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# Evaluating the adaptability and stability of common peanut varieties (*Arachis hypogaea L.*) in Northern Mozambique using the AMMI Bayesian model

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## Abstract

This study evaluated the stability and adaptability of common peanut cultivars (*Arachis hypogaea* L.) in three locations across northern Mozambique over four years, using the additive main effects and multiplicative interaction model (AMMI) under a Bayesian approach. The multi-environmental data consisted of 20 genotypes evaluated in three locations. We analyzed grain yield in tons per hectare in a complete randomized block design for each location. The results indicated that genotypes with higher marginal yield contribute to the genotype by environment interaction (GEI) and thus are not largely recommended for the entire target environment. The Namapa (NMP) location showed consistent behavior and did not contribute to the GEI effect, and in this sense, G6 and G7 would be the best indications for this location. Moreover, genotypes considered stable, with emphasis on the G20 genotype, did not have a good average yield. Mapupulo (MPPL) and Nampula (NLP) had a significant contribution to GEI, and the best genotypes for these locations were G7 and G3, respectively. In this sense, the results of the analysis specified that using genotypes in specific environments would be the best strategy to decrease the effect of GEI and increase peanut productivity in the environments considered.

**Keywords:** Bayesian inference; genetic merits; genotype × environment interaction; multi-environment data; prediction. **Abbreviations:** AMMI\_additive main effects and multiplicative interaction; AMMI-2\_ AMMI model fitted with two bilinear components; BAMMI\_Bayesian-AMMI; BAMMI-2\_Bayesian-AMMI fitted with two bilinear components; boa\_Bayesian output analysis; E\_environment; G\_genotype; GEI\_genotype × environment interaction; HPD\_highest posterior density; ICRISAT\_ International Crops Research Institute for the Semi-Arid Tropics; MET\_multi-environment trial; MPPL\_Mapupulo; NLP\_Nampula; NMP\_Namapa; NSC\_ National Seed Committee; PC1\_ first principal component; PC2\_ second principal components.

## Introduction

Peanuts are an important source of food and are either used as oil or for consumption. The Government of Mozambique periodically publishes a list of varieties that can be legally distributed or sold in the country. To enter this list, a new variety must first be registered and released by the National Seed Committee (NSC) (Rohrbach et al., 2001). Providing technical details of the evaluation and registration and releasing the varieties are responsibilities of a subcommittee whose deliberations must be confirmed by the NSC.

Variety release requires at least three years of testing at research stations and farmers' fields in Mozambique. A new variety must have higher productivity or quality compared to the existing ones. Moreover, the variety must also show less susceptibility to the main diseases and pests. Palatability and processing qualities are considered advantageous but are not required for release. Plant breeders use data from multienvironmental trials (MET) to select superior genotypes. One of the major obstacles for selecting superior genotypes is the presence of the genotype-by-environment interaction (GEI), which is characterized by the differential response of the genotypes to a change in the environment. Thus, GEI studies are extremely important in breeding programs, as they allow for the selection of widely or specifically adapted genotypes, as well as the location for the next breeding cycles, among other advantages (Vargas et al., 2015; Hernández et al., 2019; Alvarado et al., 2020). Therefore, while modelling MET data, one should consider the GEI effect accurately and include appropriate genetic and nongenetic effects according to the sources of variation associated with the experimental designs. These analyses should provide breeders with clear and accurate information to support their selection (Smith and Cullis, 2018). In general, a GEI study includes adaptability and stability. Adaptability refers to the ability of a genotype to respond positively to the stimulus of the environment, whereas stability refers to the highly predictable behavior of genotypes in the face of environmental diversity (Souza et al., 2020). Different methodologies for assessing adaptability and stability have been developed and improved. Such procedures are based on analysis of variance, linear and non-linear regression, multivariate analysis, and nonparametric statistics (Crossa, 1990; Smith et al., 2015; Nuvunga et al., 2019). Of the methodologies used in the evaluation of GEI, those based on multiplicative analysis allow for a more careful exploration of the response pattern of genotypes between environments. The advantage of multiplicative methods lies in their ability to separate noise patterns, the possibility of grouping similar environments and genotypes, and the flexibility to identify genotypes with the greatest potential in each subgroup of environments. This analysis is relatively simple owing to the use of graphic representations, named biplots (Gabriel, 1971; Yan, 2016). Among the multiplicative models, AMMI (additive main effects and multiplicative interactions) has been widely used by plant breeders in the analysis of MET data (Hadasch et al., 2017; Shahriari et al., 2018). Recent studies propose the application of the Bayesian methodology to the AMMI analysis. Bayesian-AMMI (BAMMI) provides meaningful advantages and broad perspectives for the analysis of MET data. Bayesian modeling provides flexibility to treat unbalanced data and heterogeneous environmental variance, enabling more accurate estimates of bilinear parameters (Oliveira et al., 2015; Silva et al., 2015; Romão et al., 2019; Silva et al., 2019; Nuvunga et al., 2021; Oliveira et al., 2021). Moreover, the Bayesian paradigm includes a flexible parametric method to incorporate inference in to the biplot through bivariate credible regions for genotypic and environmental scores and the incorporation of information from previous experiments, using proper prior distributions (Perez-Elizalde et al., 2012; Jarquín et al., 2016; Silva et al., 2020). The main objective of this study was to evaluate the adaptability and stability of common peanut varieties (Arachis hypogaea L.) in northern Mozambique using the Bayesian AMMI model.

