

**Local Provenance Plant Seed and Restoration:
Scientific Imperative or Romantic Diversion?**

Author: Geoff Williams

“Sarana”

Timor Rd

Coonabarabran NSW 2357

ph 02 6842 2959

email: gwillinorth@yahoo.com

Introduction

It is a widely held assumption that plants used in revegetation projects should be derived from “local provenance” seed. Throughout the last twenty years or so this notion has been a central tenet of the extension literature in government funded natural resource management programs such as Landcare. On the whole I believe this assumption is based on unjustified and tenuous interpretations of the related scientific literature. Indeed in the last five years or so some individuals and organisations have begun to acknowledge that poor or even over-excited interpretation of provenance research has stymied good operational practice for ecological restoration. It is hoped that we are now seeing the beginning of the end of a simplistic application of the phenomenon of provenance to the practice of restoration. Nonetheless an insistence on using “local” seed retains a dominant place in the thinking of many practitioners within the natural resource management sector, contributing, in my view, to wasted resources and poor conservation outcomes.

In this paper I argue that attempts at defining provenance in terms of fixed geography are unnecessary, technically unfeasible, and ultimately non-scientific, and that habitat matching is a better approach to identifying suitable sources of seed. I also attempt to use the discourse surrounding the promotion of provenance and local seed to address the broader idea of the relationship between culture, ecological knowledge and landscape-scale conservation “design”. The practice of ecological restoration represents a *cultural* aspiration that inevitably results in the creation of new kinds of ecosystems no matter how ecologically stringent or scientifically objective our criteria and strategies appear to be. The provenance issue sheds light on the negative impact that poorly thought out ideas and approaches in applied ecology have to progress in achieving restoration goals. This is particularly the case where there is a failure to candidly acknowledge our role as active landscape designers and managers, and agents of landscape change.

A frustrated NRM practitioner

I should make it clear to readers that I farm, and collect from wild stands, native plant seed as a commercial enterprise. I have many years of involvement with “ecological reconstruction” in a variety of contexts. As part of the preparation for writing this paper, I consulted widely with many of the players, including other seed collectors, seed retailers, staff involved in revegetation and seed management from almost every Catchment Management Authority (CMA) in NSW, CSIRO researchers and the coordinator of Florabank. I also have a Master of Applied Science degree in environmental horticulture. My thesis was based on an investigation of provenance variation within selected species of Australian rainforest trees. Specifically the study attempted to identify physiological variation of value for the growth and survival of those trees in urban landscapes: the amenity horticulture equivalent of the widely practised forestry provenance trial aimed at finding populations with superior growth form, timber properties and the like.

As someone trying to make a living from selling native seed and with a passion for landscape restoration, I often read and hear about the demand for seed for revegetation from the largely government funded natural resource management (NRM) sector. For example Flanery *et al.* (2006) state that in order for some CMAs to meet their existing five-year revegetation targets, they each require 200,000 kg of seed (see also DSE 2004 for more examples of predicted seed requirements). Yet, while there are calls for more seed I see no concomitant increase in actual demand through the commercial collectors and retailers of native seed. The private sector has access to thousands of kilograms of seed of the most important and desirable revegetation species, but is largely ignored by government-funded natural resource management agencies because of very strict but not strictly scientific understanding of local provenance. In contrast the mining revegetation industry, in many cases with a more balanced approach to provenance and excellent direct seeding skills and technology, is consuming increasingly large volumes of seed sourced through private seed enterprises.

An additional factor seems to be that in some areas the demand for seed is not as great as the strategies and policies of regional NRM bodies might lead us to believe. With many CMAs there is a large gap between the setting of large revegetation targets and the activity of sourcing seeds and putting them in the ground. This point seems to indicate that many CMAs and similar bodies across the most modified landscapes of south-eastern Australia have insufficient funds and/or expertise to drive the strategies they have created to improve natural resource management. For example, it is widely agreed that the adoption of direct seeding techniques is a prerequisite for successful broadscale restoration of native vegetation. Yet in NSW some CMAs do not include direct seeding as part of their programs, despite the presence of ambitious restoration targets. I have been told by various CMA personnel that “direct seeding doesn’t work in our area”. This is a defeatist position to take, perhaps largely attributable to the infancy of some NRM bodies. Yet at the same time, while basic strategies in the art and science of revegetation are being side-stepped, much money and effort is still being spent on “defining provenance boundaries” and formulating “provenance policies”, as if somehow “provenance” is actually the most important issue of all.

