

1 Identification of Stress-Resilient Maize Progenies under Drought 2 and Low Nitrogen in West Africa Using Genotype \times Environment 3 Analysis and Multi-Trait Selection Indices

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14 Abstract

15 Maize productivity in West Africa is severely constrained by recurrent drought and low soil
16 nitrogen availability, which results in strong environmental heterogeneity and complex genotype
17 \times environment interactions (G \times E). Identifying breeding materials that combine productivity, stress
18 resilience, and stability therefore requires analytical approaches that integrate multi-trait and multi-
19 environment information. In this study, 250 full-sib maize progenies generated using a North
20 Carolina Design I mating scheme were evaluated under managed drought and low-nitrogen
21 conditions across multiple environments in Nigeria to identify superior crosses for population
22 improvement. Linear mixed models were used to estimate variance components and obtain best
23 linear unbiased predictions (BLUPs) for genotypic performance. Principal component analysis
24 revealed that grain yield, flowering dates, and plant architecture contributed differentially to
25 phenotypic variation, highlighting the multidimensional nature of stress adaptation. Selection of
26 superior progenies was conducted using four complementary approaches including grain yield
27 BLUPs, multi-trait genotype–ideotype distance index (MGIDI), multi-trait stability index (MTSI),
28 and Rank-Sum index integrating genotype rankings across methods. BLUP-based selection
29 produced the highest mean grain yield (2.86 t ha⁻¹), followed by the Rank-Sum index (2.84 t ha⁻¹),
30 MTSI (2.81 t ha⁻¹), and MGIDI (2.80 t ha⁻¹), compared with the overall reference population mean
31 of 2.74 t ha⁻¹. Twenty-one out of 63 progenies selected using 25% selection intensity were
32 consistently identified across multiple selection strategies, indicating robust performance of the
33 progenies across productivity and stability criteria. The integration of G \times E analysis with
34 complementary multi-trait selection approaches provides a practical framework for identifying
35 superior progenies for advancement within drought- and nitrogen-tolerant maize populations and
36 for the development of climate-resilient cultivars adapted to stress-prone environments in West
37 Africa.

38 **Keywords:** climate resilience; drought stress; low-nitrogen stress; MGIDI; MTSI; maize
39 breeding.

40 1. Introduction

41 Maize (*Zea mays* L.) is a major staple crop in sub-Saharan Africa, where it contributes substantially
42 to food security, household income, and livestock feed [1,2,3]. Maize plays a central role in both
43 subsistence and market-oriented farming systems in West Africa, supplying a large proportion of
44 daily caloric intake for rural and urban populations [4]. Despite its importance, maize productivity
45 in the region remains considerably lower (2 t/ha) than global averages (5 t/ha) due to a
46 combination of abiotic stresses, low input use, and high environmental variability [5,6,7].

47 Among the major abiotic constraints affecting maize production in West Africa, drought stress and
48 low soil nitrogen availability are particularly widespread and yield limiting. Drought stress has
49 become increasingly frequent due to erratic rainfall patterns, shortened rainy seasons, and rising
50 climatic variability, especially in rainfed production systems [8] and could result in complete crop
51 failure if extremely severe. At the same time, nitrogen deficiency remains a chronic problem across
52 much of the region as a result of inherently poor soils, continuous cropping, low soil organic
53 matter, and limited access to mineral fertilizers [9]. Yield losses associated with nitrogen
54 deficiency alone have been reported to range from 30% to more than 60% under smallholder
55 management conditions [10,11]. The frequent co-occurrence of drought and low nitrogen stress
56 further amplifies yield instability and complicates the identification of broadly adapted maize
57 cultivars [12,13].

58 Developing maize germplasm with improved productivity and adaptation to these stress conditions
59 is therefore a major priority for breeding programs in the region. However, breeding progress
60 under drought and low-nitrogen environments is often constrained by strong genotype \times
61 environment interaction ($G \times E$), low heritability of key adaptive traits including grain yield, and
62 frequent changes in genotype performance ranking across environments [14,15]. Multi-
63 environment trials (METs) are therefore essential for evaluating breeding materials under
64 contrasting stress scenarios and for quantifying genotype performance across diverse
65 environments. Analytical approaches such as additive main effects and multiplicative interaction
66 (AMMI) and genotype plus genotype \times environment (GGE) biplot analysis have been widely
67 applied to characterize interaction patterns, identify discriminating environments, and assess yield
68 stability in maize [16]. Although these approaches provide valuable insights into interaction
69 structure, they are generally applied on a single-trait basis, most often grain yield, and therefore
70 do not fully capture the complex relationships among multiple agronomic traits contributing to
71 stress adaptation.

72 Adaptation to drought and low nitrogen conditions in maize is inherently multi-trait in nature.
73 Traits such as flowering synchrony, plant architecture, biomass allocation, and grain yield interact
74 to determine overall plant performance under stress environments [13,18]. Selection strategies that
75 focus on a single trait may therefore overlook important trade-offs among traits and limit overall
76 genetic gain. To address this challenge, multi-trait selection frameworks have been increasingly
77 adopted to integrate correlated trait information and guide breeding decisions. Among these
78 approaches, the multi-trait genotype-ideotype distance index (MGIDI) provides a practical
79 method for identifying genotypes that simultaneously approach predefined ideotypes across
80 multiple traits [18]. Similarly, the multi-trait stability index (MTSI) integrates genotype

81 performance and stability across environments, enabling the identification of genotypes combining
82 desirable trait expression with broad adaptation.

83 Despite the increasing availability of such analytical tools, their combined application to maize
84 improvement under drought and low-nitrogen conditions in West Africa remains limited. Many
85 studies continue to emphasize either single-trait $G \times E$ analysis or yield-based stress indices, with
86 less attention given to integrated multi-trait decision frameworks that better reflect the complexity
87 of stress-prone smallholder production systems. Furthermore, comparisons between different
88 selection approaches are rarely explored, limiting our understanding of how alternative selection
89 strategies influence breeding decisions and genetic gain. Most previous studies applying multi-
90 trait indices such as MGIDI or MTSI have focused primarily on identifying superior hybrids or
91 genotypes based on overall performance, without explicitly evaluating how these indices compare
92 with conventional BLUP-based selection methods or simple rank-based approaches in structured
93 breeding populations. In addition, relatively few studies have applied these multi-trait selection
94 frameworks within populations derived from mating designs such as North Carolina Design I,
95 where the primary objective is to identify superior progenies for population improvement and
96 potential development of improved open-pollinated varieties or synthetic populations.

97 In this context, the present study applied an integrated analytical framework combining mixed-
98 model $G \times E$ analysis, BLUP-based genetic evaluation, and complementary multi-trait selection
99 approaches to identify superior maize progenies under drought and low-nitrogen stress conditions.
100 The specific objectives were to: (i) evaluate the agronomic performance of 250 full-sib maize
101 progenies across multiple drought and low-nitrogen stress environments in Nigeria; (ii) quantify
102 genotype, environment, and genotype \times environment interaction effects using linear mixed
103 models; and (iii) compare alternative selection strategies based on grain yield BLUPs, the MGIDI
104 index, the MTSI index, and a Rank-Sum index to identify superior progenies for population
105 improvement under stress-prone environments.

106

107 **2. Materials and Methods**

108 **2.1. Test Population and Progeny Development**

109 The test population, TZE-Y Pop DT STR, is an early-maturing yellow-grained maize population
110 developed for tolerance to drought stress and resistance to *Striga hermonthica*. The population was
111 derived from Diallel crosses among elite tropical maize lines identified through extensive multi-
112 year evaluations across West and Central Africa. Subsequent population improvement involved
113 four cycles of S_1 family recurrent selection under artificial Striga infestation for enhanced grain
114 yield, Striga tolerance/resistance, and improved agronomic traits, followed by four additional
115 cycles of S_1 family recurrent selection under managed drought stress to improve adaptation to
116 water-limited environments [19]. To evaluate combining ability and identify superior progenies
117 for population improvement, experimental crosses were generated using a North Carolina Design
118 I (NCD I) mating scheme [20]. Seeds from the improved population were planted in single-row
119 plots (5 m long) with 0.75 m inter-row and 0.25 m intra-row spacing. Three seeds were planted
120 per hill and thinned to two plants per stand two weeks after emergence. Fifty S_1 plants were

121 randomly selected as male parents, and each male was crossed to five randomly selected S₁ female
122 parents, resulting in 250 full-sib progenies organized into 50 male families.

