CLONAL VARIATION IN THE QUALITY OF RADIATA PINE RANDOM WIDTH BOARDS

Robert Beauregard

Scientist
Forintek Canada Corp.
319 Franquet
Sainte-Foy, Qc G1P 4R4
Canada

Rado Gazo

Associate Professor
Purdue University
1159 Forestry Building
West Lafayette, IN 47907-1159
U.S.A.

Mark O. Kimberley

Research Scientist

John Turner

Research Scientist

Scott Mitchell

Research Scientist

and

Anthony Shelbourne

Research Scientist

Forest Research Institute
Private Bag 3020
Rotorua
New Zealand

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ABSTRACT

This clonal study was undertaken to analyze clonal variation in the quality of random width boards, and to document broad sense heritabilities of the board quality and the associated tree variables in radiata pine (*Pinus radiata* D. Don). Two individual trees from each of ten clones were selected based on a wide range of clone mean values for diameter at breast height (DBH), internode index, branch index, and outerwood basic density.

Several defect types and frequencies showed differences between clones; variation between clones was greater for defect frequencies than for defect areas. Also differences between clones were greater for boards from unpruned logs than from pruned logs. Knot frequency was far higher in boards coming from the clones with shorter internodes, while knot area per m^2 did not vary significantly between clones. Internode length appeared to be highly heritable. The blemish area per m^2 from pruned logs was highly variable between clones. Causes and exact configuration of this latter defect are largely unknown and unpredictable but appear to be associated with pruning.

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Differences were observed in the grade distributions between clones. For all log types, the best performing clone was a large DBH clone with the longest internodes, while a small DBH clone with the shortest internode was the worst. These results show that defect frequency and grades in appearance lumber and associated tree characteristics show high broad sense heritability. This suggests that the grades and the value of these products can be predicted, particularly from tree internode index. A breeding program for long internode radiata pine, started in 1970, has already shown that this trait responds well to selection and breeding.

Keywords: *Pinus radiata,* clones, defect frequency, DBH, internode, random width boards

INTRODUCTION

The overall objective of this project is to optimize remanufacturing technologies to improve recovery from radiata pine (*Pinus radiata* D. Don) logs and enhance product values. Several types of questions are commonly asked when discussing these issues with people involved in breeding, growing, and processing radiata pine in New Zealand.

Tree breeders and growers both ask what tree characteristics are most important for specific products or markets. The tree breeders can modify these characteristics by selection of good families of seedlings or clones for planting; the growers can modify conditions and choose sites to improve the phenotypic expression of such traits in plantation stands. Tree growers additionally want to know which parts of the tree are most desirable for different products, with the aim of modifying these through thinning and pruning regimes.

Sawmillers want to know which sawing strategy is optimal to take advantage of every part of the tree (log height class, juvenile vs. mature wood) in terms of recovery and product value. Remanufacturers want to know what recovery yields they can expect, which processing method is most suitable for a specific order, what distribution of part sizes can be obtained from radiata pine boards of given characteristics, etc.

Random width boards were studied because there is a strong demand for this type of lumber from the United States millwork industry. Millwork is one of the growing radiata pine market segments. Millwork sales were predicted to increase by 56% in 1995 to NZ$ 64 million (NZ Forest Industries 1996). The United States is a major customer in this market, taking one quarter of all millwork lumber produced in New Zealand.

The present paper has the following objectives: 1. to analyze clonal variation in the quality of random width boards; 2. to document the broad sense heritability of tree variables that matter for this type of product; 3. to assess the broad sense heritability of the board attributes themselves.

To achieve these objectives, a computer database of digitized random width radiata pine boards was developed (Gazo et al. 1998). In the past, U.S. remanufacturers of hardwood lumber were able to answer questions about yield, processing methods, parts distribution, etc. using computer modeling tools that utilized databases of digitized lumber (Gatchell et al. 1993; Gazo and Steele 1995; Harding et al. 1993; Steele and Gazo 1995; Steel et al. 1994).

METHODOLOGY

Sample material

A large proportion of the future forest establishment in New Zealand will be from progeny of the best seed orchard clones. This select group of parents is different in terms of growth and form from that currently being utilized by industry. It is known that intrinsic wood properties vary widely between clones; we actually know, for example, how wood density and branch cluster frequency vary in different seed orchard seedlots. Little is known, however, about how this variation can be used to any advantage during solid wood processing.

