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## GENOTYPE - BY - ENVIRONMENT INTERACTION FOR MARKETABLE TUBER YIELD IN ADVANCED POTATO CLONES USING AMMI AND GGE METHODS

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### ABSTRACT

Analysis of genotype-by-environment interaction (GEI) is critical in the local potato breeding and selection programme to obtain information on the performance of the genotypes for yield adaptability and stability. The objective of this study was to assess the marketable tuber yield of 18 advanced potato clones compared to the commercial variety Spunta at four locations (Bigara, Réduit, St. Antoine and Rivière du Poste), representative of four major soil types in Mauritius. They were analysed for adaptability and stability using the additive main effects and multiplicative interaction (AMMI) model and genotype main effect and genotype x environment interaction (GGE) biplot. Five clones gave significantly the highest marketable tuber yield in terms of overall ranking with yield increase of 47.4% to 59.6% over the control variety Spunta. AMMI analysis of variance detected significantly ( $P < 0.001$ ) higher proportion of variation in marketable tuber yield due to environment (42%); followed by genotype x environment interaction (21%) which justified multi-locational testing. AMMI1 biplot demarcated clones 142/161/2 and 142/161/5 as high yielding and most stable while AMMI 2 biplot identified the winning genotypes for a specific environment. Thus, clones 142/161/4 and 161/142/16 had specific adaptation to Bigara, 29/5/2 and 21/5/3 were adapted to St. Antoine, 21/5/10 to Rivière du Poste whereas 29/5/3 was adapted to Réduit. The GGE biplots identified clones 142/161/2 and 142/161/5 as the two most desirable genotypes close to the “ideal genotype”. The “which- won- where” view of the GGE biplot further pointed to the presence of two mega-environments, which corresponded to the sub-humid irrigated/humid environments (Réduit, St. Antoine and Rivière du Poste) and the high altitude super-humid environment (Bigara). These results showed that in future both AMMI and GGE methods can be integrated in the local potato breeding programme to select superior genotypes through multi-year and multi-locational yield evaluation.

**Key Words:** AMMI, GEI, GGE biplot, marketable tuber yield, potato

## RÉSUMÉ

L'analyse de l'interaction génotype-environnement (GEI) est essentielle dans le programme local d'amélioration et de sélection de la pomme de terre pour obtenir des informations sur la performance des génotypes en termes d'adaptabilité et de stabilité du rendement. L'objectif de cette étude était d'évaluer le rendement en tubercules commercialisables de 18 clones avancés de pomme de terre par rapport à la variété commerciale Spunta sur quatre sites (Bigara, Réduit, St. Antoine et Rivière du Poste), représentatifs de quatre principaux types de sols à Maurice. Ils ont été analysés pour l'adaptabilité et la stabilité à l'aide du modèle d'effets principaux additifs et d'interaction multiplicative (AMMI) et de l'effet principal du génotype et de l'interaction génotype x environnement (GGE). Cinq clones ont donné significativement le rendement en tubercules commercialisable le plus élevé en termes de classement global avec une augmentation de rendement de 47,4 % à 59,6 % par rapport à la variété témoin Spunta. L'analyse AMMI de la variance a détecté une proportion significativement plus élevée ( $P < 0,001$ ) de variation du rendement en tubercules commercialisables due à l'environnement (42 %) ; suivi de l'interaction génotype x environnement (21%) qui justifiait les tests multi-localisés. Le biplot AMMI1 a délimité les clones 142/161/2 et 142/161/5 comme étant à haut rendement et les plus stables, tandis que le biplot AMMI 2 a identifié les génotypes gagnants pour un environnement spécifique. Ainsi, les clones 142/161/4 et 161/142/16 avaient une adaptation spécifique à Bigara, 29/5/2 et 21/5/3 ont été adaptés à St. Antoine, 21/5/10 à Rivière du Poste alors que 29/5 /3 a été adapté en Réduit. Les biplots GGE ont identifié les clones 142/161/2 et 142/161/5 comme les deux génotypes les plus désirables proches du « génotype idéal ». La vision « qui-gagné-où » du biplot GGE indiquait en outre la présence de deux méga-milieus, qui correspondaient aux milieux subhumides irrigués/humides (Réduit, St. Antoine et Rivière du Poste) et aux milieux des hautes altitudes super humide (Bigara). Ces résultats ont montré qu'à l'avenir, les méthodes AMMI et GGE peuvent être intégrées dans le programme local de sélection de pommes de terre pour sélectionner des génotypes supérieurs grâce à une évaluation du rendement pluriannuelle et multi-localisée.

*Mots Clés:* AMMI, GEI, GGE biplot, rendement des tubercules commercialisables, pomme de terre

## INTRODUCTION

Potato (*Solanum tuberosum* L.) is a strategic crop grown in Mauritius to ensure food and nutrition security. The major objectives of the local potato breeding programme is to develop and select genotypes with high yield, stability and adaptability to diverse environments. While adaptability refers to good performance over a geographic region, under conditions of variable climate and environment (Stoskopf, 1981), stability of yield is generally defined as the ability of a genotype to resist substantial fluctuations in yield over a range of environmental conditions (Heinrich *et al.*, 1983). The knowledge of genotype x environment interaction (GEI) and stability of genotypes across environments is essential before cultivar release. According to Yan *et*

*al.* (2001), the performance of a cultivar is determined by three factors: genotypic main factors (G), environmental main effect (E) and genotype by environment interaction (GEI).

GEI can be defined as the difference between the phenotypic value and the value expected from the corresponding genotypic and environmental values; and is thus the variation caused by the joint effects of genotypes and environments (Dickerson, 1962., Baker, 1988). GEI has an impact on all stages of a breeding programme and has enormous implications for the allocation of resources. A large GEI reflects the need for testing cultivars in numerous environments (locations and/or years) to obtain reliable results, thus requiring increased input of resources (Kang, 2002). On the other hand, genotypes that provide high average yields

with minimum GEI (i.e., high stability) have been gaining importance over increased yields (Rosielle and Hamblin, 1981; Ceccarelli, 1989., Gauch and Zobel, 1997). GEI is also a major element in determining many important aspects of a breeding programme, including (i) whether to aim for wide or specific adaptation; (ii) choice of locations for selection; (iii) whether selection in early generations is conducted in stress or stress-free environments; and (iv) the trade-off between multi-environment testing of large numbers of genotypes and subjecting fewer lines to intensive trait-based selection (Fox *et al.*, 1997). The knowledge of GEI can also help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine-tuning the breeding programmes (Kang and Magari, 1996).