Setting the scene

One of the primary reasons given for using local seed is the need to preserve biodiversity. It is argued that the uniqueness of all local variation within a species is important. By planting more of a given “provenance” we not only enhance its stocks but also avoid “genetic pollution” with “non-local” genes. The other argument is that plants derived from local seed will do better on the site because they will be adapted to the local environment, therefore giving plantings a greater chance of success. While there is validity to both these arguments in some contexts, in others they are invalid as scientific principles and as principles guiding achievable outcomes.

The connection between a site and the genes of the organisms living there is indeed a seductive, powerful and, at times, even a moving idea. Unlike much of North America and northern Europe where the entire flora was literally wiped off the face of the earth

by glacial episodes (and where post-glacial plant colonisation has in some cases been assisted by waves of human migration), the Australian flora and landscape has that profound feel of “primitiveness” with which we are all familiar. Notwithstanding the fact that many of our “natural” ecosystems are largely artefacts of Aboriginal management, one result of this sense of natural agelessness and uniqueness has been a strong desire to restore ecosystems to their pre-European-colonisation state. I would argue that the provenance notion is culturally loaded in this way, and therefore carries a measure of romance as well as science. As I make clear below, this is not necessarily a bad thing, but I believe it is important that romance is “surfaced” as a value to allow everyone to be clear about what they are doing and why they are doing it.

There has been some progress in the understanding of provenance, helped along by recent genetic studies that have been carried out with an applied focus directed specifically at the restoration industry (see for example Broadhurst *et al.* 2006; Broadhurst, North & Young 2006; Broadhurst & Young 2006; Buza *et al.* 2000; Young 2005). Florabank and Greening Australia are both organisations that have arguably made the whole notion of provenance much more problematic and fundamentalist than it needs to be, but to their credit have begun to respond to this literature (see for example Flanery *et al.* 2006; Mortlock 2000; Mortlock 1999). Perhaps the most significant realisation is that if certain direct seeding revegetation targets are ever to be met, then existing stands of the species in question cannot be relied upon as a source of seed because they are simply too small to provide the quantity and quality of seed required (Flanery *et al.* 2006; Broadhurst, North & Young 2006). Thus even if it *was* ecologically important to take a fundamentalist approach to provenance (which I argue it is not), compromise of some kind is unavoidable (Sage 2006).

While these advances are encouraging, and while many of the points I am making have been made before, the situation on the ground in terms of practitioner attitudes remains fragmented. The idea of “maximum permissible seed collection distances” is still a major part of the policy framework being implemented or considered in several

CMA in NSW. One CMA practitioner with vast experience of direct seeding has been told by colleagues from within his CMA that “if we can’t get local seed, we’re not going to plant anything”. In this CMA even seed that was harvested from a seed orchard containing plants of known provenance was considered unsuitable for planting back into its original provenance (ie. the place from where the seed used to establish the seed orchard was collected from). This was because the seed orchard was located at some distance from the original collection location. The overall impression I get is that many recognise that the time has come for a new approach. However, in the face of twenty years of strictly local collections being considered “best practice” many still seem confused by the whole debate and are very scared of breaking what amounts to a provenance taboo.

