

Article



Assessing the Genotype-by-Environment $G \times E$ Interaction in Desi Chickpea via the Bayesian Additive Main Effects and Multiplicative Interaction Model

Ajmalud Din ^{1,2}, Rozina Gul ¹, Hamayoon Khan ³, Julian Garcia-Abadillo Velasco ^{2,4}, Reyna Persa ², Julio Isidro y Sánchez ⁴ and Diego Jarquin ^{2,*}

- ¹ Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar 25130, Pakistan; ajmalpbg@aup.edu.pk (A.D.); rozinagul@aup.edu.pk (R.G.)
- ² Department of Agronomy, University of Florida, Gainesville, FL 32611, USA; garciaabadillo.j@ufl.edu (J.G.-A.V.); r.perezsandoval@ufl.edu (R.P.)
- ³ Department of Climate Change Sciences, The University of Agriculture, Peshawar 25130, Pakistan; prof.hamayoon@aup.edu.pk
- ⁴ Department of Biotechnology-Plant Biology, Technical University of Madrid, 28040 Madrid, Spain; j.isidro@upm.es
- * Correspondence: jhernandezjarqui@ufl.edu

Abstract: Chickpea is the second most important legume crop in pulses, and its performance is greatly influenced by environmental factors inducing a change in the response patterns, complicating the selection of the best cultivar(s). The genotype-by-environment ($G \times E$) patterns of a chickpea dataset (yield and days to emergence DTE) of 36 lines evaluated in 12 environments in Pakistan were assessed in this study. The interaction patterns were evaluated using the Bayesian Additive Main Effects and Multiplicative Interaction (AMMI) model. For yield, the 95% highest posterior density (HPD) regions showed that none of the genotypes (G) were found to be stable since these did not include the null point (0, 0), while for the environments, only E-8 and E-10 included the origin. In contrast, for DTE 11, genotypes included the null point being considered stable for this trait; however, none of the environments include the origin. These results suggest that considering both traits, the genotypes G2, G6, and G17 are the best genotypes. Based on the obtained results, the abovementioned genotypes can be forwarded for further processing to be released as commercial varieties.

Keywords: Bayesian AMMI model; chickpea breeding; genotype-by-environment ($G \times E$); interaction patterns; stability

1. Introduction

Chickpea (*Cicer arietinum* L.) belongs to the Fabaceae family (Leguminosae) and the Faboideae sub-family with a diploid chromosome number 2n = 2x = 16. Chickpea is a self-pollinated, cool-season leguminous crop, which is the only cultivated species in the genus Cicer. Chickpea is one of the earliest cultivated legumes; its earliest remains are roughly 7500 years old, and these were found in the Middle East. This was also referenced in ancient manuscripts and was part of the Pre-Pottery Neolithic period, during which the first farming culture developed on our planet [1]. After the domestication of several plant species in the Near East, humans started utilizing them as food sources in 9000 BC. Nutritionally improved domesticated chickpea is the result of long trial selections and artificial mutation among a number of wild legumes of the Neolithic Near-Eastern agriculture [2].

During the 2020–2021 period, the worldwide chickpea production was 15.87 million tons in a cultivated area of 13.82 million hectares, averaging 1,148 kg ha⁻¹ [3]. India is the largest chickpea producer in the world, followed by Australia, Ethiopia, Turkey, Myanmar,



Citation: Din, A.; Gul, R.; Khan, H.; Garcia-Abadillo Velasco, J.; Persa, R.; Isidro y Sánchez, J.; Jarquin, D. Assessing the Genotype-by-Environment $G \times E$ Interaction in Desi Chickpea via the Bayesian Additive Main Effects and Multiplicative Interaction Model. *Agriculture* **2024**, *14*, 215. https://doi.org/10.3390/ agriculture14020215

Academic Editor: Rodomiro Ortiz

Received: 31 December 2023 Revised: 19 January 2024 Accepted: 19 January 2024 Published: 29 January 2024



Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). Russian, and Pakistan. In Pakistan, during the 2022–2023 period, the total crop area under chickpea cultivation was 830,000 hectares, producing 238,000 tons for an average yield of 287 kg ha⁻¹ [4], while in the Khyber Pakhtunkhwa region, an area of 33,000 hectares was cultivated, averaging 617 kg per hectare for a total production of 20,360 tons. Due to conducive environmental conditions in the southern tropical zone of Khyber Pakhtunkhwa, the average chickpea yield is higher than the overall average yield of Pakistan. This significant difference in the average yield and favorable environmental conditions have encouraged the farmers of this region to cultivate gram pulse on higher acreages [5].

