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GENOTYPE BY ENVIRONMENT ASSESSMENT IN SWEETPOTATO AS LEAFY VEGETABLE USING AMMI MODEL

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Abstract

The genotype by environment (G×E) interactions can be observed by differential genotypic responses to varied environmental conditions. Its effect is to limit the accuracy of yield estimates and complicate the identification of specific genotypes for specific environments. The objective of this study was to use the Additive Main Effects and Multiplicative Interactions (AMMI) method, with additive effects for genotypes and environments and multiplicative terms for genotype by environment interaction for analyzing data of 6 sweetpotato genotypes at 8 agro-environments. Results indicated that genotypes MIB05 and MIB14 were suitable for vegetable use for their higher shoot yield despite the root yield was low but they had low stability among agro-environments especially for 2 environments in Pontian, Johor with peat soil but these genotypes are suitable for 2 seasons of Telong, Kelantan. More breeding efforts are needed in order to improve the yield stability of these genotypes. AMMI biplot analysis has shown its advantage as helpful tool in identifying the best genotype for improving leafy vegetable for a new cycle of crossing and selection. Moreover, results indicated that MIB20 (control variety) had high stability with low interaction effects in eight agro-environments.

Introduction

Sweetpotato is grown in tropical and subtropical regions under agro-geographic conditions that vary widely and located from 15˚S to 45˚N (MacKay, 1989). It can grow on many types of soil on which other crop can grow and amazingly it can perform reasonable well on soils that are marginal to other crops such as sandy soils, peat and acid soils. Most of the cultivars are produced on marginal soil in low-input subsistence farming systems. It is hypothesized that, because of its wide distribution and large genetic diversity, sweet-potato shows large differences in genotypic expression in multi-environmental trials across regions, and G×E interactions are mainly explainable as subsets of genotypes and environments (GrÜneberg *et al*., 2005). Osiru *et al*., (2009) reported that knowledge about genotype performance and yield adaptation in diverse agro-ecological zones would be highly beneficial for cultivar development. Study of G×E interaction is important to plant breeders because it can limit the progress in the selection process, hence is a basic cause of differences among genotypes for yield stability (Asad *et al.,* 2009). Various stability techniques have been applied in different crops including sweetpatato to indentify the relative stability of individual genotype performance across environments by different workers (Denis & Gower, 1994; Gauch & Zobel, 1988; Nachit *et al.*, 1992; Manrique & Hermann, 2000; Rafii *et al.*, 2001; Mulema *et al.*, 2008; Arain *et al*., 2011; Bakhash *et al*., 2011; Mujahid *et al.*, 2011; Ali *et al*., 2012; Hikmat *et al.*, 2012; Rafii *et al.*, 2012; Roy *et al*., 2012; Shafi *et al.*, 2012; Thiyagu *et al.*, 2012; Ali *et al*., 2013).

The sweetpotato breeding program can be described as a multistage process with continuous flow of germplasm. Gene pools are improved and their best fractions are further advanced to form populations (Pandey *et al*., 1986). The superior families from each germplasm pool or population are combined to form high yielding experimental varieties. Multi-location trials play an important role in sweetpotato development program. Superior varieties are selected for two main purposes, a) use within the sweetpotato breeding program; and b) distribution to national programs for eventual use by farmers. A vital goal in breeding and agronomic research is to provide reliable guidance for selecting the best genotypes for planting in future years and at new sites. This will enable to predict yield as precisely as possible based on limited experimental data.

Statistical analysis may feature any one of three markedly different objectives for AMMI (*Additive Main effects and Multiplicative Interaction*) model namely, i) between-trial predictive success, ii) within-trial predictive success and iii) within-trial postdictive success (Gauch, 1988). If between-trial predictive is the objective, trial data, perhaps with concomint environmental data would be used to construct a model, and inferences are made for other sites and years not included in the yield trial (Crossa *et al*., 1990). However, the focus of this paper will be the within-trial objective.

In within-trial postdiction, a statistical model is constructed for a data set and success is measured in terms of the model's ability to fit the same data set. To evaluate within-trial prediction, Gauch (1988) and, Gauch & Zobel (1988) proposed that data from within a yield trial be split into modeling data and validation data. They used the AMMI model along with such data splitting method to analyze New York soybean (*Glycine max* (L.) Merr.) trial data. Success was measured in terms of the ability of the model fitted to the modeling data to predict the validation observations. They concluded that for those data, the number of multiplicative interaction terms should be one. Additional terms worsened predictive value rather than improving it. They also found that AMMI analysis with two replications was as precise as treatment (i.e., genotype × environment) means based on five replications (Crossa *et al*., 1990).

The response of a genotype in different environments may be conceptualized as a pattern in environment dimensional space, with the coordinate of an individual spatial axis being the total shoot yield or root yield/ bed of the genotype in one environment. Since genotype responses are multivariate rather than univariate (Lin *et al*., 1986; Van-Oosterom *et al*., 1993), multivariate techniques are preferable as they are usually more effective in explaining G×E interactions than linear regression models (Gauch & Zobel, 1988; Zobel *et al*., 1988; Nachit *et al*., 1992; Mulema *et al.,* 2008). Recently, multivariate techniques are being widely applied in plant breeding to describe the relationships among genotypes and environments. Hikmat *et al*., (2012) used principal component analysis (PCA) to estimate genetic variability in turmeric using scattered diagram of first two principal components. AMMI method is one of the multivariate technique briefly discussed here since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available.