At the other extreme some CMA staff appear to have almost completely rejected consideration of provenance. In some CMAs landholders who receive funding for revegetation are, vague recommendations to source local seed notwithstanding, left to source any seed they like. More than one senior CMA officer I spoke to made statements to the effect that “as long as they get the species right it doesn’t really matter”. While in some ways it is a relief to hear people espousing a “lets just get on with it and get some plants in the ground” attitude, I think this backlash is unfortunate. In particular such a free-for-all is likely to result in the use of seed collected from a narrow genetic base. For example it is not unusual for commercial collectors to sell as much as 10 kilograms of seed collected from a single large tree, and for that seed to subsequently be the only source used in a revegetation project. A further risk is that some seed may be poorly matched to the site (for example seed from coastal populations with no frost tolerance used in inland projects where severe frosts occur). Thus much of the money currently being poured into restoration projects via the CMAs could be wasted on plantings without long-term viability.

Phantom provenance boundaries

The term provenance as used or understood among many NRM workers still carries implications, often in quite subtle ways, of biological discreteness. Unlike species, which can be defined and identified on relatively solid biological ground, “provenances”, as discrete biological entities, exist only in the human imagination. That is not to say that populations of species do not vary in their genetic profiles. On the contrary, genetic variation at numerous levels between that of species and individual (region, population, neighbourhood and family) is the norm. Indeed this variation could be considered as much the dynamic engine room of evolution as variation among individuals. However, except in certain relatively unusual cases, such as an inbreeding species that occupies a distinct, isolated habitat, these patterns of genetic variation are not definable as entities in their own right. In other words, geographic variation exists, but not in accurately mappable or discrete packages. Just as importantly, the true significance of that variation for evolution is not related to arbitrary, human-defined spatial boundaries or nodes in a given landscape, and owes more of its evolutionary value to its very messiness, rather than to its neat matching of supposedly identifiable habitat types.

Gradual or abrupt spatial changes in distribution of genetic characteristics are created by several factors. In understanding the distribution of genes across a species, we have to account for contiguity in the distribution of populations (and therefore the existence of gene flow) across wide geographical areas. We also need to consider gene flow over space *and* time (see below) between *discontinuous* populations. In addition, we need to account for varying degrees of selection pressure operating on the populations. Dramatic changes in the distribution of genes can occur over very short distances, even in the face of unlimited gene flow (Jain & Bradshaw 1966; Antonovics & Bradshaw 1969; Snaydon 1984). The gradual, continuous changes (what was once fashionable to call “clinal” variation) are more problematic to provenance geographers. However, if this were the only problem then we could no doubt draw arbitrary but nonetheless useful boundaries to delineate provenances. But the critical point (and one that seems to be poorly understood or largely ignored in

much of the provenance literature) is that the difficulty of mapping within-species variation is not just a question of blurry boundaries arising from continuities in genetic variation. The more difficult and fundamental ecological fact is that the pattern of variation is unique for individual genetic traits.

Within-species variation is multi-dimensional, with the pattern of distribution of individual genes or clusters of genes spreading out across the landscape in bands, spots and smudges that cut and loop across one another. Thus, based on a single morphological attribute, we may feel we have identified a distinctive system of different populations but may find that another morphological attribute, perhaps less obvious to the eye, displays a completely different pattern (Millar & Libby 1991; Langlet 1971; Kay 1984; Turnbull & Griffin 1986). Variation in physiological adaptations is even more complex. Take for example non-morphological adaptations to “drought tolerance”. These may be influenced by a whole series of genes, each one with its *own* pattern of distribution or frequency across the range of a given species (Hawkes 1986). A single gene relating to drought tolerance may follow a pattern that matches gradual changes in rainfall distribution while a second gene may match patterns of variation in water holding capacity of various soil types. Another may have more to do with the ability of the plant to compete with other plants for moisture as a seedling, and may therefore follow a completely different pattern based perhaps on the distribution of other species or vegetation types across the range.

But what of the various methods of genetic analysis developed over the last thirty years or so, the isozyme, microsatellite, RFLP and PCR studies? Don't these give us a definitive picture of the pattern of variation within a species? As far as I can make out the answer is “no”. To begin with, these studies utilise “neutral” (ie. non-adaptive) genetic markers: the conclusions drawn from the data via mathematical models are only valid if the genetic material is non-adaptive (Charlesworth 2003; Bush & Smouse 1992). It is not yet clear what this genetic material does exactly, and the degree to which it is important in evolutionary terms.

