DIFFERENCES IN GROWTH AND WEIGHT OF GENOTYPES OF PINE WITH SPECIAL REFERENCE TO CLONES OF PINUS RADIATA

H. A. I. MADGWICK

Forest Research Institute, New Zealand Forest Service,
Private Bag, Rotorua, New Zealand

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ABSTRACT

The correlations between tree height, diameter at breast height (1.4 m), number of branch clusters, number of branches, and branch basal area for nine New Zealand clones of **Pinus radiata** D. Don. were all positive, and similar to those found for six clones in Australia. While clones could, therefore, be graded according to size, principal component analysis indicated that there was a range of "branchiness" within a given size. Current branch basal area increment per unit stem basal area increment was broadly similar for all nine New Zealand clones. Distinct differences among clones in the relationship of total branch basal area to stem basal area indicated that past growth rates of these two parameters must have been different, while slight differences among clones, if maintained, would lead to different relative rankings in the future.

Principal component analysis of component weights of genotypes of **P. radiata**, **P. elliottii** Engelm., **P. taeda** L., and **P. virginiana** Mill. suggested that genotypes could be rated in terms of both over-all size and relative branchiness. For these four species there was little indication that increasing the fraction of wood plus bark growth allocated to stems increased total stem production. However, this conclusion could reflect the relatively open-grown condition of the trees.

INTRODUCTION

Genetic variability in growth of trees, as measured by changes in height and diameter, has been widely studied. Such variation could result from a variety of causes, such as differences in photosynthetic efficiency and allocation of dry matter produced (Evans 1975). Genetic variability of tree component weight is less well understood. Forrest & Ovington (1971), working with six clones of *Pinus radiata* found that there were positive correlations between clone mean values of tree height, diameter at breast height, mean branch diameter, number of branch clusters, and number of branches per tree. They found that the relationships between individual branch constituent weights and branch basal diameter were not significantly different among clones (p not less than 10%). However, the wide variation in numbers of branches and average branch size among clones resulted in significant differences

($p = 0.01$) in the relationship between total crown weight and diameter at breast height for the different clones. Mathews *et al.* (1975) and Thompson (1976) demonstrated intra-specific variability in dry-matter allocation in *P. virginiana* and *P. contorta* Loud. while data on other *Pinus* species are available from van Buijtenen (1978) and Pope (1979). Cannell (1974) working with provenances of *P. contorta* and *Picea sitchensis* (Bong.) Carr. found that differences in the production of stem wood were related to the numbers of lateral branches produced. Roberts & Wareing (1975a) found that growth of *Pinus contorta* seedlings was related to needle production but that of *P. sylvestris* L. (1975b) to net assimilation rate.

Elucidating the complex of genetic factors affecting dry matter production of forest trees is difficult owing to the logistical problems of measurement and the intercorrelation among variables. The purpose of this study was to examine the underlying structure of data on, and related to, dry weight of genotypes of a variety of *Pinus* spp. New data are given for nine clones of *P. radiata* in New Zealand and compared with those from *P. radiata* in Australia (Forrest & Ovington 1971). Examination of genetic variability in tree biomass reported for this and other *Pinus* species (Matthews *et al.* 1975; van Buijtenen 1978) allows some general conclusions to be derived.

METHODS

New data were collected on 54 trees of *P. radiata* comprising six replicates of nine clones used to study the seasonal biomass changes of a young stand *(see* Madgwick (1983) which also contains a detailed site description). The clones were FRI No. 448, 450, 451, 454, 455, 456, 457, 459, and 460. At 4 years from planting the trees were measured for height, diameter at breast height, and the diameter of each branch 2.5 cm from the stem. At that time only a few very small branches at the base of the trees had died. The trees were remeasured 11 months later. During this interval a total of 288 sample branches was removed from 36 of the trees in eight, separate, stratified random samplings. Total branch basal area per tree was calculated at the beginning and conclusion of the 11-month period. For the final measurement date the basal area of sampled branches was taken as their basal area at time of sampling. Branch basal area accounted for 91%, 87%, and 85% of the variance of weight of branch bark, branch wood, and branch needles, respectively, when all 288 sample branches were combined. Since Forrest & Ovington (1971) found no significant differences among clones in branch diameter-weight relationships and as clones accounted for only a very small proportion of the variation in individual branch weight given branch size in the present sample, branch basal area was chosen as a variable for analysis rather than estimated weight. This approach is justified since branch constituent weights were proportional to branch basal area and the effects of clone were negligible in reducing error mean squares.

