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Susceptibility to intra-ring checking in *Pinus radiata:* potential for genetic improvement

Satish Kumar[1,*], Dave J. Cown[1], Miloš Ivković[2] and Rowland D. Burdon[1]

[1] *Scion, Private Bag 3020, Rotorua, New Zealand.*
[2] *CSIRO Plant Industry, P.O. Box E 4008, Kingston, ACT 2604, Australia.*

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*corresponding author: Satish.Kumar@plantandfood.co.nz. *Present address:*
The New Zealand Institute for Plant and Food Research Limited, Private Bag 1401, Havelock North 4157, New Zealand.

Abstract

Intra-ring ("internal") checking is one of several wood phenomena that downgrade appearance-grade products of *Pinus radiata* D.Don. A recently developed increment core-based method has proved cost-effective for large-scale non-destructive assessment. The main objectives of this paper were to document assessment methods and genetic parameters (heritability, genotype-environment interaction, genetic correlations) of internal checking. The greatest incidence of internal checking appears in sapwood outside the heartwood zone, while the heartwood itself is usually check-free. The frequency of internal checking generally decreases with log height. Estimated heritabilities (mostly > 0.30) indicated a moderate genetic control, and the estimated between-site genetic correlations (ca. 0.75) suggested that the magnitude of genotype-environment interactions would be lower compared to those generally observed for diameter, but higher compared to those for wood density. Prior estimates of genetic correlations of internal checking with diameter and wood density had been near-zero and about -0.50, respectively. Strategies for culling undesirable genotypes from the breeding and production populations are also discussed.

Keywords: intra-ring checking; heritability; genetic correlation; silviculture; *Pinus radiata*.

Introduction

"Intra-ring checking" or "internal checking" (IC) describes small cracks that are observed from time to time in partially processed wood or final wood products. In recent years, IC has arisen in products of the softwood radiata pine (*Pinus radiata* D.Don). Internal checking is a particularly undesirable defect because it is not visible on the outside of the rough-sawn wood, but is often exposed during further processing. If affected timber is not detected and rejected at an early stage, it can inadvertently be sold for high-value uses. Problems with customers then occur when the defects are exposed. Major problems can occur even at relatively low levels of IC (approximately 1 – 5% of boards). Internal checking is particularly problematic in processes involving combinations of pieces (as in laminating or finger-jointing of clearwood) followed by machining to final dimensions (Booker, 1994, 1995). The negative effect of IC wood on product reputation in established and potential markets can be substantial. New Zealand produces 3 million m^3 of pruned wood annually, and the loss of revenue from rejected, poor-quality appearance-grade clearwood is approximately NZ$ 15 million (Putoczki et al., 2007).

Internal checks have been increasingly noted in some softwood species, particularly in the 'juvenile corewood'

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of rapidly grown species with low-density earlywood and a high proportion of saturated sapwood, such as pines, spruces, and Douglas-fir (Polge, 1982, 1984; Nepveu, 1988; Persson, 1994; Pang et al., 1999; Ball et al., 2001; Rozenberg et al., 2002; Burdon et al., 2004). Normally IC occurs radially within growth rings during drying, but some radial fissures (e.g. 'old checks') in softwood tree stems and timber can span several annual rings. 'Old checks' commonly occur within the heartwood zone and are filled with resin or callus tissue. These were formed early in the life of the tree (when the wood was still sapwood) as a response to rapid stem growth and/or severe environmental conditions, such as drought and frost, and are often referred to as "drought cracks" or "frost cracks" (Day, 1954; Nepveu, 1988; Persson, 1992). Caspari and Sachsse (1990) confirmed that hot, dry weather caused an increase in stem water tension resulting in wood rupture.