Such studies measure phylogenetic relatedness, not the distribution of adaptive traits. Sometimes the phylogenetic pattern matches the adaptive patterns, sometimes not. For example in a study of *Eucalyptus marginata* in WA, it was found that patterns of variation detected via genetic marker analysis did not match those based on obvious morphological and growth characteristics clearly identified by botanists and foresters (Wheeler 2003). Ultimately, these studies are inadequate as a guide for determining patterns of genetic variation of value for use in the revegetation industry (Libby *et al.* 1997).

In emphasising the multi-dimensional complexity and difficulty of classifying within-species genetic variation I do not mean to downplay its importance. Instead, I am suggesting that attempts at defining “provenance boundaries” are misplaced and ultimately non-scientific. Nonetheless this is still a primary focus of many NRM organisations. For example, the Victorian Department of Sustainability and Environment draft native seed strategy (DSE 2004, p.31) states:

Overwhelmingly the biggest issue facing the native seed industry and revegetation more generally, is provenance and understanding the boundaries of use for plant species.

Rather than trying to define these boundaries it would be far better to spend the time and money on better habitat matching profiles via spatial data analysis. An example of such a process used with success at the species level is the climate matching work using computer modelling carried out for forestry plantation establishment (Jovanovic & Booth, 2002). In any case sophisticated tools such as computer models and GIS are often unnecessary for habitat matching in a restoration context. Understanding and observation of soils, climate and vegetation- what might be described as basic applied ecology, or simply as silvicultural or horticultural knowledge- are often all that is required. An appropriate source of seed then becomes any population of the species with a similar habitat, and we can thus ignore twenty kilometre radiuses, catchments, bioregions and all other genetically arbitrary boundaries altogether. Ultimately you can not tackle an amorphous, slippery concept with a rigid, static approach, unless that approach has proven and consistent utility.

Factors such as the site context will influence the stringency required for the habitat matching approach. For example an area adjacent to a National Park with intact native vegetation will require a different treatment to a bare paddock in a heavily cleared landscape with no adjacent remnant vegetation. Other factors that influence genetic variation (such as breeding system and distribution) and the availability of seed and project funding must also be taken into account. Thus when the *design context* indicates that very strict matching of original (remnant) genetic material and introduced genetic material (propagules used for restoration) is appropriate and feasible, then our habitat matching may be so strict as to mean that collection can only be undertaken from the site itself, provided of course that enough propagules exist to make such collection possible. I can think of restoration projects and locations where that context exists, but I can also think of many where it clearly does not.

Genetic health

Avoiding genetic pollution is a prime argument used in favour of restricting the geographic distance of seed sources. This notion is part romance and part science. The romance comes from the culturally loaded notion of primeval nature's purity. There are also valid scientific arguments centred on the phenomenon of outbreeding depression, which essentially means loss of long term genetic or adaptive viability arising from the hybridisation of distantly related provenances. This can arise from incompatible genetic architecture as well as introgression of non-adaptive genes.

In my opinion the introgression of non-adaptive traits is overrated as a threat. Given that most selection pressure is exerted on a plant during the germination and establishment phase, if plants from a non-local provenance prove to be ill adapted to the site, it is unlikely they would ever reach the reproductive stage and pass on their genes to existing or introduced adapted plants. Even if they did, over time they would be "acted upon by natural selection until they come to resemble the original local population" (Warren, 2007 p.3). Genetic divergence in the face of gene flow is not uncommon and the mechanics of divergent selection among adjacent populations in distinct habitats is in effect no different from the selection we would expect on a

single site where propagules from various populations of the same species have been introduced.

