge and Vr, variance components for genotype, interaction, and residuals, respectively.
§ E-MS and E/B-MS, mean squares for environment and and block-within-environment, respectively
¶ Mean, grand mean

Table S 3: Principal component analysis of the correlation matrix with the WAASBY values for 14 oat traits.

	Eigenvalues	Variance	Variance (%)
PC1	5.0332	35.9511	35.95
PC2	2.3656	16.8974	52.85
PC3	1.7296	12.3542	65.20
PC4	1.3388	9.5629	74.77
PC5	1.1648	8.3201	83.09
PC6	0.8236	5.8831	88.97
PC7	0.6562	4.6869	93.66
PC8	0.4472	3.1939	96.85
PC9	0.1814	1.2958	98.15
PC10	0.1576	1.1255	99.27
PC11	0.0553	0.3948	99.67
PC12	0.0236	0.1689	99.83
PC13	0.0204	0.1455	99.98
PC14	0.0028	0.0197	100.00

Table S 4: Scores for the 22 genotypes (G01-G22) and for the ideotype (ID) estimated in the first five factors. Bold values represent the selected genotypes.

	FA1	FA2	FA3	FA4	FA5	MTSI
G01	**5.71**	**-2.79**	**-2.270**	**-4.565**	**1.832**	**3.99**
G02	2.81	-1.33	-1.882	-3.385	2.055	7.00
G03	4.22	-3.60	-0.577	-2.468	2.505	6.11
G04	4.21	-4.43	0.279	-3.254	0.380	6.28
G05	3.38	-3.64	-2.820	-3.511	2.695	5.10
G06	4.76	-3.09	-3.264	-2.874	1.107	4.96
G07	4.49	-1.15	-1.163	-2.995	0.179	7.04
G08	4.97	-1.23	-2.797	-2.321	3.261	6.44
G09	3.48	-2.45	-3.477	-1.045	-0.138	7.44
G10	4.96	-3.26	-3.033	-3.545	0.032	4.79
G11	4.39	-3.38	-2.388	-3.557	2.556	4.66
G12	3.63	-2.43	-1.306	-3.613	-0.074	6.42
G13	1.55	-3.05	-2.580	-2.426	2.021	7.26
G14	4.26	-3.46	-2.939	-2.028	1.275	5.64
G15	**4.71**	**-3.50**	**-3.894**	**-3.619**	**1.034**	**4.27**
G16	**4.40**	**-4.90**	**-3.094**	**-4.158**	**1.360**	**3.61**
G17	3.77	-2.49	-2.631	-3.575	-0.272	5.99
G18	1.79	-3.76	-2.328	-4.387	1.360	6.13
G19	4.48	-2.42	-1.322	-3.076	1.746	5.84
G20	4.58	-4.56	-1.908	-0.344	1.414	6.79
G21	3.38	-3.54	-2.279	-2.663	1.018	5.87
G22	4.58	-3.34	-1.422	-2.707	1.826	5.49
ID1	7.00	-5.73	-3.949	-6.167	2.261	0.00

Table S 5: Relative contribution of each factor on the MTSI of each genotype. Bold values represent the selected genotypes.

	FA1	FA2	FA3	FA4	FA5
G01	**10.48**	**54.50**	**17.727**	**16.14**	**1.155**
G02	35.92	39.51	8.707	15.78	0.087
G03	20.63	12.16	30.431	36.62	0.159
G04	19.83	4.29	45.362	21.54	8.973
G05	50.54	16.75	4.894	27.09	0.725
G06	20.32	28.37	1.903	44.00	5.407
G07	12.79	42.45	15.681	20.33	8.754
G08	9.96	48.82	3.196	35.62	2.411
G09	22.43	19.45	0.402	47.34	10.380
G10	18.11	26.60	3.658	29.98	21.653
G11	31.55	25.39	11.236	31.43	0.402
G12	27.61	26.45	16.922	15.81	13.210
G13	56.25	13.57	3.554	26.52	0.109
G14	23.57	16.28	3.208	53.89	3.056
G15	**28.83**	**27.34**	**0.017**	**35.56**	**8.251**
G16	**51.96**	**5.33**	**5.603**	**30.89**	**6.213**
G17	29.21	29.29	4.849	18.75	17.905
G18	72.09	10.34	6.987	8.42	2.157
G19	18.72	32.18	20.270	28.05	0.777
G20	12.76	2.99	9.046	73.64	1.557
G21	37.97	13.88	8.083	35.58	4.478
G22	19.48	18.98	21.192	39.72	0.627

Table S 6: Selection differential for mean performance and stability (WAASB index).