Internal checking is attributed to collapse (physical collapse of the fibre cells) in combination with differential collapse susceptibility of earlywood and latewood cells. Collapse represents an abnormal shrinkage which can occur during drying of timber of radiata pine (and various other species). It evidently develops when the cohesive (or capillary) force of water in saturated cells generates tension that exceeds the transverse strength of the cells. Internal checking is most likely to occur in earlywood, as latewood is denser which makes it more resistant to tangential yielding within the growth ring (Booker, 1994, 1995; Pang et al., 1999). Studies (e.g. Booker, 1994, 1995) have confirmed that IC occurs when the wood is still well above the fibre saturation point. Putoczki et al. (2007) suggested that occurrence of IC may be a two-step process involving failure of the cell wall, followed by the collapsed cells opening up, resulting in the propagation of a tear along a radial cell file. They also hypothesised that altered lignin distribution is involved in the incidence of IC, by altering the strength of these wall layers. While collapse in timber is an indication of severe shrinkage, the occurrence of collapse itself does not necessarily lead to internal checking. Californian redwood frequently collapses but rarely shows internal checks (Clayton, 1952). On the other hand, collapse of radiata pine is often associated with internal checks (Booker, 1994; Booker et al., 2000). In species with high-density latewood (e.g. Douglas-fir), fissures are less likely to penetrate the latewood portion of the ring (Reid & Mitchell, 1951) than in species with low-density latewood.

The frequency of IC generally decreases with log height (McConchie, 1999; Kumar, 2004). Data from disc samples (from different stem heights) from 17 geographically diverse New Zealand sites suggested that 45% of all sample trees showed some IC, mostly in the lower stem below 5 m (D. J. Cown and co-authors, unpublished report). Even so, a near-perfect estimated genetic correlation between IC measurements at different heights within the butt log was found. This suggested that breast-height assessment of IC would provide a good representation of the butt log (Kumar, 2004). Effects of silviculture (stocking, thinning, and pruning) on IC from various unpublished New Zealand studies are inconclusive. On the other hand, occurrence of IC in Norway spruce [*Picea abies* (L.) Karst.] in Scandinavia was attributed to the increasing intensiveness of silviculture and the selection of provenances outside their "natural" habitat (e.g. Persson et al., 1987).

Since the mid-1980s, IC has become a regular, if sporadic, feature of radiata pine wood grown in New Zealand. Efforts are being made to cull the susceptible genotypes from the New Zealand radiata pine breeding programme. The New Zealand Radiata Pine Breeding Company (RPBC), which currently manages the radiata pine breeding programme, has undertaken a number of studies to understand the genetics of IC. The main objective of this paper is to document and discuss various aspects of IC including assessment techniques, and genetic parameters (heritability, genotype-environment interaction, genetic correlations) and their implications for the New Zealand radiata pine breeding programme.

Materials and Methods

Trials

Open-pollinated trials

Three different series of open-pollinated (OP) trials, namely '880', '885' and '887' have been measured for internal checking. Detailed descriptions of various selection series were reported earlier by Jayawickrama et al. (1997). Although these trials comprised a large number of OP families planted at a number of sites, the assessment of IC was carried out only on a sub-set of families at a limited number of sites (Table 1), owing to various practical and financial constraints. Sixty families in common were assessed between the two sites (Kinleith and Paengaroa) of the '887'-series, but there were no common families between the three OP series ('880', '885' and '887').

Female-Tester trials

A series of Female-Tester trials were established in 1992 and 1993, where the genotypes under test (the pollen parents) were crossed with each of five mid-to-high ranked (based on growth and form traits) Female Testers. A subset of pollen-parent families has been assessed for IC at three sites of the Female-Tester trials (Table 1). The number of offspring assessed in each pollen-parent family varied from 16 to 22, with approximately equal representation of each of the five

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TABLE 1: Details of Sites and Genetic Material used in this study. The 'variables' assessed at different sites are also shown.

