Forest Research **Project Record**

No. 6061

BRANCHING CHARACTERISTICS of RADIATA PINE in COMPARTMENT 905, KAINGAROA: DATA COLLECTION

J.C. GRACE
D. PONT
W. BLUNDELL
D. DUYVESTEYN
M. BUDIANTO

REPORT No. 63 **April 1998**

EXECUTIVE SUMMARY

A branch model is being developed that will predict the location, frequency, and growth of radiata pine branches. In this report, the procedure used to collect data from 16 trees in Compartment 905, Kaingaroa is described. These data will be used to develop the mathematical form of the functions within the branch model.

BRANCHING CHARACTERISTICS OF RADIATA PINE

IN COMPARTMENT 905, KAINGAROA: DATA COLLECTION

J.C. Grace, D. Pont, W. Blundell [1], D. Duyvesteyn, M. Budianto

1. since deceased.

INTRODUCTION

Development of a "branch model" to predict location, frequency and growth of branches will require several iterations of experimental design, data collection, function development, software implementation and testing.

Within the Central North Island, detailed branching data have already been collected on 12 trees in Experiment RO696 and 13 trees in Experiment RO905. These data are being used to develop the mathematical functions within the branch model.

One of the functions is the number of branch clusters formed per year. This characteristic appears to be under strong genetic control after the first few years (Fielding, 1960). At this stage, it is not known whether any other functions (Appendix 1) are likely to be influenced by genetics. However, it was considered important to gain an understanding of the influence of genetics on the functions within the branch model and to use known genetic material to investigate the influence of site variables on branching.

The parents within the radiata pine breeding programme have been assigned branch cluster frequency breeding value (brBV) based on the visual assessment of many trees (Kumar *et al*, 1996). The relationship between brBV and mean internode length between 6.3 m and 11.8 m has been investigated by Turner *et al* (1997).

As part of the study, Turner *et al* (1997) randomly selected 10 "crop" trees from each of ten control pollinated crosses in the "850" diallel which was planted on several sites throughout New Zealand in 1975. The parents of the trees in the "850" diallel were selected for multinodality. The 10 crosses chosen were ones that were represented on all sites where the diallel was planted; covered the range in brBV present within the trial, with an emphasis on extreme values; and had at least 10 "crop" trees on each site (ie the trees had to be above a given diameter with a low incidence of malformation).

Turner *et al* also randomly selected 10 "crop" trees from progeny of each of 10 open-pollinated parents in the 1972 uninodal progeny test in Compartment 905 in Kaingaroa Forest. The parents of the trees in this trial were from an intensive selection for long internodes, and the families were chosen to cover the range in brBV present within the trial.

On each tree Turner *et al* (1997) measured the height to the base and top of each branch cluster below 12 m, and calculated the mean internode length between 6.3 m and 11.8 m.

The objective of the current study was to more intensively measure a sample of the trees selected by Turner *et al* (1997) in Compartment 905, Kaingaroa to determine which functions within the branch growth model (see Appendix 1) are likely to be influenced by genetics.

Due to the detailed measurements required, it was only feasible to sample a few trees. Hence the results will only be an indication of likely trends. If any of the functions appear to be influenced by genetics, further sampling on more trees will be needed to develop a robust model.

In future years it is planned to sample trees from the same families in replications of the "850" diallel on other sites in order to determine the influence of site on branching characteristics.

SELECTION OF SAMPLE TREES

From the families measured by Turner *et al* (1997), four families were selected from both the 1972 uninodal progeny trial and the "850" diallel in Compartment 905 in Kaingaroa Forest, using two criteria:

to sample the range brBV present in the respective trials,
to sample both positive and negative trends in MIL with respect to increasing DBH.

From the ten trees in each family, measured by Turner *et al* (1997), two trees were selected as potential trees to fell. These trees were approximately ± 1 standard deviation in terms of both DBH and MIL and in accordance with the observed, but generally non-significant trend between DBH and MIL .