Once we understand this we can be more flexible and pro-active in the transfer of genetic material. In cases where doubts exist as to the adaptive suitability of that material we can hedge our bets by bulk-mixing a range of habitat-matched provenances in our seed mix. Those left following exposure to selection pressure will by definition be adapted to the site. As Warren (2007 p.3) points out, this “may unfortunately happen at the expense of information hidden within neutral genetic markers, but this must be balanced against the need to act to conserve the species in which the information is buried”. When the local population is close to or actually non-existent, inbred or dysfunctional in some other way, concerns about genetically polluting that population become utterly absurd: an argument about polluting something that is not there. It is as though the disruption to the notion of purity in our own minds is a greater problem than the fact that the vegetation has been obliterated, and the landscape stripped of its aesthetic values, fauna and ability to function sustainably.

The incompatibility of genetic architectures is not well studied and so far there is limited evidence that it is a widespread problem. Nonetheless, if evidence became available, it would be important to consider the implications of incompatibility for the viability of reconstituted ecosystems. But again, geographic distance is unlikely to be a useful guide in assessing risk. In certain forbs for example, outbreeding depression was shown among progeny derived from plants growing one hundred metres apart (Waser *et al.* 2000) while in another, progeny derived from hybrid populations growing 1000 kilometres apart showed equal or superior fitness to the local-only crosses to the F3 generation (Fenster & Galloway 2000). The evidence so far suggests there will be no simple and widespread patterns common to many species, so flexibility through mixing seed batches seems a far more sensible approach than constantly fretting over the degree of “localness” of each seed batch.

More importantly, the weight of evidence overwhelmingly indicates that the greatest threat to long term reproductive or adaptive viability of plantings comes from inbreeding depression rather than outbreeding depression (Frankham *et al.* 2004). In the case of many widespread species, what may be observed as a discrete local population today was, before widespread clearing, once more or less part of a continuum of plants or at least of populations with significant gene flow among them. By treating what we see today as specific “local provenances” we are in effect collecting seed from a limited gene pool, and condemning the progeny of those plants to a downward spiral of inbreeding (Broadhurst, North & Young, 2006). Again, as well as maximising the number and spread of seed-source plants within populations, the solution is to bulk-mix several habitat-matched batches.

Arguably with many species it would also be wise to include in such bulk mixes some seed from one or two populations subjected to *different* edaphic or climatic regimes. This would in effect “reconnect” older patterns of gene flow and help buffer our new population against environmental change. We need to keep in mind that diversity *within* populations is as essential to the survival of species as the diversity *between* populations.

Designing for change

By concentrating on genetic viability and adaptability rather than “purity” or “localness” we are better placed to ensure the long term survival of populations and species by maximising their ability to evolve over time in response to long term environmental change (Frankham *et al.* 2004). This is the “bottom line” function of preserving genetic diversity: not maintaining diverse populations for their own sake, but increasing the resilience of the genome to extinction. Of course, some adaptations belonging to local populations may only be revealed over longer periods of climatic cycles and so on, but I think the emphasis should be on ensuring there is sufficient diversity within the population to cope. I think it is naivety, hubris or something in between to suggest that we can even know what selection pressures may be important

at highly modified, or even relatively pristine, sites as global warming, weed invasions and other short and long term changes kick in.

In addition, a certain rate of species extinction is a natural process, and population extinctions are even more common. In fact one of the more interesting conclusions derived from many genetic marker studies is that the observed patterns of relatedness can only be explained if it is assumed that populations of the species in question have become extinct over parts of its range, and that these areas have subsequently been recolonised by other populations (Charlesworth 2003). Population extinction, migration and hybridisation are as much a part of the scene as isolation and genetic divergence. Thus plant species and populations have their own dynamic *history* and change itself is not to be feared. It is anthropocentrism in the extreme to assume that nature cannot be trusted to evolve. In fact, it amounts to a kind of pseudo ecological neo-creationism, one that manages to ignore evolution by selectively holding a certain ecological point in time and space as *the* reference point for all ecological design and reasoning.

