Keywords: Genotype stability Index, Cylas puncticolis, Resistance, Climate smart

1 Introduction

Yield is a complex quantitative trait and greatly influenced by external environment such as soil fertility or disease pathogens, which results in scale or rank shift in its performance (Dia et al. 2016a). Sweetpotato suffers yield loss caused by abiotic and biotic constraints. Sweetpotato weevil, specifically Cylas puncticolis is the major contributor to yield loss among biotic constraints affecting sweetpotato in southern Africa. Large differential genotypic responses to pests and diseases have been reported under varying environmental conditions (Bonanza et al. 1994; Mkumbira et al. 2003; Aina et al. 2007; Ssemakula and Dixon 2007). This differential sensitivity of genotype performance from one environment to another is known as genotype x environment interaction (GEI). The impenetrable interaction of a crop bio-system with the external environment introduces challenges when making breeding decisions because it complicates the demonstration of superiority of any genotype across environments (Dia et al. 2016b). GEI may result in low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This reduction leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll 1963; Alghamdi 2004; Kumar et al. 2013). Thus, the magnitude and nature of GEI is important in plant breeding and variety release (Crossa 1990; Singh et al. 2006), as they enable plant breeders to identify superior genotypes and locations that best represent production environments (Yan et al. 2000).
2 Materials and Methods

2.1 Location of the study

The proposed research was carried out at Copperbelt Research Station in Mufulira. This station is strategically located and caters for the mining population that serves as a market for sweetpotato, vegetables and fruits. The station is located at 12° 03’ 7” East, 28° 09’ 0” South, with an elevation of 1245 m above sea level.

2.2 Experimental materials

Eight varieties which included six improved and two local genotypes were evaluated in a field trial that was conducted for five seasons under rain-fed conditions.

2.3 Experimental design and Layout

The varieties were evaluated in a randomized complete block design (RCBD) with three replications. Each experimental unit (plot) consisted of 4 ridges measuring 5 m long and spaced 1 m apart. The vines measuring 30 cm each were planted on ridges at the spacing of 25 cm between stations giving a total population of 20 vines per ridge which translates to 40,000 plants ha⁻¹. A buffer distance of 2 m was left between blocks (replications) and 1 m spacing left between plots within each block. No fertilizer or herbicides were applied in the trial and weeding was done manually using a hand hoe.

2.4 Data Collection

2.4.1 Meteorological parameters

Meteorological data were collected from Kafironda Meteorological Station which is located within Copperbelt research Station. This Met Station collects data which represents the entire Copperbelt Province. The data included ground and soil temperatures and rainfall for the five year period covering 2010/11 to 2015/16 agricultural season. The daily temperatures and rainfall were averaged and summarized on a monthly basis as contained herein.

2.4.2 Root Yield

The root yield was determined by counting and weighing enlarged roots.

2.4.3 Weevil damage

Weevil incidence was measured by counting the number of weevil infested tubers and expressing as a percentage out of the total number of roots harvested in a plot. Level of damage was determined by weighing a sample (3-5 roots) of infested roots as whole tubers and also by weighing after chopping off damaged parts. The weight loss incurred after chopping off damaged parts expressed as percentage of the whole infected tubers per plot was used to determine loss due to weevil damage as indicated below:

Weevil damage (%) = \frac{\text{Wgt of whole tuber} - \text{Wgt of chopped weevil free parts}}{\text{Wgt of whole tuber}} \times 100

2.5 Statistical Analyses

2.5.1 Analysis of Variance

Yearly analyses of variance (ANOVA) were conducted using Genstat 14 (Payne et al. 2011) for all the traits evaluated in this trial. Hartley’s F-max test (Hartley 1950) based on the ratio of the largest error MS to the smallest error MS was performed for each trait to test the
homogeneity of variances across environments (season). The test indicated that the variances of the seasons were homogeneous for all the traits, and therefore there was no need for standardization of sampling data, and a combined ANOVA was carried out. For all traits, combined ANOVA was performed for eight genotypes evaluated across five seasons. The F-tests and significance of the main effects and interactions were determined using the appropriate error term and degrees of freedom.