In addition, 22 other 4-year-old trees representing seven of the clones were measured and felled. Each tree was separated into the following components: stem wood, stem bark, live (needle-bearing) branches, dead branches, and foliage. Oven-dry weight was obtained after drying at 65°C to constant weight. Practically no loss of woody dry matter had occurred through death and so weights of stem and branch wood and bark represented total above-ground production to the time of sampling.

RESULTS

Remeasured Trees

Clones differed in each of the size characteristics measured (Table 1). These were all positively inter-correlated, with correlation coefficients ranging from 0.68 to 0.90 (Table 2). Similar results were obtained from *P. radiata* data of Forrest & Ovington (1971) and correlation coefficients calculated using the data for their "1961 block" are included in Table 2 for comparison.

TABLE 1—Mean, minimum, and maximum clonal values of height, diameter at breast height, number of clusters, number of branches, and branch basal areas per tree, based on nine clones of **P. radiata** with F ratio based on the six replications per clone (F for 1% level = 3.0)

Variable	Age (yrs)	Mean	Min.	Max.	F ratio
Height (m)	4	3.7	3.2	4.3	3.3
	5	5.5	4.8	6.3	3.7
d.b.h. (cm)	4	4.7	3.3	5.5	3.9
	5	6.4	4.3	7.7	4.3
No. of clusters	4	8.3	7.0	10.7	7.1
	5	10.8	9.0	14.5	7.0
No. of live branches	4	39.5	30.5	54.0	3.7
	5	51.3	39.8	77.0	7.1
Branch basal area (cm^2)	4	33.8	19.0	47.7	3.2
	5	50.8	24.8	71.9	3.8
Total No. of branches	5	70.2	51.3	105.0	7.9

TABLE 2—Correlation coefficients among clone mean values for nine New Zealand clones (upper right triangle) and six Australian clones (Forrest & Ovington 1971) (lower left triangle)

	Variable				
	Height	d.b.h.	No. of clusters	No. of branches	Branch basal area
Variable					
Height	—	0.90	0.82	0.83	0.77
d.b.h.	0.96	—	0.69	0.71	0.89
No. of clusters	0.48	0.26	—	0.90	0.68
No. of branches	0.74	0.57	0.82	—	0.77
Branch basal area	0.91	0.98	0.16	0.54	—

The sizes of the New Zealand clones at age 5 years were similar to those for the Forrest & Ovington trees in their "1961 block". When analysed using principal component analysis both sets of data yielded similar results. The first component accounted for 73% and 84% of the variation in the Australian and New Zealand data, respectively, and the first component had high positive loadings on each variable (Table 3) indicating the importance of the general "size" variation among clones. The second component accounted for 90% and 59%, respectively, of the remaining variation in the two data sets. In both sets the loadings on the variables indicated a similar pattern with positive values for branch and cluster numbers and negative values for tree height, diameter at breast height, and total branch basal area. Thus, this second component reflected relative "branchiness". Plotting values of the second components against the first component for both Australian and New Zealand data indicates the relationships among clones (Fig. 1). Of the New Zealand clones, 451 was the largest in height and diameter while Clone 457 was the smallest and their difference in over-all "size" is indicated by having maximum and minimum values of Component 1, respectively. However, they had very similar numbers of branch clusters per metre of stem (2.2 and 1.9, respectively) and very similar values of Component 2 representing "branchiness". In contrast, Australian clones 602A and 954 were 4.4 and 4.0 m tall but carried the minimum and maximum branch clusters per metre of stem, respectively, for the Australian clones (1.7 and 2.6). These two clones had similar values of the "size" component but very different values for the "branchiness" component. The variability among clones for "size" was greatest for the New Zealand clones while the variability for "branchiness" was greatest for the Australian sample.