#### Results

#### Properties of Markov chains

All posterior samples (Markov chains) generated showed good convergence properties. Trace plots from the samples and marginal posterior densities for variance components are shown in Figure 1. Figures 1(A) and 1(C) illustrate the convergence properties. Samples can be considered independent in the posterior distribution.

#### Analyzing the main effects of genotypes

Point and interval posterior estimates for singular values and components of variance are shown in Table 1. The first two main axes explained 98% of the GEI sum of squares. The AMMI-2 biplot representation in the plane defined by the first two principal components (PC 1 and PC 2) could thus be considered representative of the analyzed data.

In Figure 2, the marginal posterior means of genotypic effects and their highest posterior density (HPD) 95% credibility regions are presented, ranked in increasing order of magnitude from left to right. Overlaps indicated similar yields. However, the interval estimate for G12 did not incorporate the zero value, indicating that, at the level of credibility considered, the yield of this genotype is likely to be higher than the general mean.

## Biplot analysis of GEI interaction

Stability information could be obtained by analyzing the AMMI-2 biplot representation (Figure 3). For this analysis, the uncertainty of the genotypic and environmental scores

was quantified by incorporating bivariate HPD (95%) credibility regions. Only regions not including the origin were represented to facilitate interpretations, as the others presented no relevant interaction.

Subgroups composed of genotypes and environments with similar GEI effects (homogeneous) are ascertained by identifying positions, directions from the origin, and overlaps in the bivariate regions in relation to the quadrants in the biplot (Júnior et al., 2018). Although there were overlaps, homogeneous subgroups of genotypes {G6, G12, G15} and {G1, G17} could be identified to the left of PC1. Another homogeneous subgroup {G2, G3, G7, G10, G11, G14} could be identified to the right of PC1. The main homogeneous subgroups of environments were {E1, E3, E15}, {E4, E10}, and {E9, E12}. The genotypes and environments not represented in the biplot comprised separable subgroups (genotypic and environmental) that did not contribute significantly to the GEI effect (stable). Adaptability and genotype recommendations to specific environments are also based on the positions and overlaps of the bivariate regions in the quadrants.

The analysis of the information from the biplot and that shown in Figure 1 shows that G6 and G12, which have the highest yield, contributed significantly to GEI and therefore are not frequently recommended. These genotypes, together with G15 and G17, were positively associated with E1 and E3 environments. Other associations included the association between the subgroup of genotypes to the right of PC1 and the subgroup {E9, E12} and the association between the G1 genotype and environments E4 and E10. However, it should be emphasized that the environments represented incorporate locations and crop seasons (Table 3), and a more detailed analysis must be conducted.

The NLP site, which corresponds to environments E1, E4, E7, and E10, made an important contribution to GEI in 2014, 2015, and 2017 crop seasons, showing consistency in the 2015 and 2017 crop seasons and stability in 2016. Similarly, the MPPL site (E3, E6, E9, E12) showed consistency in the 2016 and 2017 crop seasons, stability in 2015, and different results, compared to those in the other crop seasons, in 2014. The NMP site, in turn, showed consistency in all experiments and could be considered stable, making no important contribution to GEI.

