

UTILIZATION OF THE MULTI-TRAIT GENOTYPE IDEOTYPE DISTANCE INDEX (MGIDI) FOR SELECTING MUTANT RICE GENOTYPES FOR DROUGHT STRESS TOLERANCE

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1. INTRODUCTION

Climate changes have caused the intensification of abiotic stresses, such as the scarcity of water. Additionally, the increased demand for food in the world resulting from constant population growth, and for fertile soils for the expansion of rice cultivation, altogether have been threatening food security (KUMAR et al., 2022). This scenario creates a demand for rice cultivars that are more productive and resilient to adverse conditions. The development of new cultivars depends on the presence of genetic variability, which can be created by induced mutations (SALGOTRA; CHAUHAN, 2023).

The idea behind ideotype design is to improve crop performance by focusing on the simultaneous selection of genotypes based on multiple traits. OLIVOTO; NARDINO (2021) state that applying MGIDI (Genotype-Ideotype Distance Index) results in significant genetic gains, marking a promising advance in the field of multivariate selection indices by evaluating the strengths and weaknesses of the tested genotype. This introduction sets the stage for a more detailed investigation of MGIDI and its potential to transform breeding strategies, considering complex interactions between traits and economic factors. The main objective of this work is to select mutant genotypes with higher potential for drought tolerance during the reproductive phase, using the MGIDI for multiple traits.

2. MATERIALS AND METHODS

The experiment was conducted during the 2022/2023 crop season at the experimental field of the Terra Baixas Station of Embrapa Temperate Climate in Capão do Leão, Rio Grande do Sul.

Ten mutant rice lines in the M₆ generation were evaluated, along with the cultivars BRS Pampeira, BRSGO Serra Dourada, and BRS Esmeralda. The mutants were derived from the original genotype BRS Pampeira, which was subjected to gamma radiation (⁶⁰Co) at doses of 250 and 300 Grays.

The experiment was implemented using a randomized block design with four replications. The seeding density used was 100 seeds per row. Soil water tension was monitored using tensiometers installed at a depth of 0.10 meters. Water stress was imposed from the beginning of the R₁ stage (Panicle Initiation) to R₉ (Harvest) (COUNCE et al., 2000) by suspending irrigation, resulting in soil tension reaching -100kPa. Fertilization was applied by broadcasting according to the recommendations of SOSBAI (2018).

Three measurements were taken for each replication for plant height and days to flowering, which corresponds to the time when approximately 50% of the

spikelets are flowering. Additionally, five random panicles from each replication were selected to assess panicle length and the number of fertile and sterile spikelets. The SPAD chlorophyll index (chlorophyll a + chlorophyll b) was measured 15 days after the stress and again 15 days after the stress period. Chlorophyll index readings were taken using a ClorofiLOG chlorophyll meter, model CFL 1030.

The data were analyzed using principal component analysis with the R statistical software, version 4.3.0. MGIDI analysis was performed using the distance index to rank or select genotypes based on multiple traits. The *Metan* package (OLIVOTO; LÚCIO, 2020) was used. Firstly, the MGIDI was used to rescale the matrix X so that all the values had a 0-100 range.

$$rX_{ij} = \frac{n_{nj} - \varphi_{nj}}{n_{oj} - \varphi_{oj}} \times (\theta_{ij} - n_{oj}) + n_{nj}$$

Were, n_{nj} and φ_{nj} are the new maximum and minimum values for the trait j after rescaling, respectively n_{oj} and φ_{oj} , are the original maximum and minimum values for the trait j. θ_{ij} is the original value for the jth genotype.

For traits in which lower are desired $\eta_{nj}=0$ and $\varphi_{oj}=100$ is considered. For the traits in which higher values, we used $\varphi_{oj}=100$ and $\eta_{nj}=100$. After the rescaling procedure, a way-way table of rescaled values (rX) was realized. Each column of rX has a 0-100 range that considers the desired sense of selection (increase or decrease) and maintains the correlation structure of the original set of variables.

The second step was to compute an exploratory Factor analysis (FA) to group correlated traits into factors and then estimate the factorial scores for each genotype. The eigenvalues and eigenvectors were obtained from the correlation matrix of rX. The initial loadings were obtained considering only factors with eigenvalues higher than one. The analysis was obtained after varimax rotation (Kaiser, 1958). The scores obtained as follows:

$$F = Z(A^T R^{-1})^T$$

Were, F is a g x f matrix with the factorial scores; Z is a g x p matrix the standardized means; A is a p x f matrix between traits. g f and p are genotypes, factors retained and traits analysed respectively.

Ideotype: this step involves determining the ideal combination of trait values for a genotype. Thus, the ideotype was defined by a [1 x p] vector I such that I= [100, 100,...,100]. The MGIDI index is computed as follow:

$$MGIDI_i = \sum_{j=1}^f [(y_{ij} - y_j)^2]^{0.5}$$

Where $MGIDI_i$ is the multi-trait genotype-ideotype distance index for the ith genotype; jth is the score of the ith genotype in the jth factor (i = 1, 2, ..., g; j = 1, 2, ..., f), being g and f the number of genotypes and factors, respectively, and y_j is the jth score of the ideotype. The genotype with the lowest MGIDI is then closer to the ideotype and therefore should present desired values for all the analyzed traits. The proportion of the MGIDI index of the ith genotype explained by the jth factor (ω_{ij}) was computed as described below:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^f \sqrt{D_{ij}^2}}$$

Where D_{ij} is the best distance between the ith genotype and the ideotype for the jth factor given genotype. Low contributions of a factor indicate that traits within such a factor are close to the ideotype.