AMMI model (Denis & Gower, 1994) of the G×E interaction combining with biplot was studied by Gollob (1968); Mandel (1971); Kempton (1984) etc. Aastveit & Martens (1986) partitioned genotype × year interaction by means of the PCA. Zobel *et al*., (1988) studied and compared the conventional statistical methods (ANOVA, PCA and linear regression) with AMMI model in a soybean yield trial. In this study, a multi-location yield trials of 6 genotypes over 4 locations and over 2 seasons (i.e. eight agro-environments), and this was further partitioned to 8 agro-environmental conditions. The objectives of this study were, 1) to determine the magnitude of G×E interaction effects on both total shoot and root yield of sweetpotato but special emphasis was given for shoot tips yield for diverse agro-environments in Malaysia; and 2) to examine the results obtained by AMMI applied to six sweetpotato genotypes trials conducted in 2009 and to select environment specific or general adaptable genotypes.

Materials and Methods

Six short listed genotypes based on preliminary trial, were tested for G×E trials at four locations. They were MIB05 which was obtained from Taiwan, and the other 5 were collected from Malaysia such as MIB12 (Bawang), MIB13 (Ikan selayang), MIB14 (Pasar Borong1), MIB15 (Pasar Borong2) and MIB20 (Gendut). Commercial cultivar MIB20 (Gendut) was used as control. All 30 cm cuttings were taken from virus-free mother plants grown in Serdang, Malaysia.

Experiments were conducted in four locations over 2 seasons representing the wide agro-environmental variation found in sweetpotato growing areas in Peninsular Malaysia, between the latitudes of 6˚03'N and 1˚30'N and longitude of 102˚24'E and 103˚27'E. Moreover, the experimental sites differed in soil types. The experimental sites were, namely Telong (Kelantan) with bris soil, Serdang (Selangor) with upland mineral soil, Kundang (Selangor) with tin-tailing soil and Pontian (Johor) with peat soil at four MARDI stations. Planting was carried out in the month of February simultaneously at four locations and final harvest was done early June, 2009. The second planting season was continued from July to November, 2009.

For each experiment, a randomized complete block design (RCBD) with four replications was used. Each bed (plot) consisted of 3 rows having 20 plants. Planting distances were 1.5 m between rows and 0.25 m between plants with the bed size 1 m × 5 m and distance of 0.5 m between two beds. Total shoot yield was obtained from frequency of 6 and 7 harvests carried out at the fortnightly in first and second planting, respectively except at Pontian, where 4 and 5 frequency of harvest were obtained and root yield were recorded as kg bed^{-1}. Samples of shoot yield were taken and dried to record dry matter content of each accession. Harvesting was made from central row of every accession in the experimental plot. Ten shoots having size of 10 cm were randomly selected from central row of each replication to determine leaf area in cm^2 and number of leaves, 2 weeks before the final harvest.

Data on shoot yield were recorded at 6 week after planting in all the locations. Experiments were conducted in 2 seasons in each location and were partitioned into individual agro-environment. Thus, a total of 8 agro-ecological trials at 4 locations within the period of 10 months were conducted (Table 1).

Statistical analysis: The AMMI analysis, performed using MATMODEL (Gauch, 1987) by GENSTAT 12th edition, first fits additive effects for genotypes (G) and environments (E) by the usual additive analysis of variance procedure, and then fits multiplicative effects for genotype-environment (G×E) interaction by principal components analysis (PCA).

$$\left(Y_{ij}\right) = \mu + g_i\, e_j + \sum_{1}^{N} \lambda_k\, \gamma_{ik}\, \delta_{jk} + \varepsilon_{ij}$$

where Y_{ij} is either the total shoot or root yield bed^{-1} of the *i*-th genotype in the *j*-th environment; μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; λ_k is the eigenvalue of the principal component scores for axis *k*; *N* is the number of principal components retained in the model; and ε_{ij} is the residual term. Environment and genotype PCA scores are expressed as unit vector times the square root of λ_k (i.e., environment PCA score = $\lambda_k^{0.5}\, \delta_{jk}$; genotype PCA score = $\lambda_k^{0.5}\, \gamma_{ik}$) (Zobel *et al*., 1988).

Postdictive success was measured by approximate F-tests at the 0.05 probability level by comparing each principal component's mean square with the pooled within-environment error mean square. Those PCA axes that were not significant were pooled into a residual term. The G×E interaction sum of squares (SS) is subdivided into PCA axes where axis *k* is regarded as having $g + e - 1 - 2k$, df, where *g* and *e* are the number of genotypes and environments, respectively. Since this is the increase in the number of mathematically independent model parameters that results from incorporation of the *k*th PCA axis (Gollob, 1968). The model including one or more PCA axes is non-linear in its parameters, so the allocation of df must be regarded as an approximation. A different method of allocating the degree of freedom (df), not used here, has been suggested by Mandel (1971) and was used by Cornelius (1993) in a postdictive method for choosing a model for the analysis of an un-replicated yield trial of 49 maize cultivars grown at four plant densities.

Table 1. Agro-environmental zone, where six genotypes were evaluated.

Code	Location	Soil type	Planting season
E1	Kundang	Tin-tailing	Season 1
E2	Kundang	Tin-tailing	Season 2
E3	Telong	Bris	Season 1
E4	Telong	Bris	Season 2
E5	Pontian	Peat	Season 1
E6	Pontian	Peat	Season 2
E7	Serdang	Upland mineral	Season 1
E8	Serdang	Upland mineral	Season 2

Biplot display: In the biplot, main effects means is on the abscissa and IPCA1 values as ordinates, genotypes (or environments) that appear almost on a perpendicular line have similar means and those that fall almost on a horizontal line have similar interaction patterns. Genotypes (or environments) with large PCA1 scores (either positive or negative) have high interactions, whereas genotypes (or environments) with IPCA1 scores near zero have small interactions. The additive AMMI0 model is simply the genotype mean plus the environment mean minus the grand mean. The interaction part is simply the genotype PCA score times the environment PCA score. These two parts are added to produce the expected value of the AMMI model. Genotypes and environments with IPCA1 scores of the same sign produce positive interactions effects, whereas combination of IPCA1 scores of opposite signs have negative specific interactions.