The Additive Main effects and Multiplicative Interaction (AMMI) model (Zobel *et al.*, 1988) and the Genotype main effects and Genotype x Environment effects (GGE) model (Gauch, 2006) are the two most frequently used models for the biplot analysis (Gauch *et al.*, 2008; Yang *et al.*, 2009). AMMI model incorporates both additive (ANOVA) and multiplicative components (PCA) into an integrated, powerful, least-squares analysis (Freeman, 1985; Gauch, 1985). AMMI first applies analysis of variance (ANOVA) to partition the variation into genotype main effects (G), environment main effects (E), and genotype-by-environment interaction effects (GE), and then it applies principal components analysis (PCA) to GE. AMMI generates a family of models and the most common are AMMI1 and AMMI2 models. AMMI1 has mean on the abscissa and first principal component axis (PCA1) score on the ordinate, and it shows markers for both genotypes and environments while AMMI2 biplot shows PCA1 on the abscissa and PCA2 on the ordinate (Gauch *et al.*, 2008). GGE biplot (GGE biplot) analysis is one of the multivariate statistical models and a new technique for graphical display of GE

interaction pattern of MET data with many advantages (Yan *et al.*, 2000; Ding *et al.*, 2007). It is an effective tool for mega-environment analysis, genotype and environmental evaluation and is being extensively used in potato breeding and selection studies to assess the yield performance, adaptability and stability of genotypes (Flis *et al.*, 2014).

The local potato breeding programme at the Food and Agricultural Research and Extension Institute (FAREI) aims at identifying promising clones with adaptability and stability to different agro-ecological environments before any potential release to growers. In this study, both AMMI and GGE biplots were attempted to examine the GEI in marketable tuber yield of advanced potato clones at four locations corresponding to four major soil types in Mauritius. The objective was to use AMMI and GGE methods to identify which genotype(s) among the advanced clones had the best performance in terms of yield adaptability and stability compared to the commercially exploited variety Spunta and which environment is the best for differentiating among potato genotypes in Mauritius.

## METHODOLOGY

**Potato genotypes.** Eighteen advanced potato clones, with marketable tuber yield above the national average yield of 25 t ha<sup>-1</sup> (Cadarsa *et al.*, 2019) were evaluated, along with one widely grown commercial variety Spunta for their adaptability and yield stability under four potato environments in the year 2019. The potato clones were selected genotypes from the following pedigrees: (i) 02 - 14/2 x 01 - 16/1 (ii) 01 - 16/1 x 02 - 14/2; (iii) 05-3-10-1 x 05-8-3A; and (iv); 05-15-1 x 05-8-3A.

**Experimental details.** Four trials were set up in the first (May - June) and second (July - August) planting seasons in 2019 at Réduit, St. Antoine, Rivière du Poste and Bigara;

representing the four main agro-climatic regions and soil types (Parish and Feillafe, 1965) (Table 1).

The first season trials were established at Réduit and St. Antoine in the humid irrigated and sub-humid irrigated environments; while in the second season, the trials were set up at Rivière du Poste and Bigara in the humid rain-fed and super-humid rain-fed regions, respectively.

The experiments were established in a randomised complete block (RCB) design, with three replications. Plot size was 19.2 m<sup>2</sup>, consisting of four rows of 6 m long. Land was prepared to a fine tilth using a disc plough; followed by a rotovator. Potato furrows of 20 cm wide and 30 cm deep were made at inter-row spacing of 80 cm. Complex fertilisers 16:22:22 (N:P:K) and Diammonium Phosphate (DAP) were applied evenly in furrows at the recommended rate of 650 and 275 kg ha<sup>-1</sup>, respectively, and covered thinly with a layer of soil. Sprouted seeds (60 -120 g) were dusted with the fungicide Mancozeb 75%WP @ 3g kg<sup>-1</sup> of seeds and planted at 30 cm distance in furrows; and then covered with 5 cm of soil.

**Data collection.** During the crop cycle, data were collected on growth and yield parameters viz: (i) percentage plant stand, (ii) stem number/plant, (iii) stem thickness (mm), (iv) number of marketable tubers/plant, (v) average tuber weight (g), (vi) marketable tuber yield (t ha<sup>-1</sup>), (vii) percentage unmarketable tuber yield and (viii) total tuber yield (t ha<sup>-1</sup>). At harvest, tubers from the whole plot size were graded into marketable (>30 mm) and unmarketable (<30 mm) grades and weighed separately. Total tuber yield was computed from the sum of marketable and unmarketable yield. For the purpose of this study, marketable tuber yield (MTY) was used to assess the differential performance of genotypes across environments.

**Statistical analysis.** The effects of genotype, environment and their interactions were determined by analysis of variance (ANOVA) for each individual location, as well as across locations, using the IBM SPSS (version 20.0) statistical software. GenStat (Payne *et al.*, 2014) software was used to run the GEI analysis for marketable tuber yield. The data were checked for the homogeneity of

TABLE 1. Agro-climatic details of locations where trials were established in 2019 in Mauritius

Trial site	Réduit	St. Antoine	Rivière du Poste	Bigara
Region	Centre	North	South	Centre West
Climatic zone	Humid irrigated	Sub-humid irrigated	Humid rain-fed	Super-humidrain-fed
Date of planting	14 May	16 May	06 August	09 August
Soil type*	LHL	HL	LRP	HFL
Altitude (m asl)	203	75	180	550
Mean annual rainfall (mm)	2000	1600	2300	2500
Mean maximum temperature (°C)	24.6	26.9	25.9	23.5
Mean minimum temperature (°C)	16.9	16.9	18.9	16.0

\*LHL = Low Humic Latosol; HL = Humic Latosol; LRP = Latosolic Reddish Prairie; HFL = Humic Ferruginous Latosol

variances using Bartlett's test before AMMI and GGE biplot analyses.

