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RISK MANAGEMENT FOR CLONAL FORESTRY WITH PINUS RADIATA — ANALYSIS AND REVIEW. 1: STRATEGIC ISSUES AND RISK SPREAD

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ABSTRACT

Clonal forestry has great potential advantages for increased genetic gains and crop uniformity. However, it has inherent risks, which must be managed appropriately. Those considered important to *Pinus radiata* D.Don clonal forestry include risks stemming from reduced genetic diversity through large-scale clonal propagation, and risks stemming from technical and logistical difficulties of clonal propagation and storage, and the evaluation of clonal material. The first category of risks is addressed in this paper; the second category, plus climatic risks, is addressed in the accompanying paper.

The widely publicised risks of clonal forestry arise from the genetic uniformity of monoclonal crops and, on a broader scale, from potential restriction in total genetic diversity over clonal plantings. Both these factors are conducive to crop vulnerability to new and serious diseases, a prime hazard for *P. radiata* in New Zealand. The disease hazard, along with market risks, can be addressed by risk spread in numbers and genetic diversity of clones. This diversity can be achieved by either clonal mixtures or monoclonal mosaics, and must be addressed across landscapes and across age-classes. There are various approaches to quantitative modelling of the risks, to help devise risk-management strategies. Crop failure can be addressed in terms of probabilities. A generalised approach addresses probability distributions for adverse outcomes of varying severity. Less elaborate approaches involve standard errors (which can be applied to clonal under-performance), or the probability of any one clone failing disastrously. Ulterior risks of clonal forestry involve management of the genetic diversity that is needed for long-term breeding, as distinct from safe deployment of current crops.

No restrictive regulations exist in New Zealand concerning use of clones, unlike the situation in various European countries, nor is there a local code of practice. Such a code may not only be prudent business, but may also maintain public confidence and forestall restrictive regulations.

Keywords: clonal forestry; risk assessment; risk management; cuttings; embryogenesis; tissue culture; maturation; genetic diversity; deployment.

INTRODUCTION

Nature and Potential Benefits of Clonal Forestry

Clonal forestry represents the large-scale propagation and deployment of selected clones, which have been clonally tested. Deployment of select clonal material is nothing new. Early agriculturalists from about 15 000 years ago took advantage of the reproductive precision of cloning with species amenable to vegetative propagation, such as yams and bananas, which they had originally brought into cultivation from nature (Allard 1999). Clonal forestry has been practised for hundreds of years with some easy-to-propagate conifer species (Ahuja & Libby 1993), notably sugi (*Cryptomeria japonica* D. Don) and Chinese fir (*Cunninghamia lanceolata* Lamb.). For most of these easy-to-propagate species, vegetative propagation has become the most convenient practice. Historically, ease of propagation was often the major selection criterion. Currently, with improved technology selection is based more on silvicultural performance and wood quality. Pines (*Pinus* spp.) have been considered difficult to propagate vegetatively (Hartmann *et al.* 1990); however, even with species less amenable to vegetative propagation, clonal forestry has major attractions.

In principle, clonal forestry offers additional genetic gains from capturing non-additive effects, which are not captured via sexual propagation, plus the benefits of greater uniformity and predictability in performance resulting from a lack of genetic segregation (Burdon 1990; Aimers-Halliday *et al.* 1997). The problems with utilisation of young fast-grown plantations, which forest owners often want to produce in order to reduce growing costs, are highly relevant. With wood properties from such crops being often marginal, the advantages of tree-to-tree uniformity and predictability of wood properties become particularly attractive.

With *Pinus radiata*, which is relatively amenable to vegetative propagation for a conifer (Menzies & Aimers-Halliday in press), the attractions of clonal forestry are considerable, especially for avoiding unwanted variation. Clonal forestry has been pursued for many years, and is finally being implemented on a fairly large operational scale in New Zealand, even though the various technical problems are not fully resolved.

There are additional benefits of clonal forestry, which may currently be under-estimated. In *P. radiata* a branching habit with internodes of intermediate length, which is likely to be consistently achievable only with clonal forestry, is now appearing much more attractive in the light of utilisation problems posed by the second logs of fast-grown short-internode trees (cf. Burdon 1989). Furthermore, where uniformity of piece size is crucial, clonal forestry using monoclonal blocks can have major advantages, since it can avoid the competitional variance generated by clone-to-clone variation in growth curves. There is also the flexibility associated with the matching of individual clones (of specific physiological age) to particular sites and end-uses (Burdon 1989, 1991; Carson 1986; Libby & Rauter 1984; Menzies & Aimers-Halliday 1997; Menzies *et al.* 1991). Maturation ("physiological ageing" *), while a widespread problem with clonal propagation, can be used to advantage, especially if it can be controlled on a clone-by-clone basis. Other prospective advantages

* See the discussion on terminology regarding maturation and physiological ageing in the accompanying paper.

exist, which have been discussed previously (e.g., Libby 1987a; Burdon 1989; Miller 1991; Ahuja & Libby 1993; Aimers-Halliday *et al.* 1997).

In addition, any foreseeable application of genetic transformation, or genetic engineering, with forest trees will be in the context of clonal forestry.

Outline of Risks

While clonal forestry has major potential advantages, its adoption involves significant risks and so a major challenge is to exploit the advantages while managing the risks. If a thorough assessment of genetic gain and other benefits *versus* risk is not made by the forestry sector, clonal forestry will fall short of the promised benefits (Zobel 1993).

Risk may be defined roughly as the product of the probability of an adverse outcome and its severity or seriousness. Even a high probability of minor losses, which might be balanced against the possibility of better-than-expected performance, may therefore be of little account, particularly if the measures that may incur such minor losses served to preclude major ones. At the other end of the scale, it may be unacceptable to incur quite a low and somewhat uncertain probability of catastrophic losses. In that probabilities may often be very imperfectly known, we have to deal with uncertainty.