123 **2.2. Field Evaluation**

124 **2.2.1. Experimental Sites and Design**

125 Field evaluations were conducted across five environments representing contrasting agroecologies
126 and stress conditions in Nigeria. Drought stress evaluations were carried out at Ikenne, Kadawa,
127 and Ile-Ife, while low-nitrogen stress evaluations were conducted at Mokwa and Ile-Ife. Ikenne is
128 located in the rainforest agroecological zone (approximately 6°52'N, 3°42'E; 60 m above sea level)
129 and receives a mean annual rainfall of about 1500 mm. Drought evaluation at this site was
130 conducted during the dry season (2011/2012) under managed irrigation. Kadawa lies in the Sudan
131 savanna zone (approximately 11°45'N, 8°45'E; 469 m above sea level) and receives an average
132 annual rainfall of approximately 880 mm; drought stress at this location occurred naturally during
133 the 2012 growing season. Ile-Ife is situated in the forest–transition zone (approximately 7°18'N,
134 4°33'E; 244 m above sea level), with a mean annual rainfall of about 1200 mm; both natural
135 drought stress and low-nitrogen stress evaluations were conducted at this location during the 2012
136 and 2012/2013 seasons. Mokwa, located in the southern Guinea savanna (approximately 9°18'N,
137 5°04'E; 457 m above sea level), receives about 1100 mm of annual rainfall and was used
138 exclusively for low-nitrogen stress evaluation during the 2012 growing season. Across all
139 environments, field experiments were laid out in a 25 x 10 randomized incomplete block design
140 (RIBD). The 250 progenies were divided into 10 sets of 25 entries, with each set randomly assigned
141 to a block. Each environment consisted of two replications, giving a total of 10 blocks per
142 replication. Plots consisted of single rows 3 m in length, spaced 0.75 m apart, with 0.40 m between
143 plants within rows. Three seeds were planted per hill and thinned to two plants per stand two weeks
144 after emergence, resulting in a final plant population of approximately 66,000 plants ha⁻¹.

145 **2.2.2. Evaluation under Drought Stress**

146 Drought stress evaluations were conducted at Ikenne, Kadawa, and Ile-Ife. At Ikenne, drought
147 stress was the “managed type” where optimal moisture conditions was maintained during early
148 vegetative growth through supplemental irrigation (approximately 17 mm week⁻¹) until 28 days
149 after planting (DAP), corresponding to the V6 growth stage. This irrigation regime was sufficient
150 to support uniform crop establishment without fully replenishing evapotranspiration demand.
151 Thereafter, irrigation was stopped and crop growth depended solely on residual soil moisture to
152 induce terminal drought stress. At Kadawa and Ile-Ife, natural terminal drought stress occurred
153 when planting was scheduled such that moisture deficits coincided with the flowering and grain-
154 filling stages. Fertilizer was applied at planting at 60 kg ha⁻¹ each of N, P₂O₅, and K₂O, followed
155 by an additional 60 kg ha⁻¹ N applied as top-dressing four weeks after planting. Weed control was
156 achieved through a combination of manual weeding and the use of pre- and post-emergence
157 herbicides.

158 **2.2.3. Evaluation under Low-Nitrogen Stress**

159 Low-nitrogen (Low-N) stress trials were conducted at Mokwa and Ile-Ife, sites that are routinely
160 used for low-nitrogen screening. To maintain depleted soil nitrogen levels, maize has been
161 continuously cultivated at these locations, and following each low-nitrogen trial the above-ground
162 biomass and root residues are removed from the field after harvest to prevent nitrogen recycling.
163 Prior to establishing the present experiment, composite soil samples were collected from a depth
164 of 0–30 cm and analyzed for total nitrogen using the Kjeldahl digestion method. Based on the soil
165 test results, nitrogen fertilizer was applied at a rate of 30 kg N ha⁻¹, representing approximately
166 one-third of the recommended nitrogen requirement for optimal maize production, in order to
167 maintain uniform low-nitrogen stress conditions. Nitrogen fertilizer was applied in two equal splits
168 at two and four weeks after planting. Phosphorus and potassium fertilizers were applied at 60 kg
169 ha⁻¹ each during basal application.

170 **2.3. Data Collection**

171 Data were collected on days to 50% anthesis (DA) and days to 50% silking (DS), and the anthesis–
172 silking interval (ASI) was calculated as the difference between DS and DA. Plant aspect (PASP)
173 and ear aspect (EASP) were scored on a 1–9 scale, where lower scores indicated superior plant
174 and ear quality. Husk cover was scored on a 1–5 scale, with lower scores indicating tighter husk
175 coverage. Plant height (PHT) was measured from the soil surface to the first tassel branch, and ear
176 height (EHT) was measured from the soil surface to the node bearing the uppermost ear. Root
177 lodging and stalk lodging were recorded as the percentage of affected plants. Leaf senescence
178 (LDTH) under drought stress and stay-green (STGR) under low-nitrogen stress were evaluated at
179 70 days after planting using a 1–10 scale, where lower scores indicated delayed senescence. Grain
180 yield was estimated from field or shelled grain weight and adjusted to 15% moisture content using
181 standard conversion formulas in equations 1 and 2. Percentage data were square-root transformed
182 prior to analysis of variance to stabilize error variances.

183

184
$$\text{GYLD} \left(\frac{\text{kg}}{\text{ha}} \right) = \text{field weight} \left(\frac{\text{kg}}{\text{plot}} \right) \times \frac{(100 - \text{moisture})}{85} \times \frac{10000 \times \text{shelling \%}}{3 \times 0.75} \dots \text{eqn. 1}$$

185

186
$$\text{GYLD} \left(\frac{\text{kg}}{\text{ha}} \right) = \text{grain weight} \left(\frac{\text{kg}}{\text{plot}} \right) \times \frac{(100 - \text{moisture})}{85} \times \frac{10000}{3 \times 0.75} \dots \text{eqn. 2}$$

187 **2.4. Statistical Analysis**

188 **2.4.1. Analysis of variance and genetic parameter estimates**

189 The data obtained were analyzed using linear mixed models to quantify genetic effects, genotype-
190 by-environment interactions, and to obtain best linear unbiased predictions (BLUPs) for
191 downstream multi-trait analyses. All analyses were conducted in R using the packages lme4 [21],
192 emmeans [22], FactoMineR [23], Metan [24], and ggVennDiagram [25]. For each trait, the
193 following mixed-effects model was fitted using restricted maximum likelihood (REML) in
194 equation 3.

195

196
$$Y_{ijklm} = \mu + S_i + G_j + (GS)_{IJ} + (SE)_{ik} + (GSE)_{ijk} + Rl_{(ik)} + Bm_{(lik)} + \varepsilon_{ijklmy} \dots \dots \dots \text{eqn. 3}$$

197

198 *Where:*

199 Y_{ijklm} = the observed trait value.

200 μ = the overall mean.

201 S_i = the fixed effect of the *i*th stress condition (drought or low nitrogen).

202 G_j = the random effect of the *j*th genotype.

203 GS_{ij} = the random genotype × stress interaction.

204 SE_{ik} = the random stress × environment interaction.

205 GSE_{ijk} = the random genotype × stress × environment interaction.

206 $Rl_{(ik)}$ = the random effect of replicate nested within stress and environment.

207 $Bm_{(lik)}$ = the random effect of block nested within replicate, stress, and environment.

208 ε_{ijklm} = the residual error term.

209

210 Fixed effects were tested using Type III analysis of variance with Satterthwaite’s approximation
 211 for denominator degrees of freedom. The significance of genetic and interaction variance
 212 components was further assessed using likelihood ratio tests by comparing the full model with
 213 reduced models excluding the respective random effects. Variance components were extracted
 214 from the fitted model and used to estimate broad-sense heritability on an entry-mean basis across
 215 stress conditions and environments as shown in equation.

216

217
$$H^2 = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{GS}^2}{nS} + \frac{\sigma_{GSE}^2}{nSnE} + \frac{\sigma_e^2}{nSnEnR}} \dots \dots \dots \text{eqn. 4}$$

218

219 Where σ_G^2 , σ_{GS}^2 , σ_{GSE}^2 , and σ_e^2 are the genotypic, genotype × stress, genotype × stress ×
 220 environment, and residual variances, respectively; and nS , nE , and nR are the number of stress
 221 conditions, environments, and replications.

222

223 Best linear unbiased predictions (BLUPs) were extracted for genotypes across all environments,
 224 as well as for genotype × stress and genotype × stress × environment combinations by combining
 225 random effects with the appropriate fixed-effect estimates. Principal component analysis (PCA)
 226 was conducted on standardized genotype BLUPs to explore relationships among traits and
 227 summarize multivariate variation.