For AMMI, the model used was (Gauch, 1992):

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

Where:

$Y_{ij}$  is the observed mean yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment;  $\mu$  is the general mean,  $G_i$  and  $E_j$  represent the effects of the genotype and environment, respectively;  $\lambda_k$  is the singular value of the  $k^{\text{th}}$  axis in the principal component analysis; and  $\alpha_{ik}$  is the eigenvector of the  $i^{\text{th}}$  genotype for the  $k^{\text{th}}$  axis. Also,  $\gamma_{jk}$  is the eigenvector of the  $j^{\text{th}}$  environment for the  $k^{\text{th}}$  axis;  $n$  is the number of principal components in the model; and  $e_{ij}$  is the average of the corresponding random errors.

The GGE biplot was constructed based on the first two principal components (PCs) resulting from singular value decomposition (SVD), by estimating each element of the matrix through the following formula (Yan *et al.*, 2000; Yan and Kang, 2003):

$$Y_{ij} = \mu + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \varepsilon_{ij}$$

Where:

$Y_{ij}$  = mean response of  $i^{\text{th}}$  genotype ( $i = 1, \dots, I$ ) in the  $j^{\text{th}}$  environment ( $j = 1, \dots, J$ );  
 $\mu$  = grand mean;  
 $e_j$  = environment deviations from the grand mean;  
 $\lambda_n$  = the eigen value of PC analysis axis;

$\gamma_{in}$  and  $\delta_{jn}$  = genotype and environment PCs scores for axis  $n$ ;

$N$  = number of PCs retained in the model; and

$\varepsilon_{ij}$  = residual effect  $\sim N(0, \sigma^2)$ .

## RESULTS

**Marketable tuber yield.** Bartlett's test for homogeneity of variances for MTY was non-significant ( $P > 0.05$ ), thus validating the combined analyses (Table 2). Significant differences ( $P < 0.05$ ) in MTY among clones were as low as 2.33 t ha<sup>-1</sup> to as high as 57.03 t ha<sup>-1</sup>, indicating high genetic differences among the genotypes. At individual sites, 3 clones (142/161/2, 142/161/5 and 29/5/10) gave significantly higher MTY than Spunta at both Réduit and St. Antoine. At Bigara, ten clones produced significantly higher marketable yield than Spunta, namely four clones of the 29/5 series, five clones of the 142/161 series and clone 161142/16. At Rivière du Poste, yield was significantly higher in (18.83 t ha<sup>-1</sup>) compared to Spunta (13.17 t ha<sup>-1</sup>). The combined ANOVA showed that five clones (142/161/2, 142/161/4, 142/161/5, 29/5/10 and 29/5/16) were identified as the highest yielders with yield of 30.04 to 32.53 t ha<sup>-1</sup>. The corresponding yield increase over Spunta ranged from 47.4 to 59.6%. The environment mean yield varied from 12.36 t ha<sup>-1</sup> at Rivière du Poste to 30.37 t ha<sup>-1</sup> at Réduit.

### Correlation between test environments.

The strengths of the relationships among locations for marketable tuber yield were verified using phenotypic and rank correlations (Table 3). Significant to highly significant and positive associations of genotype means were obtained between environments. The highest correlation values were obtained between St Antoine and Bigara for both Pearson ( $r = 0.46$ ) and Spearman's rank correlations ( $\tilde{r} = 0.58$ ). However, the  $r$  and  $\tilde{r}$  values were generally

TABLE 2. Marketable tuber yield (t ha<sup>-1</sup>) of 18 advanced potato clones compared to the control variety Spunta in four potato environments in Mauritius