TABLE 3—Eigenvalues and loadings from principal component analysis of tree size data based on nine New Zealand clones and the six Australian clones of Forrest & Ovington (1971)

	Component 1		Component 2	
	Australian	New Zealand	Australian	New Zealand
Eigenvalue	3.64	4.18	1.22	0.48
Variable				
Height	0.98	0.94	–0.12	–0.03
d.b.h.	0.92	0.92	–0.38	–0.35
No. of clusters	0.58	0.89	0.80	0.40
No. of branches	0.84	0.92	0.48	0.30
Branch basal area	0.89	0.90	–0.44	–0.31

Plotting mean clonal values of branch basal area against stem basal area at ages 4 and 5 (Fig. 2) indicates that there was a general decline in the ratio of branch to stem basal area from an average of 1.87 to 1.52. There are differences in the amount of branch basal area per unit of stem basal area among clones and the ranking of clones

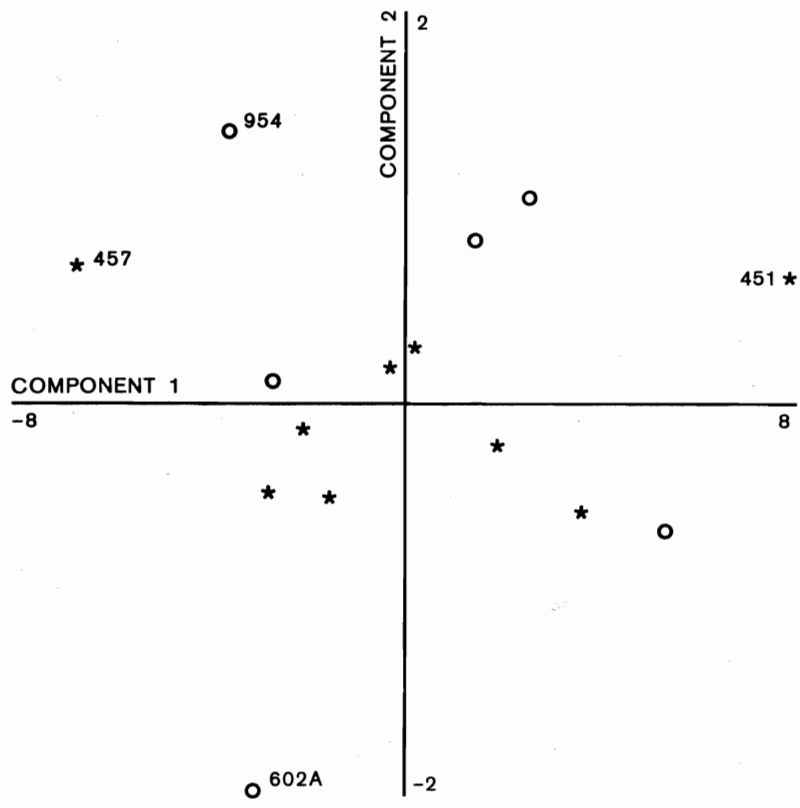

FIG. 1—Component 1 ("size") plotted against Component 2 ("branchiness") for six Australian (O) and nine New Zealand (*) clones of **Pinus radiata**. Numbers by plotted data are clone numbers referred to in text.

changed little. There is a broad similarity among clones in the slope of the lines joining the values for the 4- and 5-year-old trees, indicating that there is a similarity in current branch basal area increment per unit of current stem basal area increment but not in earlier growth.

Weighed Trees

The weights of the components of the seven clones destructively sampled also showed positive correlations (Table 4). Comparable information for the Australian clones is not available since Forrest & Ovington (1971) did not sample stems. However, foliage and branch wood plus bark can be estimated for their clones and this has been done by assuming that total crown weight was equivalent to sample component weight multiplied by the ratio of total branch basal area to sample branch basal area for each clone. Comparable correlations based on family means for 20 *P. virginiana* (Matthews *et al.* 1975), 15 *P. taeda,* and 9 *P. elliottii* (van Buijtenen 1978) are also shown Table 4. All correlation coefficients were positive, again stressing the over-all "size" difference among genotypes.

