

Stability analysis of sweetpotato (*Ipomoea batatas* Lam.) shoot tips yield for leafy vegetable across agro-ecologies using AMMI

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Abstract

Six selected sweetpotato genotypes were evaluated for yield stability over eight agro-ecological environments using the AMMI model. The experiments were conducted using RCBD, with three replications, at four locations, over two planting seasons at MARDI research stations, representing different soil type namely, bris, tin-tailing, peat, and mineral. The AMMI analysis indicated that the genotypes for the trait of shoot tips yield (t ha^{-1}) had major environmental influence. The two principal component axes (PCA1 and PCA2) were significant at $P \leq 0.01$ and cumulatively contributed to 85.24% of the total variation. The biplot technique was used to identify genotypes for general or specific adaptability. Results indicated that MIB05 and MIB14 were genotypes with highest interaction, but they were unstable; meanwhile, MIB20 (control) had the lowest interaction, and therefore, it was the most stable one. However, MIB15 was identified as the one which was mediocely stable, implying that it is more suitable for low yield environment (peat soil - AGV5 and AGV6). It was found that MIB05 was suitable for high yield planting on tin-tailing, whereas, MIB14 was suitable for bris soil.

Keywords: Sweetpotato; shoot tips; stability; AMMI; vegetable.

Abbreviations: AGV – Agro-ecology; AMMI - additive main effects and multiplicative interaction; PCA – Principal component analysis; ASV – AMMI stability value.

Introduction

Sweetpotato provide two useful food types from the same plant, namely fleshy storage roots and green tips (vine consisting of stems and leaves). The tips can be used as a nutritious food such as tropical spinach or salad green. In Japan and Philippine the shoots are also being consumed as vegetable and products are manufactured based on it. Plant breeders frequently encounter genotype x environment (G×E) when testing plant interaction across a number of environments. The magnitude of the interactions, or, different genotypic responses to the environment, mainly depends on the genotype of environmental interactions. The interactions vary greatly across agro-ecology environments. In order to quantify the interactions and describe their main effects, a combined analysis of variance (ANOVA) is usually applied. Nevertheless, since the analysis of variance does not adequately partition the G×E interactions, AMMI, also known as the additive main effects and multiplicative interaction model, can be used to describe the G×E interactions. As a matter of fact, to increase accuracy, AMMI is the proposed model of choice when effects and interactions are both important (Zobel et al., 1988). This method integrates the analysis of variance and the principal component analysis (PCA) into a united approach (Sadeghi et al., 2011). The significant feature of this analysis is that adjustment is carried out using information from other locations to refine the estimates within a given location. Moreover, it removes residual or noise variation from G×E interactions (Crossa et al., 1990a). Most importantly, Zobel et

al. (1988) reported that for AMMI analysis, no specific experimental design is required, except for a two-way data structure. The AMMI analysis provides a graphical representation (biplot) that summarises information on main effects and interactions of the genotypes and environments simultaneously (Crossa, 1990; Crossa et al., 1990a). The additive portion in AMMI is separated from the interactions by applying ANOVA. Then the PCA, which provides a multiplicative model, is applied to analyse the effect of interactions from the additive ANOVA model. The biplot display of PCA scores are plotted against each other to provide a visual view that interprets the G×E interaction components. Thillainathan and Fernandez (2001) reported that by integrating biplot display and genotypic stability statistics, it enables genotypes to be grouped based on similarity of performance across diverse agro-ecology environments. By exposing a number of genotypes to a set of contrasting environments, it is possible to identify genotypes with an average yield of high and low of G×E (Ceccarelli, 1989). Taking this into consideration, it is a norm to test selected genotypes over diverse agro-ecological environments to ensure that the chosen one has a stable performance. However, different genotypic responses to environmental conditions associated with G×E may limit the accuracy of yield estimates, as well as its identification of high yielding stable genotypes (Crossa et al., 1991; Basford and Cooper, 1998; Kang, 1998). Regarding the use of AMMI in a multi-location trial data analysis, in which partitions of

Table 1. Name and origin of sweetpotato genotypes.