Thus, although the genotypes to the left of the biplot were adaptable to the NLP and MPPL sites, only in the 2014 crop season were they usually not adequate for these locations and indicated only for NMP, which, in turn, did not contribute to GEI. The best genotypes for NMP were the two with the stronger main genotypic effect (G12 and G6; Figure 1). The best genotypes were thus G7 and G3 for NLP and MPPL, respectively.

#### Discussion

The evaluation of the productivity of peanut cultivars for different crop seasons and environmental circumstances is necessary to form inferences on the adaptability and stability for different cultivars, regions, and situations of water availability (Távora and Melo, 1991). As noted, the NLP and MPPL sites seem to have been affected by some factor in the 2014 crop season (this year was atypical), contrasting the other crop seasons, as identified by the biplot interpretation, and this might be due to low precipitation in that year. Thangthong et al. (2018) emphasized that many peanut breeding programs are seeking to improve the productivity of genotypes under

Table 1. Point and interval posterior estimates of distributions of singular values and components of variance.

Parameters	Mean	Sd	HPD interva	HPD intervals (95%)	
			LL	UL	
λ1	7.500	0.599	6.335	8.678	
λ <sub>2</sub>	4.341	0.682	3.027	5.670	
$\lambda_3$	1.292	0.962	<0.001	3.078	
$\lambda_4$	0.422	0.402	<0.001	1.255	
λ <sub>5</sub>	0.189	0.222	<0.001	0.656	
$\lambda_6$	0.090	0.125	<0.001	0.356	
λ <sub>7</sub>	0.044	0.075	<0.001	0.198	
$\lambda_8$	0.022	0.043	<0.001	0.098	
λ <sub>9</sub>	0.011	0.026	<0.001	0.051	
λ <sub>10</sub>	0.005	0.015	<0.001	0.026	
λ <sub>11</sub>	0.003	0.009	<0.001	0.013	
$\sigma_g^2$	0.064	0.037	0.014	0.144	
$\sigma_{e}^{2}$	0.6521	0.0515	0.556	0.758	

Sd, standard deviation; HPD, highest posterior density; LL, lower limit; UL, upper limit.



**Fig 1**. Trace and density plots of the marginal posterior distributions for genotypic variance in (A) and (B), and error variance (C) and (D), obtained from the markov chains generated in the sampling process.

			of the locations	where the ex	perments were cor	laactea III h	nozumbique.
District	Province	Location	Climate	Ground	Precipitation (mm)	Temp (° C)	Altitude (m)
Eráti	Nampula	13 ° 13 '17 "S, 38 ° 52 '34 "E	Tropical- humid	Sandy	800-1000	25-37	228

Alluvial

1300-1500

Semi-arid,

Subhumid

20-25

200-500

Table 2. Geographic and climatic characteristics of the locations where the experiments were conducted in Mozambique.

Temp= Temperature.

Montepuez

Cabo

Delgado

13 ° 06'18.3 "S 39

° 01'22.9" E



**Fig 2**. Highest Posterior Density (HPD) credibility intervals (95%) for the main effects of genotypes (G) for the 20 peanut hybrids evaluated in three districts of Northern Mozambique. HPDs are ranked in ascending order of their posterior averages. Genotypes with HPD that do not cross zero baseline are good to selection for average environment.

Location	Year	Environments
Nampula (NLP)	2014/15	E1
Namapa (NMP)	2014/15	E2
Mapupulo (MPPL)	2014/15	E3
Nampula (NLP)	2015/16	E4
Namapa (NMP)	2015/16	E5
Mapupulo (MPPL)	2015/16	E6
Nampula (NLP)	2016/17	E7
Namapa (NMP)	2016/17	E8
Mapupulo (MPPL)	2016/17	E9
Nampula (NLP)	2017/2018	E10
Namapa (NMP)	2017/2018	E11
Mapupulo (MPPL)	2017/2018	E12

 Table 3. Environments composed of the combination of locations with crop seasons.