228

2.4.2 Multi-Trait Selection and Comparison of Selection Strategies

229

230
 231 Superior progenies were identified using four complementary selection approaches. First, grain
 232 yield BLUP selection, based on predicted genotypic means for grain yield. Second, multi-trait
 233 genotype–ideotype distance index (MGIDI), which identifies genotypes closest to an ideal multi-
 234 trait profile. Third, multi-trait stability index (MTSI), which integrates trait performance and
 235 stability across environments. Forth, Rank-Sum index, calculated by summing genotype rankings
 236 obtained from BLUP, MGIDI, and MTSI analyses to identify progenies consistently performing
 237 well across methods. For all selection approaches, a selection intensity of 25% was applied to
 238 identify superior progenies. Mean grain yield of selected progenies was compared among methods
 239 to evaluate the effectiveness of different selection strategies.

240

241 **3. Results**

242 **3.1 Analysis of variance, variance components, and genetic parameters**

243 Table 1 showed the analysis of variance, variance components, and genetic parameters. The
244 genotype \times stress interaction variance was generally small and non-significant across most traits,
245 suggesting limited differential responses of progenies between drought and low-nitrogen stress
246 conditions. However, a moderate interaction was detected for plant aspect ($\chi^2 = 3.08$), indicating
247 some variation in genotype ranking across stress types for this trait. Variance component estimates
248 indicated that the stress \times environment interaction contributed substantially to phenotypic variation
249 for most traits. For grain yield, the variance component associated with stress \times environment
250 ($\sigma^2_{\times e} = 1.11$) was considerably larger than the genotypic variance ($\sigma^2_g = 0.03$), highlighting the
251 strong influence of environmental heterogeneity within stress categories. Similar patterns were
252 observed for flowering traits and plant height. Broad-sense heritability estimates ranged from low
253 to moderate across traits. Grain yield exhibited moderate heritability ($H^2 = 0.42$), indicating that
254 genetic improvement through selection is feasible despite environmental variability. Moderate
255 heritability was also observed for ear height (0.54), ear aspect (0.44), and days to anthesis (0.37),
256 whereas lower heritability estimates were observed for days to silking (0.15) and anthesis–silking
257 interval (0.08), reflecting stronger environmental influence on these traits under stress conditions.
258 Predicted genotypic performance based on BLUP estimates showed substantial variation among
259 progenies. Grain yield ranged from 2.47 to 2.98 t ha⁻¹, with an overall predicted mean of 2.74 t
260 ha⁻¹ across environments. The highest-performing genotype under combined environments
261 differed from those performing best under individual stress conditions, suggesting environment-
262 specific adaptation among some progenies (Table 1).

263 **3.2 Grain yield distribution under drought and low-nitrogen stress**

264 The distribution of grain yield differed markedly between drought and low-nitrogen stress
265 conditions (Figure 1). Under drought stress, grain yield values were generally lower, with a mean
266 of approximately 2.8 t ha⁻¹ and a relatively narrow inter-quartile range. In contrast, yield under
267 low-nitrogen stress showed a higher mean performance (4.1 t ha⁻¹) and a wider dispersion of
268 values, including several high-yielding observations exceeding 8 t ha⁻¹. The non-parametric
269 Kruskal–Wallis test revealed a highly significant difference between stress conditions ($p < 2.2 \times$
270 10^{-16}), indicating that the overall distribution of grain yield under low-nitrogen stress was shifted
271 upward relative to drought stress. The boxplots further illustrate this contrast through higher
272 quartile values and greater upper-tail variability under low-nitrogen environments compared with
273 drought. Despite some overlap in yield distributions, the median, mean (indicated by diamond
274 symbols), and upper range of grain yield were consistently higher under low-nitrogen stress than
275 under drought conditions. These results interpret that drought imposed a stronger limitation on
276 grain yield than nitrogen deficiency across the evaluated environments.

277

278

279 Table 1: Analysis of variance, variance components, and genetic parameters for agronomic traits of 250 maize progenies evaluated under
 280 managed drought and low-nitrogen conditions across multiple environments in Nigeria.

Effect	Statistic	GYLD (t ha ⁻¹)	DA	DS	ASI	PHT (cm)	EHT (cm)	PASP	EASP	EPP	LDTH
Stress (fixed)	Mean Sq	1.74	2.14	7.99	3.73	575.97	30.19	0.46	0.03	0.03	0.39
Gen (random)	Chisq (χ^2)	5.53*	10.65**	1.98	0.18	0.53	16.90***	1.15	6.91**	0.87	3.83
Gen × Stress (random)	Chisq (χ^2)	0.83	0.00	0.00	0.00	0.00	0.00	3.08*	0.00	0.00	0.00
Residual (random)	Variance	0.85	5.996	6.06	7.36	1545.91	106.53	0.81	0.59	0.03	0.58
Genetic Parameter											
σ^2_G		0.03	0.28	0.11	0.04	13.76	7.18	0.02	0.03	0.00	0.02
$\sigma^2_{G \times S}$		0.02	0.00	0.00	0.00	1.27	0.00	0.03	0.00	0.00	0.00
$\sigma^2_{S \times E}$		1.11	5.22	5.41	0.55	1276.46	578.18	0.26	0.31	0.01	0.22
$\sigma^2_{G \times S \times E}$		0.04	0.48	0.61	0.44	31.09	6.12	0.03	0.03	0.00	0.04
σ^2_e		0.84	6.00	6.05	7.36	1545.91	106.53	0.81	0.59	0.03	0.58
H^2		0.42	0.37	0.15	0.08	0.29	0.54	0.24	0.44	0.27	0.30
Genotype metric											
Best genotype (overall)		2.98	53.24	57.13	1.85	184.95	91.07	5.07	5.07	0.87	3.90
Predicted mean		2.74	54.68	56.80	2.13	170.78	86.26	5.20	5.38	0.83	4.06
Worst genotype		2.47	55.55	56.08	2.35	169.48	82.81	5.32	5.59	0.81	4.22
Drought winner		3.08	50.13	51.58	-1.31	185.05	92.77	4.87	4.86	1.02	3.73
LowN winner		4.52	54.57	53.43	-0.79	239.45	105.06	4.61	4.82	0.95	3.36

281 σ^2_G = genotypic variance, $\sigma^2_{G \times S}$ = genotype by stress interaction, $\sigma^2_{S \times E}$ = stress by environment interaction, $\sigma^2_{G \times S \times E}$ = genotype-by-stress-by-environment, σ^2_e = residual variance, H^2
 282 = heritability, GYLD = grain yield, DA = days to anthesis, DS = days to silking, ASI = anthesis-silking interval, PHT = plant height, EHT = ear height, PASP = plant aspect, EASP
 283 = ear aspect, EPP = ears per plant, LDTH = leaf death. *, **, *** corresponds to $P < 0.05$, 0.01, and 0.001 probability levels.

284

285

286

Figure 1. Distribution of grain yield of maize progenies evaluated under drought and low-nitrogen stress conditions across environments. Boxes represent the interquartile range, horizontal lines indicate medians, whiskers show the range excluding outliers, and diamonds represent mean values. Differences between stress conditions were assessed using the Kruskal–Wallis test.

3.3 Principal component analysis of multi-trait BLUPs

Principal component analysis (PCA) otherwise called dimensional reduction analysis was performed on standardized BLUP values of grain yield and associated agronomic traits to summarize the multivariate structure of genotype performance across stress environments. The first four principal components had eigenvalues greater than one and collectively explained approximately 73 % of the total phenotypic variation among progenies (Table 2). The first principal component (Dim1) accounted for approximately 32 % of the total variation and was primarily associated with GYLD, EHT, PASP, EASP and EPP. Grain yield, EHT, and EPP exhibited strong negative loadings, whereas PASP and EASP showed positive loadings, indicating contrasting contributions of yield-related traits and visual agronomic traits along this axis. Consequently, Dim1 largely captured variation related to overall productivity and plant architecture. The second principal component (Dim2), which explained 14.85 % of the total variation, was dominated by flowering-related traits. Days to anthesis (DA) and days to silking (DS) showed strong positive loadings, while ear height also contributed positively. This axis therefore separated genotypes primarily according to flowering time and associated plant growth characteristics. The third principal component (Dim3), accounting for 13.55 % of the variation, was mainly influenced by leaf death score (LDTH) and plant height (PHT), representing variation associated with senescence and vegetative growth responses under stress conditions. The fourth principal component (Dim4), explaining 12.76 % of the total variation, was dominated by anthesis–silking interval (ASI), capturing variation related to reproductive synchrony.

