CHAPTER 5

Results and discussion

5.1 The field performance of the elite breeding lines in the Rustenburg trial

No significant differences were detected among the genotypes in the number of days that the plants took from transplanting to physiological maturity (DTPM) (Table 5.1). This may imply that a grower would not incur additional field operational costs for substituting any one of the elite breeding lines for TL33. The differences in DTPM among replications were significant possibly due to border effects. The trial was located at the edge of the field, which boundaries on a natural bush with tall trees (Figure 4.1). Therefore, the trial might have suffered the border effect of the natural bush. It was difficult to avoid the border effect because this was the only piece of land that was available for tobacco trials according to the rotation system at the ARC-TCRI. However, efforts were made to orient the trial in such a way that only the first replication was close to the natural bush. The second replication was behind the first replication. The third replication was the furthest away from the natural bush. The first replication might have been the source of the significant differences in the DTPM among the replications.

Chlorophyll ***a*** fluorescence measurements showed non-significant differences among both the genotypes and the replications. According to Dippenaar et al. (1991), the photosynthetic rate of a green tobacco leaf is already at the maximum at a low light intensity. The hypothesis that the performances of the elite breeding lines would deviate from that of TL33 due to differences in leaf photosynthetic efficiencies was rejected at both the 0.05 and 0.01 probability levels (Table 5.1).

Table 5.1 shows differences in plant height at topping that occurred among the genotypes and replications. ODT82 (124.27 cm), OD2 (122.47 cm), ODT92

(122.20 cm), ODT100 (119.67 cm), and OD490 (118.73 cm) gave crop stands of significantly taller plants than TL33 at both 0.05 and 0.01 probability levels. The differences in PHT among replications occurred possibly due to the border effect of the natural bush on the first replication.

The differences in the number leaves per plant (NLP) were highly significant among the genotypes. ODT82 (25), OD486B (24) and ODT100 (24) gave a statistically higher number of leaves per plant than the control, TL33 (22), by 13.6%, 9.1%, and 9.1% respectively. At the 0.01 level of probability, ODT82 produced more leaves than TL33 (Table 5.1). The highly significant differences in the NLP among the treatments suggest that the treatments have different genetic backgrounds although from within the same American gene pool (Table 4.1). No significant differences existed among the replications. Physiologically, the number of leaves that a plant initiates and is able to produce is a genetically determined character (Dippenaar, personal communication). Therefore, it was not surprising to note that non-significant differences in the NLP existed among replications despite the effect of the adjacent natural bush that affected the performance of the plants in the first replication.

Table 5.2 shows lengths, widths and areas of the second-bottom leaves, which represent the lugs (the bottom leaves on the plant). The differences in the second-bottom leaf lengths were highly significant among the genotypes. Replications also showed statistical differences. OD490, OD1, and OD2 produced second-bottom leaves of statistically longer laminae (62.13cm, 59.30cm, and 58.37cm respectively) than those of TL33 (46.40cm). At the 0.01 level of probability, only OD490 showed a highly significant difference from TL33. The differences in the widths of the second-bottom leaves were statistically high among the genotypes, but not significant among the replications. However, none of the elite breeding lines produced leaves, which were statistically wider than those of TL33 (23.07cm). A comparison of the surface areas of the second-bottom leaves showed highly significant differences among the genotypes.

OD490, OD2, OD486B, and OD1 gave second-bottom leaves with larger leaf areas (1556.13cm^2, 1406.83cm^2, 1250.10cm^2 and 1204.60cm^2 respectively) than those of the control, TL33 (683.03cm^2). At the 0.01 probability level, OD490, OD2 and OD486B still demonstrated the potential to give second-bottom leaves with larger areas than those of TL33.

Table 5.3 illustrates statistical differences that occurred in the lengths of the tenth leaves, which represent the cutters (the lower-middle leaves on the plant) and the main leaves (the upper-middle leaves on the plant) of the genotypes. OD1 produced longer tenth leaves (77.03cm) than the control, TL33 (66.97cm). There were no significant differences between TL33 and each of the other elite breeding lines. Table 5.3 demonstrates that OD2 gave wider tenth-leaf blades (39.97cm) than TL33 (30.93cm). The other elite breeding lines had non-significant differences in the tenth-leaf widths from those of TL33. The tenth-leaf areas were highly variable among the genotypes. OD2 gave significantly larger tenth-leaf areas (1909.47cm^2) than those of TL33 (1320.20cm^2). No statistical differences were detected between TL33 and each of the other elite breeding lines.