**Fig 3.** Bivariate HPD credibility regions (95%) for genotypic (G) and environmental (E) scores in bayesian AMMI biplot considering the first two principal components (BAMMI-2). Multi-environmental trial for 20 peanut hybrids in three districts of Northern Mozambique. Just the regions that do not enclose the origin (0,0) are depicted to better illustrate GE interactions.



Fig 4. Map from the Northern Mozambique showing in pale yellow the provinces in which the peanut hybrids experiments were installed.

water deficiency. However, atypical climate changes have been observed recently, characterized by times with normal rainfall (ideal for cultivation), very intense rains, and severe droughts (Carrega et al., 2019). In our study, 2016 was characterized by intense (above normal) rainfall (INAM, 2017). When very heavy rains or severe droughts occur, the damage caused to crops is generally quite significant, which has increased the importance of studies on water stress within the peanut breeding programs (Paz et al., 2000; Kambiranda et al., 2011). The stress caused by water deficiency reduces the stomatal resistance, photosynthetic rate, transpiration, leaf temperature, leaf water potential, and vegetative mass, among others, causing a drop in productivity (Larcher et al., 1981) and impairments in the quality of the grains or the viability of the seeds, mainly owing to the lack of water during the filling of the pods (Carrega et al., 2019). Thus, one of the main features of a cultivar/variety of any crop is its ability to perform well when grown under different environmental conditions, which was not observed in any peanut cultivar evaluated here. Although the G20 genotype had better performance among the stable genotypes, it did not show a higher yield in any of the locations that make up the target environment. Thus, none of the tested genotypes performed well in all environments. This is due to the existence of cross-GEI, as reported here, and this represents a major challenge for breeders concerned with controlling genetic variability.

## **Materials and Methods**

#### **Plant materials**

The treatments comprised 20 genotypes (cultivars) of common peanuts (A. hypogaea L) that were made available by International Crops Research Institute for the Semi-Arid Tropics (ICRISAT-Malawi) in an advanced generation. The genotypes were as follows: ICGV-SM 01731 (G6); ICGV-SM 03590 (G14); ICGV-SM 06637 (G2); ICGV-SM 90704 (G20); ICGV-SM 07544 (G13); ICGV-SM 06518 (G1 ); ICGV-SM 08501 (G8); JL-24 (G19); ICGV-SM 05593 (G15); ICGV-SM 05688 (G12); CG-7 (G18); ICGV-SM 02724 (G10); ICGV- SM 08503(G9); ICGV-SM 07599 (G11); ICGV-SM 03710 (G7); ICGV-SM 06525 (G3); ICGV-SM 06519 (G3); ICG 12991 G16); ICGV-SM 07517 (G17); ICGV-SM 08560 (G5). These materials are the results of crosses between Spanish and Virginia lines. Crossings and selection were carried out under controlled conditions by ICRISAT-Malawi, which is one of the main suppliers of genetic material to countries in the sub-Saharan region. The objective of these crosses was to obtain tolerant or even resistant genotypes to the rosette. Material identified as promising was evaluated for adaptation to rosette tolerance in different agroecological conditions in northern Mozambique.

#### Characteristics of experimental area

The trials were carried out in Namapa (District of Eráti, province of Nampula), Mapupulo (district of Motepuez, province of Cabo Delgado), and district of Namuno (province of Cabo Delgado) located in northern Mozambique, during the 2014/15, 2015/16, 2016/17, and 2017/18 crop seasons. Geographic and climatic characteristics of the locations where the trials were performed are shown in Table 2. A map with the locations where the tests were performed is shown in Figure 4.

The different combinations between locations and crop seasons resulted in 12 different environments, as shown in

Table 3. Thus, the multi-environmental data analyzed are comprised of 20 genotypes evaluated in 12 environments.

# Experimental design

In each location, a complete randomized block design was used, with two replications and plots consisting of four rows of 5 m, spaced 0.6 m apart, with a sowing density of 20 viable seeds per linear meter, considering the two central lines as a useful plot. Basic fertilization was performed in accordance with the chemical analysis of the soil. Weed and pest control was performed according to the technical recommendations for the crop. The yield of shelled peanuts per plot was measured in t/ha and adjusted to 10% moisture.