	Mean performance			Stability (WAASB)		
Variable	Overhall	Selected	SD (%)	Overhall	Selected	SD (%)
HW	51.11	50.84	-0.54	0.642	0.233	-63.7
NEP	42.38	42.19	-0.45	1.525	0.565	-62.9
AUDPC	355.22	313.44	-11.76	5.281	2.365	-55.2
MGP	2.69	2.81	4.59	0.384	0.190	-50.4
NGP	84.36	87.60	3.84	2.226	1.130	-49.2
PM	3.03	3.21	6.08	0.400	0.211	-47.2
HI	0.72	0.76	5.02	0.116	0.063	-45.8
NG2	59.41	64.59	8.72	1.493	0.816	-45.3
TGW	30.82	31.57	2.46	0.341	0.217	-36.5
GW	1.86	1.95	4.65	0.201	0.139	-31.1
PL	20.65	21.53	4.24	0.661	0.563	-14.9
CW	1.35	1.48	10.13	0.200	0.172	-14.1
GY	3349.29	3408.95	1.78	8.900	7.671	-13.8
IGY	1402.00	1652.11	17.84	8.567	7.511	-12.3

Table S 7: Genotype ranking for GY, IGY, and AUDPC, for to the AMMI stability value (ASV) and the Weighted Average of Absolute Scores from the singular value decomposition of the matrix of BLUPs for the GEI effects (WAASB). Bold values represent the selected genotypes.

	GY		IGY		AUDPC	
Gen	ASV	WAASB	ASV	WAASB	ASV	WAASB
G1	**10**	**15**	**11**	**13**	**7**	**11**
G2	11	18	5	4	11	9
G3	1	5	7	14	16	15
G4	21	22	14	19	19	21
G5	16	3	3	1	21	20
G6	18	12	16	11	20	19
G7	12	19	17	17	6	8
G8	20	21	4	8	18	18
G9	8	17	9	6	22	22
G10	15	14	1	2	14	13
G11	4	1	6	3	5	6
G12	5	13	18	15	10	12
G13	17	9	10	16	1	7
G14	13	8	12	9	4	5
G15	**2**	**4**	**2**	**5**	**3**	**2**
G16	**14**	**16**	**19**	**20**	**8**	**4**
G17	7	11	8	7	9	3
G18	3	2	13	12	2	1
G19	19	10	20	18	12	10
G20	9	7	15	10	13	17
G21	22	20	21	21	17	16
G22	6	6	22	22	15	14

Table S 8: Genotype selection index (GSI) and genotype ranking for WAASBY index for the traits GY, IGY, and AUDPC. Bold values represent the selected genotypes.

	GY		IGY		AUDPC	
Gen	GSI	WAASBY	GSI	WAASBY	GSI	WAASBY
G1	**17**	**9**	**18**	**10**	**10**	**6**
G2	17	8	22	13	21	8
G3	6	2	28	21	22	9
G4	30	15	36	22	41	22
G5	19	1	7	1	23	11
G6	28	10	24	9	37	19
G7	31	20	37	20	25	17
G8	21	6	9	4	19	7
G9	29	22	22	12	42	21
G10	32	18	13	8	25	12
G11	12	3	16	6	10	2
G12	25	19	36	18	28	18
G13	21	5	13	7	5	1
G14	25	11	23	11	11	3
G15	**20**	**16**	**11**	**5**	**11**	**4**
G16	**16**	**7**	**20**	**2**	**20**	**10**
G17	29	21	23	14	25	14
G18	14	4	15	3	11	5
G19	34	14	36	17	26	13
G20	22	12	34	16	34	20
G21	36	17	27	15	32	16
G22	22	13	36	19	28	15