Highly significant differences from TL33 were noted among the elite breeding lines in the lengths of the eighteenth-leaves, which represent the strips (the top-most leaves on the plant) (Table 5.4). ODT92 (73.37cm), ODT19 (72.33cm), ODT100 (71.87cm), and ODT82 (71.67cm) gave longer strips than TL33 (56.30cm). The widths of the eighteenth-leaves also showed highly significant differences. OD1 and OD2 gave greater eighteenth-leaf widths (32.33cm and 32.33cm respectively) than TL33 (23.13cm). Table 5.4 also shows the considerable variation that occurred among the genotypes in the eighteenth-leaf areas. ODT92 produced the eighteenth leaves with larger areas (1476.60cm^2) than those of TL33 (825.47cm^2).

There were highly significant differences in single-leaf areas among the genotypes and replications. OD490, OD2, and OD1 had significantly larger single-leaf areas (1585.70cm^2, 1565.10cm^2, and 1429.43cm^2 respectively) than those of TL33 (942.90 cm^2) (Table 5.5). At the 0.01 level of probability, OD2 and OD490 gave leaves with statistically larger single-leaf areas than those of TL33. Mean whole-plant leaf areas, WPLA, also showed highly significant differences among the genotypes and the replications (Table 5.5). Whole-plant leaf areas which were significantly larger than those of TL33 (20408.95cm^2) were obtained with OD1 and OD490 (33263.11cm^2 and 32350.00cm^2 respectively). All the other elite breeding lines displayed whole-plant leaf areas that were non-significantly different from those of TL33.

A tobacco grower who substitutes either OD1 or OD490 for TL33 would increase the total leaf area per plant by 62.98% or 58.51% respectively (Table 5.5).

Significant differences were detected in the yield levels among the genotypes (Table 5.6). These differences were based on the statistical comparisons between the highest and the lowest performing genotypes. However, none of the elite breeding lines yielded significantly better or worse than the currently ruling cultivar, TL33 (2986.22 kg/ha). The yields were non-significantly different among replications despite the border effect on the first replication, possibly because the greater WPLA in plants of the other replications might have been accompanied by a decrease in weight per unit area (Akehurst, 1968). The effect of the natural bush might have had an impact only on the crop that was closest to the natural bush in the first replication.

Unmarketable throwaway masses described as dip masses arise from heavy disease infection, insect damage and physical damage. Harvesting the leaf when it is immature or overripe may result in large dip masses coming out of the curing oven. Poor curing process and post-cure handling of the leaf may also give rise to large dip masses. The dip masses did not differ among both the genotypes

and the replications. Consequently, the differences in the marketable yield levels followed a trend that was similar to that of the total yield levels (Table 5.6).

The correlation analyses (Table 5.7) showed that plant height at topping (PHT) and whole-plant leaf area (WPLA), PHT and yield, and WPLA and yield had significant correlations at 0.10 probability level. This may imply that PHT and WPLA are the most important yield components in these elite breeding lines.

Table 5.8 illustrates the scores of the elite breeding lines according to the visual evaluation by the representatives of the tobacco industry. ODT82, OD490, OD2, ODT100 and OD1 were generally rated better than TL33.

5.2 The market performance of the elite breeding lines in the Rustenburg trial

The F-values of the leaf quality components (Table 5.9) indicated non-significant differences among the genotypes and replications except for the Z-grade (closed grain) among the replications. This Z grade is usually of a poor quality, thin-bodied leaf with weak colour intensity, which might be punctuated with green tinges. The Z-grade is associated with harvesting of immature leaf. Possibly, some leaves in the first replication might have been harvested prematurely. The immaturity of the leaf might have been masked by the forced aging of the plants due to the border effect of the natural bush that shared boundaries with the first replication. The forced aging was evidenced by the significant differences in days from transplanting to physiological maturity and plant height at topping among the replications (Table 5.1).

There were non-significant differences among the entries and the replications in the concentration of nicotine in the cured leaves. The concentration of reducing sugars showed highly significant differences among the genotypes. However, no statistical differences could be detected between any one of the elite breeding lines and the control, TL33 (Table 5.10). The breeding lines conform to the

acceptable nicotine/reducing sugar concentration ratio of approximately 1:8, which is routinely identified in flue-cured tobacco (Hawks, 1978).