The chickpea yield is substantially influenced by environmental factors such as photoperiod and temperature. In addition, other important factors are the soil composition, the water availability, and the weather in a given location at a given time of year or over a period of years [6-8]. The time from sowing to the emergence of chickpea crops also influences the soil moisture and temperature conditions, affecting the performance of the genotypes [9]. For example, a good seed emergence and perfect early growth directly contribute to the yield [10]. One genotype may be more or less affected by a particular environment than other genotypes, or a single genotype may act differently under different environmental conditions [11]. The yield stability of genotypes under different environments can be assessed using the genotype-by-environments ($G \times E$) interaction as an index (change in the ranking patterns from a group of genotypes from one environment to another). Genotypes adaptable to diverse environments without significantly reducing their yield potential seem to be a better option than genotypes that have high potential but are locally adapted. The development of stable genotypes requires multi-location trials (METs) sequentially over a period of two to three years [12]. The main purpose of the METs is to assess the adaptability and stability of genotypes across environments. There are multiple ways to analyze such types of complex data, including the Additive Main Effects and Multiplicative Interaction (AMMI) model [13], which is extensively used in agricultural research. The AMMI model computes the main effects of genotypes, environments, and their interaction based on an iterative ordinary least squares (OLS) estimation procedure. Where the main effects of the genotypes and environments are computed first, then the singular value decomposition (SVD) is performed on the resulting matrix of residuals after correcting the matrix of phenotypes by the main effect of the genotypes and environments [14]. The AMMI model allows the display of the $G \times E$ patterns of the multi-environment trials (METs) on biplots [15]; however, the incorporation of statistical inferential tools on the bilinear effects in the biplots of the first two components is complicated under the frequentist approach (iterative OLS). The Bayesian method is an alternative statistical approach that allows the incorporation of inferential tools to the points of the biplot. The Bayesian AMMI model can be used to develop posterior density regions to incorporate uncertainty parameters into the biplot [16] via Monte Carlo Markov Chains (MCMC) obtained with the GIBBS sampling method. The Bayesian AMMI allows the use of genotypic and environmental scores to construct contour areas around the points in the biplot to make inferences [17,18] about the interaction patterns.

The main objectives of this study were to (i) interpret the $G \times E$ patterns based on the Bayesian AMMI analysis of seed yield and days to emergence DTE data and (ii) identify relatively stable and high-yielding genotypes based on the results of the AMMI model for further evaluation before commercialization.

2. Materials and Methods

2.1. Plant Material and Experimental Design

We conducted the experiment of the dataset analyzed in this study at two locations in Pakistan (Peshawar and Karak) under normal and late sowing conditions during the chickpea growing seasons of 2019/20, 2020/21, and 2021/22. We considered a total of 33 advanced lines and three check cultivars (Table 1). Each genotype was grown in three rows with three-meter lengths by keeping row-to-row and plant-to-plant distances at 30 and 10 cm, respectively. All cultural practices were uniformly carried out to all the treatments in

all the environments. The experimental material was evaluated in a randomized complete block design (RCBD) with three replications at each location. The combinations of the two locations with the two different sowing dates (normal and late) across three consecutive years were considered separate environments ($12 = 2 \times 2 \times 3$). The 12 environments (E-1, E-2, E-3, E-4, E-5, E-6, E-7, E-8, E-9, E-10, E-11, and E-12) considered for analysis of the G×E interaction are the following: E-1 Peshawar normal 2019–2020, E-2 Peshawar late 2019–2020, E-3 Karak normal 2019–2020, E-4 Karak late 2019–2020, E-5 Peshawar normal 2020–2021, E-6 Peshawar late 2020–2021, E-7 Karak normal 2020–2021, E-8 Karak late 2020–2021, E-9 Peshawar normal 2021–2022, E-10 Peshawar late 2021–2022, E-11 Karak normal 2021–2022, and E-12 Karak late 2021–2022. The information on the monthly average precipitation and the minimum and maximum temperature of the locations for the different growing seasons (from planting to harvest) are given in Table 2. In this study, seed yield (in kilograms per hectare) and DTE were used as response variables for analyses.

Table 1. Pedigree and origin of advanced lines used in this study.