Clone	Location <sup>†</sup>				Mean yield	IPCA1 <sup>‡</sup>	IPCA2 <sup>‡</sup>
	Réduit	St Antoine	Bigara	Riviere du Poste			
142/161/1	35.83 <sup>abcde</sup>	20.07 <sup>fghi</sup>	25.33 <sup>efgh</sup>	16.50 <sup>abcd</sup>	24.43 <sup>cd</sup>	1.126	1.134
142/161/2	43.83 <sup>a</sup>	34.03 <sup>ab</sup>	35.70 <sup>bcde</sup>	15.17 <sup>abcd</sup>	32.18 <sup>a</sup>	0.415	0.448
142/161/4	34.87 <sup>abcde</sup>	27.20 <sup>cde</sup>	57.03 <sup>a</sup>	11.00 <sup>defg</sup>	32.53 <sup>a</sup>	-3.582	0.831
142/161/5	41.40 <sup>ab</sup>	38.67 <sup>a</sup>	31.60 <sup>cdef</sup>	18.08 <sup>ab</sup>	32.44 <sup>a</sup>	1.138	-0.793
142/161/6	24.33 <sup>fgh</sup>	8.73 <sup>j</sup>	24.33 <sup>efgh</sup>	2.33 <sup>h</sup>	14.93 <sup>gh</sup>	-0.519	1.437
142/161/8	28.17 <sup>efgh</sup>	15.53 <sup>hi</sup>	19.73 <sup>ghi</sup>	16.67 <sup>abcd</sup>	20.03 <sup>ef</sup>	1.356	0.554
142/161/9	23.67 <sup>gh</sup>	29.73 <sup>bcd</sup>	35.00 <sup>bcde</sup>	11.42 <sup>cdefg</sup>	24.95 <sup>bc</sup>	-1.023	-1.806
142/161/15	34.90 <sup>abcde</sup>	25.00 <sup>def</sup>	30.00 <sup>defg</sup>	8.67 <sup>efg</sup>	24.64 <sup>bcd</sup>	0.088	0.503
161/142/16	28.57 <sup>defgh</sup>	23.43 <sup>defg</sup>	45.60 <sup>b</sup>	17.08 <sup>abc</sup>	28.67 <sup>ab</sup>	-2.083	0.067
21/5/3	19.30 <sup>h</sup>	23.37 <sup>defg</sup>	23.03 <sup>fghi</sup>	11.83 <sup>cdef</sup>	19.38 <sup>f</sup>	0.324	-2.047
21/5/10	23.10 <sup>gh</sup>	14.27 <sup>ij</sup>	11.67 <sup>i</sup>	6.17 <sup>gh</sup>	13.80 <sup>h</sup>	1.575	-0.012
29/5/2	20.03 <sup>h</sup>	24.87 <sup>def</sup>	20.03 <sup>ghi</sup>	7.50 <sup>fg</sup>	18.11 <sup>fg</sup>	0.637	-1.690
29/5/3	37.97 <sup>abcd</sup>	18.27 <sup>ghi</sup>	24.27 <sup>efgh</sup>	8.67 <sup>efg</sup>	22.29 <sup>cdef</sup>	0.917	1.847
29/5/10	39.23 <sup>abc</sup>	27.17 <sup>cde</sup>	42.67 <sup>bc</sup>	18.83 <sup>a</sup>	31.98 <sup>a</sup>	-0.826	0.950
29/5/11	26.37 <sup>efgh</sup>	19.57 <sup>fghi</sup>	19.33 <sup>ghi</sup>	12.08 <sup>cdef</sup>	19.34 <sup>f</sup>	1.150	-0.260
29/5/14	27.30 <sup>efgh</sup>	19.10 <sup>fghi</sup>	33.07 <sup>cdef</sup>	16.33 <sup>abcd</sup>	23.95 <sup>cde</sup>	-0.525	0.234
29/5/16	33.47 <sup>bcdef</sup>	32.87 <sup>abc</sup>	40.00 <sup>bcd</sup>	13.83 <sup>abcde</sup>	30.04 <sup>a</sup>	-0.929	-0.760
29/5/17	23.33 <sup>gh</sup>	22.83 <sup>efg</sup>	34.67 <sup>bcdef</sup>	9.42 <sup>efg</sup>	22.56 <sup>cdef</sup>	-1.287	-0.757
Spunta	31.37 <sup>cdefg</sup>	21.13 <sup>efgh</sup>	15.87 <sup>hi</sup>	13.17 <sup>bcde</sup>	20.38 <sup>def</sup>	2.047	0.121
Mean	30.37	23.47	29.94	12.36	24.03		

<sup>†</sup>Means with the same alphabet along column are not significantly different at P < 0.05

<sup>‡</sup>IPCA = Interaction principal component analysis loadings obtained using AMMI model

not high enough to explain the similarity between environments and GEI.

**AMMI analyses.** Analysis of variance (ANOVA) with the AMMI model confirmed the significance of GEI (Table 4). Treatment combinations that comprised genotype (G), location (L) and G x E accounted for 89% of total variation, the block effect accounted for 2% and the remaining accounted for 10% by the residual. Genotype explained 26% of total variation, environment 42% and G x E 21%. Three PCAs explained the total G x E variations, of which the first two interaction principal components (IPCA) captured 84.5% of the variations.

AMMI1 biplot (Fig. 1) fitted the mean yields of the genotypes and environments, along with the first dimension measure (IPAC1) of the GEI. It provided a direct measure of the yield potential and stability of the genotypes being examined. Along the X-axis, Bigara and Réduit equally had the highest mean yield and Rivière du Poste the lowest. The high yielding varieties were further to the right and the least performing ones to the left. The overall ranking of genotypes in terms of marketable tuber yield could be interpreted as follows: 142/161/4 > 142/161/5 > 142/161/2 > 29/5/10 > 29/5/16 > 161/142/16 > ..... > 142/161/6 > 21/5/10. The IPCA scores on the Y-axis is a measure of genotype-by-environment (GE)

TABLE 3. Correlation coefficients between the four locations for marketable tuber yield among potato genotypes in in Mauritius

Location	Réduit	St Antoine	Bigara	Rivière du Poste
Pearson's (r) correlations				
Réduit	1.00			
St Antoine	0.40**	1.00		
Bigara	0.31*	0.46**	1.00	
Rivière du Poste	0.34*	0.38**	0.28*	1.00
Spearman's( $\tilde{r}$ )rank correlations				
Réduit	1.00			
St Antoine	0.34*	1.00		
Bigara	0.28*	0.58**	1.00	
Rivière du Poste	0.40**	0.29*	0.30*	1.00

\*Correlation is significant at the 0.05 level (2-tailed); \*\* Correlation is significant at the 0.01 level (2-tailed)

TABLE 4. AMMI analysis of variance for marketable tuber yield (t/ha) of 18 advanced potato clones grown at four locations in Mauritius

Source	df	SS	MS	F	Fpr.	Explained (%)	Accumulated (%)
Block	8	472	55	2.96	0.004	2	
Treatments	75	25811	344.1	17.23	<0.001	89	
Genotype (G)	18	7489	416.1	20.83	<0.001	26	
Location (E)	3	12124	4041.3	68.48	<0.001	42	
GxE	54	6198	114.8	5.75	<0.001	21	
IPAC 1	20	3865	193.2	9.68	<0.001	62.36	62.4
IPCA 2	18	1367	75.9	3.8	<0.001	22.05	84.5
IPCA 3	16	966	60.4	3.02	<0.001	15.5	99.95
Error	144	2876	20			10	
Total	227	29158	128.5				

effect of each genotype. Thus, clones close to the X-axis (horizontal line at 0) had small GE effect; while those further away in either positive or negative directions had large GE effect. The most stable genotypes were: 21/5/3, 142/161/15, 142/161/2 and 142/161/5; while the least stable were 21/5/10, Spunta and 142/161/4. However, 142/161/2 followed by 142/

161/5 were the two best performing genotypes combining both stability and high yield.

