LIST OF REFERENCES

Becker, W.A. 1992. Manual of Quantitative Genetics. 5th Edition. Academic Enterprises, USA. 189pp.

Bouvet, J.M., 1992. Geno-Phenotypic Regression and Juvenile-Mature Correlations: Methodological Tools for Clonal Selection of *Eucalyptus* Hybrids in Congo. SA For. J. 160: 13-18.

Bredenkamp, B.V. and Loveday, N.C., 1984. Research note. Volume Equations for Diameter Measurements in Millimetres. SA For. J. 130: 40.

Bulmer, M.G., 1980. The mathematical theory of quantitative genetics. Clarendon Press, Oxford. 254pp.

Burdon, R.D., 1977. Genetic Correlation as a Concept for studying Genotype-environment Interaction in Forest Tree Breeding. Silvae Genetica 26 (5-6): 168-175.

Burdon, R.D. and Shelbourne, C.J.A., 1974. The use of vegetative propagules for obtaining genetic information. NZ J. For. Sci. 4 : 418-425.

Cochran, W.G. and Cox, G.M., 1957. Experimental Designs. 2nd Edition. Wiley, New York. 611pp.

Cockerham, C.C., 1954. An extension of the concept of partitioning hereditary variance for analysis of covariances among relatives when epistasis is present. Genetics 39: 859 – 882.

Cooper, D.T. and Ferguson, R.B., 1977. Removal of competition bias from forest genetics experiments. *In proceedings of the* 14th South For Tree Imp Conf, pp 70-77.

Cotterill, P., 1997. Nucleus breeding: Is it OK for *Pinus* and *Eucalyptus*? *In proceedings of the* IUFRO Conference on Silviculture and Improvement of Eucalypts. V1. Tree improvement strategies. Salvador, Brazil. pp 277- 284.

Eldridge , K., 1995. Eucalypt base populations for selection. *In proceedings of the* CRCTHF-IUFRO Working Parties S2.02-09 and P2.02-01 Conference on Eucalypt Plantations: Improving Fibre Yield and Quality. Hobart, Australia. 19-24 February 1995. pp 204-207.

Cotterill, P.P. and James, J.W., 1984. Number of offspring and plot sizes required for progeny testing. Silvae Genetica 33(6): 203-209.

Falconer, D.S., 1989. Introduction to Quantitative Genetics. Longman Scientific & Technical, U.K. 438pp.

Foster, G.S. and Shaw, D.V., 1988. Using clonal replicates to explore genetic variation in perennial plant species. Theor. Appl. Genet. 76: 788-794.

Foster, G.S, 1985. Genetic parameters for two eastern cottonwood populations in the lower Mississippi Valley. *Proceedings* 18th South. For. Tree. Improv. Conf. pp 258-266.

Foster, G.S, Campbell, R.K. and Adams, W.T.,1984. Heritability, gain and C-effects in rooting of Western Hemlock cuttings. Can. J. For. Res. 14: 928-638.

Franklin, E.C., 1979. Model relating levels of genetic variance to stand development of four North American Conifers. Silvae Genetica 28 (5-6): 207-212.

Fu, Y-B., Yanchuk, A.D., Namkoong, G., Clarke, G.P., 1999. Incomplete Block Designs for Genetic Testing: Statistical Efficiencies with Missing Observations. Forest Science 45(3): 374-379.

Gill, J.G.S., 1987. Juvenile-Mature correlations and trends in genetic variances in Sitka spruce in Britain. Silvae Genetica 36 (5-6):189-194.

Hamblin, J. and Rosielle, A.A., 1978. Effect of intergenotypic competition on genetic parameter estimation. Crop Sci. 18: 51-54.

Hodgson, L.M. 1975. Some aspects of reproductive behaviour in *Eucalyptus grandis* (Hill) Maiden. PhD Thesis. Department of General Botany, University of Pretoria.

Jacquard, A., 1983. Heritability: One Word, Three Concepts. Biometrics 39: 465-477.

Kanzler, A. and Hodge, G.R., 2000. Genotype x environment interaction in a series of provenance/progeny trials of *Pinus patula* in South Africa. *In proceedings of* Forest Genetics for the Next Millenium. IUFRO Working party 2.08.01. Durban, South Africa. 8 to 13 October 2000. pp 151-157.

Libby, W.J., 1992. Use of genetic variation for breeding forest trees. In Plant Breeding in the 1990's. North Carolina State University (Ed. H.T. Stalker, J.P. Murphy). pp 101-117.

Libby, W.J., 1964. Clonal selection, and alternative seed orchard scheme. Silvae Genetica 13:32-40.

Libby, W.J. and Cockerham, C.C., 1980. Random non-contiguous plots in interlocking field layouts. Silvae Genetica 29(5-6): 183-190.

Libby, W.J. and Jund, E., 1962. Variance associated with cloning. Heredity 17: 533-540.

Magnussen, S., 1991. A probability distribution for age-to-age correlations and it's application in early selection. Can. J. For. Res. 21: 1550-1558.

Marques, O.G., Andrade, H.B., and Ramalho,M.A.P., 1996. Assessment of the Early Selection Efficiency in *Eucalyptus cloeziana* F.Muell. in the Northwest of Minas Gerais State (Brazil). Silvae Genetica 45(5-6): 359-361.