Entire landscapes too have their own history, and change is the rule, not the exception. Mining industry restorationists deal with sites where the mutability of landscapes cannot be denied. As one such worker said to me, referring to a site comprised of bedrock 100 metres below what used to be the soil surface, “whether or not you use a local provenance doesn’t seem all that important when you are trying to replant the surface of Mars”. This is an extreme case but it is worth remembering that the environmental conditions at most restoration sites today will not closely match those of pre-European times. How many restoration sites have never been exposed to logging and/or clearing and/or grazing and/or cropping and/or weed invasion and/or altered fire regimes, to name but a few potential changes?

It is quite acceptable to assume that genetically differentiated provenances exist (at least partly) because of unique sets of selection pressures over a geographic range. However, when so many of the environmental conditions that once existed are no longer present or have been modified, we are on very shaky territory to insist that only

the provenance that existed prior to European settlement is the one that is appropriate to our revegetation site. Unless every climatic and edaphic factor, every grazer, competitor and symbiont and every disturbance and successional process that a provenance was exposed to prior to European settlement remain unchanged or can be restored, we cannot argue that in principle, the “local provenance” is better suited to our site than another may be. According to one CMA officer based in the Hunter Valley, repeated attempts at planting *Eucalyptus melliodora* (Yellow Box) in this region using locally collected seed failed because the plants were destroyed by leaf eating insects. It wasn't until more distant provenances with less palatable foliage were imported that success was achieved. A direct seeding contractor I spoke to referred to his local *Acacia dealbata* (Silver Wattle) provenance as “a dog of a thing” because it too is almost impossible to establish in modified landscapes.

Complete reconstitution of previously occurring ecosystems is of course simply not possible anyway, not only because it would be technically and economically unfeasible, but also because, as I have hinted, one cannot reconstitute something that was never fixed in space and time. The set of conditions that led to the formation of a certain “provenance” was never “set”: ecosystems are far too “fluxacious” to allow the existence of such imaginary, static states. We may refer to examples of extant native vegetation as our template, but of course they themselves are not what they were: burning regimes, climate, weeds, grazing marsupials, Aboriginal hunters and in many cases nutrient regimes are all now altered or gone altogether. Another way of putting all this is to simply say that the mutability of nature should give us cause to relax a little, and to realise that in creating something that is, in various ways, new we are not necessarily creating something that is essentially unnatural.

Implications and conclusion

The natural human response to extreme complexity is to whittle it down into a more definable, discrete formulation. This is fine with many phenomena, but in the case of within-species variation this creates all kinds of mischief, because it distorts understanding of the phenomenon to an unacceptable degree: multi-dimensional

complexity is the very *essence* of provenance variation, and therefore in turn the very stuff of evolution itself. In a context of environmental change and disturbance at all levels, from localised nutrient regimes to global climate, the complexity and value of this variation is not destroyed but rather enhanced by the designed transfer of genetic material across geographic distances. According to the provenance orthodoxy such transfer is seen as pollution, whereas in my opinion it is better viewed as evolutionary buffering. As an ecologically trained seed supplier, I hope to assist the ultimate user of seed in assessing the design context of a given project. Within that context my goal is to match the conditions at the site to appropriate (largely meaning habitat-matched) batches of seed available on the commercial market, either as stock or as *in situ* material able to be collected.

The notion of provenance as used by many is largely a cultural rather than biological one. It is largely used, I believe, as a tool for avoiding certain realities regarding inadvertent or deliberate anthropogenic change. It allows us to indulge in the idea that by protecting “ancient and sacred” genetic patterns, we are succeeding in our task of letting nature be natural. With the ostensible aim of simply facilitating the restoration of what *was* (unspoilt nature) we can avoid the uncomfortable feeling that we may in fact be “playing god”. I think it better to be up-front about the fact that in attempting to mitigate negative human impacts on the environment, we are undertaking a form of ambitious and creative ecological landscape gardening (for a definition of the word landscape as I use it here, see Williams [2004]).