S. No.	Genotypes	Parentage	Source	S. No.	Genotypes	Parentage	Source
1	UAP-11221	ICC-19181 × NDC-4-20-4	UAP	19	ICC-14831	RSB200	ICRISAT
2	UAP-12113	ICC-19181 × NDC-4-20-4	UAP	20	ICC-19181	ICC 435	ICRISAT
3	UAP-12122	ICC-19181 × NDC-4-20-4	UAP	21	NDC-122	$C-44 \times ILC-195$	NIFA
4	UAP-12412	ICC-19181 × NDC-4-20-4	UAP	22	NDC-15-01	PB-91/M	NIFA
5	UAP-12531	ICC-19181 × NDC-4-20-4	UAP	23	NDC-15-4-0	PB-91/M	NIFA
6	UAP-13642	ICC-19181 × NDC-4-20-4	UAP	24	NDC-4-20-2	C-44/M	NIFA
7	UAP-14253	ICC-19181 × NDC-4-20-4	UAP	25	NDC-4-20-3	C-44/M	NIFA
8	UAP-14322	ICC-19181 × NDC-4-20-4	UAP	26	NDC-4-20-4	C-44/M	NIFA
9	UAP-14462	ICC-19181 × NDC-4-20-4	UAP	27	NDC-4-20-5	C-44/M	NIFA
10	UAP-14531	ICC-19181 × NDC-4-20-4	UAP	28	NDC-4-20-6	C-44/M	NIFA
11	UAP-15332	ICC-19181 × NDC-4-20-4	UAP	29	NDC-4-20-40	C-44/M	NIFA
12	UAP-15421	ICC-19181 × NDC-4-20-4	UAP	30	SL-08-14	Local	ARSK
13	UAP-16242	ICC-19181 × NDC-4-20-4	UAP	31	SL-03-15	Local	ARSK
14	UAP-16411	ICC-19181 × NDC-4-20-4	UAP	32	SL-05-42	Local	ARSK
15	UAP-16534	ICC-19181 × NDC-4-20-4	UAP	33	SL-3-64	Local	ARSK
16	UAP-21241	ICC-19181 × NDC-4-20-4	UAP	34	Karak-1	Local	ARSK
17	UAP-22432	ICC-19181 × NDC-4-20-4	UAP	35	Karak-3	Local	ARSK
18	ICC-13219	P3046	ICRISAT	36	NIFA-2005	P91/M	NIFA

Note: UAP = The University of Agriculture, Peshawar; ICRISAT = International Crops Research Institute for the Semi-Arid Tropics; NIFA = Nuclear Institute for Food and Agriculture; ARSK = Agricultural Research Station Karak.

2.2. Statistical Model

The AMMI model is a statistical approach used to analyze MET data where the main effects are additive, and the interaction effects are multiplicative. The seed yield and DTE data of this research were analyzed using Bayesian AMMI model [16]. Consider that y_{ijl} represents the response of the l^{th} replication corresponding to the i^{th} genotype at the j^{th} environment. Under the cell means model, \overline{y}_{ij} , represents the average response of the i^{th} genotype g (i = 1, 2, ..., 36) evaluated in the j^{th} environment e (j = 1, 2, ..., 12), and it is modeled as

$$\overline{y}_{ij.} = \mu + \tau_i + \delta_j + \Sigma_{k=1}^t \lambda_k \alpha_{ik} \gamma_{jk} + \overline{e}_{ij}$$

where μ is a general mean, τ_i is the effect of i^{th} genotype, and δ_j is the effect of j^{th} environment; the $\lambda_k \alpha_{ik} \gamma_{jk}$ term represents the k^{th} interaction component that corresponds to the deviations of cell means from additive main effects, and it is computed using the singular value decomposition of the residual matrix comprised by $\overline{y}_{ij} - \mu - \tau_i - \delta_j$. In particular, λ_k , α_{ik} , and γ_{jk} correspond to the k^{th} singular value of the multiplicative component, the i^{th} element of k^{th} singular vector of scores for the genotypes, and the j^{th} element of the k^{th} singular vector of the score of environments, respectively; the ij term is the residual

4 of 11

error term of the i^{th} genotype in the j^{th} environment, and it addresses the non-explained variability by the other model terms.

	2019-	-2020	2020-	-2021	2021-	2021–2022		
Months	UAP	Karak	UAP	Karak	UAP	Karak		
	Rainfall (mm)							
October	0.63	0.84	3.36	0.68	3.73	2.12		
November	1.79	0.99	2.81	1.79	0.14	0.02		
December	0.24	0.17	1.20	0.83	0.71	0.49		
January	2.00	1.70	0.45	0.45	3.83	3.27		
February	5.38	7.01	3.60	4.97	1.18	0.64		
March	9.22	9.21	3.61	1.95	1.71	1.38		
April	5.68	3.75	1.66	1.44	1.44 0.70			
Total	24.94	23.67	16.69	12.11	12.00	8.21		
	Temperature (Min–Max °C)							
October	14.34–27.91	17.94–30.21	12.52–29.00	16.33–31.10	12.57–26.63	16.88–30.05		
November	8.04–19.85	11.77–23.39	6.17–19.61	10.4–22.65	7.31–21.87	11.01–24.63		
December	3.45-16.94	6.75–19.36	3.11-15.59	6.93–18.75	3.67–16.71	6.74–19.15		
January	0.44-11.03	3.93–14.78	2.3816.89	5.28-19.26	1.43–12.67	5.12-15.88		
February	4.29–17.96	7.53–21.48	6.67-20.65	9.84-23.59	2.82-15.91	6.05–19.97		
March	7.75–17.04	11.44-20.78	8.95-22.43	12.69–26.87	10.54-25.29	14.29–29.37		
April	12.11-23.60	15.95–27.13	11.46-26.25	15.73-30.90	15.51-32.29	19.60–36.86		
Mean	7.20–19.19	10.75-22.44	7.32–21.49	11.02–24.73	7.69–21.62	11.38–25.13		

Table 2. Climatic conditions at studied sites.