Trial	Year planted	Site	Age when tested (y)	Sample type	Assessment type	#Families[a] or clones	#Trees/ family[b]	Soil type	Altitude (m)
'887'-Series OP	1988	Paengaroa	15	Disc	#checks	60	15	Pumice	60
		Kinleith	13	Disc	#checks	72	15	Pumice, Organic topsoil	370
'880'-Series OP	1981	Rotoehu	25	Core	%collapse	50	15	Sandy pumice	260
'885'-Series OP	1987	Kaingaroa	17	Core	%collapse	82	18	White pumice	570
1992 Female Tester	1992	Kaingaroa	11	Disc	#checks	62	20	Black scoria	450
		Woodhill	12	Core	Score	90	16	Coastal sand	15
1993 Female Tester	1993	Esk	13	Core	Score	56	17	Pumice	425
1997 GF Elite Clonal	1997	Tarawera	9	Core	%collapse	308	3	Black scoria	200
		Woodhill	9	Core	%collapse	325	3	Coastal sand	20

[a] Represents the number of open-pollinated (OP) families or pollen-parent families or clones, depending on the trial.
[b] Represents the number of trees per OP families or offspring per pollen-parent families or number of ramets per clone, depending on the trial.

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Female-Tester parents. Although the 1992 and 1993 Female-Tester trials described above were planted at different times, these trials were well connected through common families. The numbers of common pollen-parent families between various pairs of three sites of Female-Tester trials in this study were: 56 (Kaingaroa and Esk), 32 (Kaingaroa and Woodhill), and 48 (Esk and Woodhill). There were 32 pollen-parent families common across all three sites of the Female-Tester trials.

Control-pollinated Clonal trial

A group of 33 full-sib families, involving 33 parents (representing average-to-high diameter at breast height (DBH) performance) were used for establishing a clonal test. On average, each parent was involved in two crosses, but this number varied from one to five. Ten clones from each of the 33 full-sib families were chosen for trial establishment in July 1997 at two sites, Tarawera and Woodhill. A sets-in-replicates design with single-tree plots was used, with one ramet per clone planted in each of six replicates at each site. Only three replicates (which had the highest survival, and best growth) of each clone at both Tarawera and Woodhill were assessed for severity of collapse (Table 1).

Sampling Techniques

Both non-destructive and destructive sampling techniques have been used for IC assessment of radiata pine progeny trials over the last ten years.

Non-destructive sampling (Increment core method)

The use of non-destructive samples for IC has been investigated in preliminary, unpublished studies. Several tests have been carried out to investigate a possible connection between wood (core) collapse and IC, and a good correlation has been established. Results showed that about 80% of IC was predicted from the extent of core collapse, whereas the presence of core collapse correctly identified 75% of the severely checked logs (D. McConchie and co-authors, unpublished report). The method involves collecting fresh 12-mm sapwood increment cores, then drying them for at least 12 hours at 100 °C to induce collapse. The earlywood zone of individual rings is then assessed for minimum diameter (an indication of collapse) using a pair of callipers. It is important to note that what is being measured on the dried cores in this study is actually gross sapwood shrinkage, which is a combination of (recoverable) collapse and true shrinkage. However, the term 'core collapse' (as used in this study) has widely been used in the unpublished literature (D. McConchie and co-authors, unpublished report). This method has now been recognised as a cost-effective approach (compared to the Disc Method – see next section), and is currently being used by the RPBC.

Destructive sampling (Disc method)

A quantitative assessment method was developed for use in forest and utilisation studies (McConchie, 1999). This involves obtaining fresh discs, cutting them to 60 mm thickness, and removing a 100-mm-wide strip containing the growth rings centred on the heartwood/sapwood boundary. These samples are dried overnight at 105 °C and the numbers of checks (# Checks) determined visually for each growth ring.

Assessment Techniques

Increment cores have been assessed using different methods in different RPBC trials (Table 1). Assessment methods include actual collapse, termed as %collapse (measured using a pair of callipers and then converted into percentage of the core diameter), and/or visual assessment of collapse severity. The current practice of the RPBC is to visually assess oven-dried breast-height increment cores for collapse severity on a scale of 0 (None), 1 (Slight), 2 (Moderate) and 3 (Severe). An unpublished RPBC study gave high estimated genetic correlation between Score and %collapse (independently measured on the same core samples) of about 0.9. This indicated that a relatively simple visual assessment of collapse would provide an effective tool for screening radiata pine families and clones for IC susceptibility.