# Statistical methods

#### AMMI Bayesian Model

The AMMI model for the vector  $y_{n \times 1}$ , containing n = lcr phenotypic responses, where the terms l, r, and c are the number of repetitions, number of genotypes, and number of environments, respectively, can be represented as follows:

 $y = X_1 \beta + Zg + \sum_{k=1}^t \lambda_k diag(Z\alpha_k) X_2 \gamma_k + \varepsilon$  (1) Where  $\beta_{cl \times 1}$  and  $g_{r \times 1}$  are vectors containing the effect parameters of hierarchical blocks within environments and main effects of genotypes, respectively. Bilinear terms  $\lambda_k$ ,  $\alpha_k$ , and  $\gamma_k$  are the singular values, unique genotypic, and environmental vectors associated with the *k*th principal component, respectively, with k = 1, ..., t and t = min(r, c) being the rank of the matrix of GEI. The matrices  $X_1, X_2$ , and Z are design matrices and  $\varepsilon$  is the random error effect vector, with  $\varepsilon \sim N_n(\mathbf{0}, \sigma_e^2 I_n)$  and  $\mathbf{0}$  being the null vector and  $I_n$  the n-order identity matrix.

The bilinear components of model (1) were subject to order (for singular values) and orthonormalization restrictions to singular vectors. Conditional data distribution was the normal multivariate, as follows:

$$\boldsymbol{y}|\boldsymbol{\alpha},\boldsymbol{\gamma},\boldsymbol{\lambda},\boldsymbol{g},\boldsymbol{\beta},\sigma_{e}^{2}\sim N_{n}(\boldsymbol{\theta},\boldsymbol{I}_{n}\sigma_{e}^{2})$$
(2)

with  $\theta = X_1 \beta + Z g + \sum_{k=1}^{t} \lambda_k diag(Z\alpha_k) X_2 \gamma_k$ , and  $\sigma_e^2$  being the residual variance.

### Prior distributions

The *a priori* distributions used for the model parameters were as follows:  $\beta | \mu_{\beta}, \sigma_{\beta}^2 \sim N(\mu_{\beta}, \sigma_{\beta}^2)$  with  $\mu_{\beta} = 0$  and  $\sigma_{\beta}^2 = 10^8$ ;  $g | \mu_g, \sigma_g^2 \sim N(\mu_g, I\sigma_g^2)$ , considering  $\mu_g = 0$  and  $\sigma_g^2 \sim \frac{1}{\sigma_g^2}$ ;  $\lambda_k | \mu_{\lambda_k}, \sigma_{\lambda_k}^2 \sim N^+(\mu_{\lambda_k}, \sigma_{\lambda_k}^2)$ , assuming that  $\mu_{\lambda_k} = 0$  and  $\sigma_{\lambda_k}^2 = 10^8$ . Uniform spherical densities in the corrected subspace were assigned to singular vectors  $\alpha_k$  and  $\gamma_k$ , and Jeffrey's priori was assigned to experimental variance  $(\sigma_e^2 \sim 1/\sigma_e^2)$ .

# Posterior distributions, sampling, and inference

Posterior complete conditional distributions were used in the sampling, using a Gibbs sampler. The algebraic detailing of how these distributions were obtained and a description of the iterative sampling algorithm can be found in Oliveira et al. (2015). The convergence of the generated chains was assessed based on the criteria of Raftery and Lewis (1992) and Heidelberger and Welch (1983).

Estimates for the linear parameters of the model, variances, and singular values were obtained by the posterior means of Markov chains and the implementation of HPD regions, using the boa package (Smith, 2007). The bivariate 95% credible regions for genotypic and environmental scores were implemented using the method described by Hu and Yang (2013).

All analyses were performed using the statistical software R (R Core Team 2018). To generate posterior samples (Markov chains), the first 8000 iterations were excluded (burn-in) to avoid the influence of initial values. Samples were collected after every 10 observations (thinning) to avoid autocorrelation in the chain. Highest posterior densityregions of 95% credibility were computed from marginal distributions when appropriate.

# Conclusion

The NLP site (Namapa) showed consistency over the crop seasons and is stable. The other locations contribute to the interaction, not being consistent in all years; that is, they are influenced by the genotype  $\times$  environment  $\times$  year interaction. Genotypes with the highest yield contribute to the GEI effect, having specific recommendations. Although the best stable genotype was G20, the recommendation needs to consider negative values as values that can also occur.

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