The trees selected for these studies were required to show a range of qualities typical of the crop being harvested now and in the near

future. An additional requirement was the need to sample matching stems for various processing pathways to be investigated, particularly Saw-Dry-Rip and cant sawing. A unique early clonal test in Compartment 1350 of Kaingaroa Forest, located in Central North Island of New Zealand, planted in 1968, had the capability of providing several stems of the same genotype (clones). This stand had the required characteristics for the study, i.e., it was sufficiently large and mature.

The clonal trial was established with 216 clones that had been selected for high wood density; 500 trees were originally selected at a low intensity for vigor and freedom from forking from two Kaingaroa Forest compartments (Cpt 1296, age 6 and Cpt 1301, age 5 from planting), and their density was assessed via increment cores. The lower density half of this group were discarded and cuttings collected from the remainder. These compartments had been planted with "felling select" seedlots with GF rating of about 3. The GF index is indicative of the gain in growth and form obtained from the genetic improvement program when comparing with the original radiata pine stock. A GF index of 3 corresponds to the level of genetic improvement obtained in the early sixties. The clonal test was established with 216 clones in June 1968, consisting of open-rooted 1/1 cuttings. The mean of the higher density ortets, the parent material from which clones are vegetatively propagated, was 331 kg/m^3 versus the mean of all 500 trees of 331 kg/m^3. One hundred seventy-five of the faster growing clones still remain and of these, 46 clones had adequate replication for study purposes. Tree selection excluded the smaller stems (DBH < 300 mm).

At the time of sampling, the stand was aged 27 years. Silvicultural treatment was: establishment at 1,370 stems per hectare (spha); waste thinning initially to 700 spha (7 yr) and later (13 yr), to a nominal stocking of 350 spha with a two-lift pruning to 4 m. The regime described is not representative of usual forest practice, but facilitated attainment of research priorities while maintaining tree growth

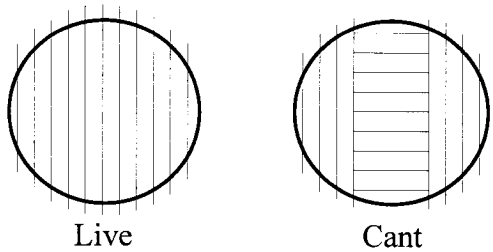

FIG. 1. Live and cant sawpatterns.

and form. Nevertheless, according to the FRI-Permanent Sample Plot database (Dunlop 1995), the average final stocking in Kaingaroa forest at the time was 318 spha and ranged from 30 to 1,492 spha, which points to a wide variation in silvicultural regimes.

Ten of the 46 available clones were selected to cover a range of diameter at breast height (DBH), internode length, branch size, and outerwood density at breast height. Since they do cover the range of tree characteristics, the selected clones are believed to be representative of the main body of the population as well as of more extreme values of stem parameters present in current plantations.

In November 1995, at age of 27 years, two replications (trees) of each of the 10 selected clones were harvested, resulting in a total of 20 trees. The two replications were needed so that each clone could be processed by two different sawing strategies (live and cant).

Log making and sawing.—Four logs were cut from each tree; these included the pruned butt log, the second log, one intermediate log, and the top log. The butt logs were on average about 4 m long, and the rest of the logs were about 4.9 m long. A top log from one tree was not suitable for sawmill processing, since it was too small and crooked, and one extra intermediate log was taken from two trees. This resulted in 20 butt logs, 20 second logs, 22 intermediate logs, and 19 top logs—a total of 81 logs.

The first 40 logs (one tree from 10 clones) were live-sawn into boards 40 mm thick (Fig. 1). This method targets the U.S. 5/4-inch random width shop boards. The second 41 logs

(second replicate set of 10 clones) were cant-sawn by flat sawing 40-mm boards leaving the central cant. Logs with small end diameter between 200–300 mm were sawn with a 100-mm cant and larger logs with a 200-mm cant. The cants were reduced to 100 × 40-mm Australian structural stock before drying. One butt log was of inferior quality and did not yield any random width boards. This log was excluded from further analysis.

As shown in Fig. 1, the cant-sawn logs did not yield any random width boards from the "cant" zone of the log, as the cants were immediately processed into structural lumber. Therefore, the random width boards that came from the same "cant" zone of live-sawn logs were excluded. Considering only the random width side boards provided a sample of two replicates (trees) per clone with comparable wood characteristics, which allowed analysis of the variation between clones, without the confounding effect of the sawpattern.