The PCA biplot based on Dim1 and Dim2 (Figure 2) illustrated the relationships among traits and the dispersion of progenies in the reduced multivariate space. Days to anthesis and days to silking were closely aligned, indicating a strong positive association between these flowering traits. Grain yield was oriented in the opposite direction to plant and ear aspect scores, reflecting the negative relationship between yield performance and visual plant quality scores. The broad distribution of progenies across the biplot further indicated substantial multivariate diversity among the evaluated materials. Overall, the PCA results highlighted that maize performance under drought and low-nitrogen stress is governed by multiple interacting traits, including productivity, flowering behavior, plant architecture, and senescence responses.

Table 2: Principal component analysis of multi-trait BLUPs from 250 maize progenies evaluated under five environments comprising drought and low nitrogen stress conditions

Trait	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
GYLD	-0.82	0.10	-0.33	0.14	-0.07
DA	0.37	0.74	-0.20	-0.41	0.20
DS	0.50	0.68	-0.10	0.43	0.19
ASI	0.30	-0.01	0.22	0.91	-0.04
PHT	-0.39	0.27	0.62	-0.02	0.11
EHT	-0.52	0.52	0.32	-0.03	-0.18
PASP	0.77	-0.24	0.12	-0.11	0.09
EASP	0.82	-0.13	0.25	-0.14	0.13
EPP	-0.57	-0.21	-0.07	0.11	0.77
LDTH	-0.19	-0.05	0.76	-0.14	0.05
Eigenvalue	3.18	1.48	1.36	1.28	0.74
Variance (%)	31.81	14.85	13.55	12.76	7.39
Cum.Variance (%)	31.81	46.66	60.21	72.97	80.36

GYLD = grain yield, *DA* = days to anthesis, *DS* = days to silking, *ASI* = anthesis-silking interval, *PHT* = plant height, *EHT* = ear height, *PASP* = plant aspect, *EASP* = ear aspect, *EPP* = ears per plant, *LDTH* = leaf death, Dim = principal component. *, **, *** corresponds to $P < 0.05$, 0.01 , and 0.001 probability levels.

Figure 2: Principal component biplot showing the relationships among agronomic traits and the distribution of maize progenies based on standardized BLUP values. PC1 and PC2 represent the first two principal components explaining the largest proportion of total phenotypic variation. *GYLD* = grain yield, *DA* = days to anthesis, *DS* = days to silking, *ASI* = anthesis-silking interval, *PHT* = plant height, *EHT* = ear height, *PASP* = plant aspect, *EASP* = ear aspect, *EPP* = ears per plant, *LDTH* = leaf death.

3.4 Multi-trait Genotype–Ideotype Distance Index (MGIDI)

The multi-trait genotype–ideotype distance index (MGIDI) effectively summarized the joint performance of progenies across all evaluated agronomic traits and enabled the identification of superior materials based on their proximity to the ideotype. The factor analysis underlying the MGIDI revealed a well-defined multivariate structure, with four latent factors explaining most of the variation among traits (Table 3 and Figure 3). High communalities for most traits (0.38–0.97) indicated that the retained factors adequately represented the original trait information and supported the robustness of the index. The first factor (FA1) was strongly associated with yield and plant architecture traits, showing high negative loadings for grain yield ($GYLD = -0.89$), plant aspect ($PASP = -0.80$), ear aspect ($EASP = -0.87$), and ears per plant ($EPP = -0.48$). This factor therefore captured variation related to productivity and overall plant quality. The second factor (FA2) was dominated by phenological traits, with strong positive loadings for days to anthesis ($DA = 0.90$) and days to silking ($DS = 0.72$), representing variation associated with flowering

dynamics. The third factor (FA3) was primarily associated with plant height, ear height and senescence traits, including plant height (PHT = - 0.76), ear height (EHT = - 0.61) and leaf death score (LDTH = 0.74), indicating variation related to vegetative growth and stress-induced senescence. The fourth factor (FA4) was mainly driven by anthesis–silking interval (ASI = -0.97), capturing variation in reproductive synchrony.

Selection based on the MGIDI resulted in measurable improvements across several traits relative to the base population mean. Grain yield exhibited a positive selection differential (SD = 0.07), corresponding to a predicted genetic gain of 2.52 % cycle⁻¹, indicating that the index successfully prioritized higher-yielding progenies while maintaining favorable performance for other agronomic traits. Improvements were also observed for ear height (SG = 1.37 %) and leaf death score (SG = 1.14 %), suggesting enhanced plant vigor and delayed senescence, important traits for adaptation under stress conditions. Conversely, negative predicted gains for traits such as ear aspect (SG = -1.13 %), plant aspect (SG = -0.76 %), and flowering time (DA and DS) indicated improvements toward more desirable phenotypic expression and earlier reproductive development. Overall, the MGIDI selection framework enabled simultaneous improvement of yield, flowering behavior, plant architecture, and stress-adaptive traits without imposing strong trade-offs among traits. These results demonstrate the utility of MGIDI as an effective multi-trait selection tool for identifying superior progenies for population improvement under drought and low-nitrogen stress conditions.

Table 3: Factor analysis loadings, population mean, selected population mean, selection differential (SD), predicted genetic gain (SG), communalities, and uniqueness estimates for agronomic traits derived from the multi-trait genotype–ideotype distance index (MGIDI).

VAR	FA1	FA2	FA3	FA4	Xo	Xs	SD	SG (%)	Communality	Uniqueness
ASI	-0.13	-0.11	-0.01	-0.97	2.13	2.10	-0.02	-1.17	0.97	0.03
DA	-0.16	0.90	-0.03	0.25	54.67	54.47	-0.20	-0.37	0.90	0.10
DS	-0.13	0.72	-0.11	-0.60	56.80	56.67	-0.14	-0.24	0.91	0.09
EASP	-0.87	0.11	-0.05	-0.07	5.38	5.32	-0.06	-1.13	0.77	0.23
EHT	-0.46	-0.25	-0.61	-0.02	86.26	87.44	1.18	1.37	0.64	0.36
EPP	-0.48	0.37	-0.05	-0.06	0.82	0.83	0.00	0.60	0.38	0.62
GYLD	-0.89	0.12	0.03	-0.09	2.74	2.81	0.07	2.52	0.81	0.19
LDTH	-0.15	-0.23	0.74	0.06	4.06	4.10	0.05	1.14	0.63	0.37
PASP	-0.80	0.01	-0.20	-0.05	5.20	5.16	-0.04	-0.76	0.68	0.32
PHT	-0.17	0.00	-0.76	0.02	170.78	171.48	0.71	0.41	0.61	0.39

GYLD = grain yield, *DA* = days to anthesis, *DS* = days to silking, *ASI* = anthesis-silking interval, *PHT* = plant height, *EHT* = ear height, *PASP* = plant aspect, *EASP* = ear aspect, *EPP* = ears per plant, *LDTH* = leaf death. *, **, *** corresponds to $P < 0.05$, 0.01, and 0.001 probability levels.

Figure 3. Ranking of maize progenies based on the multi-trait genotype–ideotype distance index (MGIDI). Each point represents a progeny positioned according to its distance from the ideotype. The red circle indicates the selection threshold corresponding to the predefined selection intensity. Progenies located inside the circle (blue) were selected, whereas those outside the circle (gray) were not selected.

3.5. Multi-trait Stability Index (MTSI)

The multi-trait stability index (MTSI) analysis revealed a clear multivariate structure among the evaluated traits and enabled the identification of progenies combining favorable mean performance with stability across stress environments (Table 4 and Figure 4). Four latent factors explained most of the variation among traits, with relatively high communalities (0.51 – 0.88) indicating that the retained factors adequately represented the original trait information.

The first factor (FA1) was primarily associated with plant architectural traits, with strong positive loadings for plant height (PHT = 0.83) and ear height (EHT = 0.89), indicating that this factor represented overall vegetative growth characteristics. The second factor (FA2) was dominated by phenological traits, with strong negative loadings for days to silking (DS = -0.91) reflecting variation in flowering time across environments. The third factor (FA3) captured yield-related variation, with notable loadings for grain yield (GYLD = 0.69), ear aspect (EASP = -0.83), and plant aspect (PASP = -0.72), indicating that this factor represented productivity and visual plant quality traits. The fourth factor (FA4) was associated mainly with reproductive traits, including ears per plant (EPP), reflecting variation in reproductive efficiency. Selection based on the MTSI resulted in measurable improvements in several key agronomic traits relative to the base population mean. Grain yield showed a positive selection differential (SD = 0.41), corresponding to a predicted genetic gain of 4.06% cycle⁻¹, indicating that the index effectively prioritized high-yielding progenies with stable performance across environments. Similarly, positive predicted gains were observed for plant height (SG = 0.30%) and ear height (SG = 2.46 %), suggesting selection toward vigorous plant types capable of maintaining productivity under stress conditions.