Data conversion

In order to correlate within- and across-sites genetic parameters with IC, it is necessary to convert existing measures of IC from different trials to a standard scale. The visual score (0 – 3 scale) system is standard practice now, so we converted existing data on %collapse (from some increment cores) and #checks (from destructively sampled discs) to the 0 – 3 scale. There are no standard rules for such data conversion, but there have been attempts/guidelines in some studies (e.g. D. McConchie and co-authors, unpublished report). We followed these guidelines, but also made some modifications depending on the observed distributions at different sites.

Increment cores were taken at six of the nine sites covered in this study (Table 1). Data from two of these sites were scored directly. At the remaining four sites, cores were assessed for %collapse. The expression/distribution of %collapse varied considerably between sites and ages. As a result, a standard conversion criterion could not be applied at every site. A distribution of %collapse data from the Kaingaroa planting of the '885'-series trial (Figure 1) is used here as an example to convert %collapse data to a 0 – 3 scale. Core samples with %collapse <3.5 were given a score of '0' and samples with %collapse >6.5 were assigned a score of '3'. This resulted in about 38% and 12% of the total samples being allocated to the Score

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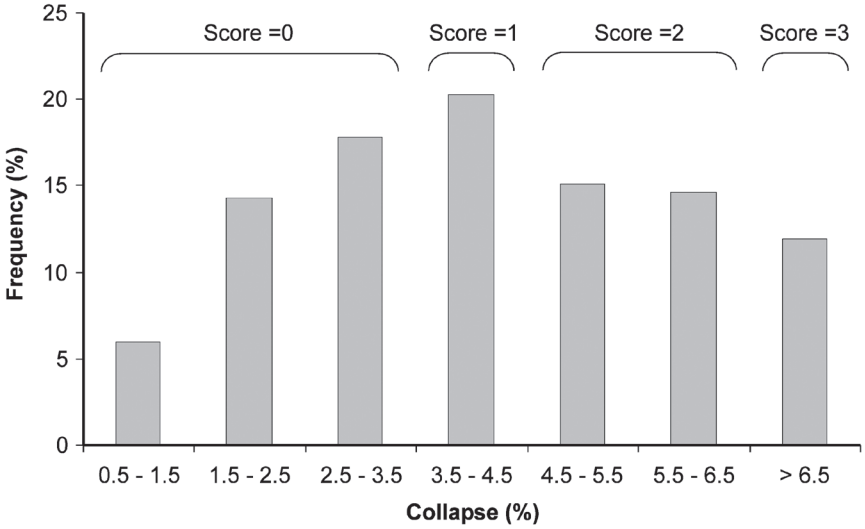

FIGURE 1: Distribution of the %collapse from increment core samples in the '885'-series trial at Kaingaroa. Allocation of Score (0 – 3 scale) is also shown.

categories of '0' or '3', respectively. A score of '1' was allocated to samples with %collapse between 3.5 and 4.5, while a score of '2' was assigned to all remaining samples.

Conversion of #checks in disc samples to a 0 – 3 scale was as follows. All disc samples with zero #checks were given a score of '0'. Approximately the worst 10% of the samples were given a score of '3', and the threshold for the #checks to be scored as '3' varied at different sites, depending on the expression of this trait. The rationale behind assigning at least 10% of the samples to a particular Score category (i.e. '3') was that Restricted Maximum Likelihood (REML) estimates of variance components would not be seriously biased when analysed assuming a normal distribution even though the actual distribution would be multinomial. The samples having #checks > 0 but ≤ 10 were given a score of '1' with a view that it would allow a reasonable sample size under the Score category '2'. An example of the '887'-series trial from Kinleith is shown in Figure 2. In this case, samples with more than 45 checks were scored as 3. The resulting 0 – 3 scale histograms at various sites are shown in Figure 3.