No	Genotype	Local name	Origin
1	MIB05	Taiwan	Taiwan
2	MIB12	Bawang	Kelantan
3	MIB13	Ikan Selayang	Perak
4	MIB14	Pasar Borong1	Kajang
5	MIB15	Pasar Borong2	Kajang
6	MIB20	Gendut	MARDI

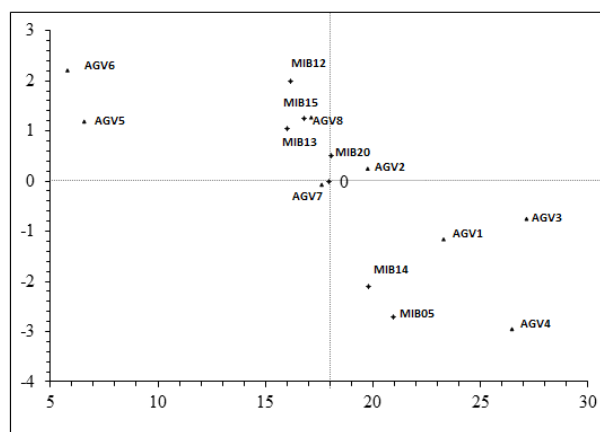
Table 2. The list of Agro-ecological environments, where 6 genotypes were evaluated.

Code	Location	Soil type	Planting season
AGV1	Kundang	Tin-tailing	Season 1
AGV2	Kundang		Season 2
AGV3	Telong	Bris	Season 1
AGV4	Telong		Season 2
AGV5	Pontian	Peat	Season 1
AGV6	Pontian		Season 2
AGV7	Serdang	Mineral	Season 1
AGV8	Serdang		Season 2

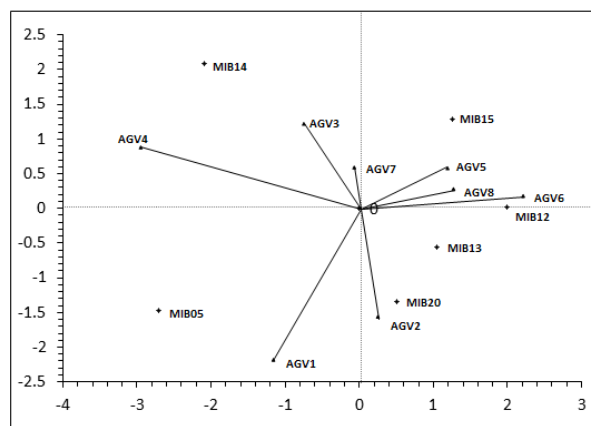
the G×E matrix was separated into individual genotypic and agro-ecological score, a good example has been provided by Zobel et al. (1988), who studied the G×E of soybean (i.e. a multi-location trial). Another example by Annicchiarico and Perenzin (1994), showed that earliness × cold stress, and plant height × drought interactions, in wheat plants were responsible for G×E. Similarly, Yan et al. (2000) applied the AMMI analysis to the yield data of winter wheat performance trials, and subsequently, suggested two winter wheat mega-environments in Ontario. Yan and Rajcan (2002) who applied the AMMI to genotypes by trait biplot analysis, soybean multiple traits and MLT data, found that the selection for seed yield was not only the simplest, but also the most effective strategy in the early stages of soybean breeding. In tandem with all such researches, the objectives of this study are: (i) to interpret G×E interactions obtained by the AMMI analysis of shoot tips yield of six sweetpotato genotypes over eight agro-ecology environments; (ii) to assess the stability of varied yield performance across agro-ecology environments based on the ASV value and biplot; and, (iii) to determine genotypes with high yields, depending on the different genotypic responses to agro-ecology environments.