The selected trees were examined in the field to determine whether they were suitable. If not, another tree was selected according to the above criteria. The revised list of trees which were selected is shown in Table 1. The actual breeding values (brBV) for the families are confidential to members of the Radiata Pine Breeding Co-operative. However the family codes 1-4 and 5-8 are correlated with the values of brBV.

Table 1. Sample trees selected.

Experiment	Family Code for analysis	Tree Number used in analysis	DBH (cm)	MIL (m)
Diallel	1	1	36.1	0.35
		2	57.7	0.51
	2	3	41.4	0.46
		4	46.0	0.34
	3	5	32.9	0.35
		6	57.0	0.87
	4	7	42.2	0.80
		8	52.4	0.35
Uninodal	5	9	37.0	0.34
		10	48.6	0.71
	6	11	29.0	0.64
		12	46.3	0.38
	7	13	33.5	1.27
		14	49.3	0.48
	8	15	29.2	0.64
		16	44.0	1.55

STAND CHARACTERISTICS

The progeny within the "850" diallel (GTI trial 320/25) were planted at 5m * 5m (400 stems/ha). At the same time filler trees were planted between the rows in one direction. However these were removed at a very young age. The trees were pruned to 6 m in three lifts. The filler trees are unlikely to have had any influence on the branches still present on the trees.

The uninodal progeny trial (GTI trial 320/16) was planted in 1972 at a spacing of 4m * 2m (1250 stems /ha). Well-stocked areas of the trial were thinned in 1978 to a nominal stocking of 600 stems/ha. The current stocking is considered to be approximately 450 stems/ha. The trees were also pruned to about 2 m, probably in 1978.

DATA COLLECTION PROCEDURE

Step 1. Prior to sample trees being felled

To estimate current growing space and local stocking for each sample tree, the following were measured:

DBH of sample tree

For all neighbouring trees within a plot whose radius gave 10 trees at the nominal stocking:

DBH of neighbouring trees
distance and bearing to neighbouring trees from sample tree

If necessary, extra neighbouring trees, outside the plot radius, were measured to ensure that there was at least one tree per quadrant for estimating growing space.

Step 2. Felling sample trees

The north side of the tree was marked to provide a reference after felling. The felling direction was identified to minimise breakage and ensure that the heads of trees did not overlap. The major vegetation along the felling path was cleared to ensure that as much of the underside of the tree (when it was on the ground) was visible for identifying branches.

The sample trees were directionally felled, and then reassembled on the ground. The branches were trimmed, perpendicular to the branch direction, to leave stubs of 10 -20 cm.

The vegetation on both sides of the stem was also cleared to provide visibility and easy access for data collection.

The northline, or an alternative reference line was then marked along the entire length of the stem to allow the position of branches between consecutive clusters to be compared.

Step 3. Position of branch clusters

Starting at the tip of the tree, the position of the base and top of each cluster was marked by a line drawn across the top surface of the stem, and the cluster numbered.

The base of the cluster is the lowest point where the branches are estimated to join the stem pith. According to D. Barthelemy (pers comm.), this point can be determined from the pattern of bark below the lowest branch in the cluster (Fig. 1). The top of the cluster is the highest point at which a branch emerges from the stem.

Care needs to be taken to ensure that each cluster is distinguished as some clusters can be close together, particularly when there is autumn extension growth (R. Burdon, pers comm.)

The position of resting buds can be distinguished, for a few years after they have expanded, by examining the patterns in the stem bark. However these buds do not necessarily represent a winter resting bud (Burdon, 1994). The cluster nearest such resting buds were noted.

The height to the base and top of each cluster, with respect to the base of the tree, was then measured using a tape.

To provide a permanent record, a series of photographs were taken of each sample tree, showing the position of the clusters along the stem.

Step 4. Measurement of clusters

Stem Growth rings

The stem was then crosscut into discs. The cuts were made just outside the marked cluster boundaries, so that each cluster was contained within a separate disc provided that clusters did not overlap. The tree and cluster number were recorded on the top surface of the disc. It is important to be consistent in the marking as this provides positive identification of the top of the cluster for future measurements.