3 Supplemental figures

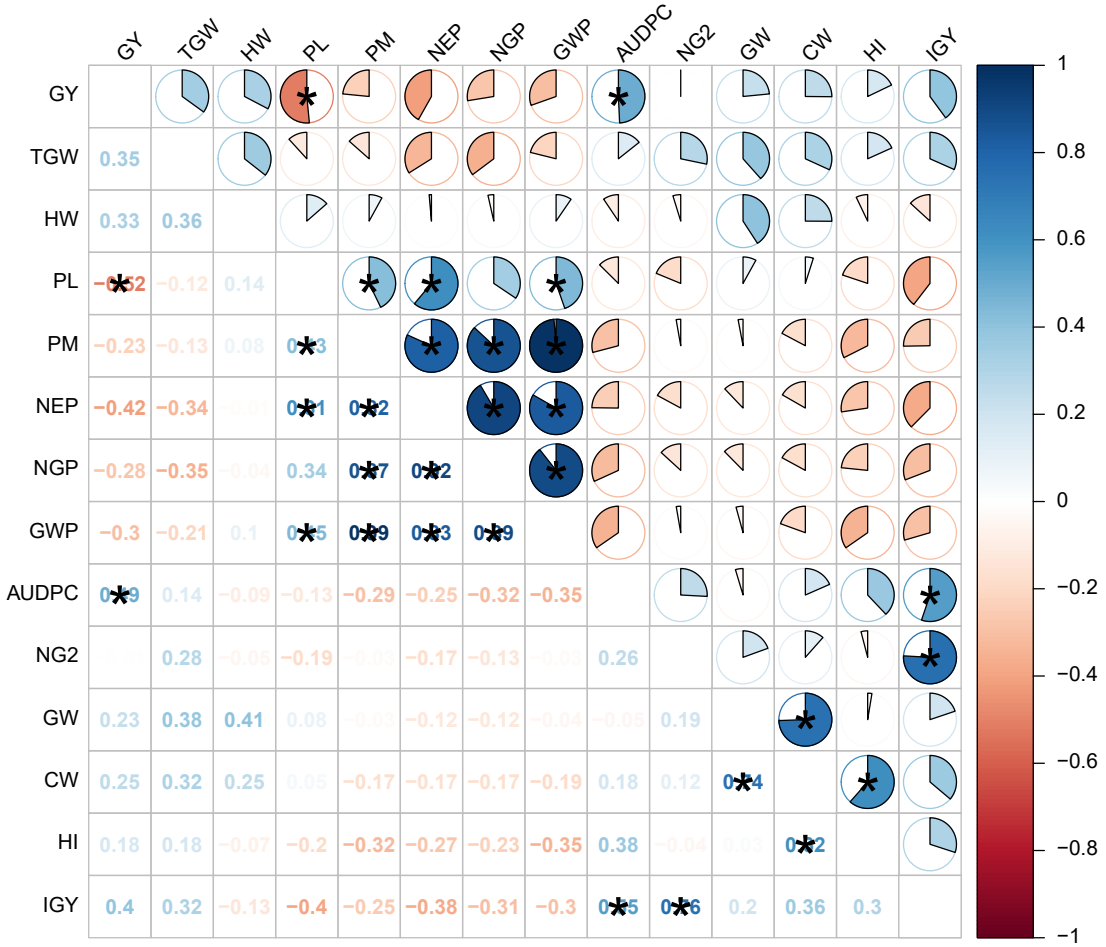


Figure S 1: Pearson correlation coefficient among the WAASBY index for 14 traits. Lower diagonal shows the correlation with fungicide whereas upper diagonal shows the ones without fungicide. Correlations with p-value < 0.05 are highlighted with an asterisk.