Mather, K. and Jinks, J.L., 1982. Biometrical Genetics. Third Edition. Chapman and Hall, London. 396pp.

Matheson, A.C. and Lindgren, D., 1985. Gains from the clonal and the clonal seed-orchard options compared for tree breeding programs. Theor. Appl. Genet. 71: 242-249.

Mullin, T.J. and Park, Y.S., 1992. Estimating genetic gains from alternative breeding strategies for clonal forestry. Can. J. For. Res. 22:14-23.

Mullin, T.J., Morgenstern, E.K., Park, Y.S. and Fowler, D.P., 1992. Genetic parameters from a clonally replicated test of black spruce *(Picea mariana)*. Can. J. For. Res. 22: 24-36.

Namkoong, G. 1981. Introduction to quantitative genetics in forestry. Castle House Publications, Kent. 342pp.

Namkoong, G., 1966. Inbreeding effects on estimation of genetic additive variance. Forest Science 12 (1): 8-13.

Nel, A., 1991. Progress report on clone bank management. CSIR Internal Report. FOR-DEA 144. 9pp.

Owen, D.L. (Ed.), 2000. South African Forestry Handbook. 4th Edition. Volume 1. Southern African Institute of Forestry, Pretoria, South Africa. 416pp.

Pandoy, R., Snedden, C.L., and Pierce, B.T., 1998. Report on the Age-Age Correlations in three second generation *E.grandis* progeny trials. CSIR Internal Report. ENV-P-I 98133. 11pp.

Park, Y.S and Fowler, D.P., 1987. Genetic variances among clonaly propagated populations of Tamarack and the implications for clonal forestry. Can. J. For. Res. 17: 1175-1180.

Patterson, H.D. and Williams, E.R., 1976. A new class of resolvable incomplete block designs. Biometrika 63(1): 83-92.

Patterson, H.D. and Thompson, R., 1971. Recovery of inter-block information when block sizes are unequal. Biometrika 58(3): 545-554.

Pierce, B.T., 2000. Personal communication. CSIR, Nelspruit.

Pierce, B.T., 1996. Status report: *Eucalyptus grandis* programme. CSIR Internal Report ENV-P-C 96086. Environmentek, Pretoria. 124pp.

Pierce, B.T., 1993. Report: Progress on the cloning of a breeding population of 300 families of *Eucalyptus grandis*. CSIR (Forestek) internal report FOR-DEA 629. 15pp.

Rosvall, O., Lindgren, D. and Mullin, T.J., 1998. Sustainability Robustness and efficiency of a Multi-generation Breeding Strategy Based on Within-family Clonal Selection. Silvae Genetica 47(5-6): 307-321.

Russell, J.H. and Loo-Dinkins, J.A., 1993. Distribution of Testing Effort in Cloned Genetic Tests. Silvae Genetica 42(2-3): 98-104.

Russell, J.H. and Libby, W.J., 1986. Clonal testing efficiency: the trade-offs between clones tested and ramets per clone. Can. J. For. Res. 16: 925-930.

SAS Software. Release 6.12, 1996. SAS Institute Inc., SAS Circle Box 8000, Cary, N.C., USA.

Schulzere, 1997. South African atlas of Agrohydrology and Climatology. Water Research Commission, PTA. Report TT82/96.

Shapiro, S.S. and Wilk, M.B., 1965. An analysis of variance test for normality (complete samples). Biometrika 52 (3-4): 591-611.

Shaw, D.V. and Hood, J.V., 1985. Maximizing gain per effort by using clonal replicates in genetic tests. Theor. Appl. Genet. 71: 392-399.

Shelbourne, C.J.A., 1992a. Genetic gains from Different Kinds of Breeding Population and Seed or Plant Production Population. SA For. J. 160: 49-65.

Shelbourne, C.J.A., 1992b. Report: Design and description of a breeding strategy for *Eucalyptus grandis* and hybrid and an implementation plan. CSIR Internal report. FOR-DEA 529. 50pp.

Snedecor, G.W. and Cochran, W.G. 1967. Statistical Methods. 6th Edition. The Iowa State University Press, USA. 593pp.

Stonecypher, R.W. and McCullough, R.B., 1986. Estimates of additive and non-additive genetic variances from a clonal diallel of Douglas-fir Pseudotsuga menziesii [Mirb.] Franco. In conference proceedings IUFRO Joint Meeting of Working Parties on Breeding Theory, Progeny Testing and Seed Orchards, 13-17 October 1986, Williamsburg,V.A. North Carolina State University - Industry Cooperative Tree Improvement Program, Raleigh, NC. pp 211-227.

Squillace, A.E., 1974. Average Genetic Correlations Among Offspring From Open pollinated Forest Trees. Silvae Genetica 23(5): 149-156.

van Wyk, G., 1990. Genetic Improvement of Timber Yield and Wood Quality in *Eucalyptus grandis* (Hill) Maiden. Part I. Genetic parameters of growth characteristics. SA For. J. 153: 1-11.

van Wyk, G., 1975. Early growth results in a diallel progeny test of *Eucalyptus grandis* W. Hill ex Maiden. Ph.D. thesis. Department of Forestry, North Carolina State University.

Verryn, S.D., 2000. Personal communication. CSIR, Pretoria.

