

SHORT, NON-REFEREED PAPER

## **ANALYSING THE NATURE AND CAUSES OF GENOTYPE X ENVIRONMENT INTERACTIONS IN THE MIDLANDS: IMPLICATIONS FOR FUTURE BREEDING AND EVALUATION**

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### **Abstract**

Commercial genotypes for the Midlands are selected at six sites. The similarities amongst these sites have never been evaluated and factors causing genotype x environment (GxE) interactions are unknown. The objectives of this study were to investigate the similarities between the selection sites and the causes of GxE interactions. Estimated recoverable crystal (ERC) yield data from eight series (1999 to 2006) of plant breeding trials were analysed using genotype + genotype x environment (GGE) biplot analysis. Soil characteristics associated with each site were determined. Results revealed that the selection sites formed a single, complex mega-environment with frequent crossover GxE interaction. Sites S2 (sandy site) and B2 (humic site) were identified as potentially redundant, raising the possibility of their removal from the trial network. The clustering of sites on the biplots was related to similarities in soil characteristics, while climatic covariates had negligible effects, and was not associated with GxE patterns.

*Keywords:* plant breeding, genotype x environment interaction, GGE biplot, site similarity

### **Introduction**

GxE interaction complicates the identification of superior genotypes in plant breeding programmes as good performance of genotypes at one selection site is not necessarily repeated at others. The success of the plant breeding programme is highly dependent on the representativeness of the test sites. To ensure the effectiveness of the selection system, it is necessary to evaluate the representativeness of the test sites.

Commercial sugarcane genotypes are selected for the midlands region from two selection programmes. The Bruyns Hill (B) and Glenside (S) selection programmes run concurrently to identify genotypes suited to humic (high potential) and sandy (low potential) soils, respectively. Each programme is represented by three permanent testing sites located either on South African Sugarcane Research Institute (SASRI) owned research farms (B1 and S1), or on grower co-operator farms (B2, B3, S2, S3) in the region, which represent conditions that are slightly different from the research farms.

Since the inception of the above selection sites in 1997 (Nuss, 1998), no study has been conducted to evaluate the relationships between the test sites in terms of genotypic performance. If the relative performance of genotypes is similar across sites, this implies that some sites may be redundant and should therefore be removed from the network in favour of

more diverse sites. The objectives of this study were (i) to investigate the similarity of the test sites used for the Midlands, and (ii) to investigate causes of GxE interactions that can inform future test site selection.

