BROAD AND NARROW SENSE HERITABILITIES IN A CLONED OPEN POLLINATED *EUCALYPTUS GRANDIS* BREEDING POPULATION

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DECLARATION

I the undersigned hereby declare that the work contained in this thesis is my own original work and has not previously in its entirety or in part, been submitted to any other university.

Signature: ..... Date: 02/08/2001

SUMMARY

Genetic variances and heritabilities in a cloned *Eucalyptus grandis* breeding population of families derived from open pollinated selections were estimated and the results are presented. The genetic variance was partitioned into additive and non-additive genetic variance components that allowed the estimation of broad and narrow sense heritabilities. Predicted gains for breeding and production population options are discussed.

The magnitude of the coefficient of relationship between sibs was shown to have a considerable impact on the estimate of variance components and the importance of understanding the level of relatedness in the population is highlighted.

Growth traits (volume, diameter at breast height/DBH, height), stem form and disease tolerance were assessed at 38 and 66 months in each of the three separate trials established as sub-populations of the breeding population. The additive genetic variance was the largest proportion of genetic variance for the growth traits (84% for volume, 94% for height and 74% for DBH), whereas the proportion of non-additive genetic variance was notably higher for stem form and disease tolerance (37% and 46% respectively). The growth traits and stem form are, economically, the most important traits and a breeding strategy that exploits the additive genetic variation by selection to increase the frequency of the alleles causing the desirable genotypes is appropriate. The higher proportion of non-additive genetic variance for disease does, however, suggest higher gains (compared with the afore mentioned strategy of selection for general combining ability) will be achieved by exploiting the non-additive variance by for example, selection for specific combining ability, using inbred lines, clones.

The composition of the genetic variance was investigated separately in the F1 and F2 families to obtain an indication of whether or not there was a change in proportion of non-additive and additive genetic variance over the two generations. A notably larger proportion of non-additive variance was found for the growth traits and stem form among the F2 families. This is probably due to the reduction in additive variance through selection for these traits in the previous generations. No

selection for disease took place in earlier generations and the proportion of non-additive genetic variance for this trait remains approximately the same over both generations. These results may indicate that with advanced generations of breeding in this population, that gains achieved through selection for additive variance will decline compared with that achieved in previous generations. A strategy for future generations that exploits non-additive variance may be appropriate.

A high proportion of error variance was estimated and in situations such as these, cloning is particularly beneficial as is shown by the high clone mean heritabilities estimated in these trials. High mortality, resulting in fewer ramets per clone, erodes the benefit of cloning in these trials.

The predicted gains showed the benefit of the cloned breeding population both in terms of breeding population gains and production population gains. Reducing the breeding cycle by bulking up clones faster will also increase gains per year. High gains in the production population were predicted, particularly for the selection of tested clones for deployment, which can be done at the same time as selections are made for the next generation. The benefit of the cloned population was therefore shown to be twofold, namely increasing the accuracy of within family selection and increasing the gains in the rapid deployment of tested clones and therefore facilitating the faster realisation of predicted gain in the plantation.

Keywords: Broad sense heritability, narrow sense heritability, cloned breeding population, additive genetic variation, non-additive genetic variation, *Eucalyptus grandis*.

OPSOMMING

Genetiese variansies en oorerflikhede in 'n gekloonde *Eucalyptus grandis* teelpopulasie van families verkry van af oopbestuifde seleksies, is bereken en die resultate word aangebied. Die genetiese variansies is opgedeel in additiewe en nie-additiewe komponente wat die skatting van breë en eng sin oorerflikhede moontlik maak. Voorspelde vordering vir die teel- en produksiepopulasies word ook bespreek.

Die grootte van die koëffisiënt van die verwantskap tussen sibbe blyk redelike groot invloed op die skatting van die variansie komponente te hê en dit is dus belangrik om die mate van verwantskap in die populasie te verstaan.