Verryn, S.D. 2000. *Eucalyptus* hybrid breeding in South Africa. *In* Hybrid Breeding and Genetics of Forest Trees. Dungey, H.S., Dieters, M.J. and Nikles, D.G. (compilers). *Proceedings of* QFRI/CRC-SPF Symposium, 9-14 April 2000, Noosa, Queensland, Australia. pp 1-13.

Verryn, S.D. 1993. Research and development report compiling estimates of genetic parameters in open pollination and diallel trials. CSIR internal report. FOR-DEA 601. 9pp.

Verryn, S.D. and Snedden, C.L. 2000. Optimising the expected genetic gains of various breeding and selection strategies. *In proceedings* Forest Genetics for the Next Millenium. IUFRO Working Party 2.08.01. Durban, 8-13 October 2000. pp 240-243.

Verryn, S.D. and Snedden, C.L. and Malan, G.J., 2000a. The early expression of splitting in *E.grandis*. CSIR client confidential report. ENV-P-C 2000-085. 19pp.

Verryn, S.D., Snedden, C.L., and Parfitt, R.C., 2000b. A program for the deterministic modelling of Genetic Gains of Tree Breeding and Seed and Clone Production Strategies. SA For. J. 189. pp 3-10.

Verryn, S.D., Hettasch, M., Pierce, B.T., 2000c. Optimising Tree Breeding Strategies Course Manual. Environmentek, CSIR. Pretoria, South Africa.

Verryn, S.D. and Snedden, C.L., 1998. G-Assist Version 3.0. A User's Manual. 31pp.

Verryn, S.D., Field, C.L., Garcia, H. and Griffin, A.R., 1997. A discussion on the relationship between heritabilities and genetic correlations and the standard errors of these parameters with a case study example of GEI in *E.grandis* over two sites in South Africa and one site in Uruguay. *In proceedings* IUFRO Conference on the Silviculture and Improvement of Eucalypts. Colombo: Embrapa:Centro Nacional de Pesquisa de Florestas, Brazil. pp 43-49.

Williams, E.R. and Matheson, A.C., 1994. Experimental Design and Analysis for use in tree Improvement. CSIRO Information Services, Victoria, Australia. 174pp.

Zobel, B. and Talbert, J., 1984. Applied Forest Tree Improvement. John Wiley & Sons, Inc., Canada. 505pp.

APPENDIX A

ASSESSMENT TECHNIQUES

Table A-1.   Procedure for the 38 month assessment of trials B1, B2 and B3.

Trait	Instrument	Method of assessment	Unit
Height	Height rods	from base to tip of tree	dm
DBH	Diameter tape	over bark at 1,3 m from ground level	mm
Stem form	Visual	on total bole from base to tip of tree	1 - 8
Coniothyrium	Visual	on total bole from base to live crown	0 - 4
Cryphonectria	Visual	on total bole from base to live crown	0 - 4
Endothia	Visual	on total bole from base to live crown	0 - 4
Botryosphaeria	Visual	on total bole from base to live crown	0 - 4
Defects	Visual	missing tree broken top forked tree runt dead tree leaning tree	M B F S D L

Table A-2.   Procedure for the 66 month assessment of trials B1, B2 and B3.

Trait	Instrument	Method of assessment	Unit
Height	Vertex Hypsometer	from base to tip of tree	m
DBH	Diameter tape	over bark at 1,3 m from ground level	mm
Stem form	Visual	on total bole from base to tip of tree	1 - 8
Coniothyrium	Visual	on total bole from base to live crown	0 - 4
Cryphonectria	Visual	on total bole from base to live crown	0 - 4
Botryosphaeria	Visual	on total bole from base to live crown	0 - 4
Endothia	Visual	on total bole from base to live crown	0 - 4
Defects	Visual	missing tree broken top forked tree runt	G B F R

Table A-3.   Industry standard subjective scale for stem form assessment in trials B1, B2 and B3.

Score	Description	Summary of defects
8	Straight stem - pole quality	STRAIGHT no defects
7	Slight sweep and/or 1 minor bend	NEARLY STRAIGHT 1 - 2 minor defects
6	One slight sweep + >1 minor bend OR More than 1 slight sweep + 1 minor bend OR More than 2 minor bends	VERY SLIGHTLY CROOKED 3 - 4 minor defects
5	Moderate sweep + 1 moderate bend OR Two moderate sweeps + minor defect OR Two moderate bends + minor defect	SLIGHTLY CROOKED 2 moderate defects OR 2 moderate + 1 minor defects
4	Moderate sweep + major bend OR More than two moderate sweeps OR More than two moderate bends OR Two major bends + minor defects	MODERATELY CROOKED 1 moderate + 1 major defect OR > 2 moderate defects OR 2 major + 2 minor defects
3	Obvious sinuosity or major crooks	CROOKED > 2 major defects OR 2 major + 2 moderate defects
2	Presence of multiple severe straightness defects	VERY CROOKED several major and moderate defects
1	Unmerchantable as a short log cork screw)	MALFORMED major defects

Table A-4. Industry standard subjective scale for the visual assessment of the diseases *Cryphonectria, Coniothyrium, Botryosphaeria* and *Endothia* in trials B1, B2 and B3.