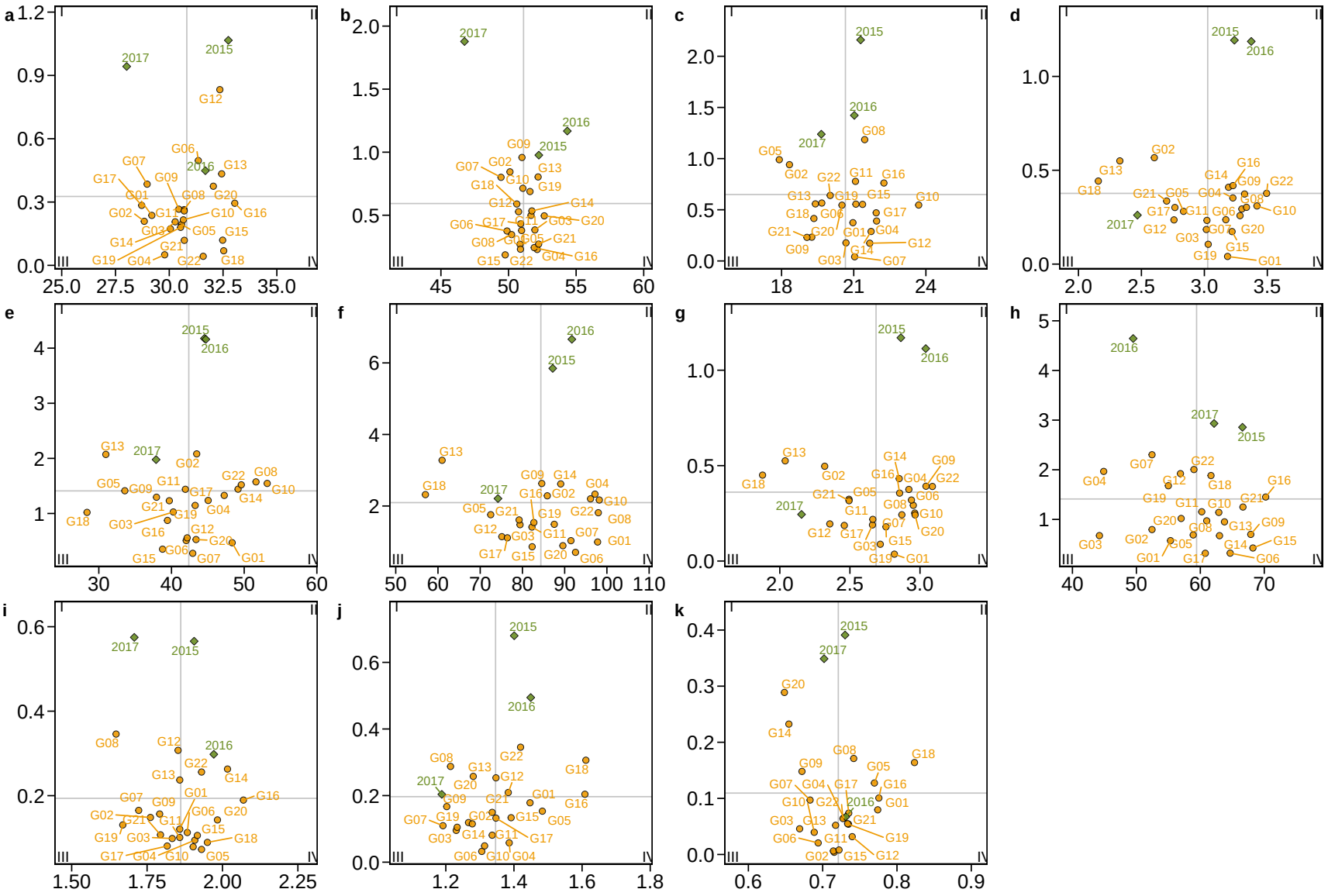


Figure S 2: Joint interpretation for mean performance and stability for thousand-grain weight (a), hectoliter mass (b), panicle length (c), and mass (c), number of spikelets per panicle (d), mass of grains per panicle (e) number of grains greater than 2mm (f) grain weight(g), cariopsis weight (h) and husking index (i).