### Materials and Methods

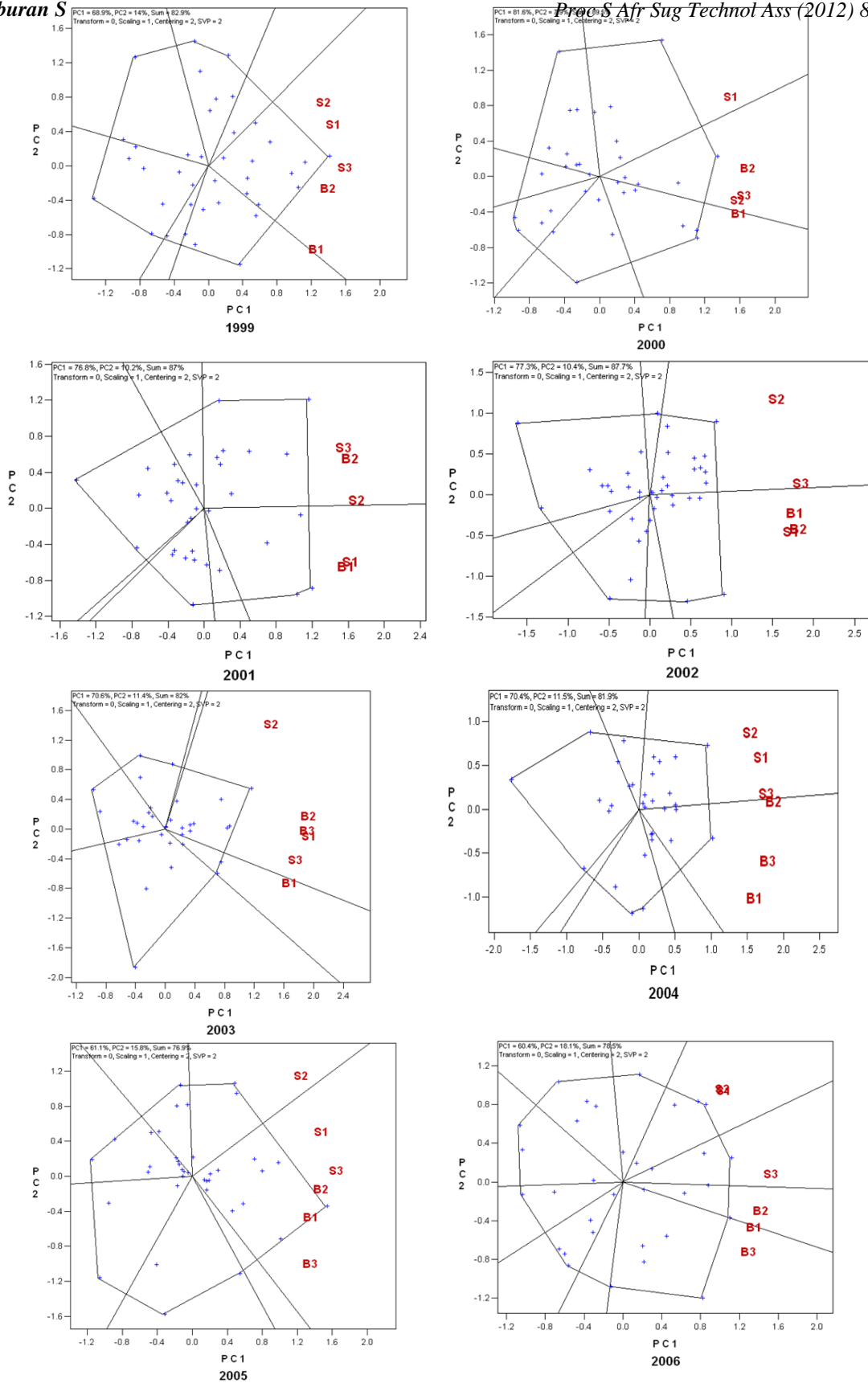
The dataset used for this study comprised advanced plant breeding selection trials established between 1999 and 2006 at six test sites (B1, B2, B3, S1, S2 and S3). Each year, a set of 32 to 41 promising sugarcane genotypes were tested in a multi-environment trial (MET). Trials established in each planting year (series) were harvested over three crops, between April and December and varied in harvest age from 18 and 24 months. The trials were planted as randomised complete block designs with three to four replicates. Plots comprised five sugarcane rows that were 10 m long, and spaced 1 m apart. At each harvest estimated recoverable crystal yields in tons/ha (TERC) was determined.

An environment was considered as a trial x ratoon combination. Within each series, the matrix of genotype x environment TERC means was analyzed using GGE biplot software (Yan, 2001), which is based on principal components analysis. In the GGE biplots, a polygon is drawn by connecting genotypes that are located furthest away from the biplot origin. A perpendicular line is drawn from each side of the polygon through the biplot origin such that the biplot is divided into sectors (mega-environments (ME)). Environments within the same sector share the same winning genotype, and environments in different sectors have different winning genotypes. Thus, the polygon view indicates the presence or absence of crossover GxE interaction, and is suggestive of the existence or absence of different MEs among the test sites (Yan and Rajcan, 2002). Ideally, different test sites should form separate MEs.