Conversely, negative predicted gains were observed for anthesis–silking interval (ASI = -1.68 %), plant aspect (PASP = -1.39 %), ear aspect (EASP = -0.97 %), and days to silking (DS = -0.24 %). These trends indicate improvements toward earlier flowering, improved plant and ear architecture, and better reproductive synchrony under stress conditions. Overall, the MTSI results demonstrate that simultaneous improvement in grain yield, flowering synchrony, plant architecture, and stability across drought and low-nitrogen environments is achievable. The index successfully identified progenies with balanced multi-trait performance and reduced sensitivity to environmental variation, making them suitable candidates for advancement in stress-resilient maize breeding programs.

Table 4: Factor loadings, population mean, selected population mean, selection differential (SD), predicted genetic gain (SG), communalities, and uniqueness values for agronomic traits derived from the multi-trait stability index (MTSI) analysis.

VAR	FA1	FA2	FA3	FA4	Xo	Xs	SD	SG (%)	Communality	Uniquenesses
ASI	-0.06	-0.94	-0.02	0.01	1.93	1.37	-0.56	-1.68	0.88	0.12
DA	0.14	-0.18	-0.08	0.73	55.19	54.81	-0.37	-0.17	0.59	0.41
DS	-0.07	-0.91	-0.10	0.12	55.81	54.99	-0.82	-0.24	0.87	0.13
EASP	-0.03	-0.05	-0.83	0.00	5.33	5.08	-0.25	-0.97	0.69	0.31
EHT	0.89	0.07	0.03	-0.12	90.96	97.72	6.76	2.46	0.81	0.19
EPP	0.28	0.00	0.20	-0.68	0.85	0.87	0.02	0.16	0.57	0.43
GYLD	0.38	0.07	0.69	-0.29	3.30	3.71	0.41	4.06	0.72	0.28
LDTH	0.26	-0.15	-0.47	-0.45	3.91	3.94	0.03	0.16	0.51	0.49
PASP	-0.19	-0.01	-0.72	0.14	5.06	4.64	-0.41	-1.39	0.57	0.43
PHT	0.83	0.06	0.26	0.00	178.76	187.08	8.31	0.30	0.76	0.24

GYLD = grain yield, *DA* = days to anthesis, *DS* = days to silking, *ASI* = anthesis-silking interval, *PHT* = plant height, *EHT* = ear height, *PASP* = plant aspect, *EASP* = ear aspect, *EPP* = ears per plant, *LDTH* = leaf death. *, **, *** corresponds to $P < 0.05$, 0.01, and 0.001 probability levels.

Figure 4. Ranking of maize progenies based on the multi-trait stability index (MTSI). Each point represents a progeny positioned according to its stability and performance across environments. The red circle indicates the selection threshold corresponding to the predefined selection intensity. Progenies located inside the circle (green) were selected, whereas those outside the circle (gray) were not selected

3.6. Comparison of Selection Strategies

The effectiveness of different selection approaches was evaluated by comparing the mean grain yield of progenies selected using BLUP-based ranking, MGIDI, MTSI, and the Rank Sum index (Table 5). The population mean grain yield across all progenies was 2.74 t ha^{-1} , while the selected groups from all methods showed improved performance relative to the base population. Direct selection based on BLUP values produced the highest mean grain yield (2.86 t ha^{-1}), reflecting the effectiveness of BLUP-based ranking for identifying high-performing progenies under multi-environment evaluation. Selection using the MGIDI and MTSI indices also improved grain yield relative to the population mean, with selected group means of 2.80 t ha^{-1} and 2.81 t ha^{-1} , respectively. Although these means were slightly lower than those obtained through direct BLUP selection, both indices simultaneously optimized multiple agronomic traits and stability components.

The Rank Sum index, which integrates genotype rankings from BLUP, MGIDI, and MTSI, resulted in a selected group mean of 2.84 t ha^{-1} , comparable to the BLUP-based selection. This result suggests that the Rank Sum approach effectively combines information from multiple selection criteria to identify progenies with favorable overall performance. Overall, the comparison

among selection strategies indicates that BLUP-based selection maximizes grain yield performance, whereas MGIDI and MTSI emphasize balanced multi-trait improvement and stability across environments. The Rank Sum index provides a complementary approach by integrating these selection signals to identify progenies with consistently superior performance.

Table 5. Comparison of selection methods based on mean grain yield of selected progenies, selection differential, relative gain, and selection coincidence index obtained from BLUP, MGIDI, MTSI, and Rank Sum selection approaches.

Method	Mean Yield (t/ha)	Population Mean (t/ha)	Selection Differential (t/ha)	Relative Gain (%)	Selection Coincidence Index (%)
BLUP	2.86	2.74	0.12	4.38	-
MGIDI	2.80	2.74	0.06	2.19	46.03
MTSI	2.81	2.74	0.07	2.55	49.21
Rank-Sum	2.84	2.74	0.10	3.65	68.25

3.7. Concordance among Selection Methods

The level of agreement among the four selection strategies (BLUP, MGIDI, MTSI, and Rank Sum) was evaluated using a Venn diagram (Figure 5). The results revealed varying degrees of overlap among the methods, reflecting their different selection criteria and objectives. A subset of 21 progenies (19 %) was simultaneously selected by all four methods, indicating a strong consensus among the different selection approaches. These progenies represent highly promising candidates combining superior yield performance, balanced multi-trait profiles, and stable expression across environments. In addition to this core set, specific combinations of methods selected several progenies. For example, MGIDI, MTSI, and Rank Sum, highlighting their favorable multi-trait performance and stability characteristics, jointly selected 15 progenies (13 %). Conversely, 18 progenies (16 %) were uniquely selected by the BLUP-based approach, reflecting the tendency of direct BLUP selection to prioritize maximum yield performance. The overall pattern of overlap indicates that while each selection method captures distinct aspects of genotype performance, there is substantial agreement among methods in identifying superior progenies. The progenies selected by multiple methods therefore represent robust candidates for advancement in the breeding pipeline.

Figure 5. Venn diagram showing the overlap of progenies selected by four selection strategies: BLUP-based ranking, multi-trait genotype–ideotype distance index (MGIDI), multi-trait stability index (MTSI), and the Rank Sum index. Numbers represent the number and proportion (%) of progenies selected by each method or shared among methods.

4. Discussion

Improving maize productivity under drought and low-nitrogen (LN) conditions in West Africa requires analytical frameworks that extend beyond single-trait evaluation to integrated assessments of performance, stability, and trait interrelationships. In this study, genotype-by-environment interaction ($G \times E$) analysis was combined with multi-trait selection indices, namely the multi-trait genotype–ideotype distance index (MGIDI) and the multi-trait stability index (MTSI), to evaluate progeny performance across contrasting stress environments. This integrative approach enabled the identification of progenies combining productivity, resilience, and stability under drought and LN stress conditions. The results demonstrate that substantial genetic variation exists among the evaluated progenies despite the absence of strong fixed stress effects, highlighting the importance of multi-trait and multi-environment analytical frameworks for identifying superior breeding materials under complex stress scenarios.

4.1. Stress Imposition and Yield Differentiation under Drought and Low-Nitrogen Conditions

The contrasting yield distributions observed between drought and low-nitrogen environments indicate that the stress environments imposed distinct constraints on maize productivity. Although the mixed-model analysis did not detect a statistically significant fixed stress effect, the non-parametric comparison of yield distributions revealed clear phenotypic differentiation between the two stress conditions. Grain yield under drought conditions was consistently lower than under low-nitrogen stress, suggesting that water limitation imposed a stronger constraint on crop performance across the evaluated environments. Similar observations have been reported in tropical maize breeding programs where drought stress frequently exerts a more severe limitation on grain yield than moderate nitrogen deficiency [26,27]. These findings highlight the importance of evaluating germplasm under multiple stress scenarios to capture the range of environmental variability encountered in smallholder production systems in West Africa.