It has long been appreciated that injudicious practice of clonal forestry can incur special risks of disease or insect attack (e.g., Kleinschmit *et al.* 1993). If an individual genotype has a genetically determined susceptibility, then every ramet of that clone will have it. (Note that a clone comprises the ortet, which represents the original seedling, and the ramets, which are vegetative propagules therefrom.) Such susceptibility can be greatly exacerbated by the way in which a clonal plantation facilitates the spread of an epidemic. Indeed, diseases and insect pests have been a classic problem with poplar plantations that were traditionally monoclonal (Zsuffa *et al.* 1993), often the problem being relieved mainly by the shortness of rotations for the poplars. Among crop plants, there is the classic, and socially catastrophic, case of the potato blight in Ireland in the mid-nineteenth century. There was almost total dependence on a single, highly productive, clonal cultivar that fell victim to a new mutant strain of the fungal pathogen. There is also the notorious disease susceptibility of many cereal crops which, being inbreeders, approach the genetic uniformity of clones. In these examples the annual nature of the crops mitigates the problem, such that "boom-and-bust" breeding for non-durable disease resistance can be a tolerable option. With a species such as *P. radiata*, however, even though it is a fast-growing conifer the rotation is still much too long to greatly mitigate biological risks. For some diseases and pests, the hazard (e.g., terminal crook disease of seedlings) can be greatly mitigated by a limited period of susceptibility. Even so, the period of susceptibility to a pathogen such as *Dothistroma pini* Hulbary, while limited, can still be too long to mitigate the risks radically.

Some of these biotic risks can be accentuated by growing an exotic species. These risks are largely shared by "family forestry", which is the deployment of groups of related individuals, generated for specific purposes, in discrete plantation blocks (Roberds & Bishir 1997). Indeed, they can also arise, to a lesser extent, with plantations from seed orchards based on limited numbers of parent clones. The release of genetic variation through genetic segregation, and any genetic contamination, may serve to mitigate the risks; on the other hand, Libby (1982) has argued that the continuum of genetic variation

arising from genetic segregation may be conducive to pathogens evolving greater virulence more readily. Even though various risks of clonal forestry may be partly shared with other systems for large-scale deployment of elite germplasm, clonal forestry may afford some special opportunities to combat certain market risks and unwanted variation arising from inter-tree competition (*see later*), and some climatic risks (Aimers-Halliday & Burdon 2003).

As well as biotic risks, there are additional risks from climatic damage and climate change. Many of these risks are understood, and can be combated by screening for resistance to the factors concerned. But with some other risks, no such forearming is readily possible, and yet risk spread appears to have limited value.

Market uncertainties represent a major risk factor. These uncertainties stem largely from the time lag between commitment to plant a set of clones and selling the harvested products. The risks considered so far relate essentially to uncertainties, where probabilities of adverse outcomes are often very low but the possible outcomes often catastrophic. In addition to these classical risks, other risks of clonal forestry figure prominently with *P. radiata*. These risks are associated, paradoxically, with the technical problems that are no longer precluding clonal forestry but are not yet fully resolved. The problems centre largely on the technical difficulties in large-scale clonal propagation, which stem mainly from problems of containing maturation in clonal storage systems (cf. Thompson 1984; Shelbourne 1991; Libby & Ahuja 1993; Ritchie 1994). Indeed, central to the success of clonal forestry is the maintenance of juvenility in clones during clonal testing or, alternatively, the ability to restore juvenility at the end of clonal testing (Aimers-Halliday *et al.* 1997).

In this paper, we address:

- The inherent nature of risks associated with major uncertainties, and their potential impacts;
- Generating factors and any cofactors;
- Available approaches to risk management.

The companion paper (Aimers-Halliday & Burdon 2003) addresses risks associated with known and generally ubiquitous problems. These involve the technical and logistical problems of storage and large-scale propagation of clonal material, and some problems of evaluating clonal performance. There are also climatic risks.

These papers are largely directed at forest managers (Paper 1); quantitative tree breeders, and those who might be involved in regulatory or policy-related agencies in New Zealand (Paper 1); and those directly involved in clonal forestry with *P. radiata* and with other species around the world (both papers). The focus on *P. radiata* is partly a direct reflection of its commercial importance. It is also an indirect reflection of that importance, which has led to *P. radiata* having effectively become a model forest-tree species that exemplifies issues and problems for various other species.

AVAILABLE APPROACHES TO RISK MANAGEMENT

Risks of clonal forestry can be addressed in various ways, which can be categorised as:

- **Active countermeasures against known risks**. These include: direct measures to counter known technical and logistical problems of clonal storage and large-scale

propagation, siting of genotypes or species, choice of management practices, quarantine systems, breeding for resistance, genetic engineering for resistance, and sundry biological control measures.

- **Forward preparation against prospective risks**. Measures include maintaining a pool of genetic diversity for future breeding work, acquiring basic research information on propagation and deployment, and having the propagation technology available for rapid deployment of resistant selections.
- **Risk spread**, which can be addressed via clonal deployment, catering for a range of currently unknown or poorly quantified risks, notably biotic risks and market risks.
- **Achieving incidental benefits of risk spread,** which centre around epidemiological protection.

The appropriate management of the two risk categories addressed in this paper, biological and market risks, is summarised in Table 1, along with the co-factors and the impacts associated with each category, and is discussed in more detail below.

BIOTIC RISKS

Where diseases or pests are involved, there are risks that may extend to crop failure (Table 1, Part A) and some highly unpredictable possibilities. True, there are known diseases, against which we can forearm using a combination of selective breeding, appropriate siting of material, and tending practice. However, there are known diseases that have not yet reached New Zealand but whose impact on arrival is highly uncertain, and almost certainly some unrecognised diseases that would be serious if they did arrive. Also, existing disease-causing fungi may mutate to produce new pathotypes.

Insect pests are often an unpredictable factor, in that we do not know which new species are going to become established and how serious they will be, even though the numbers of new species arriving per year have been so consistent as to be inherently predictable (Ridley *et al.* 2000). When insect pests do arrive in New Zealand they may be without their natural predators, parasites, and parasitoids and this can lead to severe epidemics, at least in the short to medium term. At the same time, genetic variation within tree-host populations in insect resistance has very often been insufficient to allow successful breeding for resistance (Zobel & Talbert 1984), although some variation is bound to exist at the clonal level.

Interactions with other factors may intensify biotic risks. Genetic changes in existing diseases and pests, plus incursions of new pathogens and pests, may be intensified by climatic factors, particularly climate change (Burley 2001). Also, maturation can affect susceptibility to biotic hazards. With *P. radiata*, it has been widely observed in New Zealand that adult cuttings or grafts are generally more subject to animal browsing than seedlings. On the other hand, maturation state reduces susceptibility to western gall rust caused by *Endocronartium harknessii* (J.P.Moore) Y.Hiratsuka from highly susceptible to nearly immune as *P. radiata* clones mature from early adolescent to late juvenile (Zagory & Libby 1985; Old *et al.* 1986).