Results

AMMI Model for total shoot yield (kg bed^{-1}): Additive main effects and multiplicative interaction analysis showed that environments, genotypes and G×E interaction revealed highly significant ($p \leq 0.001$) variations. The G×E interaction manifested 15.15% of the treatment sum of squares, whereas, environments and genotypes accounted for 80.11 and 4.73% of the treatment sum of squares, respectively. The first IPCA axis (IPCA1) accounted for 65.45% of the G×E interaction sum of squares, using 11 degrees of freedom. The second IPCA axis (IPCA2) accounted for 19.81% of the interaction sum of squares, using 9 degrees of freedom. The F-test indicated that IPCA1 and IPCA2 were highly significant at $p \leq 0.001$ and $p \leq 0.01$, respectively (Table 2). The criterion of postdictive success for AMMI using all the data and F-tests at the 0.05 probability level recommended including the first 2 interaction PCA (IPCA) axes in the model (Table 2).

AMMI Biplot (IPCA1 vs. mean) for total shoot yield (kg bed^{-1}): The AMMI results for total shoot yield kg bed^{-1} can be displayed in the biplot as shown in Fig. 1a. The abscissa showed the genotype and location (agro-environment) means, and the ordinate showed the IPCA1 genotype and agro-environment scores. Genotypes were shown with circle sign (labeled as MIB05, MIB12, MIB13, MIB14, MIB15 and MIB20) and agro-environments with triangle (E1-E8). The vertical dash line draws attention to the grand mean, while the horizontal dash line draws attention to zero IPCA1 score.

The Fig. 1a, captured a sum of squares of 7169 (total sum of squares for genotypes, environment and IPCA1), which was 94.75% of the treatment sum of squares (Table 2). Genotypes MIB05 and MIB14 differed only in main effects, while genotypes MIB13 and MIB14 differed in interaction effects. However, genotypes MIB05 and MIB12 differed both in main and interaction effects. As for agro-environments E5 and E6 differed in main effects, while E1 and E5 differed in interaction effects. However, E4 and E6 differed both in main and interaction effects. Environment (E7) with IPCA score near zero indicating it had small interaction effects. Most of genotypes fall within the mean of 11.77 to 15.41 kg bed^{-1}. No distinct cluster of agro-environments and genotypes was observed.

Table 2. AMMI analysis of variance for total shoot and root yield kg bed^{-1} including two interaction principal component analysis axes.

Source	df	Total shoot yield kg bed^{-1}		Total root yield kg bed^{-1}	
		SS	MS	SS	MS
Environments (E)	7	358	865.90***	2657	379.55***
Replicates within E	24	6061	10.10***	122	5.09*
Genotypes (G)	5	242	71.60***	1440	288.05***
G×E	35	1146	32.80***	1418	40.52***
IPCA1	(11)	750	68.20***	758	68.89***
IPCA2	(9)	227	25.30**	358	39.73***
Residual	(15)	169	11.30^{ns}	303	20.19***
Error	120	460	3.80	329	2.74

ns- not significant; *, ** and *** indicate significant at $p<0.05$, $p<0.01$ and $p<0.001$, respectively
SS- sum of square; MS- mean square