Data analysis

Once data from all trials were converted to a 0 – 3 scale, we used standard quantitative genetics methods for analysis. As data from OP, Female-Tester, and Clonal trials (Table 1) were used, we used models for data analysis and estimation of genetic parameters as specified in other publications (e.g. Kumar, 2004; Kumar et al., 2008a, b). Various genetic parameters estimated in this study included narrow-sense heritability (h^2), broad-sense heritability (H^2) and between-sites genetic correlation (r_B). A brief description of models is presented overleaf:

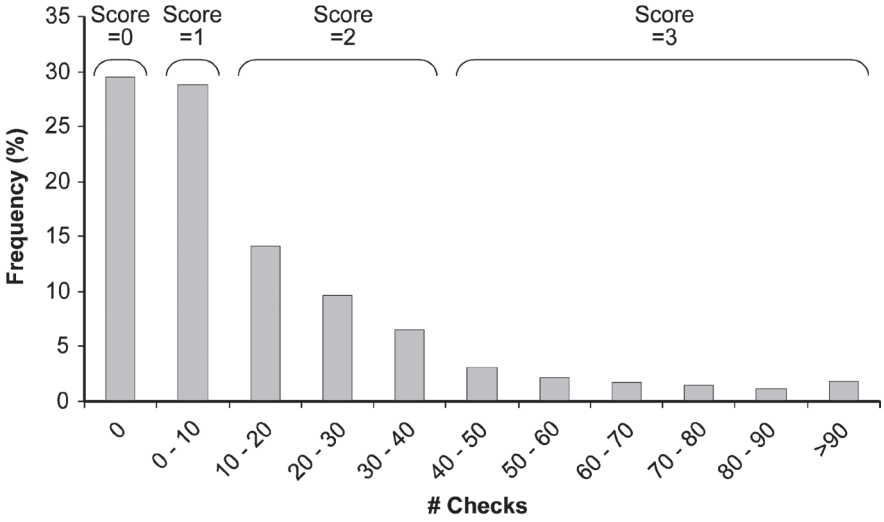

FIGURE 2: A distribution of the #checks per disc sample in '887'-series trial at Kinleith. Allocation of Score (0 – 3 scale) is also shown.

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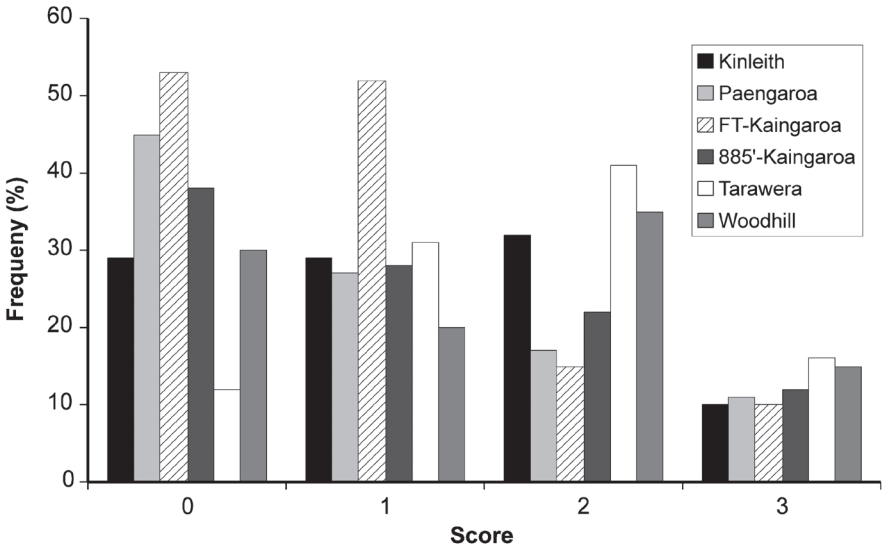

FIGURE 3: Distribution of intra-ring checking severity Score (0 – 3 scale) at different sites.