4.2. Genetic Variation, Heritability, and Implications for Selection

The detection of significant genotypic effects for grain yield, ear height, days to anthesis, and ear aspect indicates the presence of exploitable genetic variation among the evaluated progenies. Moderate heritability estimates for these traits suggest that selection for improved performance under stress conditions is feasible despite environmental variability. However, the relatively low heritability observed for traits such as anthesis–silking interval and days to silking reflects the strong environmental modulation of reproductive development under drought and nitrogen stress. Similar patterns have been documented in maize breeding programs targeting stress tolerance, where environmental effects frequently dominate the expression of reproductive traits [14,28]. The relatively small genotype \times stress interaction variance observed for most traits further suggests that genotype responses were influenced more by environmental heterogeneity within stress categories than by systematic differences between drought and low-nitrogen conditions. May also indicate the genotype resilience for the stresses.

4.3. Multivariate Trait Architecture of Stress Adaptation

The principal component analysis revealed that grain yield, flowering time, plant architecture, and senescence traits contributed differently to the overall phenotypic variation among progenies. This pattern highlights the inherently multi-dimensional nature of stress adaptation in maize. Grain yield was negatively associated with plant and ear aspect scores, reflecting the typical relationship between improved plant architecture and higher productivity. Meanwhile, flowering-related traits formed a distinct axis of variation, emphasizing the importance of reproductive timing in stress adaptation. Such trait relationships have been widely reported in drought-tolerant maize germplasm, where synchronized flowering and efficient biomass allocation are critical determinants of yield stability under stress conditions [17].

4.4. Multi-Trait Selection using MGIDI and MTSI

While multi-trait genotype-ideotype distance index (MGIDI) focuses primarily on multi-trait performance, the multi-trait stability index (MTSI) integrates both performance and stability across environments. The MTSI results demonstrated that it was possible to simultaneously improve grain yield while enhancing flowering synchrony and plant architecture. The positive predicted gain for grain yield and the reduction in anthesis–silking interval indicate that the selected progenies combined productivity with improved reproductive efficiency under stress conditions. Stability across environments is a critical attribute for maize cultivation in West Africa, where erratic rainfall and heterogeneous soil fertility frequently limit the predictability of crop performance. Several studies have used these two methods for ideotyping in maize [29,30,31], yam [32], [33], and other crops [34].

4.5. Comparison of Selection Strategies

The comparison among BLUP-based selection, MGIDI, MTSI, and the Rank Sum index revealed important differences in selection outcomes. Direct BLUP selection produced the highest mean grain yield among the selected groups, reflecting its effectiveness for identifying high-performing progenies based solely on predicted performance. However, multi-trait indices such as MGIDI and MTSI prioritize balanced improvement across multiple traits and environments, which may explain their slightly lower mean yield values relative to BLUP selection. The Rank Sum index provided an intermediate outcome by integrating genotype rankings across multiple selection criteria, resulting in selection gains comparable to BLUP while maintaining consistency with multi-trait selection results. These findings illustrate the complementary nature of single-trait and multi-trait selection strategies in maize breeding programs. The comparison among BLUP-based selection, MGIDI, MTSI, and the Rank Sum index highlights the complementary nature of different selection philosophies in maize breeding. BLUP-based ranking maximizes predicted grain yield and therefore identifies progenies with the highest expected performance across environments. In contrast, multi-trait indices such as MGIDI and MTSI emphasize balanced improvement across multiple traits and environmental stability. As a result, these indices may select progenies with slightly lower predicted yield but with more desirable trait combinations and greater resilience to environmental variability. The Rank Sum index further integrates these complementary selection signals, enabling the identification of progenies consistently favored

across different analytical frameworks. Together, these approaches provide a more comprehensive basis for selection decisions than any single method alone. Similar comparison of selection strategies was also reported several researchers [31,34,35].

4.6. Concordance among Selection Methods and Breeding Implications

The overlap observed among selection methods further highlights the robustness of certain progenies across different selection criteria. The subset of progenies selected by all four methods represents particularly promising candidates for advancement, as they combine high predicted yield performance, favorable multi-trait profiles, and stable expression across environments. Such progenies are likely to possess underlying physiological mechanisms that confer resilience to multiple stress factors, including improved flowering synchrony, efficient resource allocation, and stable reproductive development. The integration of BLUP-based performance prediction with multi-trait and stability indices therefore provides a comprehensive framework for identifying superior breeding materials for developing stress resilient hybrids.

4.7. Implications for Climate-Resilient Maize Breeding in West Africa

Overall, the results of this study demonstrate that integrating mixed-model genetic evaluation with multi-trait and stability indices provides a powerful analytical framework for identifying stress-resilient maize progenies. This approach allows breeders to simultaneously consider yield potential, trait balance, and environmental stability, thereby improving selection accuracy in complex production environments. The progenies identified through this integrated selection framework represent valuable candidates for population improvement, synthetic variety development, or further hybrid breeding efforts targeting drought- and low-nitrogen-prone agro-ecologies in West Africa. It is important to note that the evaluated materials were progenies derived from a North Carolina Design I mating scheme intended for population improvement rather than finished hybrid cultivars. Consequently, the objective of the multi-trait selection analyses was not to identify candidate commercial hybrids but to identify superior crosses and parental combinations that can contribute favorable alleles for subsequent cycles of selection and synthetic variety development.

5. Conclusion

This study demonstrated that integrating mixed-model genetic evaluation with multi-trait selection indices provides an effective framework for identifying superior maize progenies under drought and low-nitrogen stress conditions in West Africa. Despite weak fixed stress effects, substantial genetic variation was detected for several key agronomic traits, indicating opportunities for selection within the evaluated population. The application of MGIDI and MTSI enabled simultaneous consideration of multiple traits and environmental stability, while BLUP-based selection maximized grain yield performance. The Rank Sum index further integrated these complementary selection signals to identify progenies consistently favored across different selection criteria. The overlap among selection methods highlighted a subset of progenies combining superior yield performance, favorable trait profiles, and stable expression across environments. Because the materials were derived from a North Carolina Design I mating scheme, these progenies represent valuable candidates for advancing recurrent selection, synthetic variety

development, and future hybrid breeding efforts targeting drought- and nitrogen-limited production systems in West Africa.

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Supplementary Materials

Table S1: Performance of 250 S1 Progenies for Grain Yield and Other Agronomic Traits under Combined Drought and Low-N Stress and their Corresponding MGIDI and MTSI Indices

Table S2: Grain Yield of Selected Progeny under Combined Drought and Low-N Stress using BLUP, MGIDI, MTSI, and Rank Sum Index.