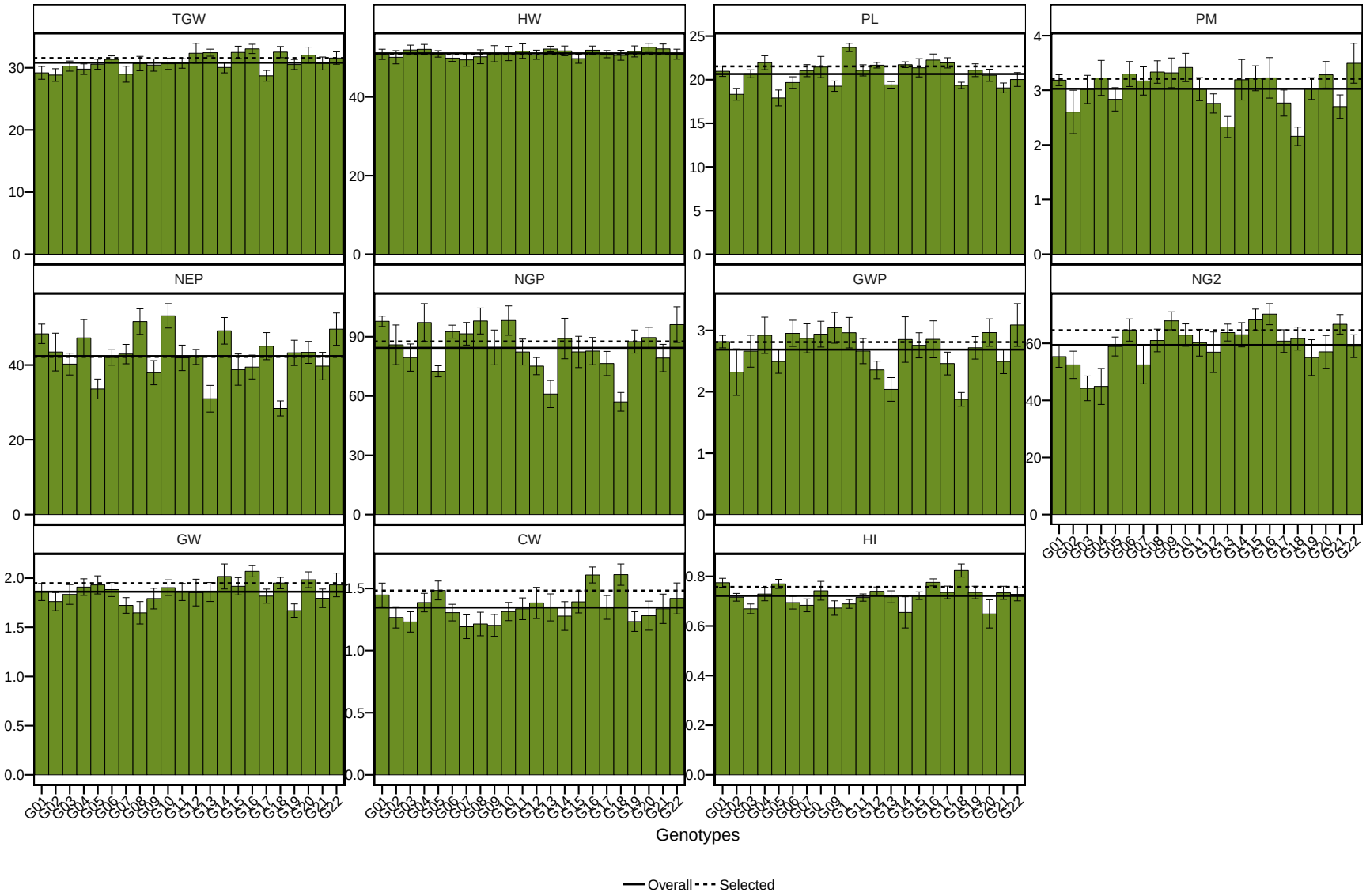


Figure S 3: Observed values for eleven oat traits. Horizontal solid lines represent the grand mean whereas dashed lines represent the mean of the selected genotypes in each fungicide use. Bars represents means±SE with n = 9.

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