

Final results from a trial to  
test the effect of plot size on  
*Eucalyptus* hybrid clonal  
ranking in coastal Zululand,  
South Africa

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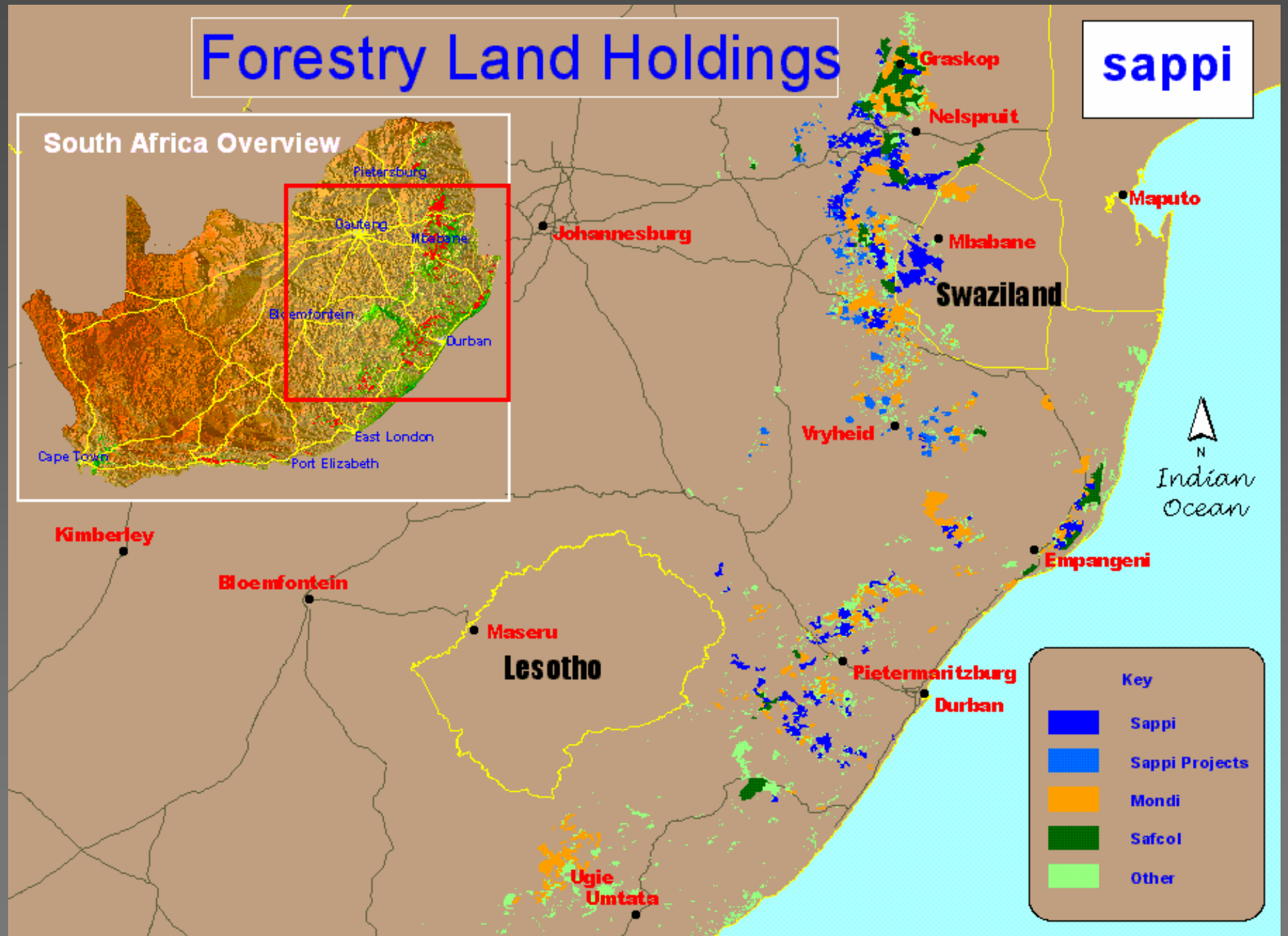
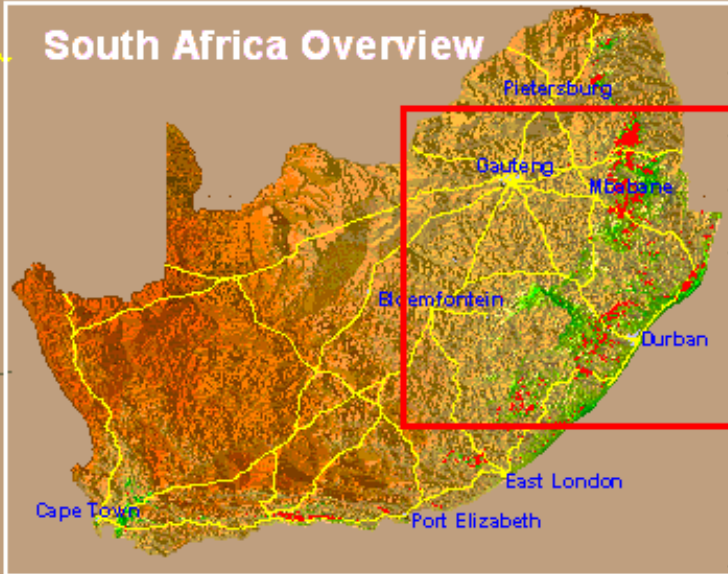
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
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# Forestry Land Holdings