### Results and Discussion

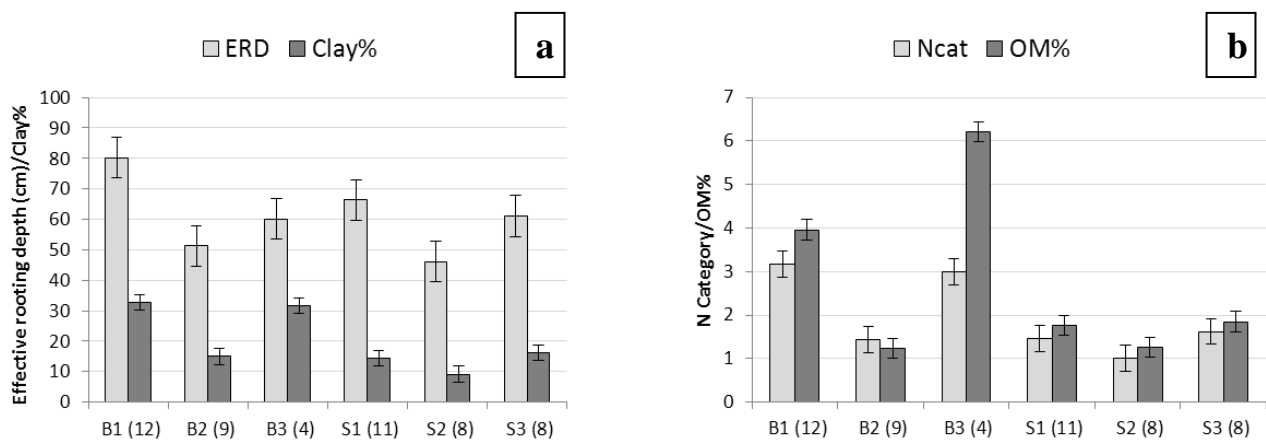
The GGE biplots for each series (1999 to 2006) are shown in Figure 1. The genotypic yields were averaged across ratoons in each trial. None of the sites consistently responded as a distinct ME across all series. Of the three S sites, S2 generally showed greater separation from the other S and B sites over the different series, particularly in 1999, 2002, 2003, 2004 and 2005. Site S2 was located further away from the B sites than S1 and S3, suggesting that it was more effective than S1 and S3 at discriminating genotypes between sandy and humic soils. Site S1 grouped together with S2 and/or S3 in four out of eight series, while sites S2 and S3 grouped together in six out of eight series. This suggests that S2 and S3 are very similar in the way they discriminate genotype performance and that one of these sites may be redundant. There was frequent correlation between sites S3 and B2, which either fell in the same ME (1999, 2000, 2001, 2003, 2005) or were in very close proximity to each other (2002, 2004, 2006). This implies that site S3 could be removed from the selection programme without much loss of information.

Of the three B sites, site B1 generally showed greater separation from the other B and S sites over the different series, particularly in 1999, 2000, 2001, 2003, and 2004. Sites B1 and B2 fell into the same MEs in four out of eight series. Although site B3 was only tested in four series, it always grouped with either B1 or B2, and never formed a unique ME. This suggests that B3 may in fact be another redundant site, which could be removed from the programme without much loss of information, as it does not provide any unique information on genotype performance.



**Figure 1. Genotype + Genotype x Environment biplots for estimated recoverable crystal yield from plant breeding trials established in the 1999-2006 series. Genotypes are depicted by '+' and trial sites are shown in bold red font.**

Figure 2 shows the soil characteristics of the six selection sites. Site B1 was characterised by fields with higher effective rooting depth (ERD) and clay percentage (Clay%) than most of the other sites. Sites B1 and B3 were characterised by similar Clay% and nitrogen mineralisation category (NCat); however, B3 showed significantly higher organic matter percentage (OM %) than all sites. The ERD of B2 was not significantly different from B3, however, B2 did show significantly lower levels of Clay%, NCat and OM% than the other B sites. Site S2 was characterised by the lowest ERD, Clay%, NCat, and OM% of all sites. Sites B2 and S3 showed no significant differences in any of the parameters measured, which may be the reason for their similarities observed in the GGE biplot analysis. Sites B1 and S1 (the SASRI selection farms) were contrasting in terms of the measured parameters, suggesting that the soil characteristics on these farms are indeed different.



**Figure 2. Average estimated rooting depth (ERD) and clay percentage (Clay%) (a), and nitrogen mineralization category (NCat) and organic matter percentage (OM%) (b) for fields at different selection sites in the Midlands region. The number of fields used for trials at each site are indicated in parentheses. Significant differences ( $P < 0.05$ ) are depicted by error bars.**

## Conclusions

In addition to identifying a redundant site (S3) that should be relocated, as well as flagging another site (B3) for possible redundancy, this study has shown that an analytical approach (including soil profile analyses) allowed for more comprehensive interpretations of the GxE interactions. A simple characterisation of soil factors gave confidence to site similarities suggested by the traditional empirical GxE analysis.

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