Results and Discussion

The AMMI analysis of variance of shoot tips yield (t ha^{-1}) of the 6 genotypes tested in eight agro-ecology environments showed that 73.31% of the total sum of squares was attributed to environmental effects; only 4.34% was attributed to the genotypic effects. The G×AGV (agro-ecology) interaction explained 15.16% of the treatment sum of squares. The large sum of squares for environments indicated that the agro-ecology environments were diverse, with large differences among agro-ecology means, causing most of the variation in shoot tips yield. The magnitude of the G×AGV sum of squares was 3.6 times larger than that of the genotypes, indicating that there were substantial differences in genotypic responses across agro-ecology environments. The result of AMMI analysis (Table 6) showed that the first principal component of IPCA axis (IPCA1), accounted for 65.44% of the G×AGV interaction sum of squares, using 11 degrees of freedom. Similarly, the second IPCA axis (IPCA2) accounted for 19.80% of the interaction sum of squares, using 9 degrees of freedom. Furthermore, PCA1 and PCA2 had



Note : ▲ = agro-ecology ◆ = genotype

Fig 1. AMMI biplot (IPCA1 vs. mean) for shoot tips yield (t ha^{-1})**Fig 2.** AMMI biplot (IPCA1 vs. IPCA2) for shoot tips yield (t ha^{-1})

sums of squares greater than that of the genotypes. The F-test indicated that IPCA1 and IPCA2 were highly significant ($P < 0.01$) at 1% level, and cumulatively contributed to 85.24% of the total $G \times AGV$. Therefore, the postdictive evaluation using an F-test at $P \leq 0.01$ suggested that the two principal component axes of the interaction were significant for the model with 20 degrees of freedom. The interaction of the 6 genotypes with eight agro-ecology environments was best predicted by the first two principal components of genotypes and environments. The most accurate model for AMMI can be predicted by using the first two PCAs (Gauch and Zobel, 1996; Yan and Rajan, 2002). Meanwhile, Sivapalan et al. (2000) had recommended a predictive AMMI model with the first four PCAs. In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa et al., 1990b).

AMMI Biplot (IPCA1 vs. Mean) for shoot tips yield ($t\ ha^{-1}$)

The AMMI model 2 biplot of the genotype trial results for shoot tips yield ($t\ ha^{-1}$), can be displayed in the biplot as shown in Figure 1. The abscissa shows the genotype and environment (agro-ecology) means, and the ordinate shows the IPCA1 genotype and agro-ecology scores. The genotypes have been shown through the diamond-shaped sign (labeled as MIB05, MIB12, MIB13, MIB14, MIB15 and MIB20), and the agro-ecology environments through the triangle-shaped sign (AGV1-AGV8). The vertical dash line draws attention to the grand mean, while the horizontal dash line draws attention to zero IPCA1 score. Figure 1, captures a sum of squares of 13,262 (total sum of squares for genotypes, environment and IPCA1), which is 94.77% of the treatment sum of squares. The agro-ecology environments showed much variability in both main effects and interactions (Figure 1). However, the high potential agro-ecology environments were distributed evenly on the right lower quadrant (AGV1, AGV3 and AGV4) with minimum interaction effects while, the lower potential agro-ecology environments were sparsely distributed on the left higher quadrant (AGV5 and AGV6) with high IPCA1 values. The lowest yielding agro-ecology environments, AGV5 and AGV6 demonstrated the highest positive interaction IPCA1 score. These two agro-ecology environments characterised as peat soil, were located in Pontian, Johor. As shown in this biplot, four groups of genotypes were evident. Group one consisted of MIB20 that showed similar main effects (mean yield) to the grand mean. MIB14, MIB20 and MIB12 showed high interaction scores that varied in direction. Whatever the direction was, the greater the IPCA scores, the more specifically adapted these genotypes were to certain agro-ecology environments (Zobel et al., 1988; Crossa et al., 1990a, 1997). Furthermore, MIB15 performed well in AGV5 and AGV6 agro-ecology environments where they interacted positively. Likewise, AGV8 favored MIB12, which interacted positively because all their interaction scores had similar signs (Zobel et al., 1988; Crossa et al., 1997). On the contrary, MIB20 had an IPCA1 score close to zero and ranked the first (least) in ASV value, reflecting a minimum $G \times AGV$ interaction or stable yield over agro-ecology environments. Group 2 consisted of MIB05 which exhibited the highest mean yield, but the IPCA1 score was not close to zero as MIB20. MIB05 showed ASV value of six. This indicated that MIB05 was not stable across agro-ecology environments but it performed well at AGV1, AGV3 and AGV4. Figure 1 shows that the genotypes of MIB05 and MIB14 had relatively the highest mean yield but their interaction scores were negative, which allowed