Score	Description	Summary of infestation
0	No visual sign of any disease infestation	NIL
1	Some visual disease infestation	25% COVERAGE
2	Mild visual disease infestation	50% COVERAGE
3	Moderate visual disease infestation	75% COVERAGE
4	Chronic visual disease infestation	100% COVERAGE

Table A-5. Model used for the estimation of volume for *Eucalyptus grandis* (Bredenkamp and Loveday, 1984).

$$\log V = b_0 + b_1 \log(DBH+d) + b_2 \log Ht$$

where,

log	is the common logarithm to the base 10
V	is the stem volume (m^3), to 75 mm tip diameter
DBH	is the diameter at breast height (mm)
d	is the correction factor (mm)
Ht	is the tree height (m).

Coefficients where diameter at breast-height (DBH) is measured in millimetres:

DBH (mm)	b_0	b_1	d	b_2
< 200	-11.16217	3.65167	100	1.14760
200 < DBH < 400	- 4.98199	1.32829	- 70	1.17827
> 400	- 5.39010	1.41460	- 60	1.29911

APPENDIX B

DATA EDITING

Table B-1. Observations deemed outliers (more than three times the Inter Quartile Range from the mean) and removed from the data sets for trials B1, B2 and B3, sorted by trial, replication and block.

| Clone | Trait | | Family | Trial | Replication | Block |
	Height at age (months)	DBH at age (months)				
AG596/9	38	38	AG596	B1	1	5
BG22/8	38	-	BG22	B1	1	7
AG535/3	66	-	AG535	B1	1	19
BG165/8	-	38	BG165	B1	2	14
AG647/9	38	-	AG647	B1	3	5
AG489/8	38	-	AG489	B1	4	1
BG128/5	38	-	BG128	B1	4	13
BG110/7	38	-	BG110	B2	1	2
AG689/1	38	38	AG689	B2	2	1
BG61/3	38	-	BG61	B2	2	2
AG643/4	38	-	AG643	B2	2	16
BG39/3	38	-	BG39	B2	2	18
AG519/8	38	-	AG519	B2	3	1
AG611/6	38	-	AG611	B2	3	5
BG111/1	66	-	BG111	B2	3	7
BG39/6	38	-	BG39	B2	3	7
AG599/8	38	38	AG599	B2	3	11
BG39/7	38	38	BG39	B2	3	20
BG152/9	38	-	BG152	B2	4	8
AG649/9	38	38	AG649	B2	4	12
AG649/8	38	38	AG649	B2	5	14
AG465/2	38	-	AG465	B2	5	17
BG71/6	66	-	BG71	B3	4	2
BG75/1	66	-	BG75	B3	4	3

Table B-2. Observations deemed outliers (more than three times the Inter Quartile Range from the mean) and removed from the data sets for trials B1, B2 and B3, sorted by family.

| Clone | Trait | | Family | Trial | Replication | Block |
	Height at age (months)	DBH at age (months)				
AG465/2	38	-	AG465	B2	5	17
AG489/8	38	-	AG489	B1	4	1
AG519/8	38	-	AG519	B2	3	1
AG535/3	66	-	AG535	B1	1	19
AG596/9	38	38	AG596	B1	1	5
AG599/8	38	38	AG599	B2	3	11
AG611/6	38	-	AG611	B2	3	5
AG643/4	38	-	AG643	B2	2	16
AG647/9	38	-	AG647	B1	3	5
AG649/8	38	38	AG649	B2	5	14
AG649/9	38	38		B2	4	12
AG689/1	38	38	AG689	B2	2	1
BG110/7	38	-	BG110	B2	1	2
BG111/1	66	-	BG111	B2	3	7
BG128/5	38	-	BG128	B1	4	13
BG152/9	38	-	BG152	B2	4	8
BG165/8	-	38	BG165	B1	2	14
BG22/8	38	-	BG22	B1	1	7
BG39/3	38	-	BG39	B2	2	18
BG39/6	38	-		B2	3	7
BG39/7	38	38		B2	3	20
BG61/3	38	-	BG61	B2	2	2
BG71/6	66	-	BG71	B3	4	2
BG75/1	66	-	BG75	B3	4	3
24			**21**			

Table B-3. Regression models used for the correction for missing trees in trials B1, B2 and B3.