Overall, fungal diseases constitute a hazard that needs to be addressed in New Zealand despite very large knowledge gaps. There are great uncertainties as to what diseases will arrive and how they would behave on arrival. Also, we are growing large areas of *P. radiata*

TABLE 1–Summary of risks of clonal forestry with *Pinus radiata* in New Zealand, including cofactors, potential impacts, and appropriate management countermeasures*.

Risk category	Cofactors	Potential impacts	Management approach	Specific countermeasures†
Biotic				
Fungal diseases	Genetic uniformity	Under-performance	Risk spread	Clonal diversity
Insect attack†	Climatic events	Crop failure		Deployment tactics
	Climate change		Forward preparation	Rapid deployment of resistant genotypes
	Pest/pathogen biology		Active countermeasure†	Clone-specific protective measures
Market				
Returns from harvested crops	Time lag to harvest	Poor returns to grower	Risk spread	Clonal portfolios
Grower reaction	Perceptions	Customer rejection of planting stock	Active countermeasures Forward preparation	Uniform planting stock Customer education
Public acceptance of clonal forestry		Public rejection		Public relations

* In addition to requirements for seedlings or vegetative multiplication
† Currently of secondary importance for *P. radiata* in New Zealand.

on sites where the considerable summer rainfall, while it is conducive to high productivity, will favour fungal pathogens.

There is a concern that clonal forestry could increase susceptibility to unknown future problems by changing the average tree physiology, or by limiting the number of genotypes that may buffer a population, therefore decreasing stand viability through loss of resistant alleles (Roberds & Bishir 1997; Namkoong 2000). Roberds & Bishir (1997) argued that the latter is not critical if the clonal forestry programme is based on a well-managed breeding programme. The breeding programme can be managed to have a variance structure that allows for future responses, even if the planted population is genetically limited. It can also be argued that a clonal forestry programme could be quickly geared to produce resistant clonal material for deployment. An early selection programme for *Cupressus* spp. (particularly *C. macrocarpa* Gordon) is currently being developed at the New Zealand Forest Research Institute for capture of clonal genotypes resistant to cypress canker (Aimers-Halliday *et al.* 2002).

Countermeasures

There is a range of active countermeasures for biotic risks that are not specific to clonal systems. These measures include deploying material that is generally adapted to the environment and selected for resistance to known and existing biotic hazards that may be important on the particular sites (e.g., dothistroma blight), and other measures such as chemical spraying and choice of silvicultural regime.

Some provision is in place for dealing with large-scale epidemics of likely new pathogens such as pine pitch canker (caused by *Fusarium circinatum* Nirenberg & O'Donnell), using early screening for disease resistance. The Forest Research Institute and the New Zealand Radiata Pine Breeding Co. have both been involved (among other organisations) in the international collaborative investigation into the genetics of resistance to pine pitch canker, the IMPACT Project, which is based in California (Devey *et al.* 2001). Elite families in the *P. radiata* breeding programmes from Australia, Chile, and New Zealand have been screened via inoculation of seedlings in greenhouse trials. Another option, which is being re-addressed, is the hybridisation of *P. radiata* with other pine species showing good resistance (Dungey *et al.* in prep.) and developing a clonal programme using resistant hybrid genotypes.

Although specific countermeasures can be taken, genetic risk spread is a key risk-management measure in the commercial deployment of clones. It will be addressed separately in terms of the quantitative considerations and strategic implementation.

The long-term success of any breeding for resistance clearly depends on the selection of many genetically diverse genotypes with multiple resistance mechanisms (Burdon 2001; Aimers-Halliday *et al.* 2002). Early greenhouse or laboratory screening of clonal material originating from the breeding programme may be the best method to efficiently screen large numbers of plants and identify and capture superior resistant genotypes, which could then become the base of a clonal forestry programme. However, the validity of any early screening method must be confirmed in field trials.

Early screening methods can also provide a platform for research into the genetic basis of resistance, at the quantitative and molecular levels. Resistant and susceptible genotypes

would provide a segregating population in which gene mapping could be used to target genomic regions controlling resistance and thereby help secure a diversity of resistance mechanisms (cf. Burdon 2001). This would open the door to molecular screening for disease resistance and also the potential for genetic manipulation.

MARKET RISKS

Market risks involve a range of time frames. Short-term risks are often relatively predictable; in this respect, they overlap with the risks addressed by Aimers-Halliday & Burdon (2003), but the longer-term risks centre around uncertainties.

Short-term market risks involve the saleability of clonal planting stock. Purchasers of such stock will want it to meet certain quality criteria, matching or surpassing standard planting stock, and they are also concerned about the cost. There are often strong expectations that genetic superiority should be manifested right from the nursery stage. Unevenness and/or indifferent early performance of planting stock are likely to outweigh in customers' minds any assurance of superior harvest-age performance. The issue of plant quality and costs is closely associated with risks due to propagation failure, and also unwanted intraclonal variation, which are addressed by Aimers-Halliday & Burdon (2003).

Medium-term market risks for clonal forestry are likely to involve public acceptance. This is largely a political issue, which will be addressed later.

Long-term market risks attach to the setting of any single breeding objective in an intensive breeding programme. Indeed, misperceptions or changes in time of economic-worth functions, as have occurred with some animal breeding, can even result in negative economic gains (Burdon in press). Because clonal forestry offers greater genetic gains, and therefore greater directional shifts in trait means, the market risks are intensified. Reliance on a very small number of clones can further intensify the risks, because it can create high exposure to any unusual and unrecognised but highly adverse wood properties that a particular clone might have.

Countermeasures

Risks involving immediate saleability of clonal stock need to be countered by measures that produce planting stock of good and even quality, as addressed by Aimers-Halliday & Burdon (2003). The same measures should make available a broader representation of top-quality clones, which should improve saleability. Educating customers concerning realistic expectations of clonal planting stock is also important, including the fact that genetic superiority is often not manifested in the nursery Burdon & Miller 1992).

The medium-term risks, involving public acceptability of clonal forestry, can be addressed by a combination of public education and adoption of responsible deployment practices.

Longer-term market risks can be addressed by deploying a portfolio of breeds or clones (Burdon 1992; C.J.A.Shelbourne unpubl. data; Aimers-Halliday *et al.* 1997), which can be differentiated on the basis of wood properties and/or branching habit for *P. radiata*. Hopefully, some of the material might command lucrative niche markets, while the remainder, by virtue of being well characterised, would command at least routine prices.

Clones being more uniform with respect to wood properties, and therefore subject to more precise characterisation, seem more amenable to this portfolio approach.

