
STATISTICAL TEST FOR GENOTYPE AND ENVIRONMENT CONTRIBUTION IN THE GENOTYPES \times ENVIRONMENTS INTERACTION MATRIX

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SUMMARY

The objective of the present work was to propose a method for testing the contribution of each level of the factors in a genotypes \times environments ($G \times E$) interaction using multi-environment trials analyses by means of an F test. The study evaluated a data set, with twenty genotypes and thirty-four environments, in a block design with four replications. The sum of squares within rows (genotypes) and columns (environments) of the $G \times E$ matrix was simulated, generating 10000 experiments

to verify the empirical distribution. Results indicate a noncentral chi-square distribution for rows and columns of the $G \times E$ interaction matrix, which was also verified by the Kolmogorov-Smirnov test and $Q-Q$ plot. Application of the F test identified the genotypes and environments that contributed the most to the $G \times E$ interaction. In this way, geneticists can select good genotypes in their studies.

In experiments in which a group of genotypes is evaluated under different environments, a characteristic may vary among genotypes as environmental conditions differ. In other words, an interaction among the factors may occur. In this way, interaction genotypes \times environments ($G \times E$) is the result of a differential response of each genotype to environmental variation (Chaves, 2001)

Presence of the significant interaction is essential for the efficiency of the process of breeding and is able to positively or negatively affect its completion (González, 1988). A problem results from a deficiency of the genotypes to maintain a consistent pattern of

performance under the environments (Allard, 1971; Kang 1998). Soon, the interaction is not just a problem, but it is also an opportunity of which to take advantage.

Plant geneticists understand that $G \times E$ interaction is of great importance in obtaining superior varieties (Duarte and Vencovsky, 1999). However, it is necessary to understand the contribution of each genotype and environment in the interaction, since evaluations of differential behavior among genotypes in function of environmental diversity may cause changes in the relative position of genotypes such as for productivity, for example, or even the magnitude of their differences (Oliveira *et al.*, 2003).

The objective of the present work is to propose a method for testing the contribution of each genotype and environment in a $G \times E$ interaction using an F test. The F test was proposed as an analytical focus in the present work due to the importance of understanding the contribution of each genotype and environment in the interaction. This information will help geneticists select better genotypes and environments in their studies.

Material and Methods

Data characterization

Data used in the present study is the same as those used by Cornelius

KEY WORDS / Genotype and Environment Contribution / $G \times E$ Interaction / Noncentral Chi-Square Distribution / Modified F Test /

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and Crossa, 1999 and Dias and Krzanowski, 2003. Data were collected by CIMMYT (Centro Internacional de Mejoramiento de Maíz y Trigo) in experiments realized in several countries but different locations, thereby characterizing the data as multi-environmental. The experiment used 20 wheat genotypes, of these one was a 'durum' type of wheat and the other nineteen were a 'bread' type of wheat, in a randomized block design with four replications, where each genotype in this group was evaluated under 34 environments.

Simulation study

Initially, the behavior of the sum of squares within rows and columns of the genotypes \times environments ($G \times E$) interaction matrix was studied by simulation using the proc IML of SAS (2003), seeking to apply a test for the effects of genotype and environment.

Suppose $Y = [y_{ij}]$ is a double-entry table for a chosen data group, which is adjusted to the analysis of variance (ANOVA):

$$Y_{ij} = \mu + g_i + e_j + (ge)_{ij} + \varepsilon_{ij}$$

where Y_{ij} : average response of the i^{th} genotype of the j^{th} environment, μ : constant common to the responses (normally the general mean), g_i : effect of the i^{th} genotype ($i = 1, \dots, g$), e_j : effect of the j^{th} environment ($j = 1, \dots, e$), $(ge)_{ij}$: effect of the interaction of the i^{th} genotype with the j^{th} environment, and ε_{ij} : mean experimental error assumed independently, and $\varepsilon_{ij} \sim N(0, \sigma^2)$.