Trial	Trait	Age	Model	Pr>F
B1	Volume	38 months	$\hat{y} = 0.00467x_1 + 0.00280x_2 + 0.12$	0.0001***
		66 months	$\hat{y} = 0.02245x_1 + 0.01281x_2 + 0.27$	0.0001***
	Height	38 months	$\hat{y} = -0.20028x_1 + 17.03$	0.0011**
		66 months	Model non-significant ($p \leq 0.05$)	
	DBH	38 months	$\hat{y} = 4.03029x_1 + 1.86632x_2 + 159.89$	0.0001***
		66 months	$\hat{y} = 8.17575x_1 + 4.20196x_2 + 198.47$	0.0001***
	Stem Score	38 months	Model non-significant ($p \leq 0.05$)	
		66 months	$\hat{y} = 0.11880x_1 + 5.31$	0.0001***
	Disease Tolerance	38 months	Model non-significant ($p \leq 0.05$)	
		66 months	Model non-significant ($p \leq 0.05$)	
B2	Volume	38 months	$\hat{y} = 0.00879x_1 + 0.13$	0.0001***
		66 months	$\hat{y} = 0.03041x_1 + 0.00774x_2 + 0.29$	0.0001***
	Height	38 months	$\hat{y} = -0.25893x_2 + 17.94$	0.0001***
		66 months	Model non-significant ($p \leq 0.05$)	
	DBH	38 months	$\hat{y} = 5.93902x_1 + 163.50$	0.0001***
		66 months	$\hat{y} = 10.53912x_1 + 2.71715x_2 + 198.05$	0.0001***
	Stem Score	38 months	$\hat{y} = 0.10973x_1 + 5.71$	0.0024**
		66 months	$\hat{y} = 0.15987x_1 + 5.59$	0.0001***
	Disease Tolerance	38 months	Model non-significant ($p \leq 0.05$)	
		66 months	Model non-significant ($p \leq 0.05$)	
B3	Volume	66 months	$\hat{y} = 0.03247x_1 + 0.02175x_2 + 0.30$	0.0001***
	Height	66 months	$\hat{y} = 0.21660x_2 + 25.26$	0.0004**
	DBH	66 months	$\hat{y} = 9.36506x_1 + 5.56324x_2 + 200.24$	0.0001***
	Stem Score	66 months	$\hat{y} = 0.09329x_1 + 0.05793x_2 + 5.51$	0.0001***
	Disease Tolerance	66 months	Model non-significant ($p \leq 0.05$)	

$\hat{y}_i$ is the predicted value for trees (observations) i=1,2, .. n

x_{1_i} is the number of missing trees adjacent to tree i ($x_1 = 1, 2, .. 4$)

x_{2_i} is the number of missing trees diagonal to tree i ($x_2 = 1, 2, .. 4$)

*   Significant at $p \leq 0.05$
**   Significant at $p \leq 0.01$
***   Significant at $p \leq 0.0001$

Table B-4. Regression models used for the correction for missing trees in the pooled data of trials B1, B2 and B3.

Trait	Age	Model	Pr>F
Volume	38 months	$\hat{y} = 0.00754x_1 + 0.12$	0.0001***
	66 months	$\hat{y} = 0.02976x_1 + 0.01607x_2 + 0.28$	0.0001***
Height	38 months	$\hat{y} = -0.14701x_1 - 0.14570x_2 + 17.57$	0.0001***
	66 months	Model non-significant ($p \leq 0.05$)	
DBH	38 months	$\hat{y} = 5.11523x_1 + 1.32590x_2 + 160.91$	0.0001***
	66 months	$\hat{y} = 9.79673x_1 + 4.72259x_2 + 197.44$	0.0001***
Stem Score	38 months	$\hat{y} = 0.06888x_1 + 0.54$	0.0120*
	66 months	$\hat{y} = 0.12672x_1 + 0.04689x_2 + 5.42$	0.0001***
Disease Tolerance	38 months	Model non-significant ($p \leq 0.05$)	
	66 months	Model non-significant ($p \leq 0.05$)	

$\hat{y}_i$ is the predicted value for trees (observations) i=1,2, .. n

x_{1_i} is the number of missing trees adjacent to tree i (x_1 =1, 2, .. 4)

x_{2_i} is the number of missing trees diagonal to tree i (x_2 =1, 2, .. 4)

*   Significant at p≤ 0.05
**   Significant at p≤ 0.01
***   Significant at p≤0.0001

APPENDIX C

ANALYSIS OF VARIANCE IN THE
SEPARATE TRIALS (B1, B2 AND B3)

Table C-1.   Analysis of variance for volume in trial B1 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.021	0.0054	2.83	0.0239*
Block within replication	75	0.19	0.0026	1.38	0.0239*
Family	55	0.25	0.0045	2.40	0.0001***
Clone within-family	419	1.30	0.0031	1.64	0.0001***
Error	694	1.31	0.0019		

Table C-2.   Analysis of variance for DBH in trial B1 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	3454.37	863.59	1.42	0.2264^{NS}
Block within replication	75	61050.90	814.012	1.34	0.0361*
Family	55	71670.50	1303.10	2.14	0.0001***
Clone within-family	419	395705.28	944.40	1.55	0.0001***
Error	698	425206.80	609.18		

Table C-3.   Analysis of variance for height in trial B1 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	100.18	25.044	12.20	0.0001***
Block within replication	75	323.079	4.31	2.10	0.0001***
Family	55	236.76	4.31	2.10	0.0001***
Clone within-family	419	1262.68	3.014	1.47	0.0001***
Error	695	1426.39	2.052		

Table C-4.   Analysis of variance for stem form in trial B1 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	17.90	4.47	2.71	0.0295*
Block within replication	75	139.91	1.87	1.13	0.2242 NS
Family	55	220.34	4.0061	2.42	0.0001***
Clone within-family	419	997.76	2.38	1.44	0.0001***
Error	694	1147.57	1.65		

Table C-5.   Analysis of variance for disease tolerance in trial B1 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	1.23	0.31	4.72	0.0009**
Block within replication	75	8.54	0.11	1.75	0.0002**
Family	55	8.46	0.15	2.37	0.0001***
Clone within-family	419	43.63	0.10	1.60	0.0001***
Error	699	45.44	0.065		