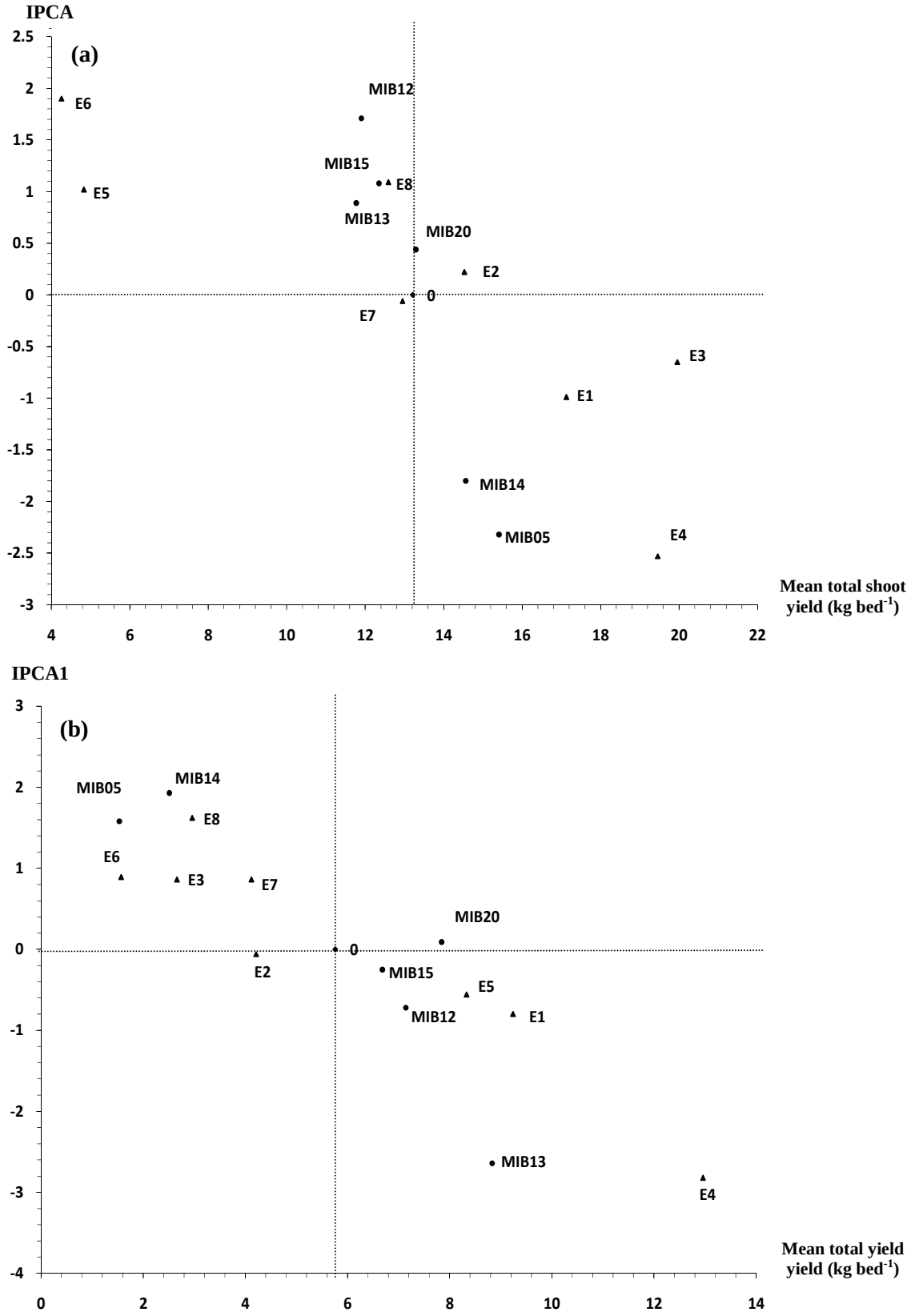


Fig. 1. AMMI biplots of principal component analysis (IPCA1) axis 1 against (a) mean total shoot yield (kg bed^{-1}) and (b) mean root yield (kg bed^{-1}) for 6 genotypes grown at 8 agro-environments. The vertical line represents the grand mean of the experiment. The numbers on the biplot refer to agro-environments (▲E) and genotypes (●MIB).

AMMI Biplot (IPCA2 vs. IPCA1) for total shoot yield (kg bed^{-1}): This biplot displays IPCA1 on the abscissa and IPCA2 on the ordinate as shown in Fig. 1b which showed that E1, E3 and E4 were displayed furthest away from the origin, suggesting that these agro-environments were associated with higher non-additivity as compared with others. Similarly, MIB05 and MIB14 were displayed farthest from the origin, and suggesting that these genotypes were also associated with maximum non-additivity. Genotype MIB05 and MIB14 had positive interaction in E1, E3, E4 and E7, but negative interaction in E2, E5, E6 and E8.

AMMI Model for total root yield (kg bed^{-1}): The G×E interaction explained 25.71% of the treatment sum of squares (Table 2). The IPCA1 accounted for 53.46% of the G×E interaction sum of squares, using 11 degrees of freedom. The IPCA2 accounted for 25.25% of the interaction sum of squares, using 9 degrees of freedom. The F-test indicated that IPCA1 and IPCA2 were highly significant ($p \leq 0.001$).

AMMI Biplot (IPCA1 vs. mean) for total root yield (kg bed^{-1}): The AMMI results for root yield (kg bed^{-1}) can be displayed in the biplot as shown in Fig. 2a, which captures a sum of squares of 4855 (total sum of squares for genotypes, environment and IPCA1, which is 88.03% of the treatment sum of squares (Table 2). Genotypes MIB12 and MIB15 differed only in main effects, while genotypes MIB12 and MIB20 differed in interaction effects. However, genotypes MIB13 and MIB14 differed both in main and interaction effects. As for agro-environments E1 and E5 differed in main effects. Meanwhile, E1 and E7 differed in interaction effects but E4 and E6 differed both in main and interaction effects. Most of genotypes fall within the mean of 6.68 to 8.83 kg bed^{-1} except for MIB05 and MIB14 which had low yield of 1.53 and 2.51 kg bed^{-1}, respectively (Fig. 1b). No distinct cluster of agro-environments and genotypes was found.

AMMI Biplot (IPCA2 vs. IPCA1) for total root yield (kg bed^{-1}): This biplot displays IPCA1 on the abscissa and IPCA2 on the ordinate as shown in Fig. 2b, which showed that E4, E5 and E8 were displayed furthest away from the origin, suggesting that these agro-environments were associated with higher non-additivity as compared with others. Similarly, MIB12, MIB13 and MIB14 were displayed farthest from the origin, and confirming that these genotypes were also associated with higher non-additivity. Genotype MIB13 had positive interaction in E1, E2, E4 and E5 but negative interaction in E3, E6, E7 and E8.

AMMI Model for leaf area (cm^2): The G×E interaction explained 11.50% of the treatment sum of squares. The IPCA1 accounted for 62.78% of the G×E interaction sum of squares, using 11 degrees of freedom (Table 3). The IPCA2 accounted for 19.26% of the interaction sum of squares, using 9 degrees of freedom. The F-test indicated that IPCA1 and IPCA2 were highly significant at $p \leq 0.001$ and $p \leq 0.01$, respectively.

Table 3. AMMI analysis of variance for leaf area and leaves/10 cm shoot including two interaction principal component analysis axes.