Consider a line over a letter to denote mean, with '·' indicating the subscript under which the total sum occurs. In this way, estimators of parameters of the above model are

$$\hat{\mu} = \frac{\sum_{ij} Y_{ij}}{ge} = \bar{Y}_{\cdot\cdot}$$

$$(\hat{ge})_{ij} = Y_{ij} - \frac{\sum_j Y_{ij}}{e} - \frac{\sum_i Y_{ij}}{g} + \frac{\sum_{ij} Y_{ij}}{ge} = Y_{ij} - \bar{Y}_{i\cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\cdot\cdot}$$

$$\hat{g}_i = \frac{\sum_j Y_{ij}}{e} - \hat{\mu} = \bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot} \quad \hat{e}_j = \frac{\sum_i Y_{ij}}{g} - \hat{\mu} = \bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot}$$

Thus, based on the original data it is possible to estimate $\hat{\mu}$, \hat{g}_i , \hat{e}_j and $(\hat{ge})_{ij}$ generating normally distributed random numbers with mean 0 and variance σ^2 for the term ε_{ij} (σ^2 is also estimated by mean square error $-MS_{Res}$). Replications that imitate the pattern of the original data can also be generated, but these have a built-in variability structure. For the data set, 10000 experiments were generated, from which the sum of squares of elements within rows and

columns of the $G \times E$ interaction matrix were obtained. A characteristic of the elements of these matrix is that the sum of squares is same the sum of squares of $G \times E$ interaction (Araújo, 2008).

To verify adhesion of the sum of squares of the simulated data to the non-central chi-square distribution used of the Kolmogorov-Smirnov test. Lastly, a Q-Q plot was constructed to visualize the adjustment of the noncentral chi-square distribution of rows and columns of the $G \times E$ interaction matrix.

Proposed statistical test to determine the contribution of G and E in the interaction

Let the interaction matrix $(G \times E)_{(g \times e)} = (\hat{ge})_{ij}$ be given as

$$(G \times E)_{(g \times e)} = \begin{pmatrix} \hat{ge}_{11} & \dots & \hat{ge}_{1e} \\ \dots & \dots & \dots \\ \hat{ge}_{g1} & \dots & \hat{ge}_{ge} \end{pmatrix}$$

Since the objective is to verify the contribution of each genotype and environment in the $G \times E$ interaction, the hypotheses tested are:

- i) H_{01} : the i^{th} genotype does not contribute to the $G \times E$ interaction, for every $i = 1, \dots, g$
- H_{a1} : the i^{th} genotype contributes to the $G \times E$ interaction, for some $i = 1, \dots, g$

The sum of squares (SS) due to the effect of genotype in the $G \times E$ interaction matrix is obtained by

$$SS_{G_i(G \times E)} = \sum_{j=1}^e (\hat{ge}_{ij})^2 \quad (i=1, 2, \dots, g)$$

with $((g-1)(e-1))/g$ degrees of freedom, and the corresponding mean square is obtained by dividing each sum of squares by their respective degrees of freedom, or rather

$$MS_{G_i(G \times E)} = \frac{SS_{G_i(G \times E)}}{(g-1)(e-1)} = \frac{g(SS_{G_i(G \times E)})}{(g-1)(e-1)}, \quad i=1, \dots, g$$

Note that $SS_{G1(G \times E)} + \dots + SS_{Gg(G \times E)} = SS_{G \times E}$, with $(g-1)(e-1)$ degrees of freedom, then these sums of squares ($SS_{G_i(G \times E)}$) are orthonormal.

The sum of squares due to the effect of genotype divided by their respective degrees of freedom follows a non-central chi-square distribution with noncentrality parameter θ_{i1} , in other words:

TABLE I
ANOVA WITH F TEST TO OBTAIN GENOTYPES THAT SIGNIFICANTLY CONTRIBUTE TO THE $G \times E$ INTERACTION

Source of variation	DF	SS	MS	F
Bd.E	$e(r-1)$	$SS_{Bd,e}$	$MS_{Bd,E}$	
G	$(g-1)$	SS_G	MS_G	
E	$(e-1)$	SS_E	MS_E	
$G \times E$	$(g-1)(e-1)$	$SS_{G \times E}$	$MS_{G \times E}$	
$G_i(G \times E)$	$((g-1)(e-1))/g$	$SS_{G1(G \times E)}$	$MS_{G1(G \times E)}$	$MS_{G1(G \times E)}/MS_{Res}$
$G_g(G \times E)$	$((g-1)(e-1))/g$	$SS_{Gg(G \times E)}$	$MS_{Gg(G \times E)}$	$MS_{Gg(G \times E)}/MS_{Res}$
Residual	$e(g-1)(r-1)$	SS_{Res}	MS_{Res}	
Total	$ger-1$	SS_{Total}		