2.3. Bayesian Framework

Under the Bayesian paradigm, the Markov Chain Monte Carlo (MCMC) method was used for sampling the parameters of the AMMI model [16]. For this, the Gibbs sampling, which is an MCMC algorithm that iteratively draws random values under certain rules/specifications, was implemented to generate full conditional posterior distributions of the model parameters [16]. For each model parameter, a prior distribution was considered to obtain the corresponding full conditional posterior. Then, the sampled values of each model term were updated at each iteration. For each MCMC, a total of 50,000 iterations were considered, with the first 10,000 removed as part of the burn-in process with the aim of obtaining a more representative distribution of the parameters. Also, a thinning of 10 was considered to avoid the repetition of highly dependent or correlated data that could influence a specific region of the posterior distribution only. Thus, for each MCMC, after removing the iterations corresponding to the burning period, 40,000 remained; however, with a thinning of 10, only 4000 were available for analysis. A total of three independent MCMCs were obtained for each trait. After mixing their values, 12,000 iterations were available for the analysis by combining the information of the three replications (3×4000).

2.4. Software

The analyses were conducted using the statistical R-software R Core Team. An example of the R code used to perform the Bayesian AMMI analysis can be found online at https://uflorida-my.sharepoint.com/:f:/g/personal/jhernandezjarqui_ufl_edu/ Ers_xdnV3IVHu6bGdMGEJl4BPpn1_dre2vlmr852kExLpQ?e=8dplTz (accessed on 23 January 2024).

3. Results

In general, the traces and histograms of the main effects showed suitable estimated densities and bell-shaped marginal posterior distributions. Supplementary Figures S1 and S2 depict the trace and histogram of the overall mean (μ) and the eigenvalues of the first two interaction components (λ_1 and λ_2), respectively. These results show good convergence of the MCMC for all of the parameters of the Bayesian AMMI model.

In addition, Figure 1 displays the cumulative distribution of the posterior density of the eigenvalues for yield and DTE. These show that the first two components explain a significant proportion of the variability of the interaction. The proportion of the variability explained by the first two interaction components λ_1 and λ_2 was about 94% for yield, while it was 78% for DTE. A total of four components are required to explain more than 90% of the variability of the interactions in DTE.



Figure 1. Cumulative posterior distribution of the eigenvalues (*y*-axis) for different numbers of components (*x*-axis) obtained from the Markov Chain Monte Carlo (MCMC) for chickpea yield (**left** panel) and DTE (**right** panel) data.

For yield, the mean marginal, their corresponding standard deviation (SD), and the upper and lower 95% highest posterior densities (HDP) of the posterior distributions of the model parameters μ , σ_e^2 , τ_i (i = 1, 2, ..., 36), and δ_j (j = 1, 2, ..., 12), are shown in Table 3. The overlapping HPD values indicate non-significant differences between genotypes or between environments. The mean of the overall mean μ and of the variance component of the error σ_e^2 were 604.42 (SD: 1.17) and 1763.35 (SD: 204.94), respectively. The posterior mean of the main genotypic effects (τ_i) ranged from -83.44 to 89.09, and the respective values for the main environmental effects (δ_i) ranged from -386.32 to 373.02.

The posterior distribution of the genotypic and environmental scores of the interaction parameters are also used to construct their corresponding HPD confidence regions for statistical inference. Figure 2 depicts the resulting 95% HPD confidence region biplot of yield for the environmental (left panel) and genotypic (right panel) scores. The elements of the scores whose regions do not include the null point (0, 0) are considered genotypes or environments that show a significant interaction effect or significantly contribute to the $G \times E$ interaction. For easy visualization, the credible 95% HPD regions of only those environments or genotypes that do not include the null point are depicted in the biplots. For the scores of the environments, the 95% HPD regions of E-8, and E-10 included the null point, and for that reason, these do not appear in the biplot (left panel). The credible 95% HPD regions of the environments E-1, E-3, and E-4 are overlapped, indicating similarities

in the response patterns between these. Similarly, the corresponding regions of the environments E-2 and E-9 show a high degree of overlapping. In contrast, the regions of the environments E-7, E-11, and E-12 do not overlap with the regions of any other environment. However, the region from environment E-11 is very close to the cluster of environments formed by E-2 and E-9. Also, the environment E-12 is located far away from the center of the biplot, forming a cluster of environments by itself.

Table 3. Mean of the marginal posterior effects, their corresponding standard deviations (SDs), and regions with 95% highest posterior density (HPD) for the overall mean (μ), dispersion parameter (σ^2_e), genotypic effects (τ_i), and environmental effects (δ_j) derived of the Bayesian AMMI model for yield (kilograms per hectare) of a chickpea dataset comprised of 36 genotypes observed in 12 environments.