According to Table 5.11, no statistical differences in grade indices (cents/kg) existed among the genotypes. The highly significant differences in grade indices among the replications might have been a direct reflection of the highly significant differences in the Z-grade among the replications (Table 5.9).

There were significant differences in total and market income among the genotypes. The differences were based on the comparison between the highest and the lowest total and market income levels. The comparisons between each elite breeding line and TL33 did not show any significant differences at all.

The non-significant differences observed between the elite breeding lines and the control, TL33, could be explained from the narrow genetic basis as well as from the inaccuracy inherent in one experiment at a single locality. Referring to the pedigrees of the elite breeding lines and the control (Table 4.1), two features can be identified. Firstly, some parents are common in certain pedigrees. Secondly, many pedigrees show that the parents were well-adapted cultivars of American gene pool. Therefore, the non-significant differences could be a consequence of common ancestry and use of well-adapted and closely related cultivars as parents to create new populations from which to make selections. The use of well-adapted parents results in cultivars that are closely related, and the use of closely related parents results in the reduction of genetic diversity and gains from selection (Thompson and Nelson, 1998; Bowman et al, 1984). On the other hand, the differences among the genotypes may be large enough to show up with experimentation that is more accurate than one at a single locality.

5.3 Genotype-locality interaction

Table 5.12 shows the mean yield, quality and income levels of the elite breeding lines at Groblersdal, Potgietersrus, Rustenburg and Vaalwater. It might be of interest to note that no significant differences existed in yield, quality and income between any one of the elite breeding lines and TL33 at the four individual sites.

5.3.1 Combined analysis of data from the four localities using the AGROBASE program

Table 5.13 shows the results of the combined analysis of the data from the four localities. The differences in the marketable yields, quality and market income levels of the entries due to the localities were highly significant. This strongly suggests that the localities are different.

The differences in yields among the entries across the localities were highly significant. ODT92 (2904.25 kg/ha), ODT82 (2873.44 kg/ha), OD2 (2826.31 kg/ha) and OD1 (2607.03 kg/ha) produced significantly higher yields than TL33 (2142.36 kg/ha) by 36%, 34% and 32% and 22% respectively. At 0.01 probability level, the difference between any one of ODT92, ODT82 and OD2 and TL33 was significant (Table 5.13). ODT92, ODT82, OD2 and OD1 were not themselves significantly different in their yielding potentials.

The grade indices, expressed as cured leaf quality and measured in cents per kilogram of leaf, did not show any statistical differences among the entries across the localities (Table 5.13).

There were highly significant differences in market income per hectare among the entries across the localities. ODT82 (R46256.03/ha), ODT92 (R43575.84) and OD2 (R40850.28/ha) were significantly more financially rewarding than TL33 (R32105.58/ha) by 44%, 36% and 27% respectively (Table 5.13). However,

ODT82, ODT92 and OD2 were not statistically different from each other. AT 0.01 probability level, ODT82 and ODT92 generated more income per hectare than TL33.

The genotype-locality interaction was non-significant for yield, cured leaf quality and income.

The combined analysis using the AGROBASE program (Table 5.13) showed three important things. Firstly, the localities are different. Secondly, the performances of the elite breeding lines did not change significantly with localities. Thirdly, although there were highly significant differences among the entries, the three elite breeding lines; ODT82, ODT92 and OD2 that were economically better than TL33 could do equally well in all the four localities.

The third general observation aroused the curiosity for further investigation of the interaction variance to see if there is any basis for the preference of specific elite breeding lines at certain localities.

5.3.2 The AMMI analysis

The results of the AMMI analyses confirmed the significant differences among the localities and among the entries and the non-significant interaction between the localities and the entries in terms of both the yield and income levels.

The partitioning of the interaction variance showed that the first Interaction Principal Component Analysis (IPCA1) was non-significant at 5% probability level for both yield and income levels (Table 5.14 and Table 5.15).

Although IPCA1 was not significant for both yield and income, the AMMI analysis demonstrated its potential application in predicting the genotypic adaptability to particular localities. The biplots (Figure 5.1 and Figure 5.2) provide graphical

summaries of the interactions among the genotypes and the localities. Various agriculturally important interaction patterns may be perceived from the biplots.