$G_i(G \times E)$: effect of the i^{th} genotype on the interaction, with $i = 1, \dots, g$; Bd.E: blocks within environments; DF: degrees of freedom; SS: sum of squares; MS: mean squares.

$$\frac{SS_{G_i(G \times E)}}{\sigma^2} \sim \chi^2_{\frac{(g-1)(e-1)}{g}}(\theta_{i1}),$$

$$\text{where } \theta_{i1} = \frac{\sum_{j=1}^e (\hat{ge}_{ij})^2}{\sigma^2}.$$

In this way, see that

$$F^*_{G_i(G \times E)} = \frac{MS_{G_i(G \times E)}}{MS_{Res}} : F_{\frac{((g-1)(e-1))/g, e(g-1)(r-1)}{((g-1)(e-1))/g, e(g-1)(r-1)}}(\theta_{i1}).$$

The hypothesis $H_0: \theta_{i1} = 0$ vs $H_a: \theta_{i1} > 0$, is equivalent to the hypothesis H_{01} vs H_{a1} . Thus under H_0 , the statistic $F^*_{G_i(G \times E)}$ has a central F distribution with $((g-1)(e-1))/g$ and $e(g-1)(r-1)$ degrees of freedom (Moser, 1996). At significance level α , H_0 or H_{01} is rejected when

$$F_{G_i(G \times E)} = \frac{MS_{G_i(G \times E)}}{MS_{Res}} \geq F_{\frac{((g-1)(e-1))/g, e(g-1)(r-1)}{((g-1)(e-1))/g, e(g-1)(r-1)}} \quad \text{for } i = 1, \dots, g$$

Results of the F test applied to ANOVA, taking into consideration the decomposition of $(g-1)(r-1)$ degrees of freedom of the GE interaction with $((g-1)(e-1))/g$ degrees of freedom for genotypes is presented in Table I.

- ii) H_{02} : the j^{th} environment does not contribute to the $G \times E$ interaction for each $j = 1, \dots, e$
- H_{a2} : the j^{th} environment contributes to the $G \times E$ interaction for some $j = 1, \dots, e$

The sum of squares due to the effect of genotype on the $G \times E$ interaction matrix is obtained by

$$SS_{E_j(G \times E)} = \sum_{i=1}^g (\hat{ge}_{ij})^2 \quad (j=1, 2, \dots, e),$$

with $((g-1)(e-1))/e$ degrees of freedom.

The corresponding mean square is obtained by dividing each sum of squares by their respective degrees of freedom, in other words:

$$MS_{E_j(G \times E)} = \frac{SS_{E_j(G \times E)}}{(g-1)(e-1)} = \frac{e(SS_{E_j(G \times E)})}{(g-1)(e-1)}, \quad j = 1, \dots, e$$

Observe that $SS_{E1(G \times E)} + \dots + SS_{Ee(G \times E)} = SS_{G \times E}$, with $(g-1)(e-1)$ degrees of freedom.

The sum of squares due to the effect of genotype divided by their respective degrees of freedom follows a non-central chi-square distribution with noncentrality parameter θ_{2j} . In other words,

$$\frac{SS_{E_j(G \times E)}}{\sigma^2} \sim \chi^2_{\frac{(g-1)(e-1)}{e}}(\theta_{2j})$$

$$\text{where } \theta_{2j} = \frac{\sum_{i=1}^g (\widehat{ge}_{ij})^2}{\sigma^2}$$

In this way, verify that

$$F^*_{E_j(G \times E)} = \frac{MS_{E_j(G \times E)}}{MS_{Res}} \sim F_{\frac{(g-1)(e-1)}{e}, e(g-1)(r-1)}(\theta_{2j})$$