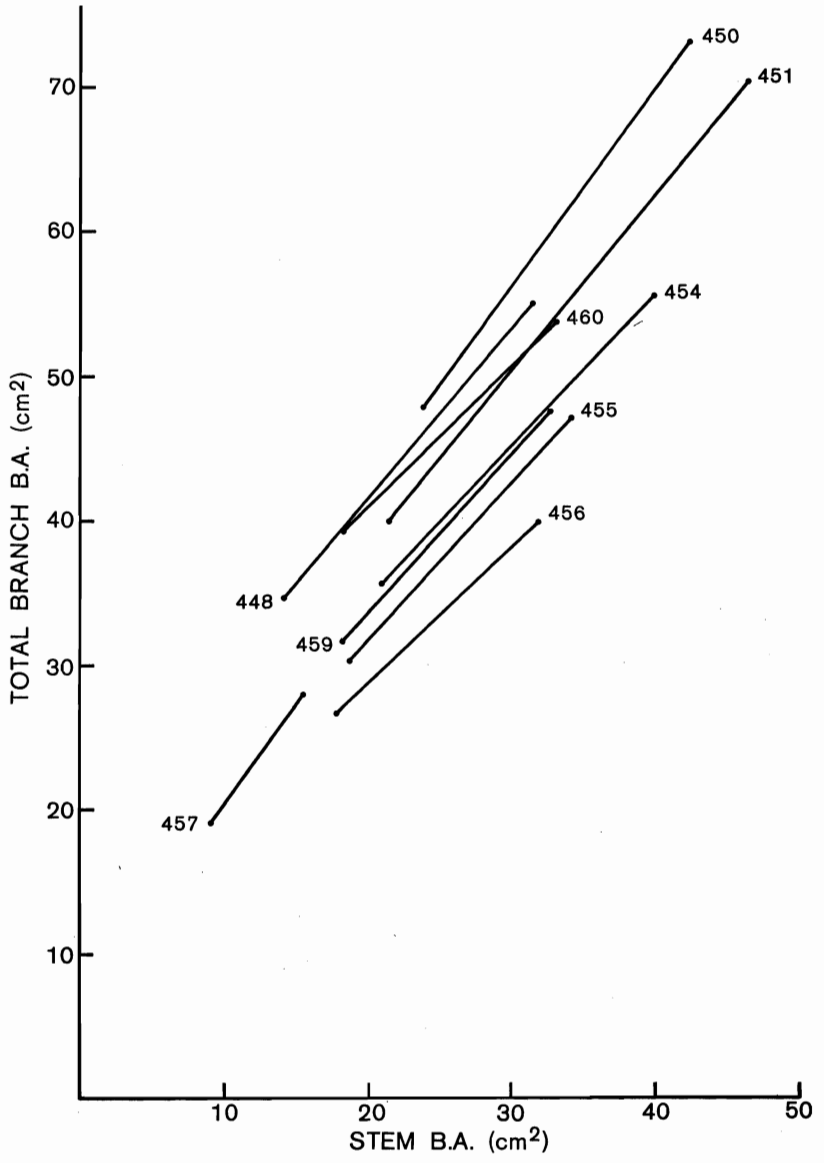

FIG. 2—The relationship between branch basal area and stem basal area at age 4 and 5 years, based on six replicates of nine clones of **P. radiata**.

