Full Length Research Paper

Genotype x environment interaction and yield stability estimate of some sweet potato [*Ipomoea batatas* (L.)Lam] breeding lines in South Africa

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Genotype x environment interaction and yield stability was evaluated for root yield for 28 sweetpotato breeding lines in South Africa using the Additive Main Effects and Multiplicative Interaction (AMMI) stability parameter. Genotype x environment interactions showed the inconsistency of the performance of the breeding lines over environments and seasons. The analysis of variance showed that the genotype x environment interaction were significant for root yield. The stability parameter used in this study identifies cultivar Monate as high yielding and stable across locations. The first two interaction principal component axes (IPCA) of the AMMI model accounted for 82.81% of the total genotype x environment interaction sum of squares for root yield. The AMMI biplot depicted the breeding lines on the bases of their adaptation patterns. Breeding lines Monate x 1999-9-4 and Khano x 1999-9-4 were found to be best adapted at Roodeplaat (A) environment while parental lines Ndou and 1999-9-4 as well as the breeding lines Monate x Khano, Khano x 1999-5-1 and 1999-9-4 x Khano were found to be the highest yielding at Fort Cox (D) environment. They were therefore recommended for cultivation in those environments.

Key words: Additive main effects and multiplicative interaction (AMMI) model, breeding lines, genotype by environment interaction, stability; sweet potato.

INTRODUCTION

Sweet potato is a root crop native to the tropics and subtropical regions in the world. On the African continent it is predominantly grown as a food crop (FAO, 2010). Sweetpotato is especially popular amongst farmers with limited resources because of its high yield, good cooking quality, early maturity, wide adaptability, resistance to diseases and pests, drought tolerance and high nutritional content (Bovell-Benjamin, 2007). The storage roots are rich sources of carbohydrates, vitamins and bio-available β-carotene (Woolfe, 1992). Sweetpotato is used for food, industrial purposes and feed. The improvement

of this crop is very important in achieving increased production and productivity in developing countries (Allemann et al., 2004).

Sweetpotato can alleviate food insecurity in areas where other crops cannot survive and provide a better yield potential. The utilization of sweetpotato as a food security crop and source of pro-Vitamin A for malnourished children has encouraged the production of the crop in diverse environmental conditions (Osiru et al., 2007, Mwanga et al., 2002).

Orange-fleshed sweetpotato plays a vital role in

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Table 1. Analysis of variance (ANOVA) based on the AMMI model for root yield (t ha^{-1}) for the two years (2009 to 2010).

Source	df	SS	MS	Total variation explained (%)	G x E explained (%)	Cumulative (%)
Total	335	114156.177				
Environments	3	43234.908	14411.636**	37.87		
Replications within environment	8	1311.002	163.875			
Genotype	27	35471.368	1313.754**	31.07		
Genotype x environment	81	21360.775	263.713**	18.71		
IPCA 1	29	9355.069	322.589**		43.80	43.80
IPCA 2	27	8332.794	308.622**		39.01	82.81
IPCA 3	25	3672.912	146.916**		17.19	100.00
Residual	216	12778.123	59.158			
Grand mean			37.319			
CV%			20.61			

**P < 0.01; IPCA=Interaction principal component axis.

alleviating micronutrient deficiencies and they have been used in food-based approaches (Hotz et al., 2011, Laurie and Faber, 2008). Sweetpotato is highly adapted to harsh environmental conditions. It was reported that significant genotype x environment interaction is present in sweetpotato in the root yield trait (Abidin et al., 2005; Grüneberg et al., 2005, Laurie, 2010). The plant breeder desires stable genotypes with good performance across all environmental situations. Understanding the knowledge of cultivar performance and yield adaptation in diverse agro-ecological zones is very important for cultivar selection and improvement. Therefore, the objective of this study was to determine stability and yield potential of some sweetpotato breeding lines in different environments of South Africa