Parameter	Mean	SD	Lower HPD	Upper HPD	Parameter	Mean	SD	Lower HPD	Upper HPD
μ	604.42	1.17	602.07	606.66	$ au_{24}$	57.51	2.58	52.59	62.72
σ^2_{e}	1763.35	204.94	1365.77	2127.01	$ au_{25}$	-65.70	2.64	-70.86	-60.52
$ au_1$	-2.14	2.60	-7.15	3.06	τ_{26}	15.31	2.60	10.16	20.38
τ_2	-18.24	2.61	-23.30	-13.05	$ au_{27}$	-14.89	2.59	-19.99	-9.80
$ au_3$	-5.59	2.61	-10.58	-0.37	$ au_{28}$	-0.22	2.61	-5.17	5.14
$ au_4$	45.14	2.57	40.25	50.39	$ au_{29}$	41.25	2.60	36.03	46.25
$ au_5$	-9.63	2.61	-14.81	-4.58	$ au_{30}$	-47.18	2.61	-52.26	-42.10
$ au_6$	11.49	2.60	6.50	16.73	$ au_{31}$	-5.55	2.59	-10.38	-0.25
$ au_7$	31.15	2.60	26.10	36.22	$ au_{32}$	-5.30	2.59	-10.40	-0.23
$ au_8$	-36.74	2.58	-41.70	-31.64	$ au_{33}$	-34.95	2.60	-39.98	-29.80
τ9	40.57	2.59	35.59	45.72	$ au_{34}$	9.94	2.61	4.89	15.01
$ au_{10}$	-83.44	2.59	-88.52	-78.40	$ au_{35}$	-13.30	2.65	-18.42	-7.97
$ au_{11}$	23.10	2.59	18.03	28.08	$ au_{36}$	36.80	2.62	31.90	42.07
$ au_{12}$	-13.28	2.58	-18.40	-8.28	δ_1	-286.91	2.53	-291.88	-281.89
$ au_{13}$	-14.57	2.63	-19.81	-9.42	δ_2	-386.32	2.50	-391.12	-381.44
$ au_{14}$	55.49	2.60	50.32	60.56	δ_3	95.27	2.54	90.31	100.23
$ au_{15}$	27.40	2.59	22.17	32.20	δ_4	-97.22	2.54	-102.09	-92.17
$ au_{16}$	-26.80	2.62	-31.90	-21.63	δ_5	-175.21	2.54	-180.25	-170.28
$ au_{17}$	-60.39	2.61	-65.42	-55.21	δ_6	-191.61	2.54	-196.84	-186.87
$ au_{18}$	89.09	2.60	83.86	94.02	δ_7	373.02	2.53	368.21	378.09
$ au_{19}$	-42.03	2.62	-47.25	-36.98	δ_8	120.67	2.54	115.70	125.62
$ au_{20}$	-9.45	2.61	-14.66	-4.47	δ_9	145.90	2.54	141.10	151.03
$ au_{21}$	28.44	2.58	23.26	33.44	δ_{10}	-13.73	2.52	-18.66	-8.84
$ au_{22}$	-28.23	2.60	-33.16	-22.98	δ_{11}	222.41	2.51	217.51	227.41
$ au_{23}$	24.93	2.59	19.95	30.12	δ_{12}	193.73	2.51	188.82	198.58

For the genotypes, a more complex overlap among their credible regions than for the environments was observed (right panel), except for genotypes G18 and G34, whose corresponding contours do not overlap with those of any other genotype. However, none of the credible 95% HPD regions of the genotypes included the null point (0, 0).

A more detailed analysis based on the clustering of the interaction components of the environments (left panel) and the genotypes (right panel) is depicted in Figure S3 in the Supplementary Materials section. The first two interaction components divide the environments and the genotypes into three and four major groups, respectively. For environments, these are [E-12], [E-1, E-3, E-4], and [E-2, E-5, E-6, E-7, E-8, E-9, E-10, E-11], while for genotypes, these are [G18, G27, G31 G35], [G1, G2, G4, G5, G6, G8, G10, G12, G14, G15, G16, G17, G23, G24, G26], [G7, G11, G19, G20, G21], and [G3, G9, G13, G22, G28, G29, G30, G32 G33, G34, G35, G36]. All the genotypes in the first group [G18, G27, G31 G35], along with the genotypes G32 and G34 from group four, are considered well-adaptable genotypes for environment E-12 since these genotypes and this environment are in the same direction on the right side of the biplot. On the other hand, the genotypes G4, G10, G12, and G23 presented in the second group (right top in panel B of Figure 2) showed specific adaptability in the second group of environments [E-1, E-3, E-4]. In addition, G1,

G2, G15, G16, and G17 of the second group of genotypes are suitable in the environments E-2, E-9, and E-11. Similarly, all the genotypes of the third group [G7, G11, G19, G20, G21] were adaptable to E-5 and E-6, while G3, G9, and G13 from the fourth cluster were specifically suitable for E-7.