This trend is more clearly discernible from the AMMI2 biplot (Fig. 2). Genotypes in a quadrant are expected to be adapted to locations in that quadrant. Genotypes that were positioned close to the biplot origin are the most stable and comprised of 29/5/14, 142/

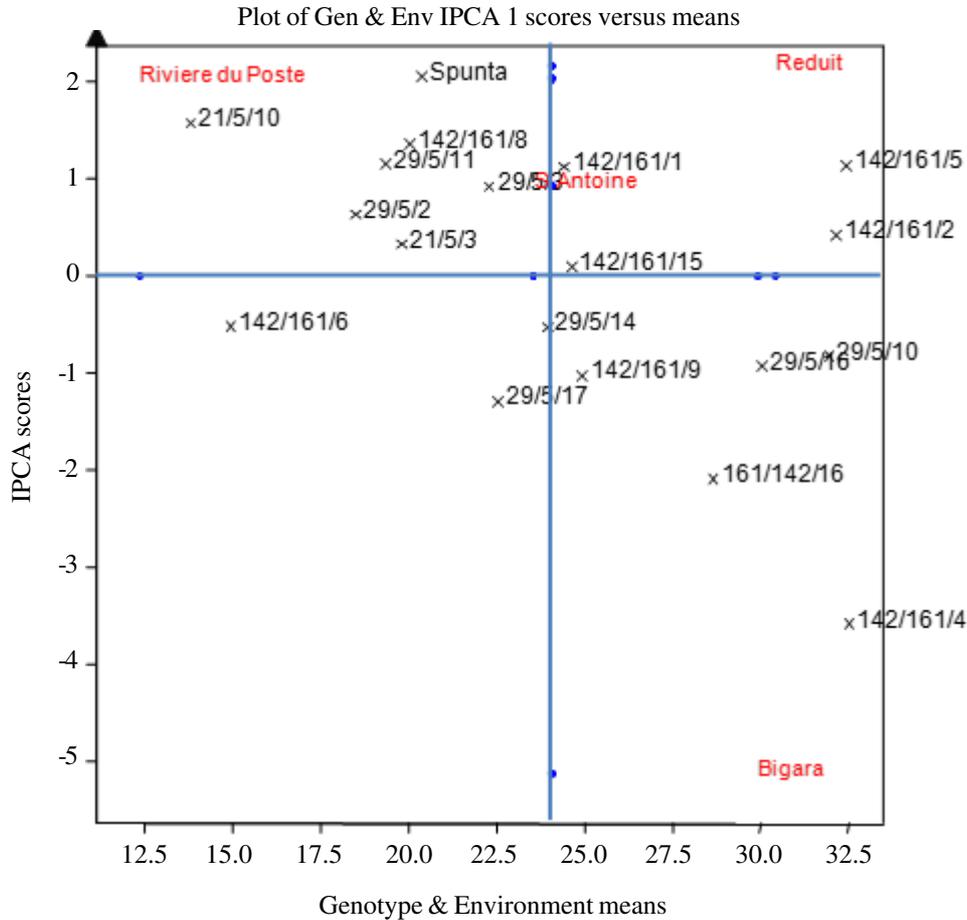


Figure 1. AMMI1 biplot for marketable tuber yield of 19 potato genotypes across locations in Mauritius.

161/2 and 142/161/5. The most unstable genotypes that were positioned distant to the biplot origin were 142/161/4 and 29/5/2. All four environments contributed to the  $G \times E$  interaction since they were positioned far from the origin. Genotypes and environments positioned close to each other in the biplot had positive associations. Thus, 142/161/4 and 161/142/16 had specific adaptation to Bigara, 29/5/2 and 21/5/3 were adapted to St. Antoine, 21/5/10 to Rivière du Poste whereas 29/5/3 was adapted to Réduit.

#### **GGE evaluation of test environments.**

Figure 3 illustrates the environment vector view of the GGE biplot for the variety-location data.

It is based on an environment-centred GE table without any scaling. The biplot explained 85% (66% by PC1 and 19% by PC2) of total variation of the genotype and  $G \times E$  combined. An Average Environment Coordination (AEC) is added in the graph that corresponds to an 'ideal environment' in Mauritius based on the four trials. The average environment (represented by a small circle) axis (AEA) is represented by a single arrowed line that passes through the origin. Test environments having smaller angle with the AEA (St Antoine and Rivière du Poste) were more representative; whereas those with wider angle (Bigara and Réduit) were less representative of ideal environment. The length of the environment

MTY: AMMI biplot (symmetric scaling)