A logical basis for constructing a clonal portfolio for *P. radiata* would be to adapt and refine our existing scheme of breed differentiation. The differentiated breeds (Jayawickrama & Carson 2000) embody various breeding goals. In these goals wood properties and branching habit (which determines size and distribution of knots) can be harmonised, with combinations that would be appropriate for either appearance- or structural-timber grades.

The strong genetic differentiation among clones, compared with seedling families, should allow far more precise targeting of alternative breeding goals. As such, it provides opportunities for countering market risks beyond any that are afforded by use of seedling families.

GENETIC RISK SPREAD

Categories of Genetic Diversity

Two aspects of the genetic diversity of plantation crops are of interest here. One is "functional diversity", which is part of the "overt diversity". Functional diversity is defined as tree-to-tree genetic variation in (a) traits that make up the breeding objective (which will include recognised adaptive features) and (b) traits that are readily assayed and of obvious potential economic significance. Overt diversity includes, in addition, clearly recognisable genetic variation for additional traits, e.g., cone size or pollination date, that are of no inherent economic significance. For many purposes, functional diversity is decidedly undesirable within stands, although much of it may provide the focus of selective breeding and the basis of developing breed or clonal portfolios. "Cryptic diversity" is the other aspect, which is generally very desirable. It typically includes genetic variability in resistance to unknown factors that may strike, such as either climatic events that go beyond the range of experience or new and serious diseases, but it also includes diversity for genetic markers.

The category into which genetic diversity for a particular trait falls can clearly change with circumstances. The arrival of a new disease pathogen can make "cryptic" diversity "functional", and a shift to vegetative propagation can change variation in propagation behaviour from cryptic to functional.

Functional diversity

Functional genetic diversity influences log or end-product values, or affects costs of growing and harvesting, thereby affecting net values. On the positive side, such diversity is captured and utilised in varying degrees through genetic gain in traits of known economic worth (which can include resistance to known diseases and pests), and it can also be used to exploit the various advantages of breed differentiation. On the negative side, functional diversity can generate unwanted tree-to-tree variation in size, form, and various wood properties. Such variation is inevitable in production populations (even in pair-crosses) that contain the segregational genetic variance that is released upon sexual reproduction.

Functional diversity seems straightforward to address, as a management response to market uncertainties, or to cope with known diversity of sites and/or markets. It may also

be used as a tool to address some biological uncertainties, to address perceived hazards of low to intermediate level. In any case, it can then serve to augment cryptic diversity.

Cryptic diversity

The very nature of this diversity leaves only one way to assure it, namely by having the equivalent of a sufficient number of unrelated genotypes represented in the crops that are deployed. If the genotypes are represented in unequal proportions (for which there may be good justification) or if some of the genotypes are inter-related, the "census" number of genotypes will need to be boosted, in order to achieve the specified effective number and the corresponding level of cryptic diversity. It may be noted that unequal representation of clones or even families can give better combinations of gain and cryptic diversity than equal representation of unrelated clones (Lindgren *et al.* 1989). This diversity can be enhanced by including additional provenances, but at a cost of some genetic gain if certain of the provenances are sub-optimal for economic traits. Even within a provenance, there will be a trade-off between gain and diversity, since increasing the effective number of parents will mean less-intensive selection and additional fiscal cost.

It might be argued that segregational variation, even with a small number of parents, will contribute materially to both cryptic diversity and overt diversity. However, the contribution of genetic segregation to the existing cryptic diversity that is of interest may be limited if genes of large, if latent, effect are predominant components of the cryptic diversity.

Cryptic diversity can, in principle, be measured by using molecular markers, but this depends on the markers being calibrated as measures of the functional diversity and the components of cryptic diversity that may eventually become important. Unfortunately, satisfactory calibration is still a long way off (e.g., Libby 1995; Burdon & Richardson 1997). Nonetheless, markers could be used as an indirect measure through revealing parental identities and relative contributions of the parents in a seedlot, although the task could be complex.

Quantitative Aspects

The issue becomes one of risk spread, or reducing sampling error with respect to susceptibility to some form of loss. Any one clone could be especially susceptible to a new and serious pathogen (be that a new species or a new strain of an existing species). And if that clone is planted to excess, the susceptibility would be reinforced by a build-up of inoculum. However, if numerous unrelated clones are used it is most unlikely that all will be especially susceptible. But the benefits of the risk spread are subject to the Law of Diminishing Returns. Thus very little gain in crop security is likely to accrue if the number of unrelated clones used exceeds about 20 (cf. Libby 1982; Hühn 1986; Roberds & Bishir 1997). Any such gains in security will be achieved at the cost of reduced selection intensity and, therefore, reduced expected genetic gain. Unlike the limited number of select clones in clonal forestry, seed-orchard offspring will show segregational variation. This would indicate that the minimum acceptable number of seed-orchard parents would be slightly below that for clonal forestry.

In addition to reducing selection intensity, the deployment of large numbers of clones can compromise management efficiency. Only with a limited number is it practicable to

tailor precisely management, processing, and utilisation to individual clones. W.J.Libby (pers. comm.) suggests that more than 20 such individual tailorings would become increasingly difficult. It may be possible to group clones that are phenotypically similar for various end-products, and thus increase the number of clones deployed without compromising management efficiency. This would result in an overall increase in cryptic diversity without increased functional diversity for the traits of interest, but would require precise characterisation of clones.

Disaster thresholds

To obtain some insights into the behaviour of risk, a minimum threshold of acceptable performance can be adopted for a particular criterion of performance, below which the forestry operation is not economically viable. Modelling can then be done from assuming a given probability that any random clone will perform below such a "disaster" threshold.

In principle, it can be easy to apply the binomial theorem to the probabilities that given numbers of clones within a group of n clones will fail simultaneously. Given a probability, p, that any random clone out of n clones will "fail", we have the expansion of

$(p + (1 - p))^n$

On this basis, we have probabilities:

p^n that all n clones will fail simultaneously

${}^nC_1(p)^{n-1}(1-p)$ = that $n-1$ will do so

${}^nC_2(p)^{n-2}(1-p)^2$ that $n-2$ will do so

${}^nC_3(p)^{n-3}(1-p)^3$ that $n-3$ will do so

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${}^nC_{n-1}(p)(1-p)^{n-1}$ that one will fail

$(1-p)^n$ that none of the clones will fail.

Note: $({}^nC_x = n!/\{(n-qx)!(x!)\})$, $n! = n \times (n-1) \times (n-2) \times (n-3) \times (n-4) \ldots\ldots 3 \times 2 \times 1$.