The number of stem growth rings on the base and top of each disc were counted as soon as possible after the discs had been cut as the rings become less clear as the sample dries. The ring closest to the pith is the hardest to discern.

These data together with the heights of the clusters are used to determine the number of clusters within an annual shoot and the relative positions of the clusters within the annual shoot (functions 1 and 2).

Cones and branches

For each cluster, the number of branches and stem cones were recorded. The horizontal diameter of each branch adjacent to the stem but avoiding any swelling was measured to the nearest millimetre using callipers. The azimuthal angle of each branch and cone with respect to the reference line was measured using a circular protractor placed on the top of the disc. There is a degree of judgment in determining the angle that the branch emerges from the stem as the point where the branch emerges from the stem is generally some distance from the top of the disc. This method only gives the azimuthal angle at the time of felling.

These data are used to derive the coefficients for functions 3-9 inclusive.

Step 5. Selection of sample branches

As there was an age difference of 3-years between the multinodal and uninodal trees, sample branches were selected from three zones in each tree:

8-10 stem growth rings below the sample branch,
11-13 stem growth rings below the sample branch,
14-16 stem growth rings below the sample branch.

This enables sample branches to be compared according to the number of stem growth rings (in 3 zones) or according to tree age when the branch was formed (in 2 zones) (Table 2).

Table 2. Tree age and number of stem growth rings by year

Year of height extension	Number of stem growth rings	Tree Age -multinodal	Tree Age- uninodal
97	1	22	25
96	2	21	24
95	3	20	23
94	4	19	22
93	5	18	21
92	6	17	20
91	7	16	19
90	8	15	18
89	9	14	17
88	10	13	16
87	11	12	15
86	12	11	14
85	13	10	13
84	14	9	12
83	15	8	11
82	16	7	10
81	17	6	9
80	18	5	8
79	19	4	7
78	20	3	6
77	21	2	5
76	22	1	4
75	23		3
74	24		2
73	25		1
72	26		

For each tree, the branches in each zone were ranked according to diameter. Sample branches, to be measured for growth, were then selected in the office, according their percentile position in the branch diameter distribution. Sample branches from the same cluster were not allowed.

For the smaller tree in each pair, branches were close to the following percentiles:
100, 90 , 80, 60 40
For the larger tree in each pair, branches were close to the following percentiles:
100, 90, 80, 70, 60, 50, 40, 30

This sampling scheme enabled the range of branch diameters to be measured for growth but avoided having too many small branches below 20 mm.

These branches were then examined in the field to see whether they were suitable, ie. not broken and not obviously curved within the stem with respect to azimuth (this may cause problems with planing). If they were not suitable, the next nearest branch in the diameter distribution was considered. Suitable branches were marked for removal from the cluster.

This sampling scheme was only feasible because the data were being recorded electronically, allowing immediate examination of the data.

Preparing sample branches for measurement

Sample branches were cut out of clusters using a chainsaw. The first cut was approximately parallel with the branch pith, but to one side of the branch. The second cut was parallel to the first cut but on the other side of the branch. The third cut was at right angles to the first two, and gives a section that includes the branch and the stem pith (see Fig. 2). This section was then numbered with the tree and cluster number.

One side of the section was planed to expose the pith of the branch and the stem. This side must be carefully chosen so that the planed surface is convex. Due to the width of the planer, it is difficult to plane a concave face. The tree and cluster number were written on the opposite side prior to planning.

Measurement of branch development

If the sample was satisfactory after planning, a reference line was drawn from the join of the stem and branch pith at approximately a right angle to the stem pith and the stem growth rings. There is some subjectivity in the position of this line, particularly if the stem pith is swept. The stem radius for each year that the stem has grown was marked and then measured along this reference line. The height of the branch pith above the reference line was measured for each year that the stem has grown. The stem growth rings were used to identify the diameter of the branch for each year that the stem has grown by following the stem growth rings through to the branch (see Fig. 3). The branch diameters were then measured. The position of defects and any bark encasement due to mortality were recorded.