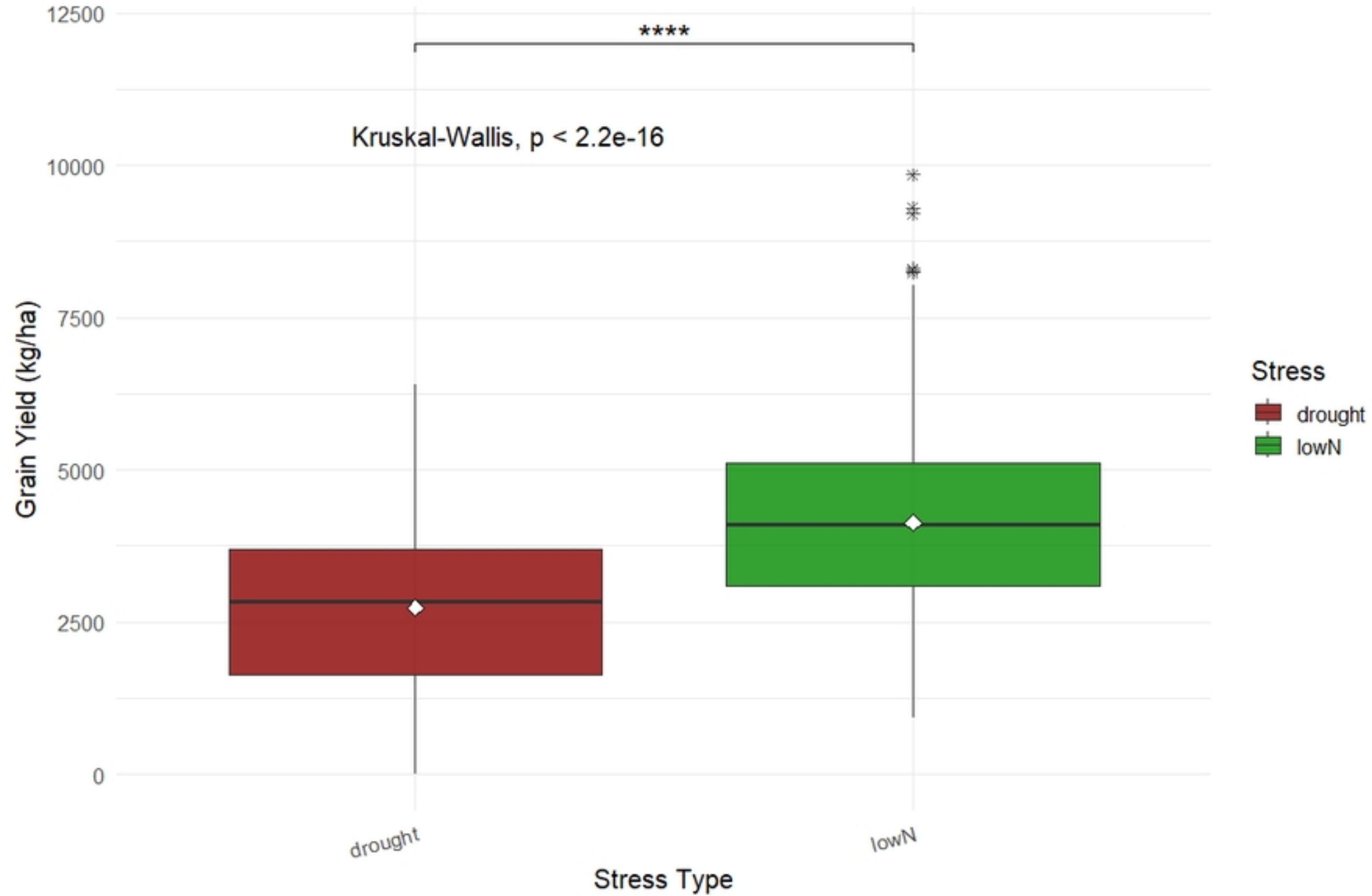


Figure 1

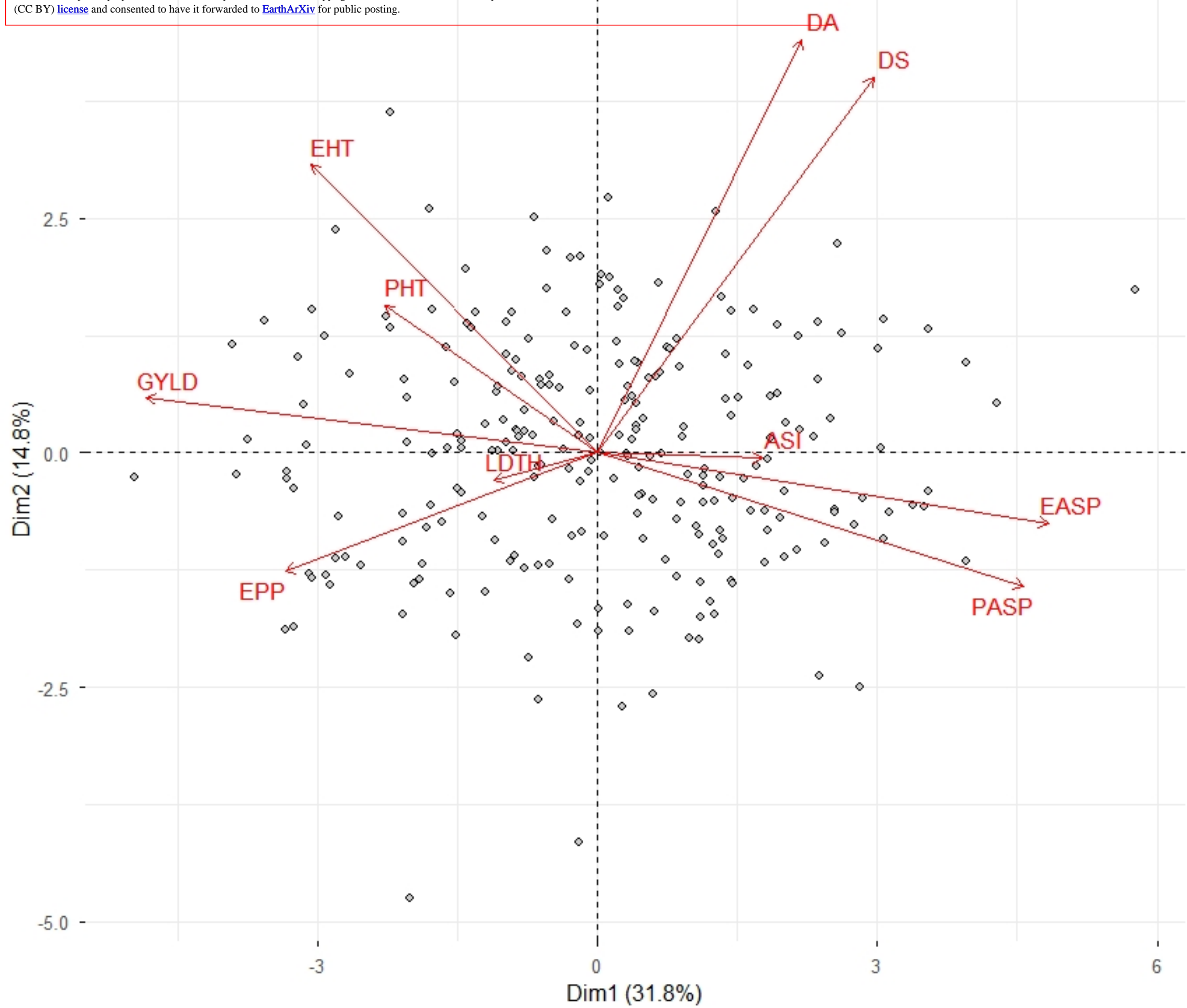


Figure 2

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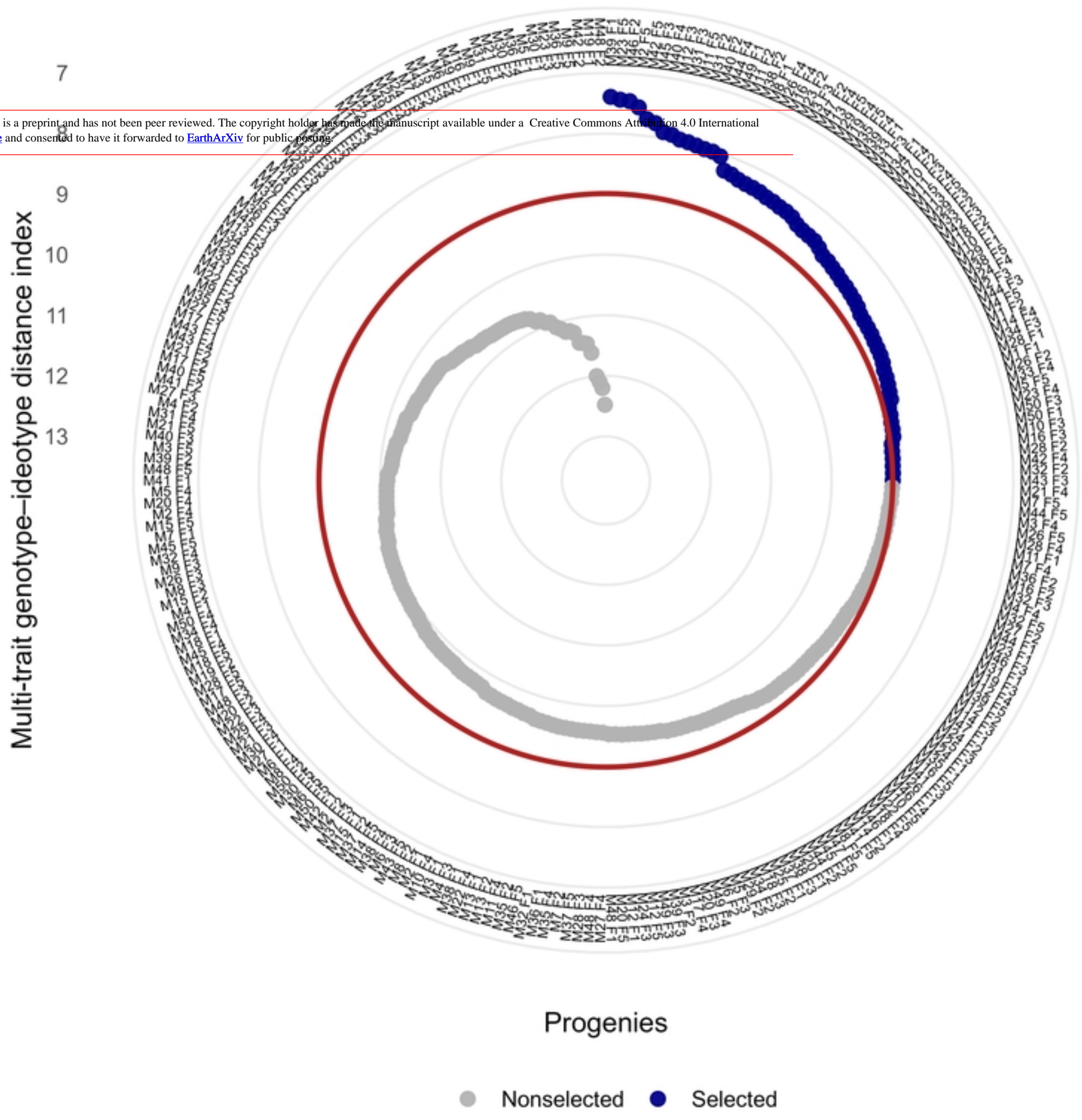