Principal component analysis of the weight data emphasised the overwhelming importance of the general "weight" component which formed the first component (Table 5) and accounted for 76% to 90% of the variation in the data. The second component accounted for the majority of the remaining variation. The stem variables had negative loadings while either one or both of the crown variables had positive

TABLE 4—Correlation coefficients between the weight components of **P. radiata**, **P. virginiana**, **P. taeda**, and **P. elliottii**

	P. elliottii*	**P. radiata†**	**P. radiata‡**	**P. taeda***	**P. virginiana§**
No. of genotypes	9	7	6	15	20
Variable pairs					
Stem wood **v.** stem bark	0.91	0.96	—	0.88	0.89
foliage	0.93	0.85	—	0.71	0.63
branches	0.87	0.75	—	0.79	0.61
Stem bark **v.** foliage	0.86	0.81	—	0.45	0.68
branches	0.79	0.84	—	0.67	0.69
Foliage **v.** branches	0.82	0.88	0.99	0.56	0.79

* van Buijtenen (1978)
† This study
‡ Forrest & Ovington (1971)
§ Matthews **et al.** (1975)

TABLE 5—Eigenvalues and loadings from principal component analysis of tree weight data based on nine **P. radiata** clones and on families of **P. virginiana** (Matthews **et al.** 1975), **P. elliottii**, and **P. taeda** (van Buijtenen 1978)

	P. elliottii	**P. radiata**	**P. taeda**	**P. virginiana**
Component 1				
Eigenvalue	3.59	3.55	3.05	3.15
Variable				
Stem wood	0.98	0.95	0.97	0.86
Stem bark	0.94	0.96	0.87	0.92
Foliage	0.95	0.94	0.77	0.87
Branches	0.92	0.92	0.87	0.87
Component 2				
Eigenvalue	0.22	0.29	0.57	0.53
Variable				
Stem wood	–0.03	–0.31	–0.07	–0.41
Stem bark	–0.23	–0.22	–0.40	–0.30
Foliage	–0.12	0.20	0.63	0.36
Branches	0.39	0.34	–0.07	0.38

loadings for this second component. The loadings for the second component suggest differences among genotypes in the relative distribution of growth between stems and crowns, i.e., "branchiness".

Needle longevity of the New Zealand *P. radiata* clones, based on the ratio of number of needles present as a fraction of total needles produced, varied among clones (Fig. 3). Thus, for needle retention in the second year the range was from 12% (Clone 460) to 54% (Clone 455). Clones 454, 456, and 459 were the only clones on which 3-year-old needles were observed. Given a uniform rate of annual needle production, which could be expected after canopy closure, these data suggest that the clone with the highest over-all retention rate would carry a total needle mass 1.3 times greater than the clone with the lowest over-all retention.