2.5.2 AMMI analysis

In order to partition the variation due to genotype, season, and the interaction thereof, the additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by Gauch and Zobel (1996) as follows:

\[ Y_{ger} = \mu + \alpha_g + \beta_e + \sum \Lambda_n \delta_{en} + \rho_{go} + E_{ger} \]

where \( Y_{ger} \) = yield of genotype \( g \) in environment \( e \) for replicate \( r \), \( \mu \) = grand mean, \( \alpha_g \) = genotype mean deviation (genotype means minus grand mean), \( \beta_e \) = environment mean deviation, \( n \) = number of principal component analysis (PCA) axes retained in the model, \( \Lambda_n \) = singular value for PCA axis \( n \), \( y_{go} \) = genotype eigenvector values for PCA axis \( n \), \( \delta_{en} \) = environment eigenvector values for PCA axis \( n \), \( \rho_{go} \) = residuals, \( E_{ger} \) = error term.

2.5.3 Stability analysis

The AMMI stability value (ASV) proposed by Purchase et al. (2000) was used to quantify and rank genotypes according to the yield stability. The ASV has been defined as the distance from the coordinate point to the origin in a two dimensional scatter-plot of first interaction principal component axis (IPCA1) scores against the second interaction principal component axis (IPCA2) (Farshadfar et al. 2012). Since IPCA1 accounts for most of the GE variation, the IPCA1 scores are weighted by the ratio of IPCA1SS (from AMMI ANOVA) to IPCA2 SS in the ASV formula as follows:

\[ ASV = \sqrt{\frac{SSIPCA1}{SSIPCA2} (IPCA1 \text{ score})^2 + (IPCA2 \text{ score})^2} \]

The lower the ASV, the more stable a genotype is.

2.5.4 Genotype stability index

A stability index was calculated for each genotype based on summing the ranking of overall mean performances for each trait and the ranking for ASV for each trait. The stability index which is normally applied to yield data and is referred to as yield stability index (YSI) (Farshadfar 2008; Farshadfar et al. 2012), was also applied in this study to the mean performances of genotypes for other traits and referred to as genotype stability index (GSI). The GSI was calculated as follows:

\[ GSI = RASV_i + RY_i \]

Where: \( GSI_i \) = genotype stability index for the \( i \)th genotype across seasons for each trait; \( RASV_i \) = rank of the \( i \)th genotype based on mean performance across seasons. The genotype with the lowest GSI was considered the best for a particular trait across seasons. To identify superior genotypes across traits, the GSI ranks of each genotype were summed for all the traits, and the genotype with smallest rank sum (\( \sum \text{rank} \)) was considered the best across traits.

2.5.5 Correlation analysis

Data on root yield and weevil damage were correlated with rainfall and temperature for each and across seasons.

3 Results and Discussion

The genotype mean squares (MS) and environment mean squares (MS) were highly significant (\( P<0.001 \)) for Root Yield (Table 1) and sweetpotato weevil damage (Table 2). The environments (season) SS accounted for 30.18% and 49.32% of the total SS for root yield and weevil damage respectively. The GEI MS were also significant (\( P<0.001 \)) for both traits and the contribution of their respective SS to the total SS were 32.56% (Table 1) and 34.61% (Table 2) for root yield and weevil damage.

IPCA 1 was highly significant (\( P<0.001 \)) for both traits and accounted for 83.11% and 97.82% of the GEI for root yield and weevil damage respectively. On the other hand, the MS for IPCA2 were not significant for either of the traits the respective SS only accounted for 14.2 and 1.56% of GEI SS for root yield and weevil damage. As none of the IPCAs beyond IPCA1 were significant for any of the traits, only the first IPCA was considered in modelling GEI for the traits. The residual SS accounted for 2.69% and 1.56% of
Genotype Stability Index for Root Yield and Tolerance to Sweetpotato Weevil \textit{Cylas puncticolls} 

169

These proportions could be attributed to random factors, which could not be explained by the experiment.