Open-pollinated trials

The following linear model was used for estimation of genetic parameters at each site:

$$Phenotype = \mu + R + F + error \quad [1]$$

where μ, R and F represent the general mean, replicate- and family effects, respectively. Replicate was considered as a fixed effect, while family- and error effects were treated as random effects. REML estimates of genetic and phenotypic variances were obtained through an iterative process in ASREML software (Gilmour et al., 1997). Estimates of individual-tree narrow-sense heritability (h^2) were obtained from:

$$\hat{h}^2 = 4\hat{\sigma}_f^2 / (\hat{\sigma}_f^2 + \hat{\sigma}_e^2) \quad [2]$$

where σ_f^2 and σ_e^2 are the among-family (or general combining ability, i.e. GCA) and within-family variance components, respectively.

Female-Tester trials

As this experiment consisted of crossing between the male-pollen-and the Female-Tester parents, the following mixed linear model was used for estimation of genetic parameters at each site:

$$Phenotype = \mu + R + T + P + T*P + error \quad [3]$$

where μ, R, T, P and $T*P$ represent the general mean, effects of replicate, tester parent, pollen parent, and interaction between the tester and the pollen parents, respectively. Replicate was considered as a fixed effect while all other effects were random effects. A pooled estimate of the GCA variance component ($\hat{\sigma}^2_{gca}$) was obtained by pooling the estimates for the tester (T) and the pollen (P) effects, weighting according to the respective degrees of freedom. The variance component for the $T*P$ effect represented specific combining ability (SCA) variance (σ^2_{sca}). Estimates of within-site narrow-sense (h^2) and broad-sense heritability (H^2) were obtained from:

$$\hat{h}^2 = 4\hat{\sigma}^2_{gca} / (2\hat{\sigma}^2_{gca} + \hat{\sigma}^2_{sca} + \hat{\sigma}^2_e) \quad [4]$$

$$\hat{H}^2 = (4\hat{\sigma}^2_{gca} + 4\hat{\sigma}^2_{sca}) / (2\hat{\sigma}^2_{gca} + \hat{\sigma}^2_{sca} + \hat{\sigma}^2_e) \quad [5]$$

Clonal trial

The following mixed linear model was used for partitioning of variance components at each site:

$$Phenotype = \mu + R + M + F + M*F + C(M*F) + error \quad [6]$$

where μ, R, M, F, $M*F$ and $C(M*F)$ represent the general mean, effects of replicate, male parent, female parent, interaction of male and female parents, and clones-within-family, respectively. Replicate was considered as a fixed effect while all other effects were random effects. Estimates of GCA variance components for the male and the female effects were $\hat{\sigma}_M$ and $\hat{\sigma}_F$ respectively, $\hat{\sigma}_{MF}$ represents estimated variance due to interaction among male and female parents, and $\hat{\sigma}_{C(MF)}$ represents estimated clones-within-family variance.

Estimates of h^2 and H^2 were obtained from:

$$\hat{h}^2 = 2(\hat{\sigma}_M^2 + \hat{\sigma}_F^2) / (\hat{\sigma}_M^2 + \hat{\sigma}_F^2 + \hat{\sigma}^2_{MF} + \hat{\sigma}^2_{C(MF)} + \hat{\sigma}_e^2) \quad [7]$$

$$\hat{H}^2 = \hat{\sigma}_C^2 / (\hat{\sigma}_C^2 + \hat{\sigma}_e^2) \quad [8]$$

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where $\hat{\sigma}_C^2 = \hat{\sigma}_M^2 + \hat{\sigma}_F^2 + \hat{\sigma}_{MF}^2 + \hat{\sigma}_{C(MF)}^2$

and represents estimated clonal variance.

Between-sites (type B) genetic correlation estimates (r_B) were obtained according to Equation [4] of Kumar et al. (2009) except that subscript "C" was used instead of subscript "gca" for clonal material.