The logs were processed in Vanner Sawmill at Reporoa, New Zealand. Processing of these 81 logs resulted in 392 random width boards. From these, 259 were side boards and were retained for the analysis of variation between and within clones. All boards were dried in a commercial dry kiln on a high temperature schedule (120°C) and surfaced on both faces.

Board digitizing.—All boards were then digitized. Digitizing consisted of recording the board dimensions (width and length), defect positions, and defect types, according to an *xy* coordinate system, for each face of the board. The board digitizing methodology is described in Gazo et al. (1998).

Defect types were organized into nine categories: intergrown knot; partially intergrown knot; loose knot/hole; spike knot; pith; bark pocket/blemish; resin pocket; needle fleck; wane. For the proper identification of the defects, the definitions, from New Zealand Ministry of Forestry (1994), were used.

The information about the clone, tree, log height class, board location within a log, sawpattern, board grade, board dimensions, defect types, and locations were entered in a computer database (Gazo et al. 1998).

The database includes: number of boards, board width and length, board volume, the location and type of each defect. The following information is derived from the database: board area, defect area, percent of clear area, count of the nine defect types, and cumulative area of each type.

Board grading.—The lumber exported to the United States for remanufacture is graded using the Western Lumber Grading Rules (WWPA 1991). The lumber is graded according to the potential recovery of clear cuttings. As the boards are intended for subsequent remanufacturing into door and window frames, moulding and millwork items, individual cuttings must also satisfy size and quality criteria. This grading rule allows for the following lumber grades: Mouldings, Factory Select, No. 1 Shop, No. 2 Shop, No. 3 Shop, and Finger Joint Common Shop.

Prior to digitizing, all the boards were graded according to the Western Lumber Grading Rules by an experienced grader. After the computer database was constructed, the boards were regraded by a computer grading program FLGRADE (Todoroki 1995). The computer results were compared to manual grading. In case of disagreement, the boards were checked and a correct grade was assigned. This procedure was done to assign the best possible grade to each board.

Tree characteristics

Some tree or clone traits are known to impact on the quality of random width boards. Gazo et al. (1998) showed that diameter at breast height (DBH), branch index (BIX), and internode index (IIX) can be used to predict one or another of the random width board characteristics. These variables were measured on each ramet, the replicas, of each clone and their variation was analyzed between and within clones.

The DBH of each tree was recorded in mm. The BIX is the average size of four branches

per quadrant per log, using the largest branch in each quadrant (Whiteside and Manley 1987). The IIX is the sum of lengths of internodes of 0.6 m or longer, expressed as a fraction of the log length (Whiteside and Manley 1987). The BIX and IIX were evaluated for each log and averaged on a per tree basis. When the trees were cut into logs, the dimensions of each log were recorded (small end, large end diameters, and length). The tree volume was then calculated using the sum of log volumes from each tree.

Incidence of defects and clear wood

In order to analyze the occurrence of defects in random width radiata pine lumber, two variables were considered: frequency and average area of the defects. The defect frequency is defined as the number of occurrences of a defect per m^2 of board surface area, and computed on a per tree basis. The number of defects of each type for each board was recorded and divided by the board surface area of each tree. Frequency of defects was calculated for all defect types except wane, as this can be found on every random width board.

The defect area is defined as the area of a defect type, in cm^2 per m^2 of board, on a per tree basis. The average defect area was calculated for all the defect types, including wane and void. The total defect area per defect type was calculated for each tree. This defect area was then divided by the total board surface area of that tree. Because the centerboards were not analyzed, the pith defect does not appear in the analysis. When calculating frequency and area of the defects, only defects on the worst face were considered.

Percentage of the clear surface area was calculated as the ratio of board clear area (board surface area minus total defect area) to board surface area.

Statistical methods

Tree and clonal averages of tree attributes and defect incidence were calculated by weighting values from individual logs by their relative volumetric contribution. The analysis of variance was used to test differences between clones versus differences between trees within clones for the various traits. Then broad sense heritability (h^2) was estimated using the following relationship:

$$h^2 = \sigma^2_c/(\sigma^2_c + \sigma^2_e)$$

where σ^2_c is the variance among clones and σ^2_e is the variance between trees within clones or the environment variance. The significance of this broad sense heritability is tested against the null hypothesis.