3.1 Adaptability of genotypes

There were no significant within-season variations among genotypes with regard to sweetpotato root yield and weevil damage in any of the first four seasons (2010-2014). However significant (analysis of \( p \)-values not presented here) differences were observed among genotypes in 2014/15 season (Figure 1). The season was also generally characterized by increased levels of weevil damage in sweetpotato. These observations could probably be attributed to the decrease in rainfall that was recorded in the season (Figure 3). Lower yields were also recorded in 2011/12, and 2012/13 seasons which coincidentally recorded low rainfall. Confirming these results, significant negative correlation (\( r=-0.5398, P=0.0209 \)) was computed between total rainfall and weevil damage indicates that reduction in rainfall resulted in increased weevil damage. Therefore breeding for drought tolerance would indirectly improve tolerance of sweetpotato to weevil damage.

In view of climate change, farmers are more interested in genotypes that perform consistently better across

### Table 1: Summary of AMMI analyses for sweetpotato root yield

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>ROOT YIELD</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>MS</td>
</tr>
<tr>
<td>Total</td>
<td>119</td>
<td>64.3</td>
</tr>
<tr>
<td>Treatment</td>
<td>39</td>
<td>137.3***</td>
</tr>
<tr>
<td>Genotype</td>
<td>7</td>
<td>78.5**</td>
</tr>
<tr>
<td>Seasons</td>
<td>4</td>
<td>577.6***</td>
</tr>
<tr>
<td>GEI</td>
<td>28</td>
<td>89.0***</td>
</tr>
<tr>
<td>IPCA 1</td>
<td>10</td>
<td>207.2***</td>
</tr>
<tr>
<td>IPCA 2</td>
<td>8</td>
<td>44.3</td>
</tr>
<tr>
<td>Residuals</td>
<td>10</td>
<td>6.7</td>
</tr>
<tr>
<td>Error</td>
<td>70</td>
<td>21.0</td>
</tr>
</tbody>
</table>

\( df = \) degrees of freedom; \( SS = \) sums of squares; \( MS = \) mean square; \( GEI = \) genotype by environment interaction; \%TSS = percentage of total SS; \%GEI SS = percentage of genotype by environment interaction SS; IPCA = interaction principal component axis; ***significantly different at \( P<0.001 \); **significantly different at \( P<0.01 \); *significantly different at \( P<0.05 \)

### Table 2 Summary of AMMI analyses for sweetpotato weevil damage

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Df</th>
<th>WEEVIL DAMAGE</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>MS</td>
</tr>
<tr>
<td>Total</td>
<td>119</td>
<td>208.7</td>
</tr>
<tr>
<td>Treatment</td>
<td>39</td>
<td>594.4***</td>
</tr>
<tr>
<td>Genotype</td>
<td>7</td>
<td>299.0***</td>
</tr>
<tr>
<td>Seasons</td>
<td>4</td>
<td>3062.9***</td>
</tr>
<tr>
<td>GEI</td>
<td>28</td>
<td>315.9***</td>
</tr>
<tr>
<td>IPCA 1</td>
<td>10</td>
<td>865.3***</td>
</tr>
<tr>
<td>IPCA 2</td>
<td>8</td>
<td>17.3</td>
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<tr>
<td>Residuals</td>
<td>10</td>
<td>5.4</td>
</tr>
<tr>
<td>Error</td>
<td>70</td>
<td>18.1</td>
</tr>
</tbody>
</table>

\( df = \) degrees of freedom; \( SS = \) sums of squares; \( MS = \) mean square; \( GEI = \) genotype by environment interaction; \%TSS = percentage of total SS; \%GEI SS = percentage of genotype by environment interaction SS; IPCA = interaction principal component axis; ***significantly different at \( P<0.001 \); **significantly different at \( P<0.01 \); *significantly different at \( P<0.05 \)
seasons (Fikere et al. 2009), indicating preference for widely adapted genotypes (Zhang et al. 2006; Singh et al. 2007), and likewise, breeders would like to consider both yield and stability of performance simultaneously to reduce the effect of GEI and to make selection of genotypes more precise and refined (Farshadfar 2008; Fikere et al. 2009).