We are not acting as an “invisible hand” on behalf of nature, reverently deferring to her rules. We are selecting species, sowing seeds, preparing the soil, planting seedlings, spraying weeds and managing the stuff that grows. Furthermore these landscapes are not just the result of our direct physical intervention: they are equally a reflection of our individual and cultural *desires*. When we act in the landscape, what we *want* is inevitably part of the mix. Whether we like it or not, our task is to design landscapes, and good design usually only comes about when the full context, the full range of values, is laid on the table for balanced consideration.

It seems there is a fear that if we admit that what we are doing is based on culture and desire, then our arguments for the value of restoration using native species somehow lose their power. If it's all open to cultural interpretation, then what is to stop people covering the landscape with thorny Gleditsias and planting creeks with Willows? If pre-existing ecosystems can never be entirely restored, does this mean we should just "give up"? The answer is "of course not". We simply need to acknowledge that what we are doing is creating new "simulacrum" ecosystems *based* on ones that existed at a certain point in time. And the arguments that underpin the use of indigenous plants to recreate these simulacrums lose none of their power couched in cultural as opposed to scientific terms: as a cultural pursuit, the act of revegetating is motivated by a plethora of worthy values. A list of such values/goals may include the following: to allow humans to enjoy biodiversity; to fulfil our moral obligation towards nature; to allow evolutionary processes to continue; to provide ecosystem services; and to recreate what existed before European settlement. The maintenance of past patterns of within-species genetic variation must be seen in the same context: one value among many.

The problem is that so long as we are unable to face up to the active role we inevitably play in shaping ecosystems (reconstituted or otherwise) we sacrifice much of our technical and strategic prowess. It is hard to do good hands-on work when the prevailing (yet not quite explicit) paradigm is "hands-off". We can only overcome the provenance taboo and others like it by embracing our role as creative and pro-active designers of landscapes that are rich in every sense of the word: in biodiversity, in beauty and in ecological processes. The point is that these landscapes can be thriving ecosystems and human artefacts at the same time. As practitioners dealing with a complex "ecotone" between science and romance, nature and culture, surely the design approach- the one that sees values as potential design criteria rather than "truths" or otherwise- is the only one that can succeed. If the modest idea of mixing a few batches of seed of a single species from a range of locations is seen as heretical then so be it. To me it just seems like good design: and good design will be required as part of our *own* adaptation to this landscape.

References

- Antonovics J. and Bradshaw A.D. (1969) Evolution in closely adjacent plant populations VIII. Clinal patterns at a mine boundary. *Heredity* 25, 349-362.
- Broadhurst L.M. and Young A.G. (2006) Reproductive constraints to the long-term persistence of fragmented *Acacia dealbata* (Mimosaceae) populations in southeast Australia. *Biological Conservation* 133, 512-526.
- Broadhurst L.M., North T. and Young A.C. (2006) Should we be more critical of remnant seed sources being used for revegetation? *Ecological Management & Restoration* 7, 211-217.
- Broadhurst L.M., Young A.G., Thrall P.H. and Murray B.G. (2006) Sourcing seed for *Acacia acinacea*, a key revegetation species in south-eastern Australia. *Conservation Genetics* 7, 49-63.
- Bush R.M. and Smouse P.E. (1992) Evidence for adaptive significance of allozymes in forest trees. *New Forests* 6, 179-196.
- Buza L., Young A. and Thrall, P. (2000) Genetic erosion, interbreeding and reduced fitness in fragmented populations of the endangered tetraploid pea *Swainsona recta*. *Biological Conservation* 93, 177-186.
- Charlesworth D. (2003) Effects of inbreeding on the genetic diversity of plant populations. *Philosophical Transactions of the Royal Society* 358, 1051-1070.
- DSE (2004) *Draft Victorian Native Seed Supply Framework*. Victorian Government. Victorian Department of Sustainability and Environment East Melbourne.

Fenster and Galloway, (2000) Inbreeding and outbreeding Depressions in Natural Populations of *Chamaecrista fasciculata* (Fabaceae). *Conservation Biology*, 14, 1406-1412.