TABLE 1. *Tree characteristics by clone.*

Clone no.	Tree	DBH (cm)	BIX (mm)	HX (%)	Volume (m^3)
1	1	51.5	47.7	12	3.090
	2	50.7	50.0	17	3.002
2	1	48.0	46.7	64	2.584
	2	48.0	49.3	54	2.447
3	1	61.2	47.9	11	5.011
	2	62.1	56.5	3	5.517
4	1	42.5	35.2	17	2.092
	2	41.5	37.4	22	2.255
5	1	47.0	55.4	43	2.921
	2	46.5	53.3	51	2.951
6	1	41.8	31.8	14	2.325
	2	42.7	38.2	18	2.335
7	1	32.5	34.6	0	1.228
	2	32.9	30.7	0	0.932
8	1	45.3	40.2	13	2.532
	2	43.5	39.4	12	1.943
9	1	39.0	30.5	0	1.663
	2	36.5	36.1	0	1.512
10	1	60.0	63.8	58	3.886
	2	61.0	66.2	61	4.339

RESULTS

The external characteristics of each tree are summarized, by clone, in Table 1. Branch index and internode index are the arithmetic mean values over three logs (second, intermediate, and top); total volume is the volume of all logs. Clone size varies between 32.7 cm in DBH and 1.080 m^3 in volume for clone 7 to 61.6 cm and 5.624 m^3 for clone 3. A wide

TABLE 2. *Broad sense heritability of clonal traits related to defect incidence in random width boards.*

Clonal trait	Mean	σ^2_c	σ^2_e	h^2	*P*-value	Significance
Diameter breast height	467	8390	71	0.99	0.0001	**
Branch index	43.9	90.2	17.1	0.84	0.0003	**
Internode index	0.240	0.0540	0.0035	0.94	0.0001	**

range of variation can also be observed for BIX, from 32.6 mm for clone 7 to 65.0 mm for clone 10, and for IIX, from 0% for clone 7 to 59% for clones 2 and 10.

Broad sense heritability was calculated for: DBH, BIX, and IIX (Table 2). The extremely high heritability value obtained for DBH is explained by the fact that once the ten clones were identified, the two ramets, the independent members of each clone, were selected to have a similar DBH in order to detect differences between the two sawing methods. However, using the data from all available ramets, before screening, a more realistic heritability of 0.61 was calculated, which is still higher than expected because the clones were selected for a wide range of growth rate. Each two ramets were not selected further for uniformity of branch size or internode length.

The cant-sawn logs (Fig. 1) did not yield any random width boards from the "cant" zone of the log. The cants were immediately processed into structural lumber. Therefore, the random width boards, which came from the corresponding "cant" zone of live sawn logs, were excluded. These boards were not considered for the statistical analysis in order to provide a sample of two replicates (trees) per clone with comparable wood characteristics. This in turn decreased the variation between the replicates and increased the likelihood of establishing differences between trees of different characteristics. All trees in the trial were pruned, which results after felling and log making, into one pruned butt log and several unpruned upper height logs. Boards from pruned butt logs and from upper logs being very different, they were analyzed in different categories. This resulted in 259 boards, from 20 trees (2 ramets per clone), available for analysis. The volume of boards included in this analysis is of 10.45 m^3 (4,429 board feet). The distribution of the trees, logs, and boards by clone is shown in Table 3. There were fewer boards per clone of the pruned (average 8.4) than for unpruned logs (17.5), which affects the precision of estimates of clone mean defect frequencies and defect areas which in turn can affect their heritability estimates.

Variability of the incidence of defects

Defect frequency.—In boards from pruned logs, there were significant differences in the frequency of intergrown and partially intergrown knots between clones (Table 4), Clone 7, of very small DBH and the lowest IIX, had the highest frequency of both, with respectively 6.127 and 1.751 knots/m^2 of boards, while clone 5, an average DBH clone with a relatively long IIX, had the least with none of each. These differences in knot frequencies on boards from pruned logs reflect partly the tree characteristics but also, the interaction with the process itself. Logs with a small end diameter (SED) smaller than 300 mm were sawn with a 100-mm cant, while the others were sawn with a 200-mm cant. It is possible that some average size trees like the one from clone 5 were exactly the size allowing the cant to remove the entire defect core from the pruned logs. This suggests that the process should be optimized carefully for the pruned logs, but this was not the objective of this trial. Hence the clonal differences here must be interpreted in the context of the interaction between the tree characteristics and the process.