Source	df	Leaf area (cm^2)		Leaf no. per 10 cm shoot (no.)	
		SS	MS	SS	MS
Environments (E)	7	67257	5475***	30.75	5.10***
Replicates within E	24	38328	360^{ns}	35.72	0.19^{ns}
Genotypes (G)	5	8648	93451***	4.56	6.15***
G×E	35	65716	1878***	73.76	2.11***
IPCA1	(11)	41259	3751***	50.04	4.55***
IPCA2	(9)	12659	1407**	12.55	1.40**
Residual	(15)	11798	787^{ns}	11.17	0.75^{ns}
Error	120	63261	527	60.00	0.50

ns- not significant; *, ** and *** indicate significant at $p<0.05$, $p<0.01$ and $p<0.001$, respectively
SS- sum of square; MS- mean square

AMMI Biplot (IPCA1 vs. Mean) for leaf area (cm^2): The AMMI results for leaf area displayed in the biplot (Fig. 3a), which revealed a sum of squares of 546844 (total sum of squares for genotypes, environment and IPCA1), which was 95.72% of the treatment sum of squares. Genotypes MIB05 and MIB13 differed only in main effects, while MIB05 and MIB20 differed in interaction effects. However, genotype MIB05, MIB12 and MIB15 differed both in main and interaction effects. Agro-environments E3 and E4 differed in main effects, while E4 and E6 were differed in interaction effects but E1 and E4 differed both in main and interaction effects. For leaf area, most of genotypes showed results between 136.5–195.07 cm^2 except for MIB15 which showed 277.87 cm^2 (Fig. 3b). No distinct cluster of agro-environment and genotype was found. Agro-environment of E7 was found nearing to point of origin suggesting that its interaction was almost negligible.

AMMI Biplot (IPCA2 vs. IPCA1) for leaf area (cm^2): This biplot displays IPCA1 on the abscissa and IPCA2 on the ordinate (Fig. 4a) which exhibited that E3, E4, E7 and E8 were displayed furthest away from the origin, suggesting that these agro-environments were associated with higher non-additivity. Similarly, genotypes MIB12 and MIB20 displayed farthest from the origin, suggesting that these genotypes were also associated with higher non-additivity. Genotype MIB12 had positive interaction at agro-environments E3, E4, E7 and E8 but negative interaction in E1, E2 E5 and E6. Agro-environments E5 and E6 have almost similar environment patterns. Genotype MIB15 was found more suitable for high leaf area index at E1 and E2. Some prefers small leaf area, which would be MIB05 and MIB14 at E1, E2, E5 and E6.