Figure 2. Bayesian AMMI biplot and the corresponding credible 95% HPD regions of the first two scores of the interaction components for environments (**left** panel) and genotypes (**right** panel) of a chickpea yield dataset comprised of 36 genotypes observed in 12 environments in Pakistan.

The same analysis of the G×E patterns was conducted for DTE. The mean (and SD) of μ and σ_e^2 for DTE are 15.36 (0.02) and 0.37 (0.03), respectively (Supplementary Table S1). Table S1 also contains the corresponding mean and SD of the main effects for genotypes τ_i and the environments δ_j . In addition, Supplementary Figure S4 displays the results of the cluster analysis of the interaction terms of the environments (left panel) and of the genotypes (right panel). Figure 2 contains the corresponding biplot for DTE, and it presents the environments and genotypes whose credible 95% HPD regions do not include the null point (0, 0). The resulting credible regions for the environments and the genotypes showed a more complex overlapping pattern than for yield. For the environments, the credible 95% HPD regions do not include the null point for any of these (left panel in Figure 3). Also, environment E-10 was the only one whose contour did not overlap with any other. Broadly, the studied environments were grouped into three clusters, and these are [E-1, E-5, E-6], [E-3, E-4, E-7, E-8, E-11, E-12], and [E-2, E-9, E-10], respectively.



Figure 3. Bayesian AMMI biplot and the corresponding credible 95% HPD regions of the first two scores of the interaction components for environments (**left** panel) and genotypes (**right** panel) of a chickpea DTE dataset comprised of 36 genotypes observed in 12 environments in Pakistan.

Similarly, the complete set of genotypes was grouped into three main clusters (right panel in Supplementary Figure S4), and these are [G10, G22, G23, G28], [G1, G2, G3, G4, G5, G6, G8, G9, G11, G12, G14, G15, G17, G19, G20, G21, G24, G25, G27, G29, G30, G31, G32, G33, G35, G36], and [G7, G13, G16, G18, G26, G34].

A mixture of genotypes (G9, G24, G26, and G27) from groups two and three (right side of the right panel) was adaptable to the first group of environments [E-1, E-5, E-6]. Genotypes in the second group (left side of right panel), except G22, were considered suitable for the second group of environments [E-3, E-4, E-7, E-8, E-11, E-12], while for the third group of environments [E-2, E-9, E-10], a mixture of genotypes (G2, G12, G33, and G34) from groups two and three (bottom in right panel Figure 3) were well suited.

4. Discussion

Pulses are the main source of the cheapest protein for human health, and their global production has remained unchanged for the past few decades [19]. Among the pulses, chickpea ranks second in importance after the common bean. Numerous biotic and abiotic stresses limit chickpea production in the world [20]. Chickpea is mostly grown in the rainfed areas of Pakistan. Unusual rainfalls and adverse climatic conditions affect its production, decreasing the production capacity, increasing prices, and limiting access for poor people to a healthier source of nutrients.

The availability of improved (more productive) and stable varieties with good-quality seeds is crucial to increasing both vertical and horizontal chickpea production [21]. Plant breeders conduct METs to identify superior and stable genotypes across environments at later stages of cultivar development [22]. When the response patterns (rankings) of the genotypes change across the different environmental conditions, there is a significant presence of the $G \times E$ interaction, complicating the selection of superior cultivars. In this study, the information of 36 chickpea genotypes evaluated under 12 different environments

was analyzed based on the Bayesian AMMI model. The main purpose of the analyses was to identify stable and superior genotypes across the studied environments.

Significant G×E interaction was revealed among all the genotypes for yield because their corresponding credible 95% HPD regions did not include the null point (0, 0). The genotypes G2, G3, G6, G13, G15, G16, G17, G22, G24, and G28 could be considered as the most stable lines, and these were present in the second and fourth groups. The performance of these genotypes across all of the environments ranged from 544 to 611 kg/ha⁻¹. The G24 genotype (611 kg/ha⁻¹) was the second most productive line among the top ten genotypes across environments.

Among environments, E-12 was totally different from the rest of the environments (Figure 2). All the environments of the first year were grouped together except E-2 (Pe-shawar late 2019–2020). E-2 was grouped with the rest of the environments in the 2nd and 3rd years. E-8 and E-10 were considered stable environments, which means that these environments do not influence significantly the performance of genotypes. Both environments E-8 (Karak late 2020–2021) and E-10 (Peshawar late 2021–2022) received the same amount of rainfall in their respective years. The average production of genotypes in E-8 and E-10 was 725 kg/ha⁻¹ and 590 kg ha⁻¹, respectively.