In the boards from unpruned logs, significant differences were also observed between intergrown knot and loose knot/hole frequen-

TABLE 3. *Number of random width boards by clone.*

Clone no.	Number of trees	Number of logs	Number of boards	Volume (m^3)	Volume (board feet)
Pruned logs					
1	2	2	9	0.366	153.3
2	2	2	8	0.333	140.9
3	2	2	17	0.713	302.2
4	2	2	6	0.163	69.2
5	2	2	8	0.260	110.3
6	2	2	7	0.239	101.4
7	2	1	3	0.073	30.7
8	2	2	7	0.259	109.8
9	2	2	5	0.153	64.9
10	2	2	14	0.632	268.0
Total	20	19	84	3.192	1,352.7
Unpruned logs					
1	2	6	18	0.722	306.0
2	2	6	14	0.580	245.9
3	2	6	27	1.309	554.7
4	2	6	13	0.451	191.3
5	2	6	18	0.685	290.1
6	2	6	13	0.499	211.5
7	2	5	12	0.385	163.2
8	2	6	16	0.628	266.2
9	2	7	13	0.449	190.1
10	2	7	31	1.551	657.2
Total	20	60	175	7.259	3,076.3

cies between clones. Again, clones 9 and 7 had the highest frequencies of intergrown knots with respectively 15.47 and 14.63/m^2, while clone 10 was the lowest with only 3.7 intergrown knot/m^2. This is in accordance with the tree characteristics from Table 1, showing that 7 is the clone with the smallest IIX and BIX, meaning it has more of smaller knots. In boards from unpruned logs, the frequency of the bark pocket/blemish category varies significantly between clones. This defect type varies between 4.08 blemish/m^2 for clone 4 and 0.54 blemish/m^2 for clone 2.

Broad sense heritability values for the defect frequencies are shown in Table 5. It appears that knot frequencies on random width boards, from the sides of unpruned logs, generally show genotype differences, strongest in the case of intergrown knots, which are by far the most frequent knot type. Needle fleck also shows a strong genotype effect in the case of boards from pruned logs. In fact, this result again has more to do with the size of the clones, which shows high heritability and which interacted with the sawpattern to exclude or not the zone where needle fleck appears in pruned butt logs. The bark pocket/blemish category also shows a relatively high heritability in the boards from unpruned logs, although only marginally significant in boards from pruned logs. This suggests that radiata pine could be selected against this defect type, although we know very little about what causes it.

Percentage of clear wood area and average defect area.—Table 6 displays the variation of clear wood and defect areas by defect type among the clones. The proportion of clear wood from pruned butt logs does vary significantly between clones; at the two extremes, clone 7 yields 59.5% and clone 5, 85.2% of clear wood. The main reason for the difference in clear wood percent is to be found in the area of wane/void where a similar pattern of

TABLE 4. *Frequency of defects in side boards from pruned and unpruned logs by clone.*

Clone no.	Defect frequency (number of defects/m² of boards)						
	Intergrown knot	Partially intergr. knot	Loose knot/ hole	Spike knot	Bark pocket/ blemish	Resin pocket	Needle fleck
Pruned logs							
1	0.78	0.17	0.45	—	2.75	0.00	0.000
2	1.04	0.19	0.17	—	0.95	0.00	0.000
3	0.69	0.52	0.24	—	2.01	0.65	0.079
4	0.15	0.15	0.00	—	1.78	0.00	0.417
5	0.00	0.00	0.00	—	0.60	0.00	0.000
6	0.58	0.81	0.39	—	0.70	0.16	0.000
7	6.13	1.75	0.00	—	3.04	0.44	0.438
8	0.49	0.12	0.12	—	1.10	0.73	0.000
9	0.86	0.26	0.52	—	0.69	0.00	0.000
10	0.39	0.10	0.00	—	0.45	0.00	0.049
ANOVA	$P = 0.01$ **	$P = 0.01$ **	$P = 0.58$		$P = 0.08$	$P = 0.19$	$P = 0.0008$ **
Average	0.85	0.34	0.20		1.37	0.19	0.080
Unpruned logs							
1	8.20	2.15	2.76	0.04	3.23	0.06	0.00
2	5.01	1.52	0.45	0.00	0.54	0.00	0.00
3	4.98	2.08	1.90	0.02	3.13	0.03	0.28
4	8.44	2.15	2.09	0.00	4.09	0.00	0.00
5	6.37	1.66	1.83	0.09	1.34	0.00	0.25
6	5.92	2.77	4.12	0.05	1.33	0.00	0.00
7	14.63	3.39	4.42	0.06	1.75	0.12	0.06
8	5.31	3.82	3.93	0.00	1.55	0.00	0.00
9	15.47	2.26	1.32	0.17	1.69	0.00	0.06
10	3.70	1.17	0.62	0.00	1.09	0.04	0.18
ANOVA	$P = 0.0006$ **	$p = 0.28$	$P = 0.005$ **	$P = 0.74$	$P = 0.03$ *	$P = 0.59$	$P = 0.29$
Average	7.804	2.295	2.346	0.043	1.973	0.024	0.083