These data are used to determine the coefficients for functions 10-13 inclusive.

It is preferable to identify the features to be measured as soon as possible after the sample has been planed as the rings are most visible immediately after planing and become less clear as the sample dries. In this experiment, all the sample branches were marked before any were measured.

DATA CAPTURE

In Experiments RO696 and RO905, data were recorded on paper, then punched and checked. This was the most appropriate approach as the methodology was still being developed, and we often needed to make comments on interesting and unusual features. Even after these two studies, the development of purpose-written data collection software was precluded by time and cost.
Near the beginning of this study, a general purpose, commercial data capture package (EASYDC, version 4.0; (White, 1996)) was purchased, and was used to record most of the data.

EASYDC allows the user to define a number of data entry forms and use them for recording data. In addition to a basic definition such as the name, type and size of fields, the user can also set up prompt text, default values, data validation, on-the-spot calculations and other sophisticated features for each data entry field. In use, several data entry forms can be open at one time, and the user can move between them, entering data.

The program was used on a HUSKY Hunter 16 computer, and the following forms were used in this data collection exercise:

COMMENT :
Any observations or notes, recorded against tree number, and where appropriate, cluster number and branch number.

CLUSTER HEADER:
Position of base and top of cluster; stem ring counts above and below the cluster; overbark stem diameters above and below the cluster.

CLUSTER DETAIL:
Diameter, azimuth and status of each branch and cone in a cluster.

BRANCH HEADER:
Pith and sapwood radii, stem ring counts, bark encasement, branch diameter and presence of bark inclusion for each planed sample branch.

BRANCH DETAIL:
Stem radius, branch diameter, branch radius below the pith, and distance of branch pith from a horizontal reference line, for each year of stem growth.

Use of direct data capture had benefits: avoidance of problems with lost, damaged or illegible data sheets; immediate validation of data in the field; removal of the need for data punching, with its associated cost and potential for errors; and immediate availability of data at the end of each days measurement.

The flexibility of EASYDC was a definite advantage. More than once, data entry forms were altered in the field, to better suit the data collection task as the methodology was improved. One potential weakness of EASYDC is that separate forms have no implicit connection, therefore data which is related must be connected by identifying fields, for example: tree and cluster number. Before field use, this was seen to be a potential problem, but in practice it was not an issue.

In summary, EASYDC was a good tool for collecting the data in this study. Data entry forms were easily set up, and changed when required. Field crew were able to use the program with a minimum of instruction. The only problem encountered was that no clear procedure was established for managing the data downloaded at the end of each day, with the result that some duplication of data occurred. This would be easily managed with a correct procedure for downloading and clearing data from the field computer.

ACKNOWLEDGEMENTS

Thanks are due to everyone who helped with the data collection.
Thanks to Fletcher Challenge Forests for allowing us to destructively sample the trees.

REFERENCES

BURDON, R.D. 1994. Annual growth stages for height and diameter in *Pinus radiata. New Zealand Journal of Forestry Science 24(1):* 11-17.

FIELDING, J.M. 1960: Branching and flowering characteristics of monterey pine. *Forestry and Timber Bureau, Canberra, Bulletin No. 37.*

KUMAR,S; CARSON, S.D; BURGER, F.C.; JEFFERSON, P.A. 1996: Best linear prediction of breeding values for straightness and branch cluster frequency in a *Pinus radiata* improvement programme. New Zealand Radiata Pine Breeding Co-operative Report No. 42 (unpublished).

TURNER, J.A.; CARSON, S.D.; MANLEY, B.R.; GRACE, J.C.; WEST, G.G. 1997: Genetic and site differences in *Pinus radiata* internode length in New Zealand. Forest and Farm Plantation Management Co-operative Report No. 39 (unpublished).

WHITE, R. 1996: EASYDC Universal Data Collection Program for MS-DOS Handheld Computers. User Guide. R. White Woods Inc. Victoria, B.C., Canada.

Figure 1. Diagram showing the pattern of bark below a branch.