Figure 3

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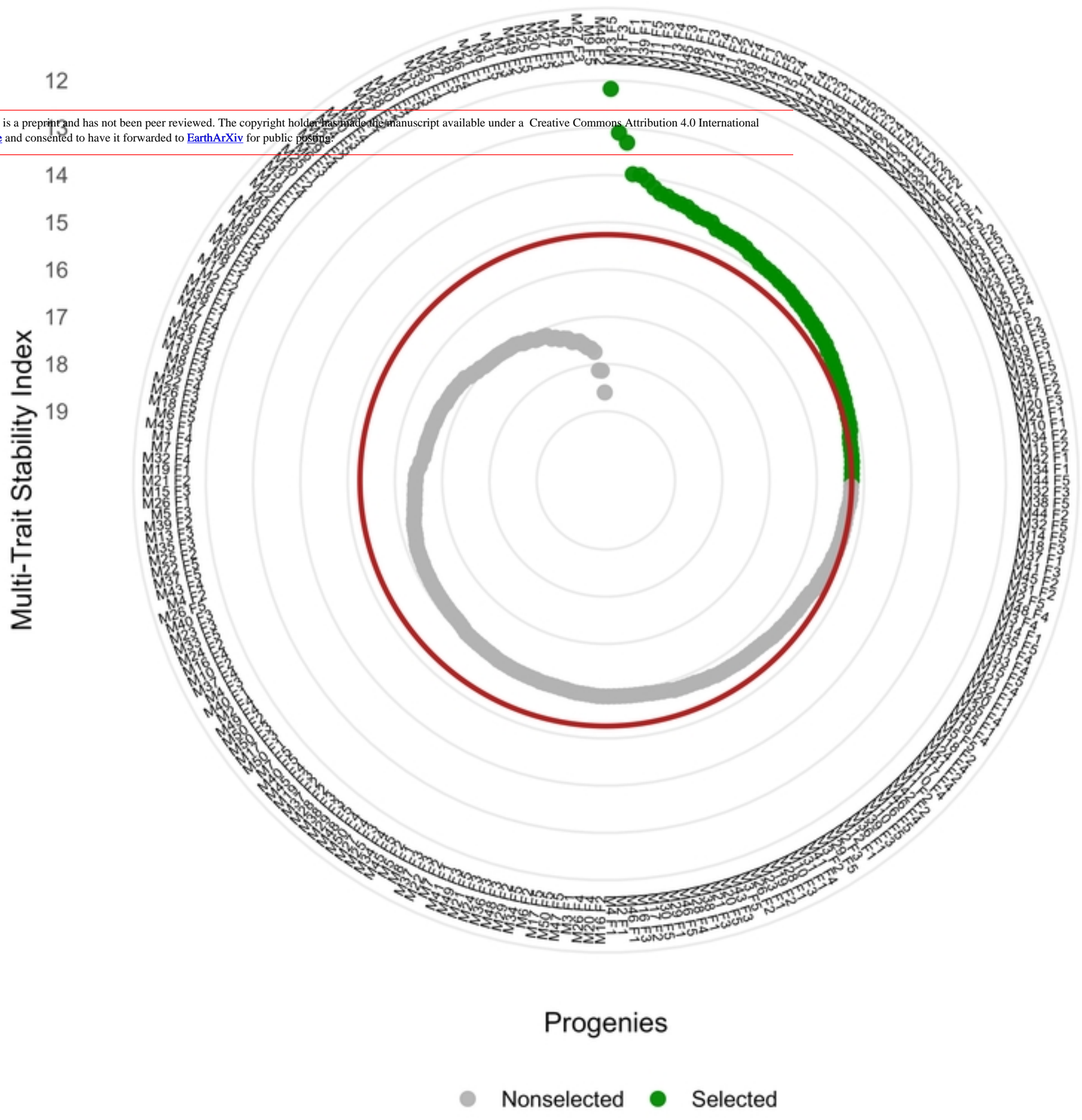


Figure 4

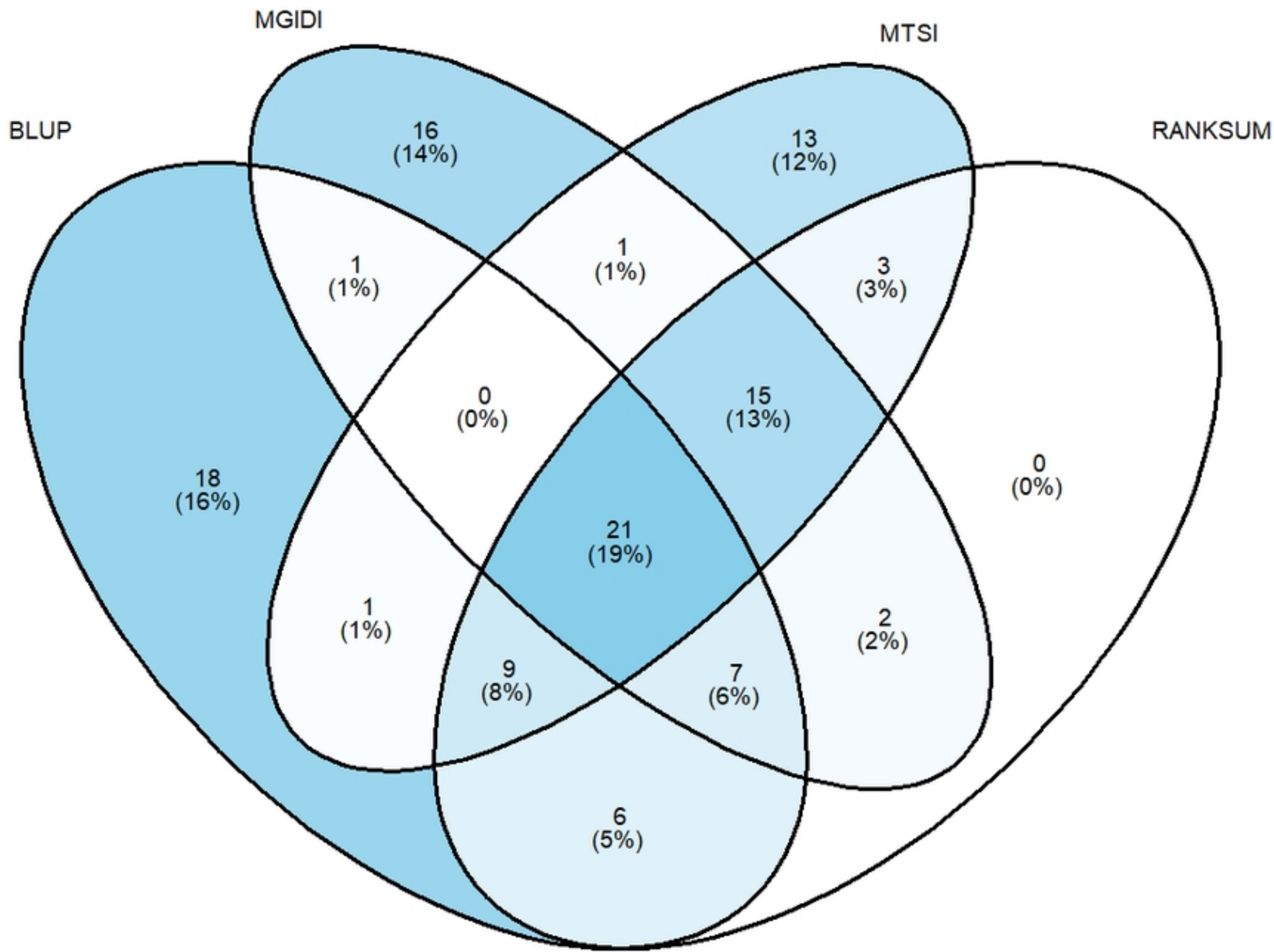


Figure 5