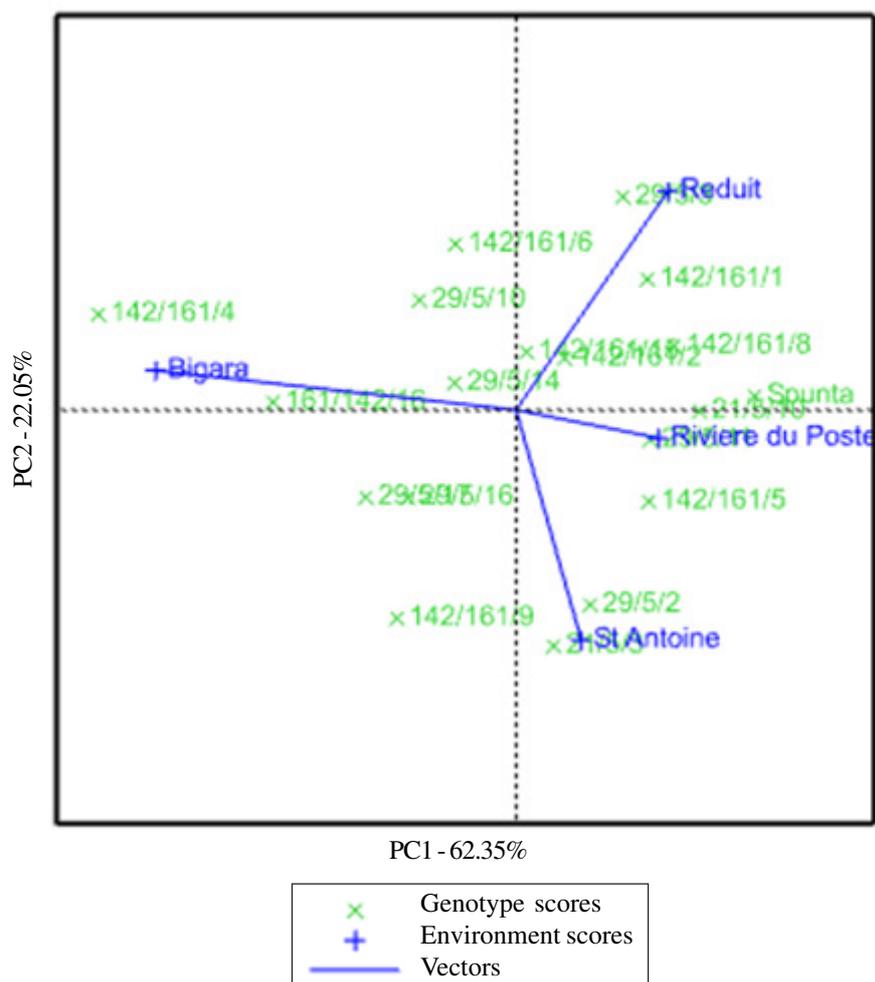


Figure 2. AMMI2 biplot showing the first two principal component axes (PCA2 vs. PCA1) for marketable tuber yield of 19 potato genotypes over four environments in Mauritius.

vectors measured the discriminating ability of the environments. Thus, Réduit and Bigara with the longest vectors were the most discriminating (informative) locations and St Antoine and Rivière du Poste the least discriminating. However, the ideal test environment should be most discriminating and most representative of the target environment. The pattern of the environments in the above biplot suggests that, for general adaptation, the environments of St Antoine and Rivière du Poste were most representative, but lacked the discriminating ability. Réduit and Bigara

represented two contrasting discriminating environments for specific adaptation.

**GGE evaluation of test genotypes.** For evaluations on genotypes with GGE biplot, genotype focused scaling was used. In order to rank the genotypes based on their performance in an environment, a line was drawn that passes through the biplot origin and the environment. Figure 4 defines an ideal genotype (the centre of the concentric circles) to be a point on the AEA (“absolutely stable”) in the positive direction and has a vector length

Ranking biplot (Total - 85.22%)

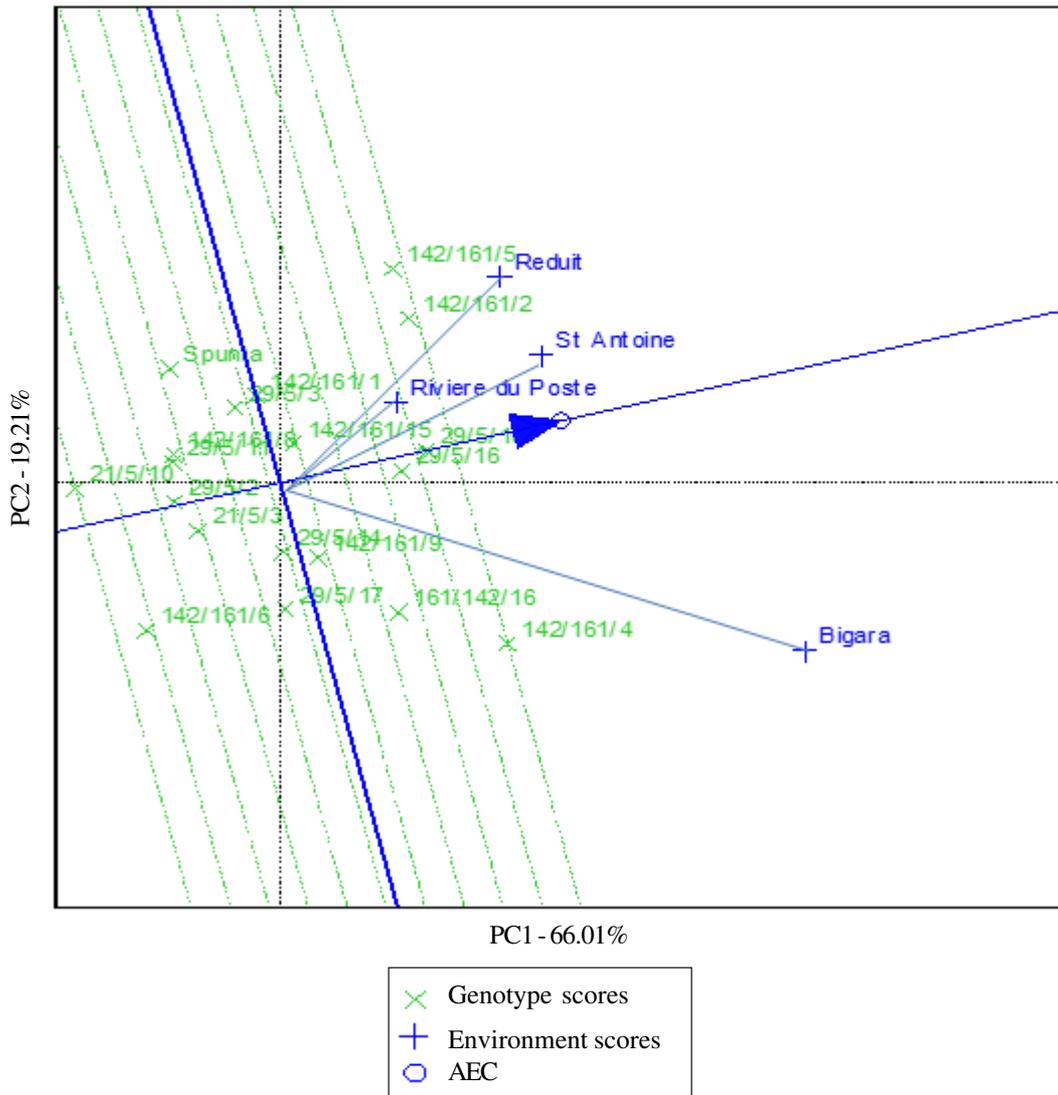


Figure 3. GGE biplot: relationship among environments. O: Average Environment Coordination.

equal to the longest vectors of the genotypes on the positive side of the AEA (“highest mean performance”). The concentric circles help visualise the distance of the different test clones from the ideal genotype.