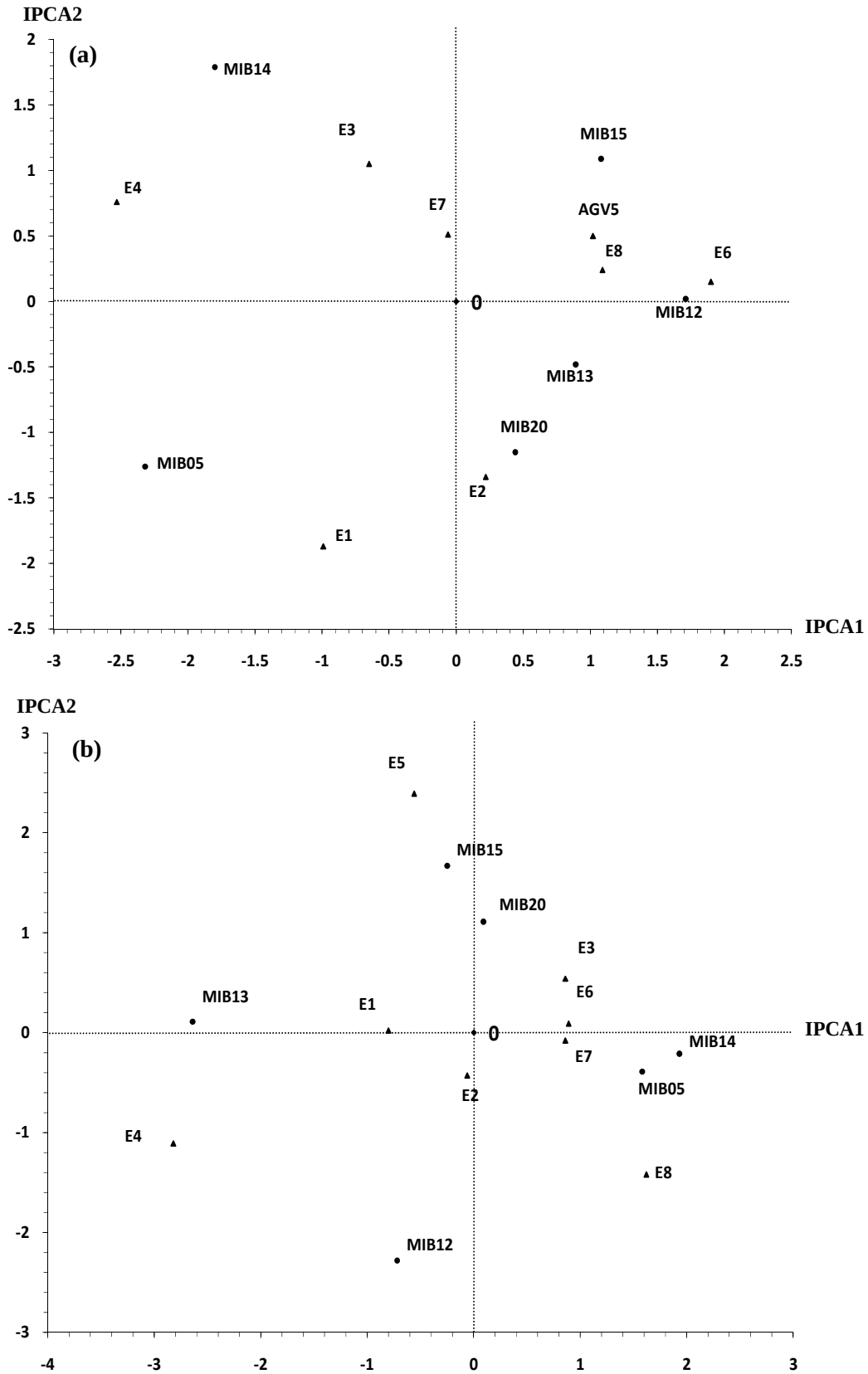


Fig. 2. AMMI biplot (IPCA1 vs IPCA2) of a set of sweetpotato genotypes in 8 agro-environments, (a) for total shoot yield (kg bed^{-1}) and (b) for root yield (kg bed^{-1}). The vertical line represents the grand mean of the experiment. The numbers on the biplot refer to agro-environments (▲ E) and genotypes (● MIB).

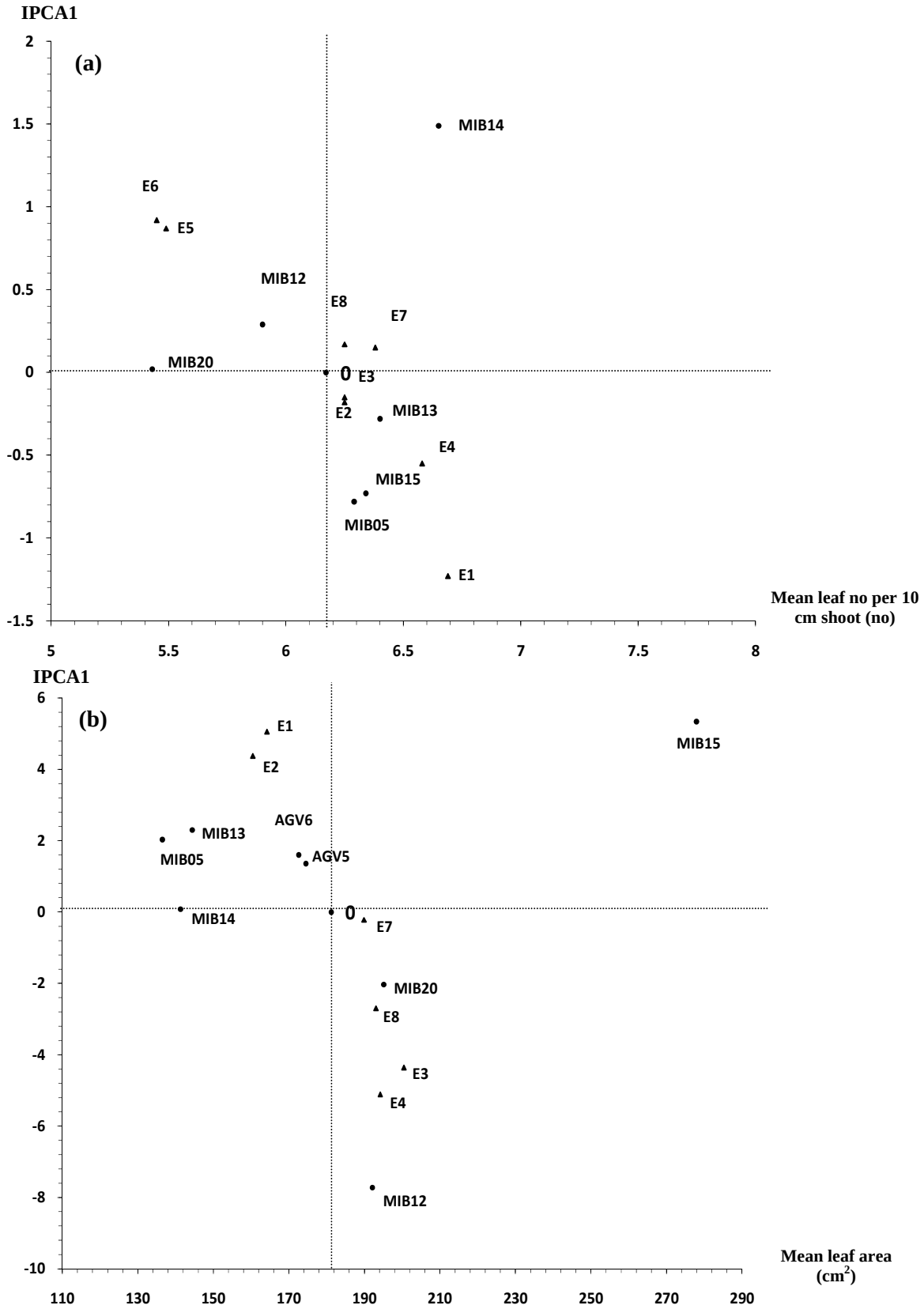
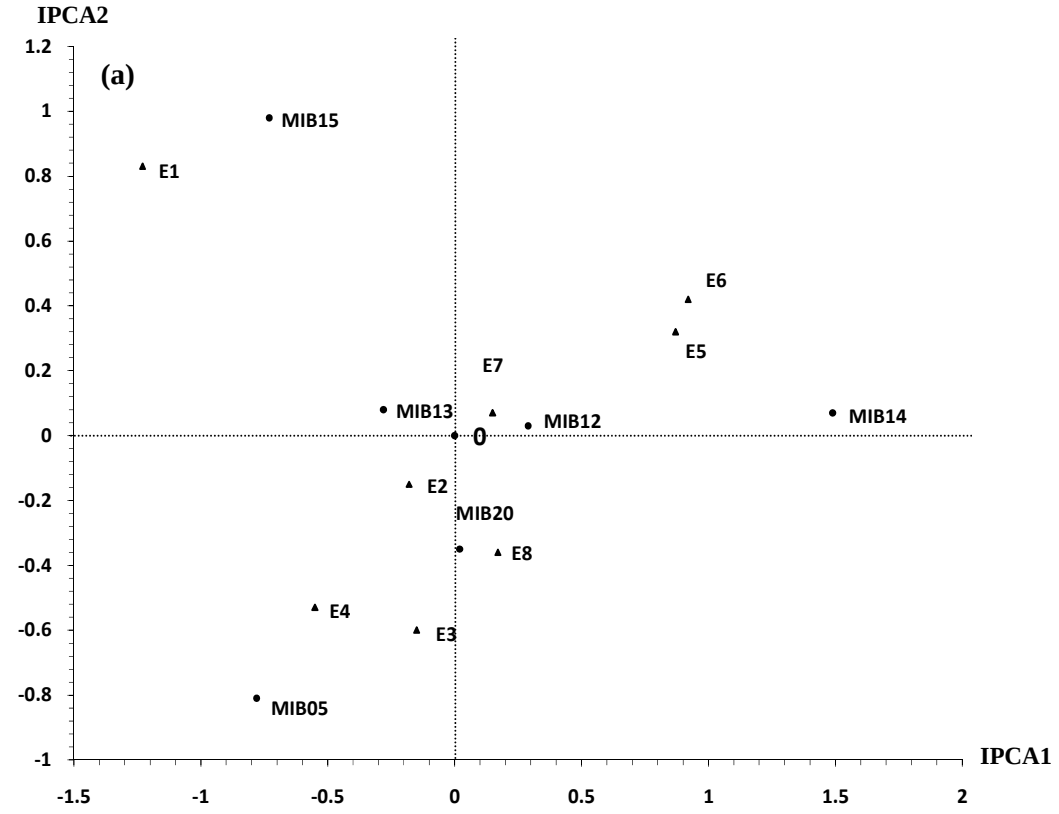