The main effects and the IPCA scores tend to be indicative of the agricultural qualities of the localities and the adaptability of the genotypes to the particular localities.

The biplot in conjunction with the AMMI model equation could serve as a useful tool for estimating the performance of the genotypes in the different localities being studied. The AMMI model equation says that the estimated genotypic performance, $Y = M_G + M_L - GM + (IPCA1_G \times IPCA1_L)$. M_G is the genotype mean, M_L is the locality mean, GM is the general mean, which together make the additive component of the AMMI model equation. The genotype IPCA1 ($IPCA1_G$) and the locality IPCA1 ($IPCA1_L$) make the multiplicative component of the AMMI model equation (Gauch and Zobel, 1996; Smith, 1995).

ODT82 (2873 kg/ha) and ODT92 (2904 kg/ha) produced almost equal mean yields (Figure 5.1 and Table 5.13) across localities. However, the AMMI selections (AMMI Table 1) predicted that ODT82 would be the best-adapted genotype at Potgietersrus while ODT92 would be the best-adapted genotype at Vaalwater.

The AMMI biplots of genotype and environment IPCA scores versus mean yields (Figure 5.1) and income (Figure 5.2) explain the reasoning behind the differences in the adaptability of the different genotypes to the different localities.

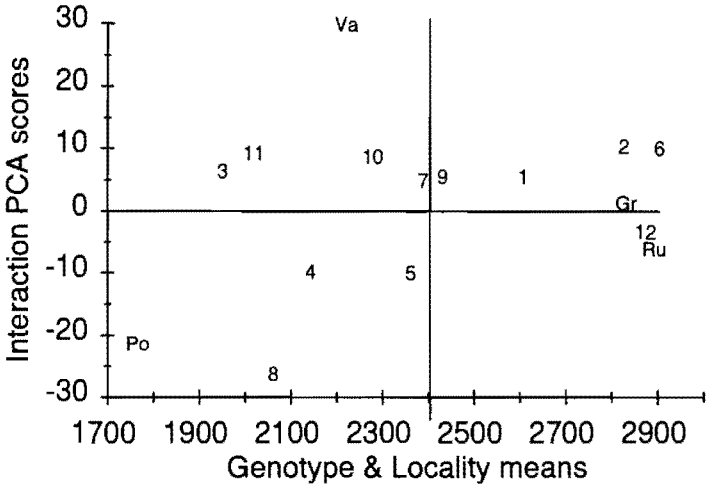

Figure 5.1: Plot of IPCA scores versus yield means for genotype and locality

Localities: Gr Groblersdal; Po Potgietersrus; Ru Rustenburg; Va Vaalwater

The treatments in Figure 5.1 have been represented by numbers 1-12 as follows, according to Table 4.5, for clarity.

1	OD1	2	OD2	3	OD486B	4	TL33
5	OD490	6	ODT92	7	ODT1	8	ODT100
9	OD313	10	ODT19	11	ODT8	12	ODT82

AMMI Table 1: Table of the AMMI genotype selections for adaptability to particular localities in terms of yield according to Figure 5.1

Locality	AMMI selections			
	Best	Second best	Third best	Fourth best
Groblersdal	ODT92	ODT82	OD2	OD1
Potgietersrus	ODT82	ODT92	ODT100	OD2
Rustenburg	ODT82	ODT92	OD2	OD1
Vaalwater	ODT92	OD2	ODT82	OD1

Figure 5.1 explains that ODT82 and ODT92 tend to be similar by main effects, but differ by interaction. Potgietersrus and Rustenburg differ by both the main

effects on the x-axis and the IPCA scores on the y-axis, but both had negative IPCA scores. ODT82 also had a negative IPCA score. Therefore, the multiplicative component of the AMMI model for ODT82 at both localities had a positive effect on yield. ODT92 had a positive IPCA score. The multiplicative component of the AMMI model for ODT92 at Potgietersrus and Rustenburg had a negative effect on yield. Hence, the AMMI selection for ODT82 as the best-adapted genotype at Potgietersrus and Rustenburg. Similarly, Groblersdal, Vaalwater and ODT92 had positive IPCA scores. The multiplicative component of the AMMI model for ODT92 at Groblersdal and Vaalwater had positive effects on yields. The multiplicative component of the AMMI model for ODT82 at Groblersdal and Vaalwater had a negative effect on yields. Hence, the AMMI selection for ODT92 as the best-adapted genotype at Groblersdal and Vaalwater.