Groei-eienskappe (volume, deursnit op borshoogte (DBH) en hoogte), stamvorm en weerstand teen siektes is op 38 en 66 maande in elkeen van die onderskeie proewe gemeet. Die additiewe genetiese variansie was die grootste proporsie van die genetiese variansie vir die groei-eienskappe (84% vir volume, 94% vir hoogte en 74% vir DBH). Die proporsie nie-additiewe genetiese variansie was merkbaar hoër vir stamvorm en siekteweerstand (37% en 46% onderskeidelik). Die groei-eienskappe en stamvorm is, ekonomies gesien, die belangrikste eienskappe en 'n teelstrategie wat die additiewe genetiese variansie ontgin deur seleksie om die frekwensie van "allele" wat die gunstige genotipes tot gevolg het te verhoog, is geskik. Die hoër proporsie van nie-additiewe genetiese variansie vir siekteweerstand wys dat 'n hoër wins gemaak sal word (in vergelyking met die bogenoemde strategie van seleksie vir algemene kombineringsvermoë) deur gebruik te maak van nie-additiewe variansie.

Die samestelling van genetiese variansie is afsonderlik in die F1 en F2 families ondersoek om 'n indikasie te kry of daar verskille tussen die proporsie nie-additiewe en additiewe variansies vir die verskillende generasies, bestaan. 'n Merkbare groter proporsie van nie-additiewe variansie is vir die groei-eienskappe en stamvorm in die F2 families gevind. Dit is moontlik te wyte aan die vermindering in additiewe variansie weens seleksie vir hierdie eienskappe in die vorige generasie. Geen seleksie vir siekteweerstand het in die vorige generasies plaasgevind nie en daarom kan dit wees dat die proporsie nie-additiewe genetiese variansie vir hierdie eienskap nie-merkbaar tussen

die twee generasies verskil nie. Hierdie resultate kan moontlik daarop dui dat, in gevorderde generasies van hierdie teelpopulasie die vordering deur seleksie vir additiewe variansie sal afneem in verhouding tot die vordering verkry deur seleksie in die vorige generasies. 'n Strategie vir die seleksie van toekomstige generasies wat die nie-additiewe variansie gebruik mag dan toepasliker wees.

'n Hoë proporsie vir die oorblywende foutvariansie was beraam en in sulke gevalle kan klonering hoogs voordelig wees, soos bewys deur die hoë erfbaarheidsyfers vir die klone verkry in hierdie proef. Die hoë mortaliteit wat tot gevolg gehad het dat minder ramette per kloon oorleef het bederf egter tot 'n mate die voordeel van klonering in hierdie proewe.

Die voorspelde vordering wys die voordeel van die gekloonde teelpopulasie in terme van beide die teel- en produksiepopulasie vordering. Verkorting van die teelsiklus deur klone vinniger te vermeerder sal ook bydra om vordering per jaar te verhoog. Hoë vordering in die produksiepopulasie is voorspel, veral vir die seleksie van getoetste klone vir aanwending wat plaas kan vind wanneer seleksie vir die volgende generasie gedoen word. Die voordeel van die gekloonde populasie is bewys tweeledig te wees, namelik verhoging van die akkuraatheid van binne familie seleksie en vermeerdering van die vordering deur die vinniger aanwending van getoetste klone en daarom die vinniger verhoging van voorspelde vordering in die plantasie deur die ontplooing van getoetste klone.

Sleutelwoorde: Breë sin oorerflikheid, eng sin oorerflikheid, gekloonde teel- populasie, additiewe genetiese variansie, nie-additiewe genetiese variansie, *Eucalyptus grandis*

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NOMENCLATURE AND DEFINITIONS

A list of abbreviations, contractions and definitions frequently used in the text is included for ease of reference; others are expanded in the text:

A	Additive genetic variance component
DBH	Diameter at breast height (1.3metres) in millimetres
Disease	Disease tolerance (Mean tolerance to *Coniothyrium, Crypohonectria, Botryosphaeria* and *Endothia* scored on a 5 point scale.)
P0	Parental generation
F1	First generation
F2	Second generation
Fam	Family
G	Genetic variance component
Ht	Height in metres
NA	Non-additive genetic variance component
SE	Standard error
Stem	Stem form (8 point scale)
VAR	Variance
h^2	Narrow sense heritability
H^2	Broad sense heritability
σ	Standard deviation
σ^2	Variance component

Subscripts:

A	Additive genetic variance component
c(f)	Clone within family
F	Family
G	Genotypic or genetic variance component
NA	Non-additive genetic variance component
P	Phenotypic

Definitions:

Clone:	a group of genetically identical individuals
Family:	Genotypes raised from the seed of a single tree
Provenance:	the original native origin (geographic) of a population
Ramet:	an individual member of a clone