Table C-6.   Analysis of variance for volume in trial B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.044	0.011	4.45	0.0015**
Block within replication	77	0.23	0.0030	1.22	0.1112 NS
Family	58	0.34	0.0058	2.35	0.0001***
Clone within-family	428	1.50	0.0035	1.42	0.0001***
Error	677	1.68	0.0025		

Table C-7.   Analysis of variance for DBH in trial B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	13413.67	3353.42	4.85	0.0007***
Block within replication	77	65065.23	845.0030	1.22	0.1043 NS
Family	58	94007.92	1620.83	2.34	0.0001***
Clone within-family	428	409987.31	957.91	1.39	0.0001***
Error	685	473492.51	691.23		

Table C-8.   Analysis of variance for height in trial B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	21.87	5.47	2.72	0.0288*
Block within replication	77	373.00	4.84	2.41	0.0001***
Family	58	240.11	4.14	2.06	0.0001***
Clone within-family	428	1318.36	3.08	1.53	0.0001***
Error	677	1361.56	2.011		

Table C-9.   Analysis of variance for stem form in trial B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	28.55	7.14	5.35	0.0003**
Block within replication	77	129.18	1.68	1.26	0.0764 NS
Family	58	107.71	1.86	1.39	0.0328*
Clone within-family	428	789.66	1.85	1.38	0.0001***
Error	685	914.44	1.33		

Table C-10.   Analysis of variance for disease tolerance in trial B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	1.22	0.30	7.00	0.0001***
Block within replication	77	3.39	0.044	1.01	0.4534 NS
Family	58	5.015	0.086	1.99	0.0001***
Clone within-family	428	30.42	0.071	1.64	0.0001***
Error	687	29.84	0.043		

Table C-11.   Analysis of variance for volume in trial B1 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.16	0.040	3.70	0.0054**
Block within replication	84	1.17	0.014	1.28	0.0542 NS
Family	55	2.16	0.039	3.60	0.0001***
Clone within-family	418	9.82	0.024	2.15	0.0001***
Error	741	8.089	0.011		

Table C-12.   Analysis of variance for DBH in trial B1 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	21999.30	5499.83	5.76	0.0001***
Block within replication	84	118348.79	1408.91	1.48	0.0052**
Family	55	160154.52	2911.90	3.05	0.0001***
Clone within-family	418	813209.65	1945.48	2.04	0.0001***
Error	742	708155.071	954.39		

Table C-13. Analysis of variance for height in trial B1 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	25.67	6.42	1.84	0.1198 NS
Block within replication	84	515.62	6.14	1.76	0.0001***
Family	55	622.37	11.32	3.24	0.0001***
Clone within-family	418	2690.24	6.44	1.84	0.0001***
Error	741	2589.13	3.49		

Table C-14. Analysis of variance for stem form in trial B1 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	6.52	1.63	3.21	0.0125*
Block within replication	84	47.045	0.56	1.10	0.2565 NS
Family	55	69.72	1.27	2.50	0.0001***
Clone within-family	418	330.85	0.79	1.56	0.0001***
Error	740	375.64	0.51		

Table C-15. Analysis of variance for disease tolerance in trial B1 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.23	0.057	1.57	0.1800 NS
Block within replication	84	4.14	0.049	1.37	0.0209*
Family	55	5.92	0.11	2.98	0.0001***
Clone within-family	418	30.66	0.073	2.03	0.0001***
Error	742	26.77	0.036		

Table C-16.   Analysis of variance for volume in trial B2 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.15	0.038	2.80	0.0253*
Block within replication	77	1.42	0.018	1.34	0.0346*
Family	58	2.20	0.038	2.75	0.0001***
Clone within-family	420	9.16	0.022	1.59	0.0001***
Error	630	8.66	0.014		

Table C-17.   Analysis of variance for DBH in trial B2 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	9909.71	2477.43	2.38	0.0506^{NS}
Block within replication	77	122045.95	1585.012	1.52	0.0041**
Family	58	147231.058	2538.47	2.44	0.0001***
Clone within-family	420	672872.80	1602.078	1.54	0.0001***
Error	631	657127.39	1041.41		

Table C-18.   Analysis of variance for height in trial B2 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	148.26	37.064	9.04	0.0001***
Block within replication	77	597.00	7.75	1.89	0.0001***
Family	58	521.22	8.99	2.19	0.0001***
Clone within-family	420	2446.57	5.83	1.42	0.0001***
Error	631	2588.16	4.10		

Table C-19. Analysis of variance for stem form in trial B2 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	4.23	1.057	1.97	0.0972^{NS}
Block within replication	77	57.25	0.74	1.39	0.0204*
Family	58	56.96	0.98	1.83	0.0003**
Clone within-family	420	327.65	0.78	1.46	0.0001***
Error	632	338.65	0.54		

Table C-20. Analysis of variance for disease tolerance in trial B2 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.32	0.081	2.36	0.0526^{NS}
Block within replication	77	2.89	0.038	1.09	0.2855^{NS}
Family	58	6.46	0.11	3.24	0.0001***
Clone within-family	420	23.11	0.055	1.60	0.0001***
Error	632	21.70	0.034		