MATERIALS AND METHODS

Cuttings of six parental lines were obtained from the Agricultural Research Council-Roodeplaat Vegetable and Ornamental Plant Institute sweetpotato gene bank and 22 progenies were produced in conventional crosses. Twenty eight genotypes of sweetpotato (Table 1) including locally released standard check and parents were tested in two environments (Roodeplaat and Fort Cox) during 2009 and 2010 cropping seasons in South Africa. Roodeplaat lies at 25°59'S latitude and 28°21' E longitude at an altitude of 1164 meter above sea level (masl). The soil is clay loam with a pH of 7.08. The location receives a total precipitation of 686 mm, and an average maximum and minimum temperature of 25.8°C and 10.5°C, respectively, during the growing season. The Fort Cox site lies between 32°46'S latitude and 27°20' E longitude at an altitude of 400 masl. The type of the soil is loam with a pH value of 7.2. The total precipitation during the growing season was 606 mm and the mean minimum and maximum temperatures were 23.8°C and 12.3°C, respectively. The experiments were laid out as randomised complete block design (RCBD) with three replications at each location. Each plot consisted of four rows (ridges of 40 cm high) which were 5 m in length. Stem cuttings (30 cm in length with 6 nodes) were planted at a spacing of 30 cm apart within rows and 100 cm between rows. A total of 20 cuttings were planted in each row. As per general recommendation (Allemann et al., 2004), 500 kg/ha 2: 3: 4 (6.7% N, 10% P, and 13.3% K) fertilizer was broadcasted before planting with topdressing of 150 kg/ha limestone ammonium nitrate (LAN 28%) at Fort Cox; but in the case of Roodeplaat 200 kg/ha 1: 0: 1 (18.5% N, 18.5% K) and a top dressing of ammonium sulphate (21% N) was used. Crop management practices such as fertilizer application, weeding, pests and diseases control were carried out during the cropping seasons. The middle two rows were used for data collection and analysis. Harvesting was done five months after planting.

Data analysis

The total root yield data were subjected to the Additive Main Effects and Multiplicative Interaction (AMMI) statistical model (Purchase, 1997) using Agrobase Generation II (Agronomix, 2008). Furthermore, AMMI's stability value (ASV) was calculated (Purchase, 1997) as shown as follows:

$$\text{AMMI Stability Value (ASV)} = \sqrt{\left[\frac{\text{IPCA1 sum of squares}}{\text{IPCA2 sum of squares}}(\text{IPCA1 score})\right]^2 + [\text{IPCA2 Score}]^2}$$

Where: IPCA1 = interaction principal component analysis axis 1; IPCA2 = interaction principal component analysis axis 2.

RESULTS AND DISCUSSION

Analysis of variance using the AMMI model showed that there was highly significant variation among the genotypes (Table 1). This observed variation will be useful when selecting parental lines for use in sweetpotato breeding programme. The highest yield was recorded in parents Monate (63.25 t/ha), 1999-9-4 (57.00 t/ha) and Ndou (53.79 t/ha) while the lowest yield was obtained in hybrid W-119 x Khano with 20.22 t/ha and check Resisto (22.07 t/ha) (Table 2). These yield values were higher than those reported by Osiru et al. (2007) but, comparable to that of Laurie (2010). The variation in yield might be due to genetic and environmental

Table 2. Mean root yield, IPCA1, IPCA2 scores, graph ID and AMMI stability value (ASV) for 28 sweet potato genotypes evaluated in two environments.

No.	Hybrids	Graphic ID	Mean root Yield	Rank	IPCA1	IPCA2	ASV
1	W-119 x Ndou	a	35.64	13	-1.1400	-0.6760	1.447
2	W-119 x Khano	b	20.22	28	-0.9288	0.8653	1.355
3	W-119 x 1999-9-4	c	45.37	7	1.0672	-0.4047	1.265
4	W-119	d	34.33	15	1.7407	1.1332	2.259
5	Resisto	e	22.07	27	-1.3691	0.2806	1.562
6	Ndou x W -119	f	29.78	24	-1.3857	1.0168	1.883
7	Ndou x Monate	g	32.23	18	-1.5797	-1.8724	2.579
8	Ndou x Khano	h	32.15	19	-1.7310	0.1632	1.95
9	Ndou x 1999-9-4	i	24.54	26	-1.9465	-1.0591	2.428
10	Ndou x 1999-5-1	j	30.11	22	0.3106	-0.3362	0.485
11	Ndou	k	53.79	3	0.6310	-0.7926	1.063
12	Monate x Ndou	l	31.49	20	-0.7815	-0.1647	0.893
13	Monate x Khano	m	48.23	5	2.5039	-0.4846	2.853
14	Monate x 1999-9-4	n	45.19	8	-0.7929	-2.0038	2.193
15	Monate x 1999-5-1	o	34.30	16	0.9323	-0.0671	1.045
16	Monate	p	63.25	1	-0.3841	4.5460	4.566
17	Khano x Monate	q	37.87	11	-1.4966	0.7269	1.831
18	Khano x 1999-9-4	r	41.21	9	-1.4373	1.0815	1.943
19	Khano x 1999-5-1	s	47.28	6	1.5285	-1.886	2.55
20	Khano	t	38.85	10	2.0860	-0.8409	2.488
21	1999-9-4 x W-119	u	29.88	22	0.8850	1.1542	1.523
22	1999-9-4 x Ndou	v	32.27	17	-1.3014	0.1492	1.469
23	1999-9-4 x Khano	w	48.69	4	0.4371	1.2415	1.335
24	1999-9-4	x	57.00	2	1.0918	-0.2227	1.246
25	1999-5-1 x W-119	y	27.48	25	1.4815	0.3071	1.691
26	1999-5-1 x Ndou	z	30.74	21	-1.5142	-2.7385	3.223
27	1999-5-1 x Monate	!	35.02	14	0.2638	1.3625	1.394
28	1999-5-1	~	35.98	12	2.8294	-0.4760	3.212
Mean squares			1313.754**				
LSD			8.7607				
CV%			20.61				
Locality means:							
Fort Cox 2009		D	51.13	1	6.28	1.51	
Fort Cox 2010		B	21.56	4	-3.56	5.25	
Roodeplaat 2009		A	44.36	2	-1.18	-3.43	
Roodeplaat 2010		C	32.23	3	-1.55	-3.44	