Results and Discussion

The destructive method (Disc Method) has been used in some published studies for comparing families and sites (e.g. Ball et al., 2001; Kumar, 2004). However, thousands of trees would need to be assessed to undertake progeny tests and this would be prohibitively expensive using disc sampling. The use of increment cores is both a non-destructive and cost-effective way of obtaining data useful in the selection of trees for resistance to IC. Converting all the data to a 0 – 3 scale ("Score") allows us to compare data from wider range of trials than would otherwise be possible.

Genetic parameters

Site means and heritabilities

The average Score varied from 0.52 (Rotoehu; age 25) to 1.61 (Tarawera; age 9) (Table 2). Owing to the confounding of effects of age (older crops contain more heartwood which does not show checking) and site, the comparisons among site means are not straightforward. Estimated genetic coefficients of variation (CV) varied from 20 to 56 percent, while phenotypic CV were greater than 50 percent (Table 2). The genetic parameters at each site were estimated using converted data (0 – 3 scale), so the different conversion methods at various sites could also have contributed to the site differences in parameter estimates. Estimated h^2 varied from 0.04 (at Rotoehu) to 0.61 (at Kaingaroa) (Table 2). Approximate standard error of estimated h^2 varied from 0.06 to 0.15 (details not shown). Various factors, such as age, site and silviculture, would have contributed to the lower incidence of IC and observed non-significant estimates of h^2 at Rotoehu. High stocking (600 stems/ha) resulted in narrow growth rings, especially in the outerwood, which might have considerably suppressed the expression of h^2 at Rotoehu. There have been few earlier published studies to estimate genetic control of IC in radiata pine. Ball et al. (2001) reported high narrow-sense heritability (h^2 = 0.64) for IC checking in an unreplicated family-block trial of 18 full-sib families. Kumar (2004) using data from larger replicated seedling progeny trials, reported across-site estimated h^2 as 0.40 and 0.16 from two separate experiments. Both these studies used #checks assessment of disc samples.

There are only a few reported studies on genetic control of IC in other conifer species. Rozenberg et al. (2002) presented evidence for relationship between internal checks in one ring and peaks in wood density profile caused by water deficit. For two 19-year-old Norway spruce trials in Sweden, the estimated H^2 of the number of checks in a single growth ring was either

TABLE 2: Average Score (intra-ring checking severity on a 0 – 3 scale) at different sites, and estimated within-site heritabilities ($\hat{h}^2$ or $\hat{H}^2$). Phenotypic (CV_p) and genetic (CV_g) coefficients of variation (%) are also shown.

Trial	Year planted	Site	Age when tested (y)	Average Score	$\hat{h}^2$ or $\hat{H}^2$	CV_p	CV_g
1997 GF Clonal	1997	Tarawera	9	1.61	0.31[a]	51	28
	1997	Woodhill	9	1.45	0.34[a]	68	39
1992 Female Tester	1992	Kaingaroa	11	0.82	0.25	77	35
	1992	Woodhill	12	0.85	0.49	60	40
1993 Female Tester	1993	Esk	13	0.84	0.17	68	28
'887'- Series	1988	Kinleith	13	1.23	0.42	66	43
	1988	Paengaroa	15	0.94	0.49	73	51
'885'-Series OP	1987	Kaingaroa	17	1.08	0.61	72	56
'880'-Series OP	1981	Rotoehu	25	0.52	0.04	101	20

[a] Broad-sense heritability ($\hat{H}^2$).

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0.37 or 0.64. Using data from the same trials, (Hannrup et al., 2004) reported H^2 estimates of the total number of checks in disc samples to be similar (0.45 and 0.57) to those reported by Rozenberg et al. (2002).