variation is observed, which is due mainly to process-related, geometric constraints. Small clone size combined with higher taper causes higher proportions of void (Gazo et al. 1998). In boards from pruned logs, the area of intergrown and partially intergrown knots is only marginally variable between clones, with again clone 7 tending to produce larger areas of knots and clone 5 presenting none. Also in boards from pruned logs, the area of bark pocket/blemish varies among clones with, at the two extremes, clone 1 producing 45 cm²/m² of boards and clones 9 and 10 producing only around 1 cm²/m².

In boards from unpruned logs, no significant differences can be observed in defect area between clones for any defect except needle fleck, where differences can be explained by the relationships between the tree geometry and saw patterns used. Needle flecks tend to be absent outside the inner two to four growth rings (Kininmonth and Whiteside 1991). In the case of larger trees, being of the same age as smaller trees, these four inner rings occupy a wider zone inside the log and are likely to show outside the center zone that is excluded in this analysis.

The only area trait showing an appreciable board sense heritability is the area occupied by the bark pocket/blemish defect type in boards from pruned logs (Table 7). The only other traits showing high heritability values (clear wood percent and wane/void in boards from pruned logs and needle fleck in boards

TABLE 5. *Broad sense heritability of the defect frequencies in side boards from pruned and unpruned logs.*

Defect type	Mean	σ^2_c	σ^2_e	h^2	*P*-value	Significance
Pruned logs						
Intergrown knot	0.849	0	0.448	0.00	0.923	n.s.
Partially intergrown knot	0.338	0.030	0.068	0.30	0.185	n.s.
Loose knot/hole	0.198	0	0.084	0.00	0.536	n.s.
Spike knot	—	—	—	—	—	—
Bark pocket/blemish	1.369	0.258	0.708	0.27	0.216	n.s.
Resin pocket	0.186	0.045	0.093	0.33	0.167	n.s.
Needle fleck	0.080	0.016	0.005	0.78	0.002	**
Unpruned logs						
Intergrown knot	7.804	15.027	3.347	0.82	0.001	**
Partially intergrown knot	2.295	0.216	0.924	0.19	0.279	n.s.
Loose knot/hole	2.346	1.688	0.689	0.71	0.005	**
Spike knot	0.043	0	0.007	0.00	0.738	n.s.
Bark pocket/blemish	1.973	0.893	0.737	0.55	0.034	*
Resin pocket	0.024	0	0.003	0.00	0.591	n.s.
Needle fleck	0.083	0.004	0.017	0.18	0.287	n.s.

from unpruned logs) reflect differences between clones in diameter growth and thus are artifacts of geometry.

Grade distributions

The grade distribution yielded by each clone was computed on a "grade and better" basis. For boards from both pruned and unpruned logs, significant differences between clones appear only for the lower grades, mainly because the very few boards represented in the highest grades provide an inadequate sample to characterize a clone. The precision of estimate of frequencies of boards in any one grade would have been improved by sawing additional trees in each clone. Also there are only two pruned logs per clone versus six unpruned logs and on average 8.4 versus 17.5 boards per clone, respectively.

On boards from pruned logs, a significant difference in grade yield was observed between the clones for the "No. 3 Shop and better" and "Finger Joint and better" categories. In the "No. 3 Shop and better" category, the best were clones nos. 1, 5, 6, and 10 and the worst was by far clone No 7. The difference between the best and worst performing clones was 71%.