3. RESULTS AND DISCUSSION

The principal component analysis resulted in a total of seven eigenvalues, with the first two components explaining 81.20% of the total variance. Indicating high genetic variability among the studied genotypes. The values obtained for PCA1 and PC2 were 49.3% and 31.8%, respectively (Table 1).

Table 1. Principal component analysis, eigenvalues, and percentage of variance for seven studied traits.

PCA	PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7
Eigenvalues	3.45	2.23	0.62	0.41	0.16	0.11	0.01
Variance (%)	49.30	31.80	8.92	5.81	2.27	1.61	0.21
Cum.variance (%)	49.30	81.20	90.10	95.9	98.20	99.80	100

Principal component analysis (PCA); cumulative variance (Cum.variance (%))

To assess the strengths and weaknesses of the genotypes, a selection intensity of 20% was used. The evaluation using the MGIDI selection index revealed desirable selection gains for eight out of the eleven traits analyzed. The genotypes selected based on the MGIDI index were m66, m364 and m689 (Figure 1A). Notable traits and their respective selection differentials (DS) were as follows: positive values for NFS (33.5%), SPAD_i (1.71%) and PH (1.56%) (Table 2).

The analysis of both table 2 and figure 1B provides a comprehensive understanding of the strengths and weaknesses of different genotypes, based on their contributions to the Multi-Characteristic Genotype-Ideotype Distance Index (MGIDI). For factor 1 (FA1), which includes traits such as SPAD_i, DFL, and PL, mutant m689 exhibits a weakness, while m66 and m364 demonstrate a strength. In factor 2 (FA2), which highlights traits like SPAD_f, PH, NFS and NSS, genotype m689 shows strength, m66 and m364 exhibit weaknesses.

The selection of genotypes using MGIDI to evaluate strengths and weaknesses can help breeders identify superior genotypes that combine different desired traits (JALALIFAR et al., 2023). MAMUN et al. (2022) used the MGIDI method to identify ideal genotypes among rice mutants. In this study, the identified mutants emerge as ideal genotypes for future breeding programs, playing a crucial role under drought conditions. This strategic use of factors and attributes contributes to the development of tolerant and high-performing rice varieties.

Table 2. Factorial loadings (FA), original value (X_o), selected value (X_s), selection differential (SD) and selection differential in percentage (SD%), based on the multi-trait genotype–ideotype distance index (MGIDI) in 13 rice genotypes.

Traits	Factor	X _o	X _s	SD	SD (%)	Sense	Goal
SPAD _i	FA1	36.20	36.80	0.61	1.71	increase	100
DFL	FA1	110	106	-4.66	-4.23	decrease	100
PL	FA1	22.50	21.70	-0.80	-3.56	increase	0.00
SPAD _f	FA2	39.40	37.60	-1.88	-4.77	increase	0.00
PH	FA2	89.30	90.70	1.39	1.56	increase	100
NFS	FA2	30.50	40.80	10.20	33.50	increase	100
NSS	FA2	30.80	27	-3.80	-12.30	decrease	100

The initial SPAD chlorophyll index (SPAD_i), the SPAD chlorophyll index after stress (SPAD_f), days to flowering (DFL), panicle length (PL), plant height (PH), number of fertile (NFS) and sterile spikelets (NSS).

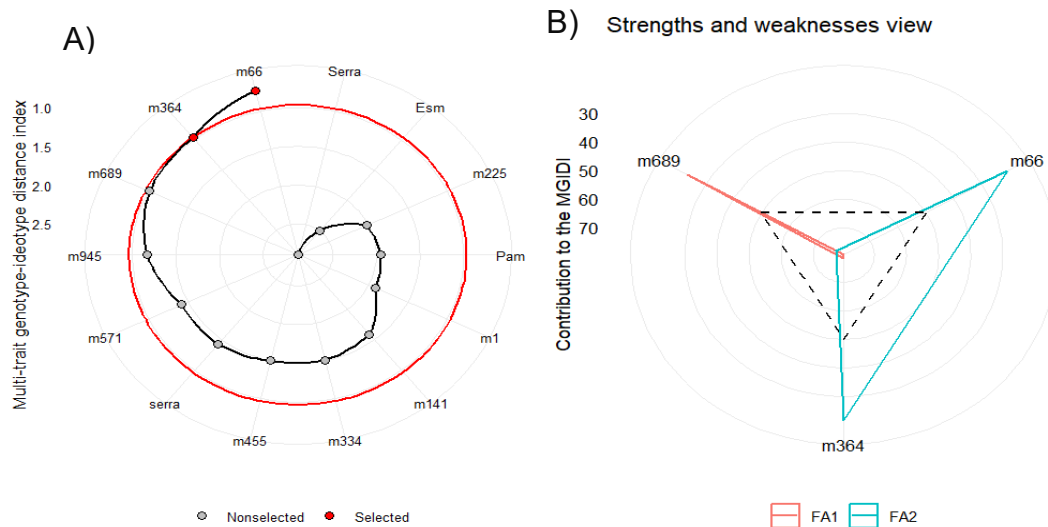


Figure 1. The strengths and weaknesses of the selected genotypes are illustrated by the proportion of each factor on the calculated Multi-Trait Genotype–Ideotype Distance Index (MGIDI). The smaller the proportion assigned to a factor (closer to the outer edge), the closer the attributes of that factor are to the ideal. The black dashed circle at the center represents the theoretical value, assuming all factors contributed equally.

4. CONCLUSION

The Multi-Trait Genotype–Ideotype Distance Index (MGIDI) has proven highly effective in selecting rice genotypes across various environments. The genotypes identified through MGIDI, such as m66, m364, and m689, show considerable potential for use as key materials in breeding programs for rice tolerant to water deficit stress during the reproductive phase.

5. REFERENCES

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