Fig. 3. AMMI biplots of interaction principal component analysis (IPCA1) axis 1 against (a) mean leaf no per 10 cm shoot and (b) mean leaf area (cm^2) for 6 genotypes grown at 8 agro-environment. The vertical line represents the grand mean of the experiment. The numbers on the biplot refer to agro-environments (▲E) and genotypes (● MIB).



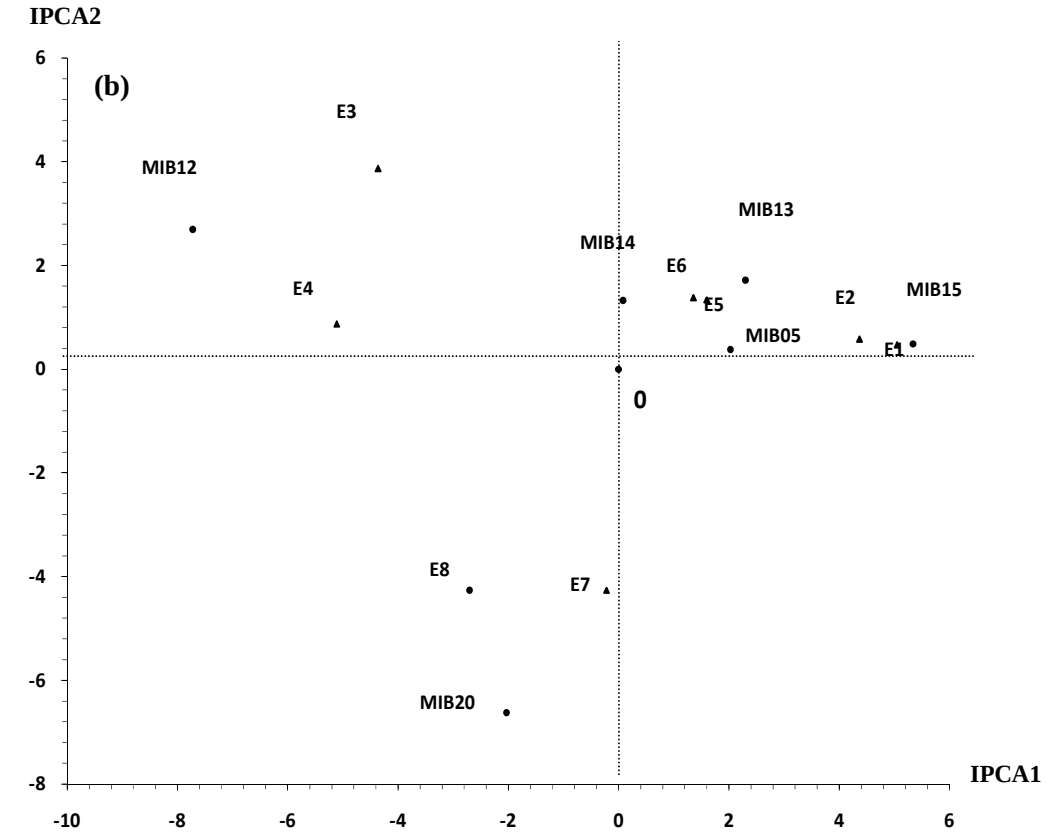


Fig. 4. AMMI biplot (IPCA1 vs IPCA2) of a set of sweetpotato genotypes in 8 agro-environments, (a) for leaf no per 10 cm shoot and (b) for leaf area cm^2. The vertical line represents the grand mean of the experiment. The numbers on the biplot refer to agro-environments (▲E1) and genotypes (●MIB).