Genotypes located on the ideal genotype axis were most stable; whereas those further away (perpendicular to the AEA in both positive and negative directions) were more unstable. Clones 21/5/3 and 142/161/15, which crossed

the single arrowed line (AEC), were the most stable clones, but were only average yielders. From the biplot, the AEC points to higher mean yield across environments. Thus, 142/161/2 and 142/161/5, which were located in the innermost concentric circles, ensured high yield and higher stability; and can therefore, be exploited for wide adaptability. On the other hand, Spunta which was very far from the AEC conferred lower stability.

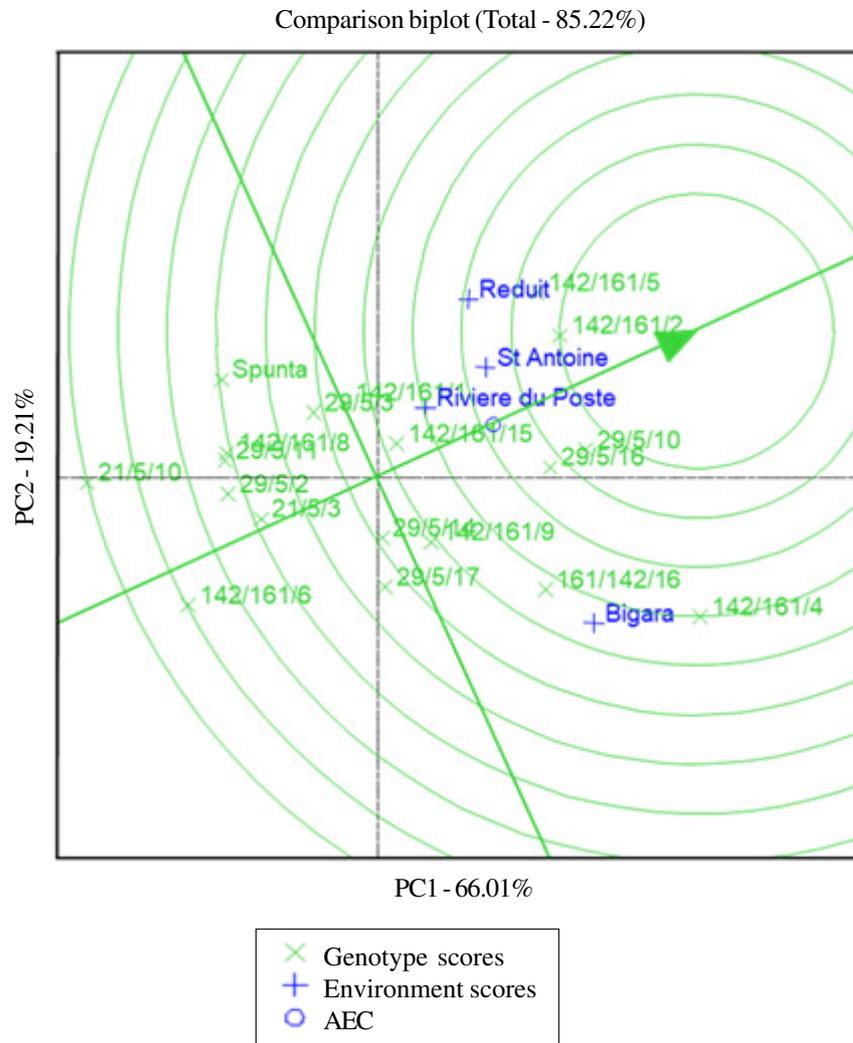


Figure 4. GGE biplot mean yields and stability of genotypes.

#### Polygon view of the GGE biplot analysis.

To explore the possible existence of mega-environments within the regions, a polygon graph (Fig. 5) was constructed to visualise the interaction patterns between genotypes and environments. The polygon connects the furthest genotypes from the biplot origin such that all other genotypes are contained within the polygon. Since these genotypes possess the shortest vectors, they are relatively less responsive to interaction with the environment.

The equality lines, which originate from the centre of biplot and are perpendicular to the sides of polygon, divide the graph into five sectors. Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. The winning genotype for each sector was the one located on the respective vertex. In consequence, 142/161/5 was the winner at Réduit, St Antoine and Rivière du Poste, followed by 142/161/2, 29/5/10 and 29/5/16.

Scatter plot (Total - 85.22%)