If clones are grown in intimate mixtures, low (individual-tree) failure rates will have very little impact on crop performance, because the failures can effectively disappear quite harmlessly as part of a routine thinning process. Beyond a certain failure rate (which will depend strongly on the thinning ratio) additional failures will start to affect crop performance, increasingly so as the failure rate rises. As indicated earlier, there can eventually be a threshold failure rate above which the crop performance becomes unacceptable, so constituting crop failure. Where the probability of failure is low ($p \leq 0.1$) and a proportion of individual failures (which can depend on the thinning ratio, natural or artificial) can be readily tolerated, the probability of an unacceptable failure rate will decline with increasing n. With large n, the expected individual failure rate will not only approach p, but will also have a variance approaching zero. Given p well below the threshold of crop failure, there will be essentially no likelihood of such crop failure.

If p is high, corresponding to crop failure, the highest probability of avoiding unacceptable losses can paradoxically arise with a single clone (Libby 1982; Roberds & Bishir 1997; Bishir & Roberds 1999). This is because multiple clones will virtually guarantee that the proportion of loss approaches p, whereas with a single clone there is no assurance that the

level of loss will actually equate to p. This is a situation where a single clone might be right when everything else is wrong, instead of the more usual situation of being the worst option for risks. However, when this situation arises the general risks of growing the species are probably unacceptable in the first place.

This approach of addressing risk in terms of disaster thresholds has some important limitations. First, it imposes the artificial assumption that there are just two discrete categories of performance, acceptable and unacceptable, rather than continuous variation. How that assumption may apply may depend on whether a particular clone is deployed in mixture or mosaic, since performance that is tolerable in a component of a mixture may not be so in a monoclonal block, or vice versa. It could also depend on factors affecting the logistics and costs of replacing failed monoclonal blocks.

Generalised probability-density functions

Risks may be specified in terms of risk profiles, which can be described quantitatively as the distribution of probability in relation to the magnitude of loss or under-performance. Typically, the probability distribution would be characterised by high probabilities of minor losses, trailing off to progressively lower probabilities of more serious losses, somewhat like an exponential-decay curve. (If probabilities of serious losses are high, then the general operation is almost certainly too risky, unless there were some combination of very high potential returns and ulterior risk spread.) Such distributions can conveniently be specified by appropriate choice of parameters for Weibull distributions, for instance (Libby 1982). Given such a distribution for a single clone, it is in principle possible to derive a risk profile for a set of any given number of clones (Libby 1982). In the absence of a well-defined risk profile for any single clone, it is still possible to explore the multi-clone risk profile under alternative assumptions.

In practice, there will be two types of risk component:

(1) Relating to losses (e.g., due to disease) that generate under-performance (which may extend to outright failure), as outlined in the preceding paragraph. Such a component will be bounded by zero, this corresponding to the case where the clone in question is performing at its potential.

(2) Relating to imperfect evaluation, leading to inherently symmetrical variation about the predicted genotypic value, the predicted value being effectively the departure of test performance from the test mean reduced by the repeatability of the clonal mean (Aimers-Halliday & Burdon 2003, Eq. 2). This component can thus include "negative losses" for individual clones.

In practice, these two components may be impossible to separate cleanly, but the former is liable to generate a markedly non-normal distribution for any one clone.

"Central-limit" approach

While individual clones may show highly asymmetric risk profiles (probability density functions for different levels of loss) the mean performance for a large number of clones will, according to the Central Limit Theorem, be normally distributed. In principle, this makes the computation of risk much simpler, since the expected standard deviation for the mean of a population of n clones (σ_n) represents the standard error of the mean for an

individual clone (σ_ε) divided by the square root of the number of (unrelated random) clones (n), i.e.,

$$\sigma_n = \sigma_\varepsilon/\sqrt{n} \quad (1)$$

This asymptotic solution, however, may only be a crude approximation, since we are likely to be using only a very finite number of clones. Moreover, it will depend on knowing enough about the risk profile for a random individual clone to allow a realistic expected mean and variance to be computed. Under these conditions, it may be readily practical to compute a generalised probability density function (above).

Our own agenda

Another option for quantifying risks is the use of generalised probability distributions, extending the approach of Libby to cover distributions that appear relevant to our circumstances in New Zealand. With such a framework established, simple cases can be addressed incidentally.

Simulations of expected impacts can be either deterministic or stochastic. The latter approach, while more computer-intensive, is typically well within the capacity of modern computers, is often inherently easier to model, and gives not only mean expectations but also distributions about those means which are based on minimal assumptions.

Main Deployment Options

Decisions must be made on the number of clones deployed in forests, taking a mid-course between the increased risks *versus* increased gains in using a finite number of selected clones (Burdon 1989; Libby 1982; Timmis 1985). Important considerations are: land area planted in clones and capital investment involved; the amount of information on each clone; whether the clones are grown in pure stands or mixtures; genetic diversity of the clones; adaptability of each clone deployed; and risk factors such as market shifts, pathogens, pests, and climatic and edaphic changes (Burdon 1989; Lindgren 1993; Zobel *et al.* 1987; Zobel 1992).

The options for achieving risk spread in deploying clones are various, and several can be used in combinations. Options include:

- Numbers of clones, in equal or unequal representation;
- Equal or varying proportions in which individual clones are used;
- Inter-relatedness among the clones that are used;
- Growing clones in intimate mixtures or mosaics of monoclonal blocks;
- Deployment of clones at the "landscape" level rather than in immediate locality;
- Staggering of clonal deployment in time.

Numbers, proportions, and relatedness of individual clones

The effective level of risk spread in commercial crops, assuming a single population, will be governed by the effective population size of deployed material. This size reflects not only the number of genotypes used, but also the proportions in which they are used and the patterns of inter-relatedness. Unequal proportions and inter-relatedness will reduce the effective number.

There are several possible measures of effective population size (Libby 1998). The classical measure, generally denoted N_e, is based on a norm of an idealised population in which size remains constant over generations and family size shows a Poisson distribution (Falconer & Mackay 1996; Libby 1998). Thus, if clones or parents make equal contributions, the effective number will exceed the census number (N). The application of this concept has been developed for a wide range of "metapopulation" structures, in terms of the interrelated factors of subdivision, relatedness and inbreeding, and restrictions on mating patterns (*see* review by Caballero 1994). It is appropriate for studying the long-term dynamics of populations that are subject to fluctuations in size.