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## South Africa Overview



Key	
	Sappi
	Sappi Projects
	Mondi
	Safcol
	Other

# Introduction

## *E. grandis*

- historically an important forestry species in South Africa
- has desirable wood properties for pulp production
- poor survival in subtropical climate due to fungal diseases

## *E. urophylla*

- disease tolerant

## *E. grandis* x *E. urophylla* hybrid clones

- combines good survival, disease tolerance and rapid early growth of parents
- currently deployed operationally in monoclinal blocks of average size 20-40 ha

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# Background

Fasoula and Fasoula (1997) identified ecosystems in which genotypes are grown by plant breeders



**competition environment**  
interactions between  
genetically dissimilar  
genotypes

**crop environment**  
interactions between  
genetically identical  
genotypes



poor negative correlation between the best yield producers in a competition environment and the best yield producers in a crop environment

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## Competition environment

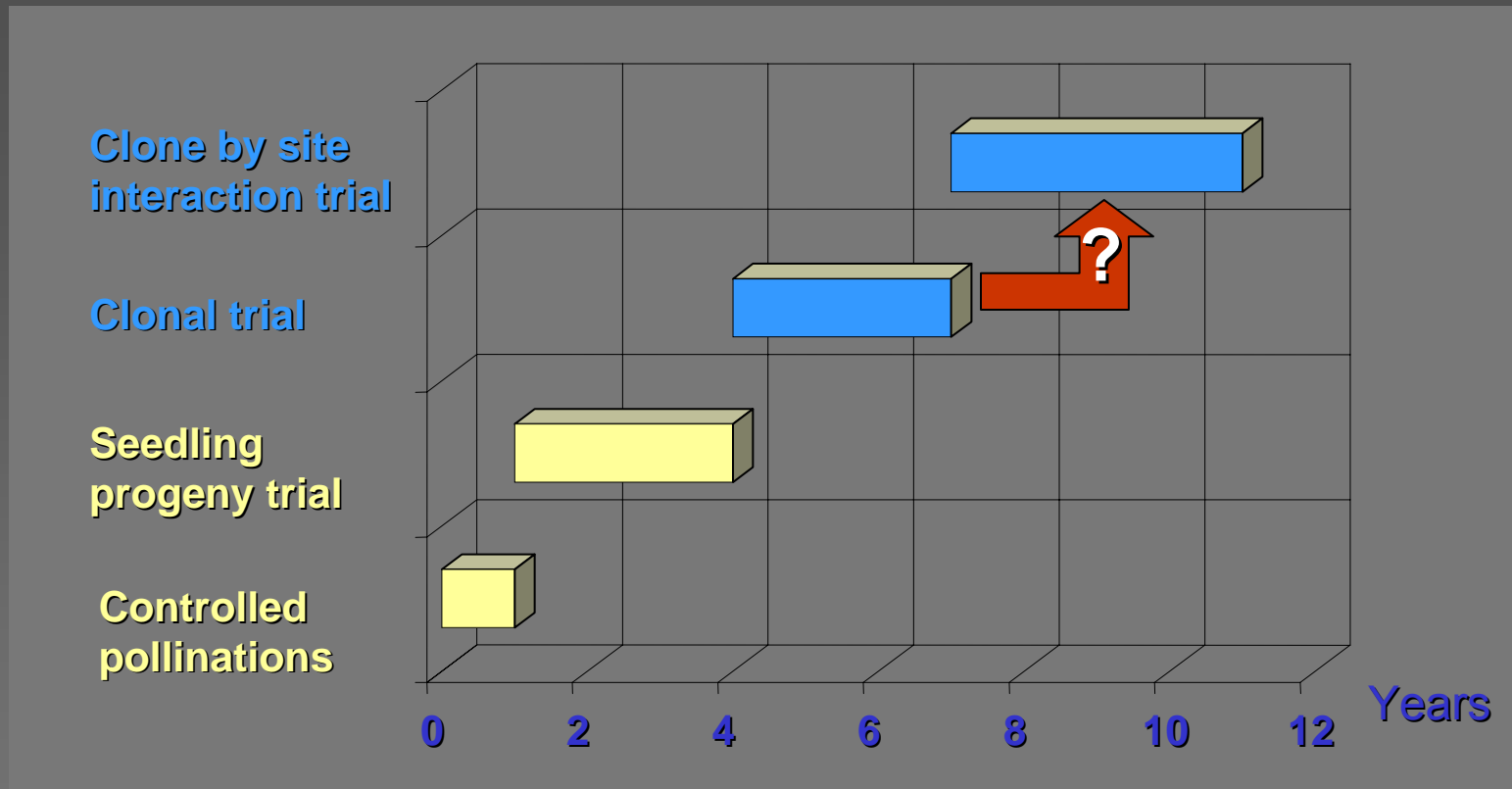


## Crop environment





# Selection and deployment of clones



## Clonal trials

design: 6 replications  
3 tree line plots  
purpose: rapidly screen large number of clones

## Clone by site interaction trials

design: 4 replications  
6 x 6 tree square plots  
purpose: screen small number of clones comprehensively

# Objective

to evaluate the effect of  
different **plot size/type**  
on clonal ranking

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# Trial site details

<b>Planting date</b>	<b>17/09/1998</b>
<b>Site Quality</b>	<b>High productivity site</b>
<b>MAT</b>	<b>21 °C</b>
<b>MAP</b>	<b>1149 mm</b>
<b>Climate</b>	<b>Sub-tropical</b>
<b>Age</b>	<b>94 months</b>



# Trial design

randomised complete block design

8 clones: 7 *E. grandis* x *E. urophylla* clones

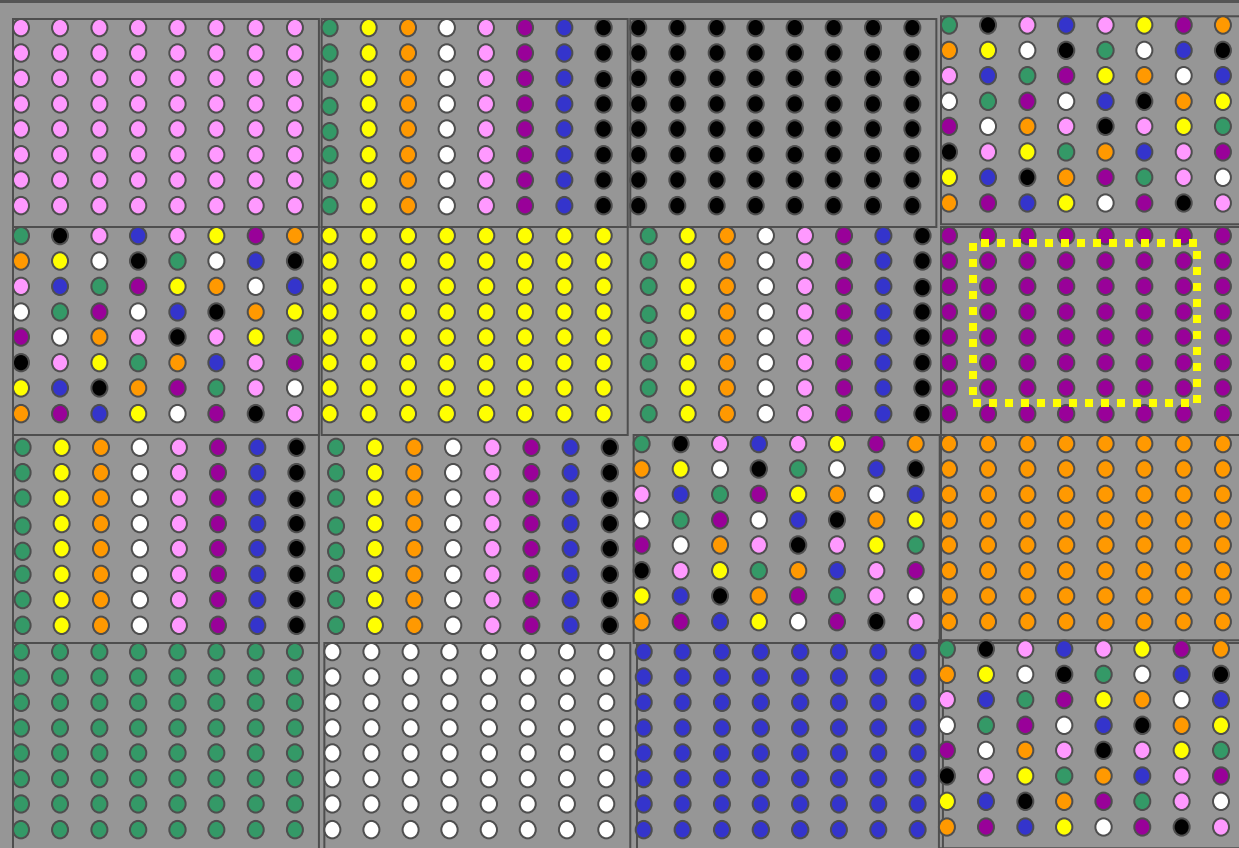
1 *E. grandis* x *E. camaldulensis* clone