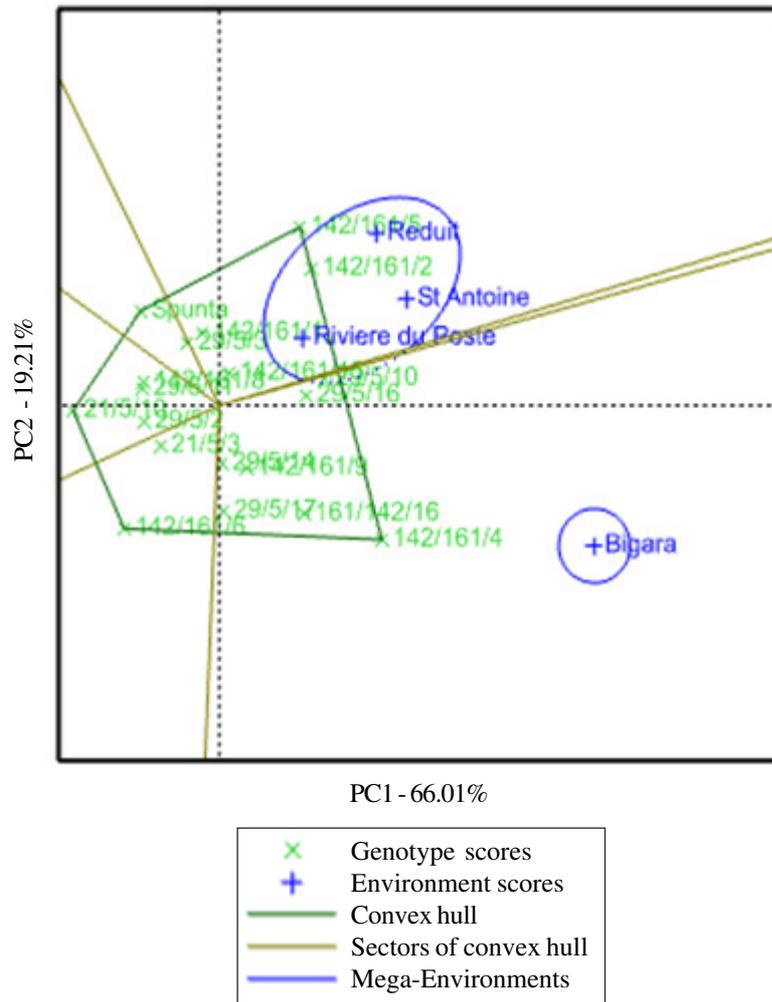


Figure 5. Polygon view of the GGE biplot to show which genotype performed best in which test environment.

At Bigara, the winning genotype was 142/161/4 followed by 161/142/16. Other vertices represented by Spunta, 21/5/10 and 142/161/6 were poor yielding genotypes generally showing negative interactions (obtuse angles) with the four locations. Furthermore, the test environments could be delineated into two mega-environments. Réduit, St Antoine and Rivière du Poste formed one group and the high altitude, super-humid region of Bigara; a second group.

## DISCUSSION

Both AMMI and GGE biplot techniques (Figs. 1 - 4) provided similar results on GEI. The AMMI ANOVA partitioned the total variation into genotype main effect (26%), environment main effect (42%), and GEI (21%). Therefore, the environment and GEI combined (63%) had greater influences on yield than individual genotypes. Similar results were obtained by Abalo *et al.* (2001), Dixon and Nukenine

(1997) and Arinaitwe *et al.* (2018). The highly significant environment effect and its variance component could be attributed mainly to differences in air temperatures and rainfall pattern. The high marketable yield at Bigara could be due to cool temperatures while the relatively high temperature at Rivière du Poste could explain the low marketable yield (Table 2). Potato is a cool season (C3) crop and cool conditions lead to high tuber yields (Haverkort *et al.*, 1990). Previous research on yield of potato clones has shown similar results on GEI effects (Flis *et al.*, 2014; Gedif and Yigzaw, 2014; Muthoni *et al.*, 2015). Furthermore, the high variation (84.5%) explained by the first two PCA due to GEI implied the need to examine stability through multi-locations to investigate whether there are any repeatable GE patterns, and certainly multi-year trials to verify the stability of new varieties across years. AMMI1 biplot was found to be very useful in showing mean yield versus stability of potato genotypes. Thus, it differentiated the high yielding from low yielding, as well as the unstable to the more stable genotypes. AMMI2 biplot was helpful in detecting G x E interaction, as well as its magnitude (Silveria *et al.*, 2011). In the present study, all four environments contributed largely to the GEI since they were far from the biplot origin.

According to Negash *et al.* (2013), GGE biplots of multi-environment trial data enable visualising the inter-relationship among genotypes, including the ranking of genotypes based on both mean performance and stability, inter-relationship among environments as well as interaction between genotypes and environments, including the which-won-where view. In the present study, GGE methods (genotype centered biplot, comparison biplot, ranking biplot and “which-won-where” view) were helpful in identifying, firstly the winning genotypes in a specific environment; secondly the “ideal test environment” which is most representative and most discriminative; thirdly the “ideal genotype” which is associated with high mean yield and high stability; and lastly

the presence of mega-environment. Broadly, out of the 18 advanced clones, six of them were identified as high yielding namely: 142/161/4, 142/161/5, 142/161/2, 29/5/10, 29/5/16 and 161/142/16. Yan *et al.* (2007) and Yan and Holland (2010) showed the accuracy of GGE biplot analysis for discriminating test environments and genotypes. Nevertheless, since no ideal environment could be identified by the GGE methods, additional years of trials are warranted to confirm that a specific test environment is ideal (Yan and Tinker, 2006). The AEC view of the GGE biplot revealed that 142/161/2 and 142/161/5 were the two most desirable genotypes being located closer to the ideal genotype; while the “which-won-where” approach provided clear graphical displays of the winning genotypes for each environment. The evaluation of test environments distinguished them in two mega-environments; the very humid central upland (Bigara) and the remaining three (Réduit, St. Antoine and Rivière du Poste) located in lower altitudes with lesser mean annual rainfall as the second mega-environment. Similar results were obtained by Santchurn *et al.* (2016), who worked on GEI of sugarcane crop in the island. The angle between the environment vectors of Réduit and St. Antoine being small, suggests that very similar yield data could be obtained from each of them. Therefore, one of them could be eliminated while optimising resources without losing information on the genotypes in future trials.

In Mauritius, recommendations for potato cultivation have traditionally been based on soil types and annual precipitation. In consequence, super-humid regions were not recommended for potato cultivation mainly because of the high incidence of the late blight disease to which all commercial varieties, including Spunta are highly susceptible. The fact that the majority of the clones outperformed Spunta at Bigara provided tangible evidence that the latter is a key testing site for evaluation of local potato genotypes for cultivar release. However, more precise

analysis of genotype performance and delineation of mega-environments require a full-fledged field investigation, with additional years of information from several locations.

### CONCLUSION

The findings of this study showed that the AMMI methods were very appropriate in detecting GEI, as well as identifying the high yielding and stable potato genotypes. The GGE biplots gave similar results and provided additional useful visualisation techniques in ranking genotypes based on their performance in a specific environment, delineation of mega-environments; and selection of desirable genotypes which are close to the ideal genotype. Therefore, both AMMI and GGE models can effectively be employed in the local potato breeding and selection programme to analyse multi-locational trial data and select superior potato genotypes for commercial cultivation. This study needs to be further strengthened with additional years of evaluation; whereby genotype x year interaction, which is equally highly important, can be similarly addressed using the biplot techniques. A high genotype year interaction would certainly be less desirable as growers expect new varieties to remain productive and stable across a long time span.

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