In the boards from unpruned logs, there was also a significant difference between clones for the "No. 1 Shop and better", "No. 2 Shop and better" and "No. 3 Shop and better" levels. The "No. 2 Shop and better" grade being the middle of the grading range, it can be used to characterize clones for grade performance. For that category, the best clones were nos. 10 and 2 and the worst was no. 9. The difference between the best and the worst was 78%. In all cases, clone 10, a large DBH clone with the longest internodes (Table 1), was among the best performing clones while clone 7, a small DBH clone with the shortest internodes, was the worst.

For pruned logs the heritability values (Table 8) are generally low and nonsignificant, reflecting the inadequate board sample size for these logs. For unpruned logs, very high heritabilities were evident for "No. 2 and No. 3 Shop and better" indicating that selection of clones for high yields of U.S. random width boards would be feasible. This result would probably hold true for any other type of appearance grade where the production of clear

TABLE 6. *Clear wood percent and defect areas in side boards from pruned and unpruned logs by clone.*

Clone no.	Clear wood area (%)	Defect area (cm^2/m^2)							
		Intergrown knot	Partially intergr. knot	Loose knot/ hole	Spike knot	Bark pocket/ blemish	Resin pocket	Needle fleck	Wane/ void
Pruned logs									
1	79.78	11.57	0.53	2.52		44.90	0.00	0.00	1,962.41
2	78.06	7.51	1.25	0.12		7.56	0.00	0.00	2,177.69
3	76.81	3.87	7.53	8.08		18.98	8.12	193.81	2,078.97
4	78.30	0.64	0.10	0.00		4.42	0.00	134.85	2,030.30
5	85.24	0.00	0.00	0.00		2.42	0.00	0.00	1,473.95
6	78.17	2.36	11.76	2.08		8.56	5.28	0.00	2,153.30
7	59.52	34.52	15.63	0.00		13.48	0.34	201.47	3,782.76
8	74.41	7.39	0.59	0.96		2.48	3.00	0.00	2,543.89
9	68.67	1.77	1.47	0.72		1.42	0.00	0.00	3,127.69
10	81.94	0.94	0.98	0.00		1.43	0.00	5.27	1,797.25
ANOVA	$P = 0.006$ **	$P = 0.06$	$P = 0.06$	$P = 0.62$		$P = 0.01$ **	$P = 0.62$	$P = 0.46$	$P = 0.01$ **
Average	76.96	5.66	3.37	1.52		10.41	1.74	45.75	2,235
Unpruned logs									
1	74.64	148.62	47.33	25.81	0.23	13.62	0.37	0.00	2,300.42
2	75.70	104.90	18.78	5.48	0.00	5.05	0.00	0.00	2,305.47
3	74.34	99.80	45.66	23.23	0.34	12.80	0.08	488.49	1,995.49
4	75.30	87.70	30.58	22.78	0.00	17.05	0.00	0.00	2,312.33
5	70.69	129.01	68.36	18.45	5.38	21.04	0.00	122.47	2,566.24
6	80.63	87.84	43.99	26.54	0.94	4.03	0.00	0.00	1,774.15
7	72.50	159.14	25.32	26.42	0.90	5.08	0.09	41.06	2,491.78
8	77.89	70.52	58.77	15.93	0.00	8.37	0.00	0.00	2,057.43
9	76.19	174.12	29.33	4.35	2.93	7.24	0.00	43.33	2,120.15
10	79.66	121.57	30.81	3.39	0.00	4.62	0.15	1.29	1,744.64
ANOVA	$P = 0.47$	$P = 0.42$	$P = 0.42$	$P = 0.15$	$P = 0.64$	$P = 0.51$	$P = 0.54$	$P = 0.002$ **	$P = 0.57$
Average	75.74	118.3	39.89	17.24	1.07	9.89	0.07	82.43	2,156.81

TABLE 7. *Broad sense heritability of clear wood and defect area, on side boards, from pruned and unpruned logs.*