The temperature, including maximum (Figure 4) and soil temperatures (Figure 5), were not significantly different among seasons. These observations seem to suggest that exclusive changes in rainfall can affect growth performance and quality characteristics of sweetpotato. However, progressive decrease in mean ground minimum temperatures were recorded across seasons (Figure 6). This result seems to suggest that farmers are likely to face serious challenges due to shortage of planting materials. If the decrease in ground temperatures continues in subsequent seasons, sweetpotato vines will fail to overwinter in the field leading to insufficient availability of planting materials at the beginning of the next rainy seasons. Therefore, research aimed at developing improved and cost effective methods of conserving planting materials becomes important.

Figure 1: Variability in root yield among sweetpotato genotypes in different seasons

Figure 2: Variability in tolerance to weevil damage among sweetpotato genotypes in different seasons
Figure 3: Rainfall (mm) recorded in five seasons (2010-2015)

Figure 4: Maximum temperatures recorded in five seasons (2010-2015)

Figure 5: Soil temperatures recorded at 30 cm depth over five seasons (2010-2015)
3.2 Selection of genotypes

Based on genotype selection index, two genotypes namely Kokota and Lunga which had the least GSI score were identified as the best exhibiting high stability for increased root yield across seasons, while Chingovwa, Chumfwa and Kalungwishi were identified as least stable and low yielding genotypes (Table 4).

On the other hand, the genotypes Kokota and Kalungwishi proved to be highly stable and most tolerant to weevil damage, while Chingovwa and Luapula had the highest GSI score and were, therefore, identified as least stable and most susceptible to sweetpotato weevil damage (Table 5).

Summing up the GSI for root yield and GSI for weevil damage, the genotype with least sum of GSI was considered to be the best which combined stability and best trait mean for root yield and tolerance to weevil damage. In this regard, at least two genotype namely; Kokota and Kalungwishi were identified as the best genotypes with combined stability and best trait mean for root yield and weevil damage (Table 6).

4 Conclusion

In the current study, genotype Kokota had high yield and weevil resistant stability. Genotypes Lunga and Kalungwishi were stable for yield and weevil resistance, respectively. These genotypes have the potential for tolerance to drought and weevil damage. Considering the seasonal variations, such genotypes were regarded to be

Table 4: Ranked genotype stability indices for sweetpotato root yield

<table>
<thead>
<tr>
<th>Genotype</th>
<th>ASV</th>
<th>RASV</th>
<th>Root Yield</th>
<th>Rank RY</th>
<th>GSI</th>
<th>Rank GSI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chingovwa</td>
<td>1.986559</td>
<td>8</td>
<td>10.97</td>
<td>5</td>
<td>13</td>
<td>7</td>
</tr>
<tr>
<td>Chumfwa</td>
<td>0.445302</td>
<td>3</td>
<td>8.98</td>
<td>8</td>
<td>11</td>
<td>6</td>
</tr>
<tr>
<td>Kokota</td>
<td>0.321564</td>
<td>2</td>
<td>14.12</td>
<td>2</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>Lunga</td>
<td>0.184586</td>
<td>1</td>
<td>15.16</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>Kalungwishi</td>
<td>1.38111</td>
<td>6</td>
<td>9.09</td>
<td>7</td>
<td>13</td>
<td>7</td>
</tr>
<tr>
<td>Luapula</td>
<td>0.516941</td>
<td>4</td>
<td>9.78</td>
<td>6</td>
<td>10</td>
<td>4</td>
</tr>
<tr>
<td>Lukusashi</td>
<td>1.904934</td>
<td>7</td>
<td>12.5</td>
<td>3</td>
<td>10</td>
<td>4</td>
</tr>
<tr>
<td>Olympia</td>
<td>0.88497</td>
<td>5</td>
<td>11.52</td>
<td>4</td>
<td>9</td>
<td>3</td>
</tr>
</tbody>
</table>

ASV=AMMI stability value; RASV= Rank of AMMI stability value; RY= Root Yield; GSI=genotype selection index
climate smart and could be used as parents in a breeding programme aimed at enhancing resilience of sweetpotato to drought and weevil damage. However, there is need to increase the number of sites to better reveal the difference among genotypes.

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