them to perform well in agro-ecology environments with negative interaction values (AGV1, AGV3 and AGV4). In the biplot showing IPCA1 scores against the mean yield, MIB05 appeared to be the best, but it was not stable in all agro-ecology environments. Meanwhile, MIB20, relatively third in mean yield, had the least $G \times AGV$ interaction.

AMMI Biplot (IPCA2 vs. IPCA1) for shoot tips yield ($t\ ha^{-1}$)

The AMMI 2 model, IPCA2 scores was considered in interpreting $G \times AGV$ interaction that captured 19.8% of the interaction sum of squares as suggested by Gauch and Zobel (1996). This biplot displays IPCA1 on the abscissa and IPCA2 on the ordinate as shown in Figure 2. The vertical dash line represents IPCA1 score=0, while the horizontal dash line represents IPCA2 score=0. Purchase (1997) pointed out that the closer the genotypes score is to the center of the biplot when IPCA1 is plotted against IPCA2 (Figure 2), the more stable they are. According to Figure 2, it shows that AGV1, AGV4 and AGV6 are displayed farthest from the origin, which suggests that these agro-ecology environments were associated with higher environmental interactions compared to the others. Similarly, MIB05 and MIB14 were displayed farthest from the origin, which suggest that these genotypes were associated with higher environmental interactions effect or were unstable in performance as indicated in both biplots. Genotype MIB05 and MIB14 had positive interaction in AGV1, AGV3, AGV4 and AGV7 but negative interaction in AGV2, AGV5, AGV6 and AGV8. MIB12 and MIB20 were relatively close to the center.

Materials and Methods

This study was carried out to determine performance of six sweetpotato genotypes for shoot tips yield ($t\ ha^{-1}$) across eight agro-ecological environments, during the two growing seasons of 2009. Gendut (MIB20), a variety released by MARDI, was used as the control (Table 1). All the experiments were arranged in accordance to a randomised complete block design (RCBD) with three replicates. Sweetpotato cuttings of 30 cm were used as the planting materials. The experimental plots consisted of 5 m long three rows in each replicate, with 0.5 m row spacing. Experiments were carried out in Malaysia in four locations namely, Telong (Kelantan), Kundang (Selangor), Serdang (Selangor), and Pontian (Johor). Each location represented a different soil type vizs bris, tin-tailing, mineral, and peat (Table 2). All agronomic applications such as, weeding and fertilising were practised according to the standard procedure recommended for sweetpotato planting. Irrigation was carried out for the first two weeks after planting, followed by rain-fed. The yield data was only collected from the middle bed of each plot of replication. Harvest commenced 6 weeks after the initial planting, and continued with two weeks of interval until the final eight harvests.

Statistical analysis

GenStat, 12th edition, was applied to perform the data analysis of AMMI on the values of shoot tips yield obtained from each bed across the agro-ecological environments. The AMMI model equation according to Gauch and Zobel (1996) is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + P_{ge} + \varepsilon_{ger}$$

Where Y_{ger} = the observed yield of g^{th} genotype in e^{th} environment for r^{th} replicate; μ = the grand mean; α_g = the

Table 3. AMMI model for shoot tips yield (t ha⁻¹).