Clear wood and defect type	Mean	σ^2_c	σ^2_e	h^2	*P*-value	Significance
Pruned logs						
Clear wood proportion	76.96	15.6	11.9	0.57	0.036	*
Intergrown knot	5.66	0	46	0.00	0.130	
Partially intergrown knot	3.37	8.9	16.1	0.36	0.144	
Loose knot/hole	1.52	0	14.4	0.00	0.560	
Bark pocket/blemish	10.41	165	69.1	0.70	0.008	**
Resin pocket	1.74	0	19.4	0.00	0.558	
Needle fleck	45.75	1,240	8,360	0.13	0.352	
Wane/void	2,235	149,000	139,000	0.52	0.054	
Unpruned logs						
Clear wood proportion	75.74	0.41	17.72	0.02	0.468	
Intergrown knot	118.3	143	2,046	0.07	0.418	
Partially intergrown knot	39.89	30	431	0.06	0.418	
Loose knot/hole	17.24	45	90	0.33	0.147	
Spike knot	1.07	0	7	0.00	0.636	
Bark pocket/blemish	9.89	0	71	0.00	0.509	
Resin pocket	0.07	0	0.0297	0.00	0.537	
Needle fleck	82.43	20,040	5,670	0.78	0.002	**
Wane/void	2,157	0	176,871	0.00	0.571	

TABLE 8. *Broad sense heritability of the grade distribution of side boards from pruned and unpruned logs.*

Grade and value	Mean	σ^2_c	σ^2_e	h^2	*P*-value	Significance
Pruned logs						
Moulding	18.74	31.3	486.6	0.06	0.427	n.s.
Factory select and better	21.17	186.8	427.6	0.30	0.184	n.s.
No. 1 Shop and better	43.60	292.5	620.5	0.32	0.171	n.s.
No. 2 Shop and better	83.07	0	290.9	0.00	0.623	n.s.
No. 3 Shop and better	90.51	0	146.7	0.00	0.721	n.s.
Finger jointing and better	97.90	0	0.755	0.00	0.494	n.s.
Unpruned logs						
Moulding	—	—	—	—	—	—
Factory select and better	1.18	0	27.8	0.00	0.495	n.s.
No. 1 Shop and better	3.04	28.9	29.8	0.49	0.054	n.s.
No. 2 Shop and better	26.28	642.0	138.3	0.82	0.001	**
No. 3 Shop and better	48.28	680.1	117.1	0.85	0.000	**
Finger jointing and better	81.28	84.4	260.6	0.24	0.224	n.s.

wood would matter and where a premium would be given to long clears.

This has practical implications for the tree breeder and the forester using the clones. It tells us which characteristics to seek for producing high grade random width lumber for millwork applications. Basically, trees bred for size and long internode produce significantly higher proportions of high grade factory lumber. Size and internode length are heritable, and the resulting yield in high grade lumber is as well.

CONCLUSIONS

The main objective of this report was to analyze clonal variation and broad sense heritability of the random width board traits and of the tree characteristics themselves that have a bearing on these types of products. There were greater differences between the clones in the boards from unpruned logs than in boards from pruned logs. The frequencies of several types of defects differed between clones, particularly knot and bark pocket/blemish frequencies, and showed moderate to high broad sense heritability, indicating possibilities for selection against them. Differences were much less between clones for defect areas, except notably the area of bark pockets and blemishes in boards from pruned logs.

The grading results of the boards provide a useful summation of defect incidence. Differences were observed in the grade distributions between clones. In all log types, clone 10, a large DBH clone with the longest internode, was among the best performing ones while clone 7, small DBH with the shortest internode, was the worst one. For pruned logs, heritability values were low and nonsignificant, reflecting the inadequate board sample size for these logs. For unpruned logs, very high heritabilities were evident indicating that selection of clones for high yields of U.S. random width boards would be feasible.

In our analysis, differences between clones for different traits were often nonsignificant but marginal. This was probably due to small sample size of boards per tree possibly combined with an insufficient spread of tree characteristics. It would probably be worth examining more clones because more clones would allow quantification of these relationships more reliably. Also in selecting clones for clonal forestry and breeding, large numbers of clones would need to be evaluated to get good gains, and external tree morphological traits would be the first basis for such selection. Thus predictive relationships between these and appearance lumber grade distributions are needed.

The study so far leaves many questions unanswered. It was based on the grading rules for the U.S. random width boards. This tells us very little about the behavior of this wood in use. The lumber produced by this trial has been stored, and it is planned later to remanufacture it into generic products (long clears, finger-joined clears, and edge-glued panels) to evaluate their behavior in use. They should at least be assessed for stability in use through cycles of moisture content. The relationships between the clones' intrinsic wood properties such as density, spiral grain, and microfibril angle (which have been measured on these clones) and the behavior of the products would be of utmost importance. These relationships will provide additional guidance to a breeding program that would aim at producing appearance or millwork lumber.

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