An alternative measure is Status Number (N_s) (Lindgren *et al.* 1996, 1997). It has the properties of never exceeding N, with a lower bound of 0.5 under complete inbreeding. In a closed population it will always decline in time, since it is based on identity by descent and assumes zero mutation, which means that it can decline in a way that is intuitively alarming (*see* Lindgren *et al.* 1996). However, being based on co-ancestry values, it can be readily adapted to an initial state of some inbreeding and consequent co-ancestry among founding parents.

Yet another measure of effective population size is one that has been applied in forestry to seed orchards, but is equally applicable to clonal deployment (Lindgren 1993). In the simplest form, with a set of N unrelated seed-orchard parents, or commercially deployed clones, which are represented in unequal proportions

$$N_{e'} = 1/\sum(p_i^2) \qquad (\sum p_i = 1) \tag{4}$$

where p_i denotes the proportion in which the i^{th} parent or clone is represented in a seed orchard or in clonal deployment respectively. If $p_i = 1/N$ for all parent clones, $N_{e'} = N$. This solution can readily be extended to a relatively complex pedigree, provided the founding parents can be assumed to be unrelated, by the proportional contribution of each founder (p_{if}) on the basis of:

(1) Its pedigree contribution to the ancestry of each parent/clone;
(2) The proportion in which each clone or immediate parent contributes (p_i);
(3) Summing p_i over all parents/clones descended from that founder;
(4) Applying p_{if} in place of p_i in Eq. 2.

Effective population size ($N_{e'}$) is seen as the most convenient measure of the genetic base to use in connection with clonal diversity, although it does depend on two key assumptions:

- That there was a set of unrelated founder parents*,
- That genetic contributions of founders are reflected in pedigree, whereas selective forces and stochastic variations due to the mechanisms of genetic recombination can lead to representation of genes from individual ancestors departing from pedigree-based expectations.

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* The assumption of completely unrelated founding parents is unlikely in the New Zealand *P. radiata* land race, given the uncertainties of their origins (i.e., number and relatedness of founding parents). Although the early seed importations are known to have been quite large, they would have represented a very incomplete sample of the species' natural range. This has been recognised by New Zealand Forest Research Institute breeders, with genetic infusions from the five native populations being seen as important.

Neither assumption will be completely fulfilled. However, trying to adjust for departures from the former complicates the computation of $N_{e'}$. The inevitable departures from the latter will lead to increasing downward departures from the theoretical $N_{e'}$ over successive generations. It seems unlikely, however, that actual departures from these assumptions will be crucial.

In addition, this treatment does not account for the roles of mutation and certain recombinational events in offsetting any run-down of genetic diversity. However, with the numbers of parents and selection candidates that would be involved in a good breeding programme, and the limited number of generations, such effects are unlikely to be important.

The simplest approach is to achieve risk spread by using a number of unrelated clones in equal proportions, which is a convenient basis for studying basic relationships between risk and number of clones. In practice, various clones will be used in different proportions. Reasons for this include factors influencing the availability of ramets, and a desire to have the very best clones more heavily represented. In any event, it is in principle possible to juggle the numbers of clones and the proportions in which they are used to give a prescribed $N_{e'}$ value. Deploying individual clones in proportions that trail off down the list of clonal rankings can be expected to give an optimal combination of genetic advance and genetic diversity (Lindgren *et al.* 1989; Lindgren 1993). It can actually mean that more clones may be used, but the lowest-ranking selections would each be used in only very small proportions.

Mosaic versus *intimate mixtures*

A basic decision is whether to deploy clones in a mosaic of monoclonal stands or in mixtures. Monoclonal stands have major potential advantages for marketing, processing, and utilisation, and significant potential advantages for establishment and tending and harvesting (Libby 1987b; Burdon 1989; Aimers-Halliday *et al.* 1997). They also offer possible gains in production through exploiting any divergences between competitive ability and crop productivity, a phenomenon that has underlain much of the yield gains in breeding traditional crop plants. However, they do have the increased risks of loss through biotic damage and possibly climatic damage, because there is no opportunity for better adapted clones to take advantage of reduced competition. The importance of this aspect may depend greatly on the feasibility and economics of salvage harvesting.

Intimate mixtures of clones will sacrifice various advantages of tree-to-tree uniformity and predictability in wood properties, although monoclonal blocks will not overcome certain troublesome within-tree variations. Zobel (1993) reported that growers of clonal eucalypt plantations favour monoclonal blocks for their uniform growth and wood properties (cf. Denison & Quaile 1987), while Zsuffa *et al.* (1993) cited unacceptable variability of growth in intimate mixtures of poplar clones. A mixture of clones can surely buffer stand performance against the presence of a minority of maladapted clones, but a difficult question arises as to whether a set of well-adapted clones can perform better in mixture than in monoclonal blocks, through complementary exploitation of the resources of the environment. However, the actual evidence for the latter effect in forest trees appears to be very limited and, at best, equivocal (von Weuhlisch *et al.* 1990; Zsuffa *et al.* 1993; DeBell & Harrington 1997; Zhou *et al.* 1998).

A mixture of clones can allow the relatively painless elimination of disease- or pest-affected clones in the course of thinning, without greatly compromising yields. Nevertheless, some growers of clonal eucalypt plantations have decided that removal and immediate replacement of whole blocks of single disease- or pest-ridden clones is an easier option (e.g., Zobel 1993). If too many clones fail, and deferral of harvest of surviving clones is not a satisfactory option, this approach may prove unsatisfactory. In any event, where outright failure of clones is involved, the production losses with mixtures would be less than proportional to the clonal failure rate, in contrast to monoclonal blocks.

The choice between deployment in mixtures or in mosaics of monoclonal blocks can, therefore, depend on several operational factors. Factors that favour the use of monoclonal blocks include:

- Terrain and roading network that allow single clones to be deployed in blocks that can readily be salvage felled;
- The material that allows premature harvest without undue losses;
- Silvicultural regime that does not allow for thinning (despite the terrain);
- The major utilisation advantages in processing defined batches of individual clones.

Conversely, factors that favour intimate mixtures of clones include:

- Terrain that makes salvage felling of blocks inconvenient;
- Tree-to-tree uniformity of wood properties not greatly enhancing the economics of processing and utilisation;
- Precommercial thinning being needed near the end of the risk period in stand development;
- Major epidemiological protection being conferred by the use of intimate clonal mixtures.