Source	df	SS	MS	F	Probability (p)
Genotypes (G)	5	663	132.50	18.68	0.00000
Environments (AGV)	7	11211	1601.50	85.79	0.00000
Block within AGV	24	448	18.70	2.63	0.00030
G×AGV Interactions	35	2121	60.60	8.54	0.00000
IPCA1	11	1388	126.20	17.78	0.00000
IPCA2	9	420	46.70	6.58	0.00000
Residuals	15	312	20.80	2.93	0.00055
Error	120	851	7.10	-	-
Total	191	15293	80.10	-	-

IPCA = Interaction Principle Component Analysis; df=degrees of freedom; SS=Sum Square; MS= Mean Square

Table 4. Genotype and agro-ecology means and IPCA scores for shoot tips yield (t ha⁻¹).

Genotype	Shoot tips yield (t ha ⁻¹)		IPCA[1]	IPCA[2]	ASV	
	Mean	Rank			Value	Rank
MIB05	20.96	1	-2.71	-1.47	9.07	6
MIB12	16.19	5	2.00	0.02	6.61	4
MIB13	16.01	6	1.04	-0.56	3.48	2
MIB14	19.81	2	-2.09	2.08	7.21	5
MIB15	16.80	4	1.25	1.28	4.32	3
MIB20	18.08	3	0.51	-1.34	2.15	1

IPCA = Interaction Principle Component Analysis

Table 5. Agro-ecology means and IPCA scores for shoot tips yield (t ha⁻¹).

Agro-ecology	Agro-ecology mean	IPCA[1]	IPCA[2]
AGV1	23.29	-1.16	-2.18
AGV2	19.76	0.25	-1.56
AGV3	27.15	-0.75	1.22
AGV4	26.47	-2.95	0.88
AGV5	6.57	1.19	0.58
AGV6	5.79	2.21	0.18
AGV7	17.62	-0.07	0.59
AGV8	17.13	1.27	0.28

IPCA = Interaction Principle Component Analysis

deviation of mean of the gth genotype from grand mean m; β_e = the deviation of mean of the eth environment from the grand mean m; λ_n = the singular value for the nth interaction principal component axis; V_{gn} = the genotype eigenvector for nth PCA axis; U_{en} = the environment eigenvector values for the nth PCA axis; P_{ge} = the residual effects; and ϵ_{ger} = the error term.

Furthermore, AMMI's stability value (ASV) was calculated in order to rank genotypes in terms of stability using the formulae suggested by Purchase (1997):

$$\text{AMMI stability value (ASV)} = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_{score1})^2 + [IPCA_{score2}]^2 \right]}$$

Where, SS = Sum of squares; IPCA1 = interaction principal component analysis axis 1; IPCA2 = interaction principal component analysis axis 2.

In general, an absolute AMMI stability value (ASV) was determined using a procedure that combines IPCA1 and IPCA2. In addition, the AMMI adjusted mean shoot tips yield (t ha⁻¹) for each genotype was estimated from the untransformed data to demonstrate the mean performance. For each genotype and environment, the genotypic and environment scores of the principal component axes were extracted and statistically tested by Gollob (1968) using F-

test procedure (Vargas and Crossa, 2000). These components were used to obtain a biplot. Predictive and postdictive approaches were applied to the data analysis to assess the suitability of the AMMI model of Zobel et al. (1988).

Conclusion

The best genotype in the context of agro-ecology environments AGV5, AGV6 and AGV8, was MIB15. Genotype MIB20 was the best for AGV2; meanwhile, genotype MIB05 was the best fit for AGV1. Evidently, for AGV3, AGV4 and AGV7, the best genotype was MIB14. Thus, based on Figure 2 and ASV ranking, as well as mean yield (Table 7), MIB05 and MIB15 were identified to be superior and MIB20 (control) as the most stable genotype in shoot tips yield (t ha⁻¹).

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