In an operational procedure it will be sufficient to look for the base of the pattern, marked by a horizontal line. It is considered that the actual join between the stem and branch piths is a few millimetres above the marked point. However the actual join is more difficult to determine.

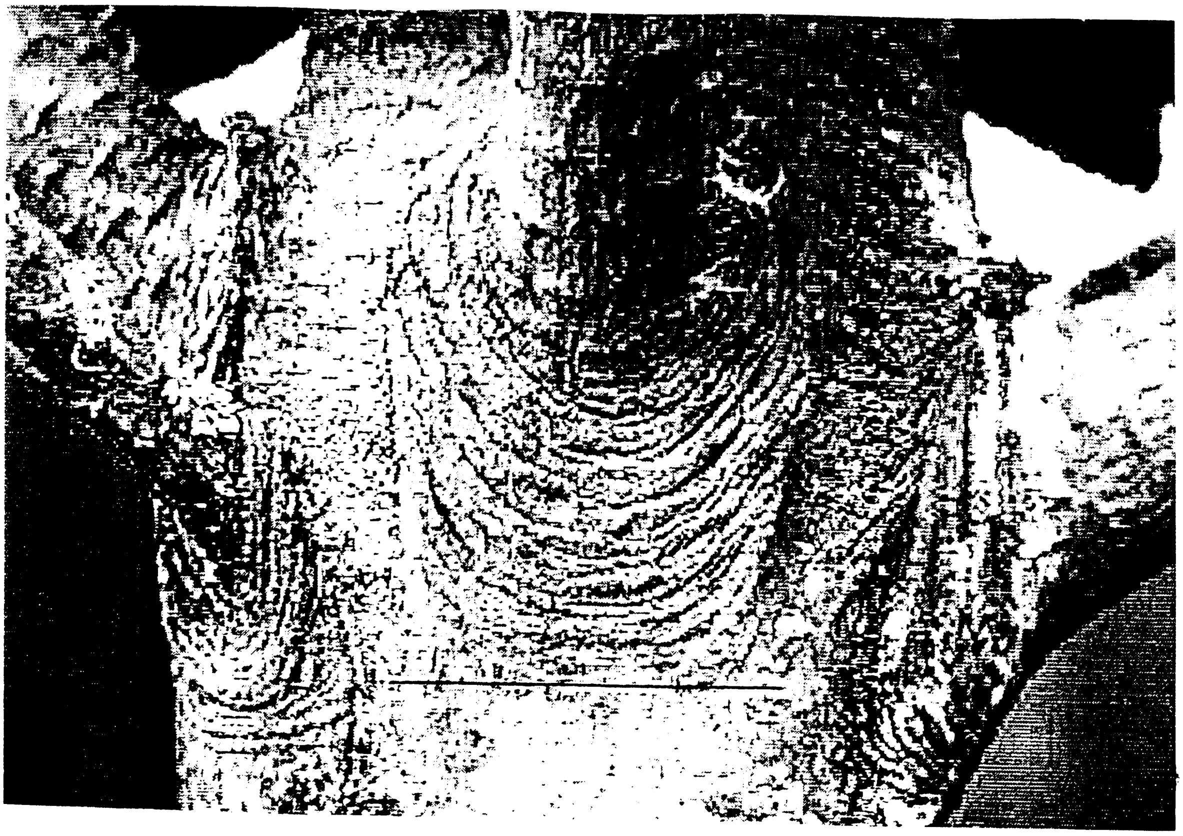


Figure 2. Diagram showing how a sample branch is cut from a stem disc.