The hypothesis $H_0: \theta_{2j} = 0$ vs $H_a: \theta_{2j} > 0$, is the same as hypothesis H_{02} vs H_{a2} . Thus, under H_0 , the statistic $F^*_{E_j(G \times E)}$ has a central F distribution with $\frac{(g-1)(e-1)}{e}$ and $e(g-1)(r-1)$ degrees of freedom (Moser, 1996). At significance level α , H_0 or H_{02} are rejected when

$$F^*_{E_j(G \times E)} = \frac{MS_{E_j(G \times E)}}{MS_{Res}} \geq F_{\frac{(g-1)(e-1)}{e}, e(g-1)(r-1)} \quad \text{for } j=1, \dots, e$$

Results of the F test, applied to ANOVA, taking decomposition of $(g-1)(e-1)$ degrees of freedom of the $G \times E$ interaction with $\frac{(g-1)(e-1)}{e}$ degrees of freedom for environments into consideration, are presented in Table II.

Results and Discussion

Simulation study

Figures 1 and 2 represent histograms of the 10000 simulated experiments for the sum of squares of some row and columns in the $G \times E$ interaction matrix.

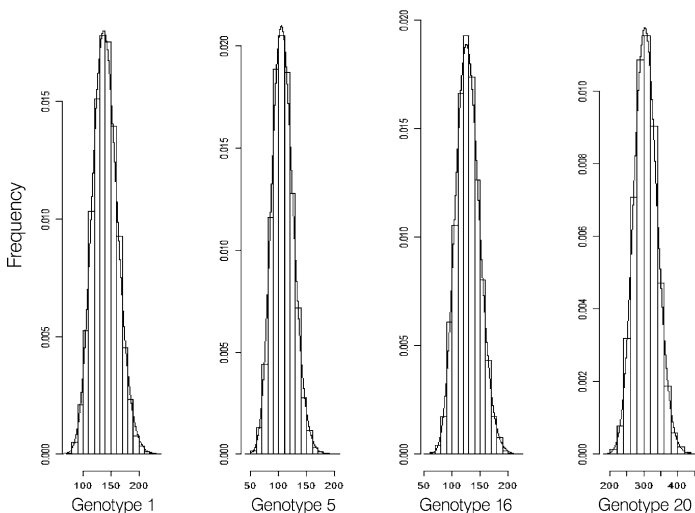


Figure 1. Histograms for SS of genotypes 1, 5, 16 and 20 with 10000 simulated experiments.

A continuous line represents a noncentral chi-square distribution and vertical bars represent an empirical distribution of the simulated genotype/environments sum of squares. Observe that distribution of the genotype sum of squares is nearly a non-central chi-square distribution.

Table III presents maximum likelihood estimates for noncentrality parameters and p-values for the Kolmogorov-Smirnov test. Note that θ varies among the genotypes, indicating that each genotype be tested with a specific noncentral F distribution to verify its contribution to the interaction. The p-value also shows that almost all the sum of squares due to genotypes within the $G \times E$ interaction follow a noncentral chi-square distribution. This was only not true for genotype 7 at a 5% significance level.

Quantile-quantile plot (Q-Q plot; Figures 3 and 4) illustrate that

TABLE II
ANOVA WITH F TEST TO OBTAIN ENVIRONMENTS THAT SIGNIFICANTLY CONTRIBUTE TO THE $G \times E$ INTERACTION

Source of variation	DF	SS	MS	F
Bd.E	$e(r-1)$	$SS_{Bd.E}$	$MS_{Bd.E}$	
G	$(g-1)$	SS_G	MS_G	
E	$(e-1)$	SS_E	MS_E	
$G \times E$	$(g-1)(e-1)$	$SS_{G \times E}$	$MS_{G \times E}$	
$E_1(G \times E)$	$\frac{(g-1)(e-1)}{e}$	$SS_{E_1(G \times E)}$	$MS_{E_1(G \times E)}$	$MS_{E_1(G \times E)} / MS_{Res}$
$E_e(G \times E)$	$\frac{(g-1)(e-1)}{e}$	$SS_{E_e(G \times E)}$	$MS_{E_e(G \times E)}$	$MS_{E_e(G \times E)} / MS_{Res}$
Residual	$e(g-1)(r-1)$	SS_{Res}	MS_{Res}	
Total	$ger-1$	SS_{Total}		

$E_j(G \times E)$: effect of the j^{th} environment of the interaction, with $j=1, \dots, e$; Bd.E: blocks within environments; DF: degrees of freedom; SS: sum of squares; MS: mean squares.

the points are arranged nearly in a straight line, which leads to the conclusion that these sum of squares have a noncentral chi-square distribution with a noncentrality pa-

rameter θ . This was true even for the sum of squares regarding genotype 7, which was rejected by the Kolmogorov-Smirnov test, showing a good adherence to a noncentral chi-square distribution.