conditions that prevailed during the growing periods.

The combined ANOVA for 28 breeding lines evaluated over two years and two locations according to AMMI model showed highly significant (P < 0.01) differences among environments, genotype and G x E interactions for root yield trait (Table 1). This indicated the different responses of different breeding lines to the environmental conditions of the localities in the cropping seasons. The largest contributor to variance was the environment complicating selection and performance of root yield (Table 1). This interaction could suggest that some of the breeding lines were not stable across environments, responding differently to the different environments. The

G x E interaction was partitioned into three interaction principle component axis (IPCA). The IPCAs were ordered according to their importance. All the IPCAs axes were highly significant. The IPCA 1 alone explained 43.80% of the total G x E interaction sums of squares percentage while IPCA 2 explained 39.01% of the total G x E interaction sums of squares percentages. The third IPCA axis accounted 17.19% of variation. The total variation explained (%) by the main effects of genotypes and environments accounted a variation of 31.07% and 37.87%, respectively, the G x E interaction accounted for 18.71% for root yield. In this study, environment contributed higher variation than the genotype on the root
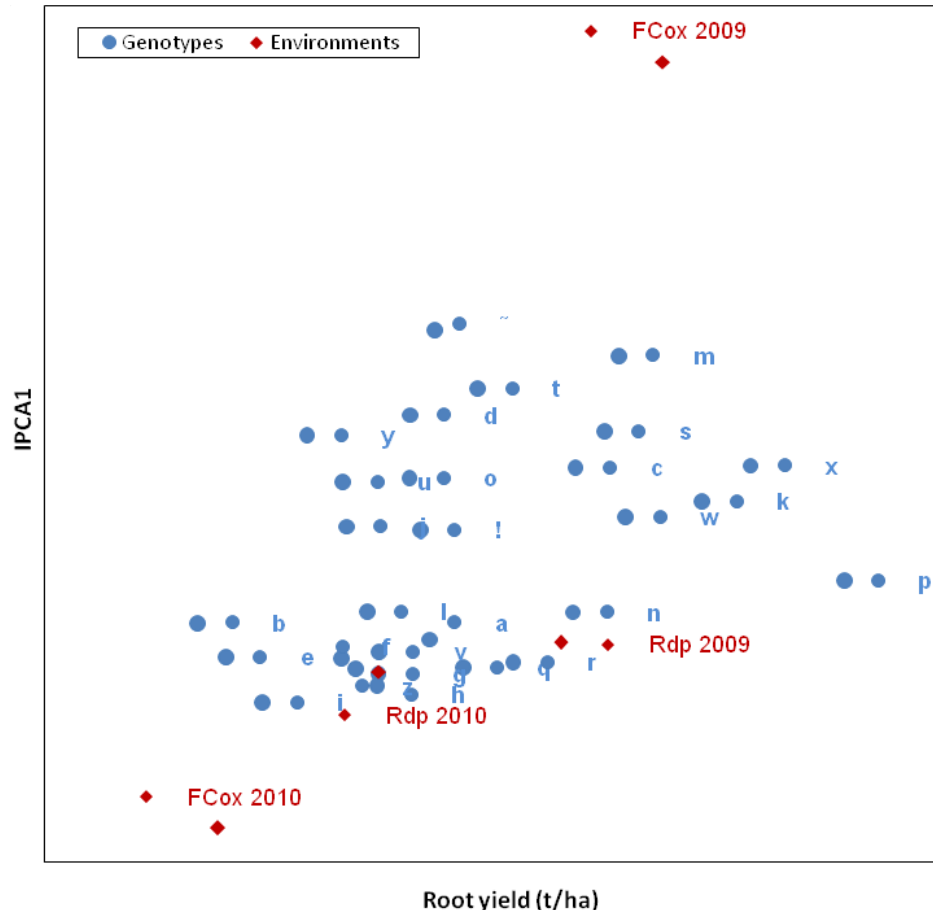
Figure 1. Biplot of interaction principle component axis 1 (IPCA1) score versus total root yield for 28 sweet potato genotypes. The names of genotypes were indicated in Table 2 under graph ID.