Similarly, genotypes and environments showed significant interactions for DTE (Figure 3). The biplot analysis identified genotypes G1, G2, G5, G6, G14, G17, G25, G30, G31, G33, and G35 as stable for this trait because their corresponding credible 95% HDP intervals included the null point (0, 0). The genotypes G1, G2, and G5 were among the top ten genotypes, showing the lowest number of days to emerge across environments. The results of the AMMI biplot grouped all the environments (E-3, E-4, E-7, E-8, E-11, and E-12) of the second location in one cluster. The remaining environments were divided into two different groups, presenting E-10 as a suitable environment due to its closest position to the null point.

Based on the results of the Bayesian AMMI model for yield and DTE, the genotypes G2, G6, and G17 were commonly considered the best genotypes across environments, while E-8 and E-10 were identified as the most stable environments for both traits. These three genotypes were selected based on their 95% HPD confidence regions with the closest appearance near the origin of the biplot for yield, while for DTE, their corresponding HPD regions included the null point (0, 0). With respect to the environments, similarly, as for the genotypes, the 95% HPD confidence regions of E-8 and E-10 included the null point for yield but not for DTE, although these were the closest among all environments. Therefore, these environments were recommended as the most stable environments for all genotypes. The main reason for their stability is the minimum difference between the performance of genotypes within these environments.

Supplementary Materials: The following supporting information can be downloaded at: https://www. mdpi.com/article/10.3390/agriculture14020215/s1. Figure S1. Trace and histogram of the overall mean (μ) obtained from the Bayesian-AMMI model for a chickpea yield dataset comprised of 36 genotypes evaluated in 12 environments in Pakistan. Figure S2. Traces and histograms of values of the first and second singular values (λ_1 and λ_2) obtained from the Bayesian-AMMI model for a chickpea yield data set comprised of 36 genotypes evaluated in 12 environments in Pakistan. Figure S3. Clustering of genotypes and environments based on the interaction parameters derived from the Bayesian-AMMI model for a chickpea yield dataset comprised of 36 genotypes observed in 12 environments in Pakistan. Figure S4. Clustering of genotypes and environments based on the interaction parameters derived from the Bayesian-AMMI model for a chickpea DTE dataset comprised of 36 genotypes observed in 12 environments in Pakistan. Table S1. Mean of the marginal posterior effects, and their corresponding standard deviations (SDs), and 95% highest posterior density HPD regions for the overall mean (μ), dispersion parameter (σ_e^2), genotypic effects (τ_i), environmental effects (δ_j) of the Bayesian-AMMI model for DTE of a chickpea dataset comprised of 36 genotypes observed in 12 environments.

Author Contributions: R.G. conceived and designed the experiments with supervision. A.D. conducted the field trials and collected the data. H.K. provided guidance and technical support during

agronomic practices carried out in the fields. J.G.-A.V. and D.J. helped in data arrangement and analysis using R packages. A.D. prepared the first draft of the manuscript, and it was reviewed and edited by D.J., J.G.-A.V., R.P., J.I.y.S. and R.G. All authors have read and agreed to the published version of the manuscript.

Funding: This research was part of AD's PhD research, and all the expenses were covered by his program.

Institutional Review Board Statement: Not applicable.

Data Availability Statement: The morphological data and Supplementary Materials used in this study will be made available by the corresponding authors.

Acknowledgments: The authors want to thank Agricultural Research System, Khyber Pakhtunkhwa, Pakistan, for providing research space at their Agricultural Research Station, Ahmad Wala, Karak (ARSK). We are thankful to the technical and field staff of The University of Agriculture, Peshawar, Khyber Pakhtunkhwa, Pakistan.