Application to real data

Table IV presents the ANOVA results for a data set with 20 wheat genotypes and 34 environments in a randomized block design with four replications.

Table V contains results of the F test applied to ANOVA, taking into consideration the decomposition of $(g-1)(e-1) = (20-1)(34-1) = 627$ degrees of freedom of the $G \times E$ interaction with $\frac{(g-1)(e-1)}{g} = \frac{(20-1)(34-1)}{20} = 31.35$ degrees of freedom for the genotypes.

Note that only genotypes 3, 4, 6 and 15 were not significant at a 5% significance level. In other words, these genotypes did not contribute significantly to $G \times E$ interaction. The remaining genotypes were significant and contributed more to the interaction. And these genotypes may be better evaluated by breeders.

Table VI takes into consideration the decomposition of the same 627 degrees of freedom of the $G \times E$ interaction with $\frac{(g-1)(e-1)}{e} = \frac{(20-1)(34-1)}{34} \approx 18.44$ degrees of freedom for the environment with application of the F test in ANOVA.

Note that environments 2, 3, 8, 11, 13, 17, 21, 28, 30 and 31 do not contribute to the $G \times E$ interaction; conse-

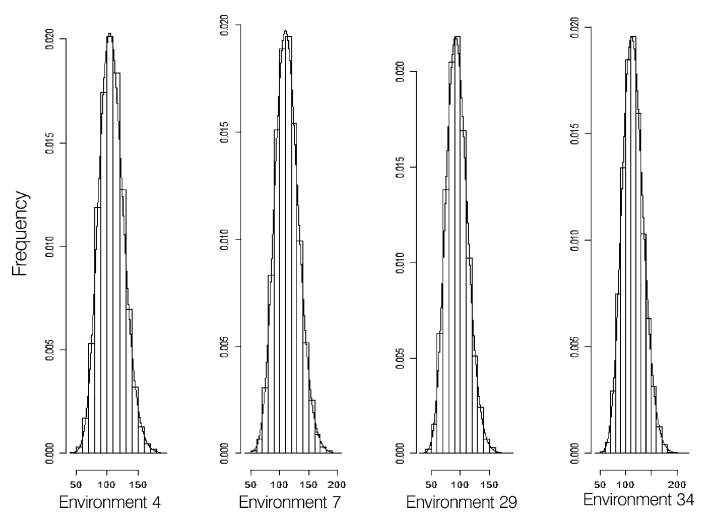


Figure 2. Histograms for SS of environments 4, 7, 29 and 34 with 10000 simulated experiments.

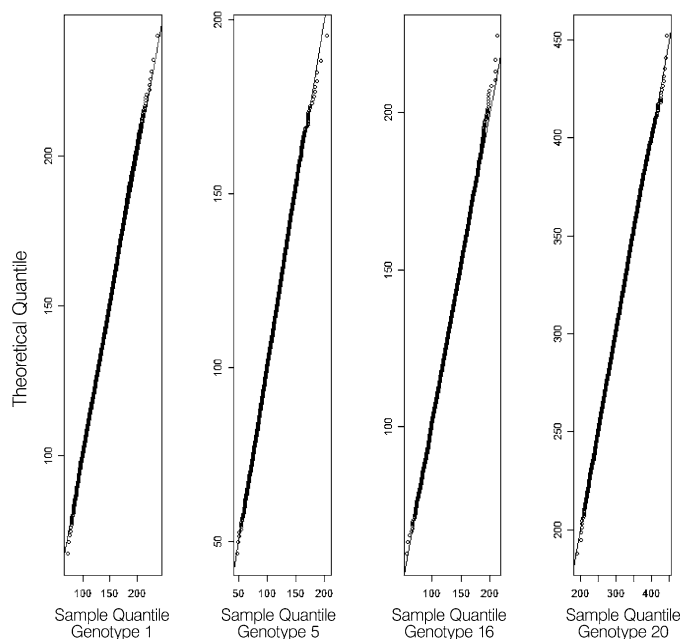


Figure 3. Q-Q plot for SS of genotypes 1, 5, 16 and 20 with 10000 simulated experiments.