- 96 replications single tree plots (96 trees)
- 12 replications 8 tree line plots (96 trees)
- 3 replications 8x8 tree square plots (inner 6x6 analysed, 108 trees)

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# Field layout



**8 square plots:**  
each clone  
represented once

**4 line plot blocks:**  
each clone  
represented once

**4 Single tree plot  
blocks:**  
each clone  
represented 8 times

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# Parameters calculated

## Clonal heritability

$$H^2 = \sigma^2_{\text{clone}} / (\sigma^2_{\text{clone}} + \sigma^2_{\text{plot}} / b + \sigma^2_w / nb)$$

## Environmental portion of the variance of a clonal mean (Loo-Dinkins & Tauer, 1987)

$$E_{c \text{ mean}} = \sigma^2_{\text{plot}} / b + \sigma^2_w / nb$$

## Relative efficiency of a design

$$RE = E_{c \text{ mean}} \text{ STP} / E_{c \text{ mean}} \text{ design}$$

where  $n$  = number of trees/plot

$b$  = number of reps

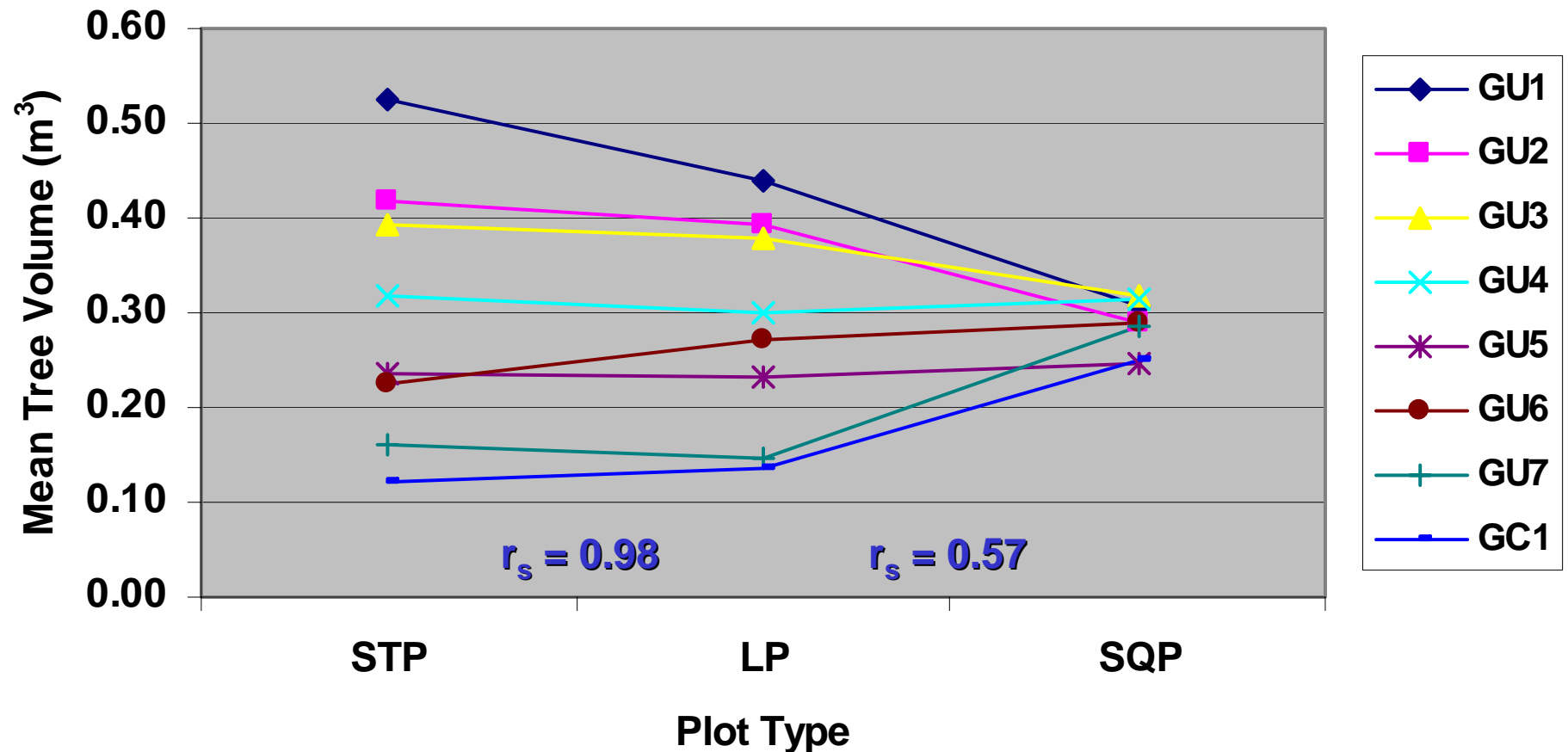
# Summary of trial parameters

	Single tree	Line	Square
$\sigma^2_{\text{block}}$	0.00064	0	0
$\sigma^2_{\text{clone}}$	0.01841	0.01208	0.0004478
$\sigma^2_{\text{plot}}$	0.0278	0.00157	0
$\sigma^2_w$	-	0.02816	0.02876
$H^2$	0.98	0.97	0.63
$\sigma^2_{\text{clonal mean}}$	0.019	0.013	0.001
$E_c \text{ mean}$	0.028	0.030	0.029
RE	1.00	0.94	0.97

- $H^2$  lowest for square plots
- $E_c \text{ mean}$  very similar for all three plot types
- RE only marginally better for STP



# Mean volume at 94 months for each clone for the three different plot types



# Trial results

Clone	Single Tree Plot		Line Plot		Square Plot	
	Vol94	Rank	Vol94	Rank	Vol94	Rank
GU1	0.5245	1	0.4380	1	0.3081	3
<b>GU2</b>	<b>0.4180</b>	<b>2</b>	<b>0.3943</b>	<b>2</b>	<b>0.2878</b>	<b>5</b>
GU3	0.3919	3	0.3777	3	0.3178	1
GU4	0.3180	4	0.3017	4	0.3145	2
GU5	0.2371	5	0.2318	6	0.2469	8
GU6	0.2250	6	0.2723	5	0.2910	4
GU7	0.1599	7	0.1474	7	0.2874	6
GC1	0.1203	8	0.1366	8	0.2499	7
Mean	0.3043		0.2915		0.2877	
LSD <sub>0.05</sub>	0.05371		0.04926		0.04692	