There are variations of the mixtures option, such as assigning particular clones to individual rows, which might facilitate systematic thinning but may contribute little to risk management. Alternatively, mixtures of different subsets of clones could be deployed in mosaics. However, while the principles can easily be set out for making a choice, they may not be straightforward to apply. For instance, the very conditions that facilitate salvage felling of blocks will also facilitate thinnings, especially commercial ones. Moreover, since the biological risk spread in clonal deployment is directed largely at unknown problems, it cannot be tailored specifically to the epidemiological behaviour of particular diseases or other problems.

A mixture of clones that represent a single ideotype, in effect a genetically diverse but phenotypically similar multi-clonal line, should be an effective option for risk management, especially where there is a known serious pathogen. The clones would have to be well characterised, so this option would be probably be possible only in a well-established clonal programme. Such a clonal mixture should ideally be known to have multiple resistance mechanisms that would be able to counter genetic shifts in the pathogen.

Mosaics of monoclonal blocks, used in forest management by "clonal portfolio" (Burdon 1992; C.J.A.Shelbourne unpubl. data; Aimers-Halliday *et al.* 1997), are another option which can address market risks (see earlier). The essential elements are the planting of sub-compartment-sized management units of many single well-characterised clones. Hundreds of clones should be under test in various stages. It is recommended that numerous

clones are deployed at any one time, covering a range of breeding objectives, and of wide genetic diversity. They should be evaluated for a wide variety of characteristics including growth, form, disease resistance, site adaptation, basic wood properties, and wood-processing and end-product traits. This portfolio-management strategy is aimed at minimising biological and marketing risks by managing and eventually exploiting a large, genetically diverse and well-characterised group of clones. Efficiency and profitability will be much enhanced, not only from the growing, harvesting, marketing, and processing of logs, but also from the production and sale of a range of end-products. A dossier of each clone grown in the forest would allow clones to be optimally managed and the out-turn channelled to processing plants and markets existing at the time of harvest.

Trying to maximise genetic gains from extremely intensive clonal selection may be unnecessary, as well as undesirable from a genetic diversity standpoint, and may also increase market risks. Maintaining a wide diversity among production clones is necessary to fulfil the requirements of "clonal-portfolio" forest management for different end-uses. By doing this, the biological risks from reduced diversity, such as increased susceptibility to catastrophic loss or damage from fungal and insect pests and environmental causes, can also be reduced. The in-built diversity of clonal-portfolio management should allay fears that clonal forestry might increase biological risks of disastrous attack by pests and diseases. Economic risk factors relating to uncertain future markets and end-products are likely to be another driving force in maintaining a reasonably large number of clones in production forests (Aimers-Halliday *et al.* 1997).

A third deployment option has been proposed by Park *et al.* (1998). It involves planting mixtures of tested clones and seedlings from selected families. This would reduce the cost of planting stock and increase the initial genetic diversity of the plantation, at least prior to thinning. Exceptional seedlings could fill gaps created by poorer-performing clones or ramets, which could be removed at thinning. However, this deployment option may result in an undermining of some critical benefits of clonal forestry, i.e., the predictability and uniformity in performance of well-tested clones.

Issues of landscape-scale clonal deploymnent

Given that clonal risk spread need not necessarily be adopted at the level of the individual block or plantation, there remains the question of the appropriate scale of the geographic units within which the desired clonal risk spread needs to be achieved. This scale is likely to vary according to local factors, which may include the business circumstances of the forest grower(s). For instance, for a grower with a large forest estate, the appropriate unit is likely to be larger than for a smaller grower. However, other factors of the grower's business interests, such as ulterior forms of risk spread (e.g., outside forestry), may influence rational decisions as to the appropriate scale of "landscape" diversification in clonal deployment. If the grower's risk spread is beyond the region, or even well outside the forestry operation, it may be appropriate to consider what is acceptable risk exposure for the communities on which a forestry operation depends.

Spread in time

Some spread in time for clonal diversification should be acceptable. For instance, current plantings using very few clones may be acceptable if in coming years a different set

of unrelated clones is to be used. To some extent, this may happen automatically with the genetic obsolescence of existing select clones, if new and better clonal selections are coming from unrelated lineages. However, any lack of diversification in time should almost certainly be confined to fairly narrow time bands — the fewer clones used in a time band the narrower the acceptable band. A high rate of failure within an age-class of more than 5 years, say, could prove very disruptive of forest out-turn with a species such as *P. radiata*, especially under short rotations. Moreover, with age-dependent hazards, such as certain diseases, increased exposure to risk within age-classes may be inherently undesirable.

GENETIC DIVERSITY CONCERNS AND REGULATION OF PRACTICE FOR CLONAL FORESTRY

Concerns about Genetic Diversity

The need for retaining genetic diversity will be all the more critical if clonal forestry of *P. radiata* is widely adopted by industry (Burdon 1997). However, using clones does not necessarily decrease genetic diversity (Mullin 1992; Aimers-Halliday *et al.* 1997) which can be maintained, and even much enhanced, by judicious composition of clonal mixtures or mosaics of monoclonal blocks. High genetic diversity will be maintained, in any case, in breeding* and gene-resource populations. This allows for high selection differentials in selecting parents for future production populations, and the conservation of useful alleles that are in low frequency in the population (Aimers-Halliday *et al.* 1997). In other words, the breeding population will be managed to have a variance structure to allow for future responses, even if production population is genetically limited at any one point in time.

Massive adoption of clonal forestry could pose a problem in the event of a biotic crisis that could not be countered by sufficient unrelated selections from breeding populations and dedicated gene-resource populations (Burdon 1997). Such a development could force tree breeders to abandon the position that commercial plantations represent a genetic dead-end, in the hopes that the sheer numbers of segregant genotypes would provide a worthwhile pool of favourable genetic mutations. In nature, such mutations, while occurring at extremely low frequencies, may be provided by dense natural regeneration over large areas and long time periods, with mixed mating (allowing some inbreeding) providing opportunites for expression of favourable recessives. While the very large numbers of *P. radiata* trees grown in New Zealand might be sufficient to provide enough favourable mutants, this potential could be negated if only limited numbers of clones are being planted .

Overseas Legislation, Regulations, and Internal Rules

Some countries have legal or regulatory restrictions specifying the minimum effective number of unrelated clones or seed parents for use in single commercial plantations (e.g., Table 2). Mondi Forests in South Africa declared a policy of using at least 30 clones for a species within a geographic area (Denison & Quaile 1987). The formal restrictions for some

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* It is the breeding population in which progressive genetic gain can be achieved by intercrossing parents and selecting among their progeny over successive generations.