AMMI Model for leaves per 10 cm shoot: The G×E interaction explained 52.6% of the treatment sum of squares (Table 2). The first IPCA axis accounted for 67.84% of the G×E interaction sum of squares, using 11 degrees of freedom. The second IPCA axis accounted for 17.01% of the interaction sum of squares, using 9 degrees of freedom. The F-test indicated that IPCA1 and IPCA2 were highly significant at $p \leq 0.001$ and $p \leq 0.01$, respectively.

AMMI Biplot (IPCA1 vs. Mean) for leaves per 10 cm shoot: The AMMI results for leaves per 10cm of shoot can be observed in the biplot as shown in Fig. 3b, which expressed a sum of squares of 116.51 (total sum of squares for genotypes, environment and IPCA1), which is 83.08% of the treatment sum of squares. Genotypes MIB05 and MIB15 differed only in main effects, while MIB05 and MIB12 differed in interaction effects. However, genotypes MIB05 and MIB14 differed both in main and interaction effects. According to agro-environments, E2 and E3 differed in main effects, while E2 and E7 differed in interaction effects. However, E1 and E6 differed both in main and interaction effects. Most of the genotypes showed values ranged from 5.43- 6.41 number of leaves except MIB14 which had 6.65 (Fig. 3a). No distinct cluster of agro-environment and genotype was found. Agro-environment E3 was noted near to point of origin suggesting that its interactions was almost negligible within genotypes to grand mean.

AMMI Biplot (IPCA2 vs. IPCA1) for leaves per 10 cm shoot: This biplot displays IPCA1 on the abscissa and IPCA2 on the ordinate shown in Fig. 4b, which showed that E1, E5 and E6 were displayed furthest away from the origin, suggesting that these agro-environments were associated with higher non-additivity compared to others. Similarly, genotypes MIB05, MIB14 and MIB15 were displayed farthest from the origin, confirming that these genotypes were associated also with higher non-additivity. Genotype MIB15 had positive interaction at agro-environments E1, E2, E3 and E4 but showed negative interaction with E5, E6, E7 and E8. Agro-environments E5 and E6 had almost similar environment patterns. Genotype MIB15 was found more suitable for high number of leaves per 10 cm shoot at E1.

Discussion

According to AMMI biplot analysis, genotypes MIB05 and MIB14 were found relatively prominent for total shoot yield, while MIB13 had good root yield. Osiru *et al*., (2009) had reported that in Uganda sweetpotato root yield was ranged from 14.75 to 41.1 t ha^{-1}, where planting was done only for root yield. In this study, root yield was obtained on an average of 11 t ha^{-1} after 7 shoot tip harvests. Genotype MIB20 maintained stability in unfavorable agro-environment as well as in favourable agro-environment with average shoot and root yields because its IPCA1 scores were near zero. Based on AMMI models, Osiru *et al.*, (2009) identified the genotypes Dimbuca, Tanzania, Naspot-2, Naspot-6 and Araka Red with positive interactive principal component scores (IPCA1) and Araka Red, Old Kawogo and Naspot-1 with IPCA scores close to zero indicating only small interaction with environment at Uganda. Similarly, Mwololo *et al*., (2009) identified sweetpotato genotypes Jonathan, Exshimba, SPK-004 and Kemb-10 as highly adapted across environment while Ejumula, Jewel, Jubilee, Bungoma and Sponge as stable genotypes with less interaction effects at Kenya.

Highly significant G×E interactions for all the studied traits suggested that genotypes varied across the agro-ecological zones E1 to E8. Results were also in confirmation with findings of Osiru *et al.*, (2009); Mcharo *et al.*, (2001); Naskar & Singh (1992) for root yield traits. Genotypes MIB05 and MIB14 showed the largest negative IPCA1 scores (2a). The root yield indicated that genotypes MIB15 and MIB20 showed good stability across both low and high-yielding agro-environments. Genotype MIB13 was productive as well established but its yield showed poor stability in agro-environments E6 and E8. So, more breeding efforts are needed to improve yield stability. Genotype MIB14 had highest number of leaves in 10 cm shoot tips. It is a good indication to be used as vegetable according to the study of Villareal *et al.*, (1979). But this genotype had high interaction effects and breeding efforts are needed to improve its stability. Genotypes MIB05 and MIB14 produced high shoot yield due to having higher number of shoot tips though these two genotypes had smaller leaves.

Two genotypes, MIB05 and MIB14 proved to be the most widely adapted for total shoot yield in most of the agro-environments despite low root yield recorded in their plots. Low shoot yield was not favorable as it would decrease the farmers income. So, to develop genotypes with high root and shoot tips yields, research works through breeding are needed to combine these two valuable traits to increase farmers income. Results obtained with AMMI method were useful for comparing the different genotypes, which authenticated that which genotype was found capable to produce good and stable yield across agro-environments. For genotypes and agro-environments study, the AMMI biplot analysis provided satisfactory findings in detecting genotypes that perform well and remain stable under various environmental conditions.

Conclusion

Two genotypes, MIB05 and MIB14 were found suitable for planting as a leafy vegetable for their high shoot tips yield despite their low root yield. However, AMMI analysis indicated that these two genotypes were able to produce high shoot tips but had low stability in most of the agro-environments as compared to genotype MIB20 (control) having relatively high stability effects. Nevertheless, these two genotypes are to be recommended for specific planting at Telong, Kelantan (Malaysia) for their best shoot tips yield. In future, further research is needed to include these genotypes in breeding program to improve their stability and root yield traits.

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