## Predicted gain from single tree plots vs. realized gain from square plots

Clone	STP	Gain	Predict Yield	Predict Gain	Actual Yield	Realized Gain
GU1	0.5245	0.216	0.5201	74%	0.3081	7%
GU2	0.4180	0.111	0.4157	39%	0.2878	0%
GU3	0.3919	0.086	0.3901	30%	0.3178	10%
GU4	0.3180	0.013	0.3177	6%	0.3145	9%
GU5	0.2371	-0.066	0.2384	-20%	0.2469	-14%
GU6	0.2250	-0.078	0.2266	-24%	0.2910	1%
GU7	0.1599	-0.142	0.1628	-46%	0.2874	0%
GC1	0.1203	-0.180	0.1240	-59%	0.2499	-13%
Mean	0.3043		0.2994		0.2877	

- Gains predicted using STP data were overestimates

# Discussion

## competition environment

- genetically dissimilar genotypes
- single tree and line plots
- in the competition environment the sharing of resources can never be equal, as the interacting plants are genetically different

## crop environment

- genetically identical genotypes
- square plots
- in a crop environment resources are shared evenly by all plants, thus the yield of all plants is evenly suppressed

The  $r_s = 0.57$  between the single tree and square plots, suggests a genotype by plot type interaction.



## Discussion (continued)

The best performers in a competition environment are the strongest competitors

Results have shown that they can be poorer yield producers in pure stands

Gains are overestimated in single tree and line plots

A much younger follow up trial with 25 clones is showing similar trends

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# Conclusions

**For clones in coastal Zululand, square/rectangular plots may be the most reliable and efficient way of identifying suitable commercial clones.**

**Based on field experience, the arguments of Fasoula and Fasoula (1997) with regard to crop breeding, warrant further investigation in forestry.**

**Clonal forestry with eucalypts offers an opportunity to further understand some of the mechanisms that may be involved in “between genotype” competition.**

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# *Improving fibre per hectare*