Although ODT92 had a negative effect on yield at Potgietersrus and Rustenburg, the AMMI selections rated it the second best-adapted genotype at Potgietersrus and Rustenburg due to its high level of the main effect. Similarly, ODT82 was rated the second best-adapted genotype at Groblersdal.

OD2 and ODT92 tended to be similar in interaction on the y-axis, but different in main effects on the x-axis. The AMMI selections rated OD2 second to ODT92 in its adaptability at Vaalwater possibly due to the high level of its main effect and its positive IPCA score. Similar arguments account for the subsequent AMMI selection of genotypes for particular localities.

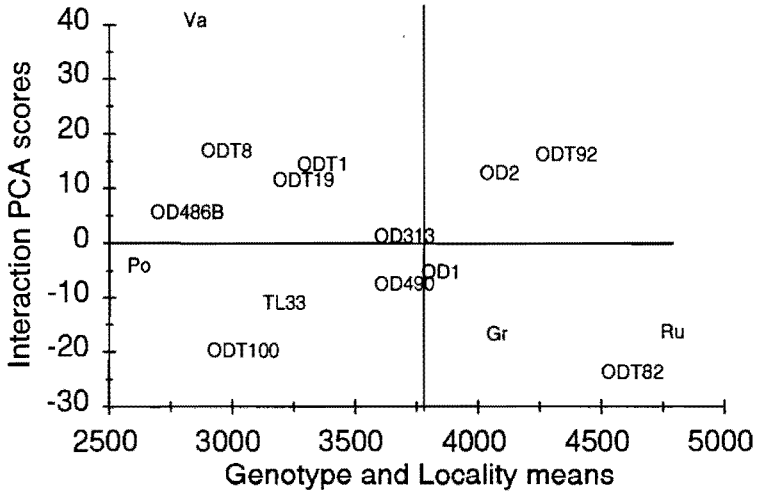

Figure 5.2: Plot of IPCA scores versus income means (in tens) for genotype and locality.

Localities: Gr Groblersdal Po Potgietersrus,
Ru Rustenburg Va Vaalwater

AMMI Table 2: Table of the AMMI genotype selections for adaptability in particular localities in terms of income according to Figure 5.2.

Locality	AMMI selections			
	Best	Second best	Third best	Fourth best
Groblersdal	ODT82	ODT92	OD1	OD2
Potgietersrus	ODT82	ODT92	OD2	OD1
Rustenburg	ODT82	ODT92	OD1	OD2
Vaalwater	ODT92	OD2	ODT1	ODT19

Figure 5.2 shows that although Groblersdal, Potgietersrus and Rustenburg tend to differ mostly by the main effects on the x-axis, they have negative IPCA scores. ODT82 had a high level of the main effect and a negative IPCA score. The multiplicative component of the AMMI model for ODT82 at Rustenburg, Groblersdal and Potgietersrus had positive effects on income levels. ODT92 had

its main effect just below that of ODT82, but had a positive IPCA score. The multiplicative component of the AMMI model for ODT92 at Groblersdal, Potgietersrus and Rustenburg had negative effects on income levels, whilst at Vaalwater it had a positive effect on income. Therefore, the AMMI selected ODT82 as the best-adapted genotype at Groblersdal, Potgietersrus and Rustenburg; and ODT92 at Vaalwater.

The multiplicative component of the AMMI model for ODT92 at Groblersdal, Potgietersrus and Rustenburg had negative effects on income levels. However, the AMMI selections indicate ODT92 as the second best-adapted genotype to Groblersdal, Potgietersrus and Rustenburg possibly due to the high level of the main effect.

OD2 had a positive IPCA score and tended to be similar to ODT92 in interaction. Therefore, the multiplicative component of the AMMI model for OD2 at Vaalwater had a positive effect on income. Hence, the AMMI selection for OD2 as the second best-adapted genotype to Vaalwater.

Likewise, the level of the main effects and the IPCA scores explain the agricultural qualities of the localities and the adaptability of the other different genotypes to the particular localities.