TABLE 2–Regulations affecting deployment *. For legislative/regulatory requirements in Sweden, Federal Republic of Germany, and Canada, ca 1992 *see* Muhs (1993)

Country	Description of Federal law
Germany	NO clonal plantings. 500 clonal mixture for major species, 100 clones for minor species, 100 clones of major species and 20 clones of minor species for specific situations. Families planted only with permission. Poplars excluded. (Established 1957, modified 1979, 1981)
Sweden	NO clonal plantings. Mixtures of 29 clones from 10 families. Planting block limited to 20 ha for vegetative material. (Established 1979, modified 1994)
Finland	Registration and trade of clonal material. Testing specified. Tested clones — 33 in blocks or mixtures. (Established 1980, modified 1992)
Denmark	Deals with trade of approved seed source. Self imposed: NO monoclonal plantings, 30-clone mixtures, sufficiently unrelated. CANNOT plant half-sib families. (As of 1994)
	Description of policy*
Canada	
Ontario	Status changing. Regulates the deployment of clones (100 clones from 10 unrelated families), open-pollinated and full-sib families (15) through control of pedigree and magnitude of planting. Mixtures or blocks. (Established 1988)
BC	NO monoclonal or full-sib blocks on crown land, except for hybrid poplar. $N_e \geq 10$ for seedlot or clonal lot for crown land ($N \geq 20$ for clones) (Established 1997)
Alberta	NO clonal forestry on public lands (most forest land is public)
Quebec	NO monoclonal plantings. Vegetative multiplication of ≥20 families mixed before planting (self-imposed)
Australia (Qld)	≥10 clones or families (full-sib or half-sib) of introduced *Pinus* sp. deployed at any one time (self-imposed)
NZ	No regulations on clones
France	NO clonal or full-sib family plantings. Accepts tested open-pollinated families. (Established 1989)
Norway	Regulates only vegetatively-propagated material. NO monoclonal plantings. 30 clonal mixtures. 10 unrelated families in bulk propagation; maximum of 100 seed per family. (pending 1994)
USDA Forest Service—PNW	NO monoclonal plantings; 30-clone mixtures only for *Populus trichocarpa* (self-imposed)
	Particulars of "rules"
Weyerhaeuser Co.†	Seed from individual orchard trees <10% of any annual planting. Planting blocks ≤120 acres

* From information kindly provided by Dr Barbara McCutchan, Manager, Sustainable Development, MeadWestvaco Corporation, Stamford, CT, U.S.A.
† From "Generations of Quality. The Tree Improvement Story." Undated newsletter, Weyerhaeuser Co., WA, USA: p.7

European countries include some extremely restrictive provisions, for which we see no technical justification, but their very existence gives them legitimacy. If the New Zealand forestry sector is not seen to lead in this area, we may have similar provisions imposed. However, since *P. radiata* is exotic to New Zealand, there is less public sentiment than with native species grown in plantations in North America and Europe. Thus it is less likely that public pressure groups will lobby for restrictive Government legislation for clonal deployment in New Zealand's plantation forests.

Issues for Implementation in New Zealand Forestry

To gain support in the politics and social pressures of the modern society, any organisation involved in applying new biotechnology must communicate its benefits, and management of associated risks, to decision-makers and the public (Mátyás 2000). Clonal forestry (and application of other new technologies) must be seen as part of sustainable development and not as a threat to the genetic diversity and long-term stability of our forest resources.

A large corporate grower can have much flexibility in achieving the appropriate level of cryptic diversity. Achieving it for the large new forest estate being created by the numerous 'small players' could be another matter. Moreover, the emergence of the small players (growers or investors) could lead to a seed supplier, or supplier of tested clonal material, coming under commercial pressures that might not reward responsible practice.

For an individual small player, genetic risk spread may or may not be important, depending on whether, and in what way, the forestry venture fits into a wider scheme of diversification. But, while a genetic risk spread may not be imperative for the individual player, it will still be needed for the regional subsector. In any case, there are likely to be different requirements for different customers for nursery stock, which will pose a marketing challenge.

If large suppliers of clones deal directly with individual growers, it might be quite straightforward. However, there will be the nurserymen in between, often able to produce large volumes of narrowly-based stock by vegetative propagation. The situation is potentially complicated by the larger forestry companies being able to sell pair-cross lots to nurserymen. Some protection against the worst of the potential problems does exist. This comes partly through restrictions within the New Zealand Radiata Pine Breeding Co. on release of top-ranking material. Protection also comes partly in the current practice of downgrading the improvement ratings of narrowly based lines on the grounds that ratings for individual families are less precise than those for groups of families.

It must be acknowledged that clonal forestry is likely to be deployed on only part of the plantation estate, i.e., on more uniform, higher-quality, readily accessible sites. There the initially higher costs of clonal forestry can be recouped. The main benefit of clonal forestry, the delivery of a uniform and predictable product, is unlikely to be achieved on highly variable sites, which comprise much of New Zealand's forestry estate.

Initial Proposals for a New Zealand Code of Practice

We urge against any hurry to be quantitatively prescriptive, given the complexities of the issues, the obvious folly of some of the prescriptions within the European Community,

and the lack of other, widely accepted, codes of practice (the Weyerhaeuser Co. "golden rules" are still only in unreleased draft).

Notwithstanding, we would suggest the following basic guidelines:

Clones (unrelated): at least 20 in a 5-year age cohort in a major forest estate unit, (perhaps 25–30 if monoclonal blocks are used);

Seedlings: at least 16 unrelated parents in a similar entity.

These represent effective numbers (N_e). Arriving at them, despite unequal representation and/or inter-relatedness, should be reasonably straightforward. Less straightforward may be developing detailed prescriptions for ensuring that the requisite risk spread is achieved in practice. Prescribing more clones than seed parents is admittedly arguable. Intercrossing among seed parents, while releasing segregational variation, will mean less variation among pair-cross families than among their parents. One might choose clones for more than random diversity, but at increased risk of including sub-optimal clones.

Setting minimum numbers of clones for monoclonal blocks is complicated by two conflicting considerations:

(1) Monoclonal blocks incur greater exposure to failure of individual clones than intimate mixtures, and

(2) The advantage of such blocks for management, processing, and utilisation depends on using very finite numbers of clones.

Any code of practice would need to be complemented by education. That in turn can be backed up by the availability of fingerprinting tools to verify the genetic composition of crops. In theory, the Resource Management Act could be brought into play, but that is a speculative matter.

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