Table C-21. Analysis of variance for volume in trial B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.26	0.064	3.69	0.0055**
Block within replication	85	2.0082	0.024	1.37	0.0206*
Family	67	2.37	0.035	2.05	0.0001***
Clone within-family	411	7.75	0.019	1.09	0.1586^{NS}
Error	697	12.052	0.017		

Table C-22. Analysis of variance for DBH in trial B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	8947.00046	2236.75	1.96	0.0990^{NS}
Block within replication	85	126168.13	1484.33	1.30	0.0433*
Family	67	146920.70	2192.85	1.92	0.0001***
Clone within-family	411	510951.015	1243.19	1.09	0.1631^{NS}
Error	698	796709.94	1141.42		

Table C-23. Analysis of variance for height in trial B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	381.17	95.29	23.93	0.0001***
Block within replication	85	443.73	5.22	1.31	0.0387*
Family	67	605.30	9.034	2.27	0.0001***
Clone within-family	411	1887.83	4.59	1.15	0.0508^{NS}
Error	697	2776.12	3.98		

Table C-24. Analysis of variance for stem form in trial B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	8.33	2.082	3.85	0.0042**
Block within replication	85	45.36	0.53	0.99	0.5127^{NS}
Family	67	44.94	0.67	1.24	0.1000^{NS}
Clone within-family	411	242.13	0.59	1.09	0.1595^{NS}
Error	698	377.054	0.54		

Table C-25. Analysis of variance for disease tolerance in trial B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Replication	4	0.36	0.091	2.31	0.0568 ^{NS}
Block within replication	85	4.96	0.058	1.48	0.0050**
Family	67	4.75	0.071	1.80	0.0002**
Clone within-family	411	22.73	0.055	1.40	0.0001***
Error	698	27.52	0.039		

SS	Type III Sum of Squares
NS	Non-significant
*	Significant at $p \leq 0.05$
**	Significant at $p \leq 0.01$
***	Significant at $p \leq 0.0001$

APPENDIX D

ANALYSIS OF VARIANCE IN POOLED DATA
WITH TRIAL EFFECT

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Table D-1.   Analysis of variance for volume (m^3) in the pooled data of trials B1 and B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	1	0.015	0.015	6.70	0.0098**
Family	113	0.62	0.0055	2.43	0.0001***
Clone within-family	844	2.84	0.0034	1.48	0.0001***
Error	1534	3.49	0.0023		

Table D-2.   Analysis of variance for height (m) in the pooled data of trials B1 and B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	1	0.018	0.018	0.01	0.9303 NS
Family	113	514.77	4.56	1.94	0.0001***
Clone within-family	844	2807.92	3.33	1.42	0.0001***
Error	1535	3601.43	2.35		

Table D-3.   Analysis of variance for DBH (mm) in the pooled data of trials B1 and B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	1	5295.00	5295.00	7.84	0.0052**
Family	113	171446.018	1517.22	2.25	0.0001***
Clone within-family	844	812006.57	962.093	1.42	0.0001***
Error	1546	1043912.39	675.23		

Table D-4. Analysis of variance for stem form (1-8 point scale) in the pooled data of trials B1 and B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	1	0.011	0.011	0.01	0.9339^{NS}
Family	113	341.85	3.025	1.95	0.0001***
Clone within-family	844	1847.99	2.19	1.41	0.0001***
Error	1542	2388.53	1.55		

Table D-5. Analysis of variance for disease tolerance (0-4 point scale for each disease) in the pooled data of trials B1 and B2 at age 38 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	1	0.017	0.017	0.29	0.5906^{NS}
Family	113	15.0049	0.13	2.29	0.0001***
Clone within-family	844	80.72	0.096	1.65	0.0001***
Error	1549	89.89	0.058		

Table D-6. Analysis of variance for volume (m^3) in the pooled data of trials B1, B2 and B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	2	0.093	0.047	3.17	0.0422*
Family	176	7.28	0.041	2.81	0.0001***
Clone within-family	1222	27.49	0.023	1.53	0.0001***
Error	2357	34.68	0.015		

Table D-7.   Analysis of variance for height (m) in the pooled data of trials B1, B2 and B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	2	129.0051	64.50	14.84	0.0001***
Family	176	2009.72	11.42	2.63	0.0001***
Clone within-family	1222	7523.51	6.16	1.42	0.0001***
Error	2358	10249.68	4.35		

Table D-8.   Analysis of variance for DBH (mm) in the pooled data of trials B1, B2 and B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	2	3925.46	1962.73	1.77	0.1711^{NS}
Family	176	480888.45	2732.32	2.46	0.0001***
Clone within-family	1222	2072873.74	1696.30	1.53	0.0001***
Error	2360	2622036.63	1111.03		

Table D-9.   Analysis of variance for stem form (1-8 point scale) in the pooled data of trials B1, B2 and B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	2	2.56	1.28	2.35	0.0955^{NS}
Family	176	185.51	1.054	1.94	0.0001***
Clone within-family	1222	925.38	0.76	1.39	0.0001***
Error	2359	1282.083	0.54		

Table D-10. Analysis of variance for disease tolerance (0-4 point scale for each disease) in the pooled data of trials B1, B2 and B3 at age 66 months.