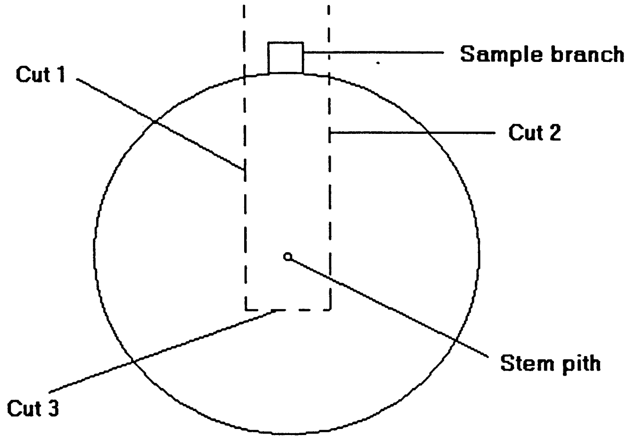
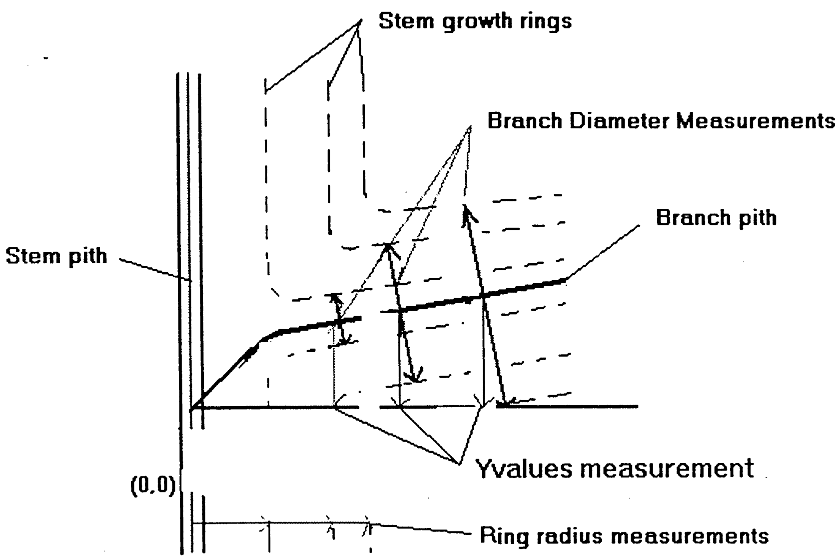


Figure 3. Diagram showing how the stem growth rings merge with the branch growth rings.



APPENDIX 1. FUNCTIONS WITHIN THE BRANCH GROWTH MODEL

A. Position of branch clusters along the stem

We have chosen to model the position of clusters within annual stem growth units as it allows us to utilise the extensive knowledge of annual height growth in radiata pine.

The first function with the model calculates:

the number of branch clusters within the annual shoot (1)

Knowing the number of branch clusters within the annual shoot, the models calculates:

the relative position of the branch clusters within the annual shoot (2)

B. Number of branches and stem cones within each cluster

Prior to reproductive maturity, a cluster contains only branches. After reproductive maturity, a cluster can contain only branches, branches and cones, or only cones.

For each cluster the model calculates:

the number of branches within each cluster (3)

the probability of stem cones occurring within the cluster (4)

If there are stem cones within the cluster, the model calculates:

the number of stem cones present (5)

C. The diameter of branches within each cluster

As it is relatively easy to observe the branch of largest diameter within a cluster in the field, it was decided to model branch diameter relative to the diameter of the largest branch. This approach means only the largest branch diameter would need to be recorded in an operational procedure. These measured values would be used in place of predictions from function 6.

The model therefore calculates:

the diameter of the largest branch within the cluster (6)

then it calculates

the relative diameter of the other branches within the cluster (7)

D. Azimuthal location of branches within clusters and between clusters

The azimuthal location of branches within and between clusters is important for determining what parts of the log can be used for different products. It is important to know whether the larger branches occur in the same azimuthal sector of the stem or whether they are distributed all round the stem.

The model contains two functions, one which calculates:

the azimuthal angle of branches in each cluster (8)

the other function calculates:

the azimuthal angle between largest branches in adjacent clusters (9)

E. Branch Development over time.

Several functions are needed to predict the size and location of the branch within the stem.

One function calculates:

the change in branch diameter over time (10)

A second function which calculates:

the vertical distance between the base of the branch and the current position of the branch pith. (11)

There are also functions to predict:

the occurrence of bark encasement due to mortality (12)

the occurrence of defect above the branch, not due to mortality (13)