Conflicts of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- 1. Hirst, K.K. The Domestication History of Chickpeas; ThoughtCo, Dotdesh Meredith. 2016. Available online: https://www.thoughtco.com/the-domestication-history-of-chickpeas-170654/ (accessed on 18 July 2022).
- 2. Zohary, D.; Hopf, M. Domestication of Plants in the Old World: The Origin and Spread of Cultivated Plants in West Asia, Europe and the Nile Valley, 3rd ed.; Oxford University Press: Oxford, UK, 2000; ISBN 0198503563.
- 3. FAO. Crops. Available online: http://www.fao.org/faostat/en/#data/QC/ (accessed on 22 August 2023).
- PBS. Pakistan Statistical Yearbook 2023. In *Pakistan Bureau of Statistics (PBS), Ministry of Food Security & Research*; Government of Pakistan: Islamabad, Pakistan, 2023; pp. 19–30. Available online: https://mnfsr.gov.pk/PublicationDetail/OTRjNDA0M2QtYjE4 My00NzA1LThhNDMtMmNmZjg5YjBmZTAy (accessed on 29 September 2023).
- 5. Raja, S.; Tauqir, A.; Qureshi, T.; Rana, A.W. *Khyber Pakhtunkhwa Food Outlook Report Rabi Crops* 2021–2022; International Food Policy Research Institute: Washington, DC, USA, 2022. [CrossRef]
- 6. Velu, G.; Shunmugavalli, N. Genotype × environment interaction in sesame (*Sesamum indicum* L.). *Sesame Safflower Newsl.* 2005. Available online: https://www.cabdirect.org/cabdirect/abstract/20093312604 (accessed on 2 October 2023).
- 7. Crossa, J. Statistical analyses of multilocation trials. *Adv. Agron.* 1990, 44, 55–85. [CrossRef]
- 8. Purchase, J.L.; Hatting, H.; Van Deventer, C.S. Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *S. Afr. J. Plant Soil* **2000**, *17*, 101–107. [CrossRef]
- Hosseini, N.M.; Palta, J.A.; Berger, J.D.; Siddique, K.H.M. Sowing soil water content effects on chickpea (*Cicer arietinum* L.): Seedling emergence and early growth interaction with genotype and seed size. *Agric. Water Manag.* 2009, *96*, 1732–1736. [CrossRef]
- 10. Maiti, R.K.; Moreno-Limon, S. Seed and seedling traits in bean (*Phaseolus vulgaris* L.) and its relation to abiotic stress resistance. *Legum. Res. Int. J.* **2001**, *24*, 211–221.
- 11. Falconer, D.S. Introduction to Quantitative Genetics, 2nd ed.; Longman Group Ltd.: London, UK, 1981; pp. 1–133. [CrossRef]
- Farshadfar, E.; Sadeghi, M. GGE biplot analysis of genotype × environment interaction in wheat-agropyron disomic addition lines. *Agric. Commun.* 2014, 2, 1–7. Available online: https://api.semanticscholar.org/CorpusID:43589803 (accessed on 11 October 2023).
- 13. Gauch, H.G., Jr.; Zobel, R.W. Optimal Replication in Selection Experiments. Crop Sci. 1996, 36, 838–843. [CrossRef]
- 14. Gauch, H.G., Jr. Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 2006, 46, 1488–1500. [CrossRef]
- 15. Luo, J.; Pan, Y.B.; Que, Y.; Zhang, H.; Grisham, M.P.; Xu, L. Biplot evaluation of test environments and identification of mega-environment for sugarcane cultivars in China. *Sci. Rep.* **2015**, *5*, 15505. [CrossRef] [PubMed]
- 16. Crossa, J.; Perez-Elizalde, S.; Jarquin, D.; Cotes, J.M.; Viele, K.; Liu, G.; Cornelious, P.L. Bayesian estimation of the additive main effects and multiplicative interaction model. *Crop Sci.* **2011**, *51*, 1458–1469. [CrossRef]
- 17. Bernardo, L.A.Y., Jr.; de Silva, C.P.; de Oliveira, L.A.; Nuvunga, J.J.; Pires, L.P.M.; Von Pinho, R.G.; Balestre, M. AMMI Bayesian models to study stability and adaptability in maize. *Agron. J.* **2018**, *110*, 1765–1776. [CrossRef]
- 18. Antonio de Oliveira, L.; Pereira da Silva, C.; Nuvunga, J.J.; Da Silva, A.Q.; Balestre, M. Credible intervals for scores in the AMMI with random effects for genotype. *Crop Sci.* 2015, 55, 465–476. [CrossRef]
- Foyer, C.H.; Lam, H.M.; Nguyen, H.T.; Siddique, K.H.M.; Varshney, R.K.; Colmer, T.D.; Cowling, W.; Bramley, H.; Mori, T.A.; Hodgson, J.M.; et al. Neglecting legumes has compromised human health and sustainable food production. *Nat. Plants* 2016, 2, 1–10. [CrossRef] [PubMed]
- 20. Sadras, V.O.; Lake, L.; Li, Y.; Farquharson, E.A.; Sutton, T. Phenotypic plasticity and its genetic regulation for yield, nitrogen fixation and δ13C in chickpea crops under varying water regimes. *J. Exp. Bot.* **2016**, *67*, 4339–4351. [CrossRef] [PubMed]

- 21. Singh, V.; Chauhan, Y.; Dalal, R.; Schmidt, S. Chapter 9—Chickpea. In *The Beans and the Peas*; Pratap, A., Gupta, S., Eds.; Woodhead Publishing: Cambridge, UK, 2021; pp. 173–215. ISBN 978-0-12-821450-3.
- 22. Dia, M.; Wehner, T.; Hassell, R.; Price, D.S.; Boyhan, G.; Olson, S.; King, S.; Davis, A.; Tolla, G.; Bernier, J.; et al. Mega-environment identification for watermelon yield testing in the US. In Proceedings of the Cucurbitaceae 2012, Proceedings of the Xth EUCARPIA Meeting on Genetics and Breeding of Cucurbitaceae, Antalya, Turkey, 15–18 October 2012; University of Cukurova: Adana, Turkey, 2012; pp. 385–390.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.