Flanery F., Carr, D. & Rawlings K. (2004) Thinking bush thinking seeds. *In: Thinking Bush 4. Greening Australia and Native Vegetation Research and Development Program*, Canberra.

Frankham R, Ballou J.D. and Briscoe D. (2004) *A Primer in Conservation Genetics*. Cambridge University Press, Cambridge.

Hawkes J.G. (1986) Intraspecific classification- the problems. *In Intraspecific Classification of Wild and Cultivated Plants* (ed B.T. Styles) pp.87-98. Clarendon Press, Oxford.

Jain S.K. and Bradshaw A.D. (1966) *Evolutionary divergence among adjacent plant populations. I. The evidence and its theoretical analysis*. *Heredity* 21, 407-441.

Jovanovic T. and Booth T.H. (2002) Improved species climatic profiles. *Report for the RIRDC/L&W Australia/FWPRDC/MDBC Joint Venture Agroforestry Program*. Rural Industries Research and Development Program, Canberra.

Kay Q.O.N. (1984) Variation, polymorphism and gene-flow within species. *In Current Concepts in Plant Taxonomy* (eds V.H. Heywood and D.M Moore). pp 181-199. Academic Press, London.

Langlet O. (1971) Two hundred years of genealogy. *Taxon* 20, 653-722.

Libby W.J., Bridgewater F., Lantz C. and White, T. (1997) Genetic diversity in commercial forest tree plantations: introductory comments to the 1994 SRIEG meeting papers. *Canadian Journal of Forestry Research* 27, 397-400.

Millar C.I. and Libby W.J. (1991) Strategies for conserving clinal, ecotypic and disjunct population diversity in widespread species. *In Genetics and Conservation of Rare Plants* (eds D.A. Falk and K.E. Holsinger). pp123-134. Oxford University Press, New York.

Montalvo A.M. and Ellstrand, N.C. (2001) Nonlocal transplantation and outbreeding depression in the subshrub *Lotus scoparius* (Fabaceae). *American Journal of Botany* 88, 258-269.

Mortlock W. (1999) Native Seeds in Australia: a Community Perspective. Florabank, Canberra.

Mortlock W. (2000) Guidelines 10, Seed collection ranges for revegetation. Flora Bank, Canberra.

Sage C. (2006) Land management tradeoffs. *Thinking Bush* 4. 30-32. Native Vegetation Research and Development Program, Canberra.

Snaydon R.W. (1984) Intraspecific variation and its taxonomic implications. *In Current Concepts in Plant Taxonomy* (eds V.H. Heywood and D.M Moore) pp.203-218. Academic Press, London.

Turnbull J.W. and Griffin A.R. (1986) The concept of provenance and its relationship to infraspecific classification in forest trees. *In Intraspecific Classification of Wild and Cultivated Plants* (ed B.T. Styles) pp. 157-189. Clarendon Press, Oxford.

Warren J. (2007) The geographic spread of genetic variation and the case for local provenance. Farmland Ecology Unit, Scottish Agricultural College
<http://www.floralocale.org/content.asp?did=23928>

Waser N.M., Price M.V. and Shaw R.G. (2000) Outbreeding depression varies among cohorts of *Ipomopsis aggregata* planted in nature. *Evolution* 54, 485-491

Wheeler M. A., (2003) Reproductive and molecular biology of *Eucalyptus marginata* Donn ex Smith. Thesis presented for the Degree of Doctor of Philosophy, Murdoch University, Perth.

Williams C.C. (2004) *Old Land New Landscapes*. Melbourne University Press, Melbourne.

Williams M. and Price, P. (2002) Strategic framework for investment in native seed for revegetation in Australia. Michael Williams and Associates Pty Ltd for Florabank, Canberra.

Young A. (2005) Non-provenance genetic issues for native seed sourcing. *In: Fifth Australian Workshop on Native Seed Biology*, 21-23 June, 2004. (eds S.W. Adkins, P.J. Ainstey, S.M. Bellairs, D.J. Coates and L.C. Bell). Australian Centre for Minerals Extension and Research, Brisbane, Queensland.