Across-sites heritability and genotype-environment (G×E) interaction

The across-sites h^2 estimates were 0.38 and 0.32 for the '887'-series trial and the Female-Tester trial series, respectively, while the across-sites H^2 estimate for the clonal trial was 0.28 (results not tabulated). The estimated type-B between-site genetic correlations (r_B) were 0.84, 0.74 and 0.74 for the '887'-series trial, the Female-Tester trial series, and the Clonal Trial, respectively. The estimated between-site genetic correlations suggested that the magnitude of rank-change G×E would be lower compared to those generally observed for diameter but higher compared to those for wood density (Kumar, 2004; Kumar et al., 2008b). The inclusion of the coastal Woodhill site in both the Female-Tester and the Clonal trials has evidently contributed to the somewhat lower observed between-sites genetic correlation compared to that between the two pumiceland sites (Kinleith and Paengaroa) of the '887'-series trial. In comparison with other economic traits (e.g. growth, form, needle retention), r_B between Woodhill and other sites is reasonably high for IC.

Genetic correlation with other traits

In a radiata pine clonal study (P. Beets and co-authors, unpublished report), clone mean correlations between IC and basic wood density (DEN), and IC and shrinkage were -0.59 and 0.59, respectively. Kumar (2004) and Kumar et al. (2008a, b), using data from most of the sites considered in this study, reported that the estimated genetic correlation of core-based collapse assessment with DBH was close to zero, and was highly favourable with DEN (ranged from -0.30 to -0.60). Research has indicated that IC may be less severe at wood density levels >460 kg/m^3 (Chafe, 1996; McConchie, 1999; Ball et al., 2005) and in earlywood rings of density >400 kg/m^3 (Ilic, 1999). Grabner et al. (2006) reported that tree rings with lower earlywood density had a higher number of radial checks in Norway spruce, and this was supported by the work of Ball et al. (2005) in radiata pine.

Within-site predicted parental breeding values (BV) for Score (0 – 3 scale) were compared with those for the observed trait (e.g. #checks or %collapse) in order to check the influence of data conversion on family ranking. Results suggested that the family or clones selected based on Score BV would be very similar (i.e. correlation between predicted BVs varied from 0.89 to 0.99 at different sites) to those based on the observed trait. These results suggested that visually assessed collapse Score could provide a non-destructive cost-effective method for ranking families or clones.

Implications of these results for the New Zealand radiata pine breeding programme.

The availability of an increment core-based visual assessment technique has been a major step forward in order to screen germplasm for its susceptibility to internal checking. As discussed earlier, this scoring protocol cross-referenced very well with other assessment measures. Moderate-to-high heritability (Table 2) of core collapse Score has opened up the possibility to effectively select/cull genotypes on the basis of phenotype.

The New Zealand radiata pine breeding programme is based largely on multi-trait (e.g. DBH, straightness, branching, and DEN) selection. Achieving simultaneous improvement for traits involved in adverse genetic correlations (e.g. DBH and DEN) is always a challenge for tree breeders. Adding more traits (such as internal checking) could reduce the individual-trait gains from index selection even further. White et al. (2007) suggested a combination of selection index and independent culling, with the high-priority traits (e.g. DBH, DEN, etc.) included in the selection index and independent culling levels set for the second-priority traits (e.g. internal checking, external resin bleeding, etc).

As a long-term measure, the RPBC could cull genotypes with undesirable IC scores (say, 3) from next-generation breeding parents of the main breeding population. This option is currently being implemented. Formation of an elite population (Jayawickrama & Carson, 2000) with an appearance-grade breeding objective would also be a long-term solution, where IC could be a selection trait along with other traits such as DBH, internode length, spiral grain, external resin bleeding and heartwood. In the meantime, seed producers could use parental BV information to avoid including highly susceptible parents in commercial seedlots. Involving high-wood-density parents would help reduce the problem of IC because of a favourable estimated genetic correlation (about -0.55).

Studies on age-age genetic correlations are required because the corewood zone, which is normally used for family or clonal ranking, will become heartwood (which prevents IC) by harvest age. This would, however, require a modified trial design, preferably using clones.

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