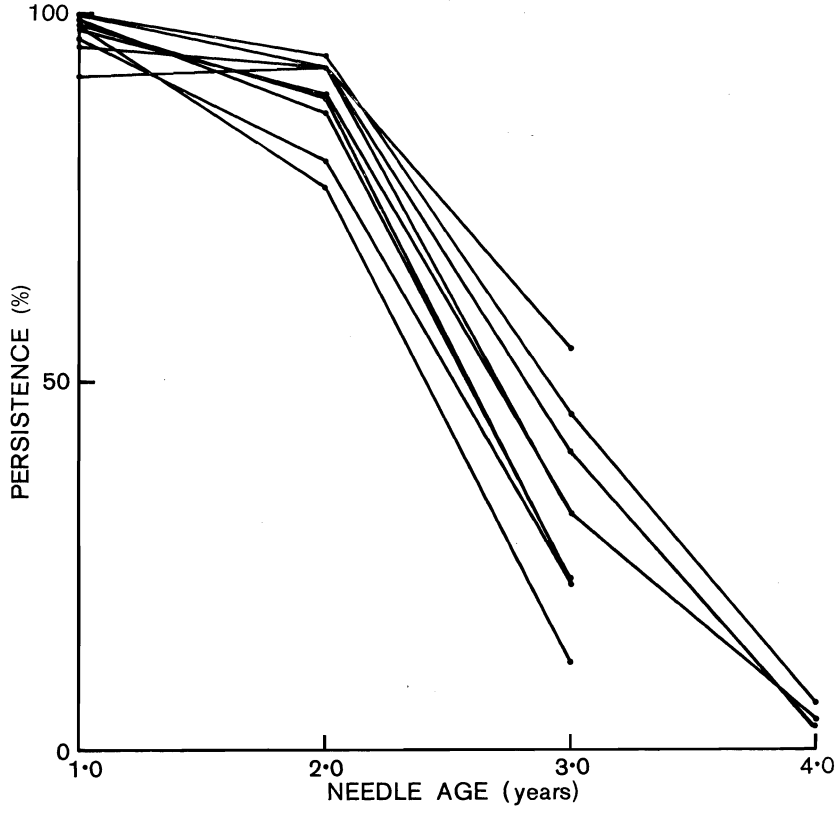

FIG. 3—The relationship between needle retention and needle age for nine clones of **P. radiata.**

DISCUSSION

Agricultural experience suggests that crop yields can be increased by genetic selection in such a way that a higher percentage of dry matter increment is allocated to the harvested component (Evans 1975). Matthews *et al.* (1975) found significant differences

in dry matter allocation among the above-ground wood and bark components of 20 half-sib families of *P. virginiana.* They found between 32% and 43% of the above-ground woody dry matter in stems, depending on family. This compares with 53% to 68% for *P. radiata* in this study, 36% to 59% for *P. elliotti,* and 69% to 72% for *P. taeda* (van Buijtenen 1978).

The question arises, how does the relative allocation of wood plus bark growth within pine trees relate to their total stem production? For *P. radiata* and *P. virginiana* the relationship is weak, with correlation coefficients of 0.09 to 0.17 respectively, and associated probabilities considerably greater than 0.05. For *P. taeda* the correlation was 0.58 but this result was primarily the effect of one family with an unusually low stem weight and percentage of dry matter allocated to stems. For *P. elliottii* the correlation was –0.80, stem weight increasing with a decrease of the percentage of growth allocated to stems.

Under the relatively open-grown conditions in which the trees in these studies were grown there are obvious advantages in the development of large crowns if the goal is to maximise growth in size. When canopy closure is complete, total foliage weight is likely to be constrained by site conditions (Satoo & Madgwick 1982). If we assume that stand foliage weight is unaffected by genotype within a species then individuals with high stem-wood weight/foliage weight ratios would be able to carry the highest stem-wood weights per hectare. Based on the data for the four species considered in this paper, stem wood weight would vary by a factor of 1.4 to 1.6 given constant foliage weight per hectare. However, foliage weight per hectare varies among genotypes. Pope (1979) found a maximum ratio of 2 : 1 in foliage weight between 11-year-old stands of four families of *P. taeda.* The maximum foliage weight was shared by two of the four stands and they had only 27% and 52% more stem biomass than the stand with minimum foliage.

Zavitkovski *et al.* (1981) examined four provenances of *P. banksiana* Lamb. at three locations. Within any one location the reported stem dry matter formed an almost constant fraction of above-ground total trees. The location with the lowest site index had the lowest percentage of dry matter in stems. These results probably reflect the methods used to estimate stand weights based on pooled regressions and the relative constant canopy weights associated with closed stands. (Zavitkovski and co-workers did not estimate foliage weight as a separate value.)

Two primary physiological factors influence the rate of tree dry matter growth – assimilation per unit of photosynthesising tissue and the quantity of such tissue on the tree. In evergreen species the quantity of photosynthesising tissue will be influenced by the relative distribution of dry matter increment between components and by needle longevity (Roberts & Wareing 1975b) and, in closed stands, by shade tolerance. Given uniform rates of assimilation and needle longevity, total dry matter production would be positively correlated with the fraction of growth allocated to needles in open-grown conditions. Allocation to needles appears to be positively related to allocation to branch wood. After canopy closure, trees with large crowns may allow lesser packing of stem material per hectare in untended stands. They would then appear relatively less productive. Such a change in relative performance could account for observed spacing-genotype interactions (Campbell & Wilson 1973).

These results are based on a relatively small number of genotypes per species and no conscious effort was made to select the genotypes for a wide range of any single characteristic described. However, there is a similarity in underlying variation in dry matter distribution in all four species which suggests that more intensive investigation may prove rewarding.

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