yield of sweetpotato hybrids.

Table 2 presents the results of the AMMI analysis with the IPCA1 and IPCA2 scores for the sweet potato genotypes. The higher the IPCA scores either positive or negative, the more specifically adapted a genotype is to certain environment. The more IPCA scores approximate to zero, the more stable the genotypes are over all environments sampled (Gauch and Zobel, 1988). Genotypes with lower AMMI stability values are considered more stable than those with higher AMMI stability value (Purchase, 1997). According to the ASV ranking the most stable genotypes were Ndou x 1999-5-1 (j), Monate x Ndou (l) and Monate x 1999-5-1 (o) (Table 2). The most unstable genotypes according to the ASV were Monate (p), 1999-5-1 x Ndou (z) and 1999-5-1 (~). The biplot generated by AMMI model for G x E interaction permits the visualization of differences in the interaction main effects (Figure 1). The IPCA1 scores for both the parents and hybrids (lower case) and the environments (upper case) were plotted against the mean root yield for the hybrids and the environments, respectively. Table 2 shows the names and graph ID of the hybrids. Plotting of

both sweet potato hybrids and the environments in the biplot using IPCA scores clearly showed the relationship between the hybrids and the environments. In the biplot, genotypes and environments were distributed from low yielding in quadrants II (top left) and III (bottom left) to the high yielding in quadrants I (top right) and IV (bottom right). The high yielding environments classified according to the AMMI model were Fort Cox 2009 (D) and Roodeplaat 2009 (A). The low yielding environment was Fort Cox 2010 (B). The genotypes categorized under favourable environmental condition with above average root yield means were Monate (p), 1999-9-4 (x), Ndou (k), 1999-9-4 x Khano (w), Monate x Khano (m), Khano x 1999-5-1 (s), W-119 x 1999-9-4 (c), and Monate x 1999-9-4 (n). Among them 1999-9-4 (x), Ndou (k), 1999-9-4 x Khano (w), W-119 x 1999-9-4 (c), Monate x 1999-5-1 (o) and Khano x 1999-9-4 (r) were found to be more stable (low ASV) and these genotypes were the most stable, high yielding hybrids across locations. Genotypes lying in close proximity to specific environments indicate better adaption to that environment, e.g. Khano x 1999-9-4 (r) was better adapted at Roodeplaat. Hybrids which are

close to each other tend to have similar root yield reaction to environment.

Conclusion

The AMMI model is an important technique in analysing G X E interactions helping plant breeders in the identification and selection of promising genotypes that perform better in terms of yield potential to specific environmental situations or specific locations. In this study, 28 sweet potato genotypes were evaluated in two locations across two years. Highly significant differences were recorded between the genotype, environment and their interaction for root yield. The best yielding hybrids with the highest stability across localities were 1999-9-4 x Khano (w) and W-119 x 1999-9-4 (c). The AMMI biplot depicted the breeding lines on the bases of their adaptation patterns. Hybrids best adapted to Roodeplaat (A) with higher yield were Monate x 1999-9-4 (n), 1999-9-4 x Khano (w) and Khano x 1999-9-4 (r), while parental lines best adapted to Fort Cox (D) environment were Ndou, and 1999-9-4. They were therefore recommended for cultivation in those environments.

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