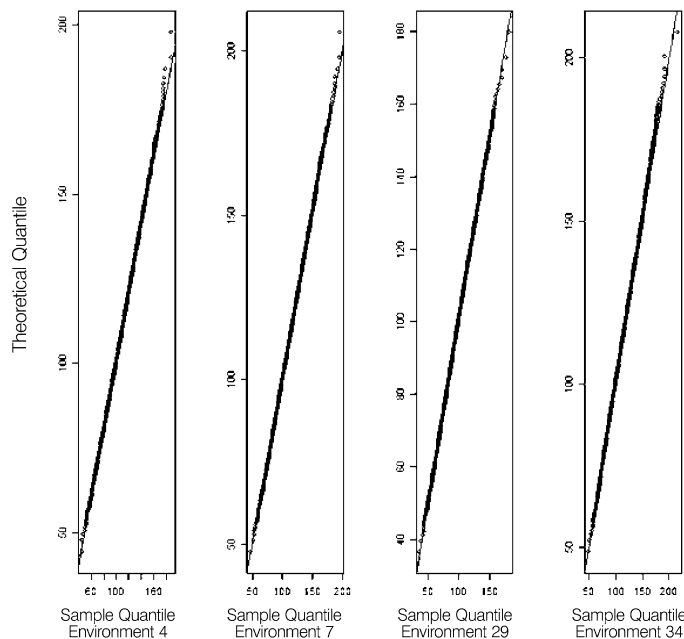


Figure 4. Q-Q plot for SS of environments 4, 7, 29 and 34 with 10000 simulated experiments.

TABLE III
ESTIMATES OF NONCENTRALITY PARAMETERS ($\hat{\theta}$) AND P-VALUES FOR THE KOLMOGOROV-SMIRNOV TEST FOR ADHERENCE TO A NONCENTRAL CHI-SQUARE DISTRIBUTION OF GENOTYPE SUM OF SQUARES FROM 10000 SIMULATED EXPERIMENTS

	$\hat{\theta}$	p-value		$\hat{\theta}$	p-value
G ₁	108.5437	0.1027	G ₁₁	52.0944	0.5212
G ₂	50.8489	0.2220	G ₁₂	109.3350	0.2460
G ₃	42.5279	0.2833	G ₁₃	56.5189	0.4606
G ₄	38.0294	0.1671	G ₁₄	108.9042	0.1850
G ₅	76.1384	0.1337	G ₁₅	37.1842	0.1471
G ₆	44.4034	0.3644	G ₁₆	97.0332	0.4719
G ₇	96.7086	0.0207	G ₁₇	116.6613	0.1173
G ₈	73.8949	0.8790	G ₁₈	58.8805	0.2883
G ₉	52.6225	0.2367	G ₁₉	106.1936	0.2299
G ₁₀	76.4783	0.7882	G ₂₀	274.4027	0.2886

quently, these environments can be better evaluated by geneticists due to the genotypes homogeneous response to this variable. The remaining environments contributed significantly (at a 5% significance level) to the interaction.

TABLE IV
ANOVA FOR DATA SET WITH 20 WHEAT GENOTYPES, 34 ENVIRONMENTS WITH IN A RANDOMIZED BLOCK DESIGN WITH FOUR REPLICATIONS

Source of variation	DF	SS	MS	F	p-value
Bd.E	102	257862519	2528064	7.14	<0.0001
G	19	89066441	4687707	13.23	<0.0001
E	33	4333925428	131331074	370.67	<0.0001
G×E	627	594108485	947541	2.67	<0.0001
Residual	1938	686646195	354307		
Total	2719	5961609068			

Bd.E: blocks within environments; DF: degrees of freedom; SS: sum of squares; MS: mean squares.

Conclusions

The sum of squares of rows and columns of a genotypes × environments interaction matrix follows a noncentral chi-square distribution that was detected by a combination of the Kolmogorov-Smirnov method and Q-Q plot. The test proposed to detect which genotypes and environments contribute the most to an interaction has many advantages. Not only is it easy to apply and interpret, but it also does not require many calculations and can easily be implemented on a computer.