Source	DF	SS	MS	F Value	Pr > F
Trial	2	0.27	0.13	3.46	0.0316*
Family	176	19.22	0.11	2.84	0.0001***
Clone within-family	1222	80.32	0.066	1.71	0.0001***
Error	2361	90.75	0.038		

SS	Type III Sum of Squares	*	Significant at p≤ 0.05
NS	Non-significant	**	Significant at p≤ 0.01
		***	Significant at p≤0.0001

Table D-11. T-test for volume in the pooled data of trials B1 and B2 at age 38 months.

Trial	Mean	n	T-Test Grouping
B2	0.14	1245	A
B1	0.13	1248	B

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-12. T-test for height in the pooled data of trials B1 and B2 at age 38 months.

Trial	Mean	n	T-Test Grouping
B2	17.71	1245	A
B1	16.91	1249	B

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-13. T-test for DBH in the pooled data of trials B1 and B2 at age 38 months.

Trial	Mean	n	T-Test Grouping
B2	172.62	1253	A
B1	168.65	1252	B

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-14. T-test for stem form in the pooled data of trials B1 and B2 at age 38 months.

Trial	Mean	n	T-Test Grouping
B2	5.88	1253	A
B1	5.44	1248	B

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-15. T-test for disease tolerance in the pooled data of trials B1 and B2 at age 38 months.

Trial	Mean	n	T-Test Grouping
B1	0.65	1253	A
B2	0.56	1255	B

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-16. Student-Newman-Keuls test for volume in the pooled data of trials B1, B2 and B3 at age 66 months.

Trial	Mean	n	SNK Grouping
B3	0.39	1265	A
B2	0.35	1190	B
B1	0.32	1303	C

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-17. Student-Newman-Keuls test for height in the pooled data of trials B1, B2 and B3 at age 66 months.

Trial	Mean	n	SNK Grouping
B3	25.62	1265	A
B2	24.30	1191	B
B1	23.35	1303	C

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-18. Student-Newman-Keuls test for DBH in the pooled data of trials B1, B2 and B3 at age 66 months.

Trial	Mean	n	SNK Grouping
B3	222.85	1266	A
B2	218.95	1191	B
B1	215.82	1304	C

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Table D-19.   Student-Newman-Keuls test for stem form in the pooled data of trials B1, B2 and B3 at age 66 months.

Trial	Mean	n	SNK Grouping
B2	5.84	1192	A
B3	5.74	1266	B
B1	5.49	1302	C

Means grouped with the same letter are not significantly different (α=0.05)

Table D-20.   Student-Newman-Keuls test for disease tolerance in the pooled data of trials B1, B2 and B3 at age 66 months.

Trial	Mean	n	SNK Grouping
B1	0.59	1304	A
B2	0.53	1192	B
B3	0.50	1266	C

Means grouped with the same letter are not significantly different (α=0.05)

APPENDIX E

T-TEST FOR
GENERATIONS F1 AND F2

Table E-1.   T-test for volume (corrected for missing trees) at age 38 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1 and B2).

Generation	Mean	n	T-Test Grouping
F1	0.0024	1156	A
F2	-0.0020	1361	B

Table E-2.   T-test for height (corrected for missing trees) at age 38 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1 and B2).

Generation	Mean	n	T-Test Grouping
F1	0.14	1156	A
F2	-0.12	1361	B

Table E-3.   T-test for DBH (corrected for missing trees) at age 38 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1 and B2).

Generation	Mean	n	T-Test Grouping
F1	0.46	1156	A
F2	-0.39	1361	A

Table E-4.   T-test for stem form (corrected for missing trees) at age 38 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1 and B2).

Generation	Mean	N	T-Test Grouping
F1	0.025	1156	A
F2	-0.021	1361	A

Table E-5. T-test for disease tolerance (not corrected for missing trees) at age 38 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1 and B2).

Generation	Mean	n	T-Test Grouping
F2	0.61	1356	A
F1	0.60	1152	A

Table E-6. T-test for volume (corrected for missing trees) at age 66 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1 B2, and B3).

Generation	Mean	n	T-Test Grouping
F1	0.016	1803	A
F2	-0.015	1962	B

Table E-7. T-test for height (not corrected for missing trees) at age 66 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1, B2 and B3).

Generation	Mean	N	T-Test Grouping
F1	24.77	1801	A
F2	24.092	1958	B

Table E-8. T-test for DBH (corrected for missing trees) at age 66 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1, B2 and B3).

Generation	Mean	N	T-Test Grouping
F1	3.37	1803	A
F2	-3.10	1962	B

Table E-9.   T-test for stem form (corrected for missing trees) at age 66 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1, B2 and B3).

Generation	Mean	N	T-Test Grouping
F1	0.011	1803	A
F2	-0.010	1962	A

Table E-10.   T-test for disease tolerance (not corrected for missing trees) at age 66 months for the F1 and F2 groups of families (subsets of the pooled data of trials B1, B2 and B3).

Generation	Mean	N	T-Test Grouping
F2	0.55	1960	A
F1	0.53	1802	B

Means grouped with the same letter are not significantly different ($\alpha=0.05$)

Note: Due to the correction for missing trees where applicable, the "means" are in fact effects and although as such they should sum to zero, the two groups do not as the subsequent grouping into F1 and F2 is imbalanced. Without the grouping of families into F1 and F2 generation categories, the sum for each of the corrected traits is zero.