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TABLE V
F TEST APPLIED TO DATA SET TO OBTAIN GENOTYPES THAT CONTRIBUTE SIGNIFICANTLY TO THE G×E INTERACTION

Source of variation	DF	SS	MS	F	p-value	Source of variation	DF	SS	MS	F	p-value
G ₁ (G×E)	31.35	38419779	1225511.30	3.46	<0.0001	G ₁₁ (G×E)	31.35	18457831	588766.55	1.66	0.0122
G ₂ (G×E)	31.35	18000775	574187.39	1.62	0.0164	G ₁₂ (G×E)	31.35	38927562	1241708.50	3.50	<0.0001
G ₃ (G×E)	31.35	15051875	480123.62	1.35	0.0910	G ₁₃ (G×E)	31.35	20045716	639416.78	1.80	0.0042
G ₄ (G×E)	31.35	13438384	428656.59	1.21	0.1970	G ₁₄ (G×E)	31.35	38666042	1233366.60	3.48	<0.0001
G ₅ (G×E)	31.35	26944156	859462.70	2.42	<0.0001	G ₁₅ (G×E)	31.35	13098543	417816.37	1.18	0.2278
G ₆ (G×E)	31.35	15771832	503088.74	1.42	0.0619	G ₁₆ (G×E)	31.35	34294875	1093935.40	3.09	<0.0001
G ₇ (G×E)	31.35	34115953	1088228.20	3.07	<0.0001	G ₁₇ (G×E)	31.35	41353606	1319094.30	3.72	<0.0001
G ₈ (G×E)	31.35	26152950	834224.88	2.35	<0.0001	G ₁₈ (G×E)	31.35	20927058	667529.76	1.88	0.0022
G ₉ (G×E)	31.35	18638713	594536.31	1.68	0.0109	G ₁₉ (G×E)	31.35	37625900	1200188.20	3.39	<0.0001
G ₁₀ (G×E)	31.35	27052040	862903.98	2.43	<0.0001	G ₂₀ (G×E)	31.35	97124895	3098082.80	8.74	<0.0001

TABLE VI
F TEST APPLIED TO DATA SET TO OBTAIN ENVIRONMENTS THAT CONTRIBUTE SIGNIFICANTLY TO THE G×E INTERACTION

Source of variation	GL	SS	MS	F	p-value	Source of variation	GL	SS	MS	F	p-value
E ₁ (G×E)	18.44	16838211.0	913076.83	2.5770810	0.0002	E ₁₈ (G×E)	18.44	34465014.0	1868916.20	5.2748558	<0.0001
E ₂ (G×E)	18.44	6501297.7	352542.46	0.9950209	0.4628	E ₁₉ (G×E)	18.44	21472712.0	1164389.50	3.2863895	<0.0001
E ₃ (G×E)	18.44	6448827.2	349697.17	0.9869903	0.4724	E ₂₀ (G×E)	18.44	30798200.0	1670077.80	4.7136514	<0.0001
E ₄ (G×E)	18.44	31408385.0	1703166.00	4.8070400	<0.0001	E ₂₁ (G×E)	18.44	7480479.7	405640.05	1.1448843	0.2997
E ₅ (G×E)	18.44	37599852.0	2038907.50	5.7546415	<0.0001	E ₂₂ (G×E)	18.44	18406653.0	998127.92	2.8171305	<0.0001
E ₆ (G×E)	18.44	26887597.0	1458019.60	4.1151354	<0.0001	E ₂₃ (G×E)	18.44	10940424.0	593260.61	1.6744272	0.0356
E ₇ (G×E)	18.44	33399579.0	1811141.50	5.1117914	<0.0001	E ₂₄ (G×E)	18.44	16740586.0	907782.95	2.5621395	0.0003
E ₈ (G×E)	18.44	8687710.9	471103.94	1.3296505	0.1566	E ₂₅ (G×E)	18.44	21066198.0	1142345.70	3.2241727	<0.0001
E ₉ (G×E)	18.44	20359469.0	1104022.20	3.1160081	<0.0001	E ₂₆ (G×E)	18.44	17427185.0	945014.82	2.6672233	0.0001
E ₁₀ (G×E)	18.44	12093933.0	655811.38	1.8509714	0.0150	E ₂₇ (G×E)	18.44	13639858.0	739641.45	2.0875746	0.0043
E ₁₁ (G×E)	18.44	9053531.4	490941.10	1.3856391	0.1258	E ₂₈ (G×E)	18.44	10275510.0	557204.67	1.5726624	0.0569
E ₁₂ (G×E)	18.44	18406587.0	998124.34	2.8171203	<0.0001	E ₂₉ (G×E)	18.44	27022757.0	1465348.90	4.1358215	<0.0001
E ₁₃ (G×E)	18.44	4906271.5	266049.81	0.7509028	0.7630	E ₃₀ (G×E)	18.44	3011783.5	163318.40	0.4609522	0.9752
E ₁₄ (G×E)	18.44	15826596.0	858220.51	2.4222538	<0.0001	E ₃₁ (G×E)	18.44	4996776.7	270957.59	0.7647545	0.7471
E ₁₅ (G×E)	18.44	12162492.0	659529.07	1.8614642	0.0142	E ₃₂ (G×E)	18.44	10857237.0	588749.69	1.6616955	0.0378
E ₁₆ (G×E)	18.44	16377350.0	888085.98	2.5065465	<0.0001	E ₃₃ (G×E)	18.44	28897327.0	1567000.20	4.4227237	<0.0001
E ₁₇ (G×E)	18.44	5595639.5	303431.81	0.8564103	0.6357	E ₃₄ (G×E)	18.44	34056454.0	1846761.50	5.2123258	<0.0001

PRUEBA ESTADÍSTICA PARA LA CONTRIBUCIÓN DE LOS GENOTIPOS Y AMBIENTES EN LA MATRIZ DE LA INTERACCIÓN GENOTIPO × AMBIENTE

Mirian Fernandes Carvalho Araújo, Lúcio Borges de Araújo, Priscila Neves Faria y Carlos Tadeu dos Santos Dias

RESUMEN

El presente trabajo tiene como objetivo proponer un método para evaluar la contribución de cada genotipo y el medio ambiente en la interacción genotipo × ambiente (G×E) en ensayos multi-ambiente mediante una prueba estadística F. Se analizó un conjunto de datos referente a 20 genotipos y 34 ambientes con cuatro bloques. Se simuló las sumas de los cuadrados de las filas (genotipos) y columnas (ambientes) de la matriz G×E, generando 10000 experimentos para verificar la distribución empírica. Los resultados muestran una

distribución chi-cuadrado no central para las filas y columnas de la matriz de interacción G×E, que también se verificó mediante la prueba de Kolmogorov-Smirnov y el gráfico Q-Q plot. En la aplicación de la prueba F fueron identificados los genotipos y ambientes que más contribuyeron a la interacción G×E. De esta forma, los seleccionadores pueden escoger buenos genotipos y ambientes en sus estudios.

TESTE ESTATÍSTICO PARA CONTRIBUIÇÃO DE GENÓTIPOS E AMBIENTES NA MATRIZ DE INTERAÇÃO GENÓTIPOS × AMBIENTES

Mirian Fernandes Carvalho Araújo, Lúcio Borges de Araújo, Priscila Neves Faria e Carlos Tadeu dos Santos Dias

RESUMO

O presente trabalho teve por objetivos propor um método para testar a contribuição de cada genótipo e ambiente para a interação genótipos × ambientes (G×E) em ensaios multi-ambientais pr meio de um teste F. O estudo avalia um conjunto de dados, com vinte genótipos e trinta e quatro ambientes com quatro blocos. Simulou-se as somas de quadrados das linhas (genótipos) e colunas (ambientes) da matriz de interação G×E gerando-se 10000 experi-

mentos para verificar a distribuição empírica. Os resultados indicaram distribuição qui-quadrado não-central para as linhas e colunas da matriz de interação G×E, verificados também pelo teste de Kolmogorov-Smirnov e o gráfico Q-Q plot. Na aplicação do teste F identificou-se os genótipos e ambientes que contribuíram mais para a interação G×E. Dessa forma, os melhoristas podem selecionar bons genótipos e ambientes nos seus estudos.