



## Genetic Indicators for State of the Environment Reporting

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## **Preface**

Commonwealth State of the Environment Reporting was established in 1992 in response to the national strategy for ecologically sustainable development. The system's first major product, *Australia: State of the Environment 1996* (the first ever independent and comprehensive assessment of the state of Australia's environment), was presented to the Commonwealth Environment Minister in 1996.

The next step in the evolution of the reporting system is to develop a set of environmental indicators that, properly monitored, will help us track the condition of Australia's environment and the human activities that affect it. In the course of developing these indicators, Environment Australia has commissioned a number of specialist technical papers. After refereeing, they are being published as the State of the Environment Technical Paper Series (Environmental Indicators).

## **Acknowledgments**

This paper was reviewed by R. Crozier, School of Genetics and Human Variation, La Trobe University, and C. Moritz, Department of Zoology, University of Queensland.



# Abstract

Seven indicators of genetic diversity for state of the environment reporting in Australia are described. These are: number of sub-specific taxa, population size, numbers and isolation, environmental amplitude of populations, genetic diversity at marker loci within individual populations, quantitative genetic variation, inter-population genetic structure, and mating. A rationale, monitoring strategy, and list of potential data sources are given for each indicator. The selection of target taxa against which to monitor the indicators, interpretation of the indicators, and research needs are discussed.

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## Summary

1. A workshop was convened to review monitoring requirements for State of the Environment (SoE) reporting and nominate indicators of the state of biodiversity of Australian biota at the gene level (genetic diversity).
2. Genetic diversity refers to variation among individuals in their genetic endowment and is a crucial level of concern for the survival of species in the wild and the improvement of domesticated species.
3. Pressures on genetic diversity are due to changes in the environment that affect the five main evolutionary processes: 1) mutation, 2) selection, 3) random genetic drift, 4) migration and 5) mating and genetic recombination. The goal of conserving 'appropriate' genetic diversity is best achieved by trying to prevent drastic alteration of the pace and direction of these processes.
4. Genetic diversity is unique relative to species and ecosystem biodiversity because it is generally cryptic and evolutionary processes themselves are difficult to quantify.
5. The indicators of choice for the state of genetic diversity fall into three main categories: 1) population characteristics of species that affect evolutionary processes such as population size and isolation, 2) direct quantification of genetic diversity either using single-gene markers to estimate the level of heterozygosity within populations, or by counting the numbers of recognisable infraspecific types occurring within a fixed set of species, 3) measurements of evolutionary processes such as mating.
6. It is impossible to measure all indicators of genetic diversity on all taxa. Instead a small suite of taxa should be chosen for analysis to represent the responses of other species with which they share genetic, biological and ecological traits (functional groups). As far as practicable, these taxa should be representative of both taxonomic and biological or ecological species diversity at the bioregional level. Rare species merit special but not exclusive attention.
7. The most appropriate reporting scale for indicators of genetic diversity is at the bioregion level as defined by the Interim Biogeographic Regionalisation for Australia (IBRA).
8. Seven overall indicators are proposed that reflect both the actions of the main evolutionary processes and the range of genetic diversity likely to exist within a species. These are: 1) number of sub-specific taxa, 2) population size, numbers and spatial isolation, 3) environmental amplitude of populations, 4) genetic diversity at marker loci within individuals and populations, 5) quantitative genetic variation, 6) inter-population genetic structure and 7) mating. Two additional indicators that may have potential, but at present lack a sufficient knowledge base, are: 8) population turnover and 9) fluctuating asymmetry. Several measures are available for any of these indicators.
9. Interpretation of the biological significance of changes in values of indicators between SoE reporting periods requires a framework of baseline data that represent expected and acceptable norms. Such baselines can be drawn from three sources: 1) indicator values assessed in the first reporting period against which future values can be assessed, 2) data from previous genetic studies of 'healthy' populations of target taxa in the very few cases where such prior studies are available, 3) new baseline data, which, however, limits the selection of target taxa to those

species for which undisturbed populations still exist.

10. Research goals are to: 1) elucidate linkages between different indicator groups, 2) understand how different functional groups of organisms respond to various pressures at the gene level, 3) provide baseline data on genetic diversity for groups of species for which this information is

currently missing (e.g. arthropods, fungi, bacteria). These goals require a substantial research effort. However, without such information, the monitoring of the state of Australia's genetic environment is open to misleading conclusions.

# 1 Introduction

## 1.1 What is genetic diversity?

Genetic diversity is the variation among the various copies of related genes present in different individuals or different species of organisms.<sup>1</sup> Levels and patterns of genetic diversity are the result of both evolutionary and ecological processes and as such reflect the integrity and functioning of evolutionary and ecosystem processes within species.

## 1.2 Why report on genetic diversity?

Genetic diversity is a crucial level of concern in the maintenance of biological diversity for three main reasons: short-term viability of individuals and populations, evolutionary potential of populations and species, and direct use of genetic resources.

### *Short-term viability of individuals and populations*

The ability of individuals to survive and reproduce (i.e. their fitness) depends largely on their genetic makeup (genotype). Individuals carrying more than one form (allele) of a particular gene (heterozygotes) are on average ‘fitter’ than individuals carrying identical copies for that gene (homozygotes), particularly when this effect is summed over the many thousands of genes in the genome of a single individual. In addition, certain alleles of particular genes are deleterious in their effect on fitness when homozygous, whereas heterozygotes can often mask this deleterious effect if they also carry non-deleterious alleles of these genes.

Genetic diversity can enhance population fitness because populations that harbour a range of genotypes are, on average, able to occupy a broader range of habitats than genetically uniform populations. This is because the products of genes and gene interactions enable an individual to survive and reproduce under a limited set of environmental conditions. Products from one form of a gene may adapt an individual to one set of environmental conditions better than products of another form of the same gene, which in turn, is better adapted to a different environment.

### *Evolutionary potential of populations and species*

Evolution is fully dependent on the level of genetic variation within a species. Because of genetic differences among individuals within a variable population, particular individuals will be favoured when environmental conditions change. This is essentially the theory of evolution by natural selection. Populations or species depauperate in genetic diversity are less able to respond to environmental change than their more variable counterparts and are thus more prone to extinction.

### *Direct use of genetic resources*

Genetic diversity also has utilitarian value. The variety of animals and plants that humans use reflects underlying genetic diversity. Plant and animal breeders have manipulated genetic diversity within populations and species to breed an enormous number of different breeds and varieties (genetic forms) for a wide variety of environmental conditions. Exploitation of genetic diversity has also led to disease-resistant and stress-tolerant forms of many crop varieties and animal breeds. The ability to grow wheat and maize and graze cattle and sheep in areas far removed from their native habitat has resulted from direct use of genetic diversity within these species. Many of the world’s most effective medicines have been extracted from genetically distinct varieties of a number of species. More recently, the development of genetic engineering has provided the means whereby any useful genes from a wild species can be transferred into a domesticated species.

## 1.3 How does genetic diversity differ from species or ecosystem diversity?

Genetic diversity is unique relative to the other two levels of biodiversity considered in the SoE Report for several reasons. First, unlike species or ecosystem level diversity, it is frequently cryptic, and requires an experimental effort to detect.<sup>2</sup> Second, genetic diversity expresses itself at several structural levels—individual, subpopulation, population, and metapopulation. All of these levels may play a role in management for long-term conservation. Third, genetic diversity is not a static resource, but is more dynamic both spatially and temporally than either species or ecosystem biodiversity. In sexually

reproducing organisms, individuals are genetically unique and are not the object of conservation per se.

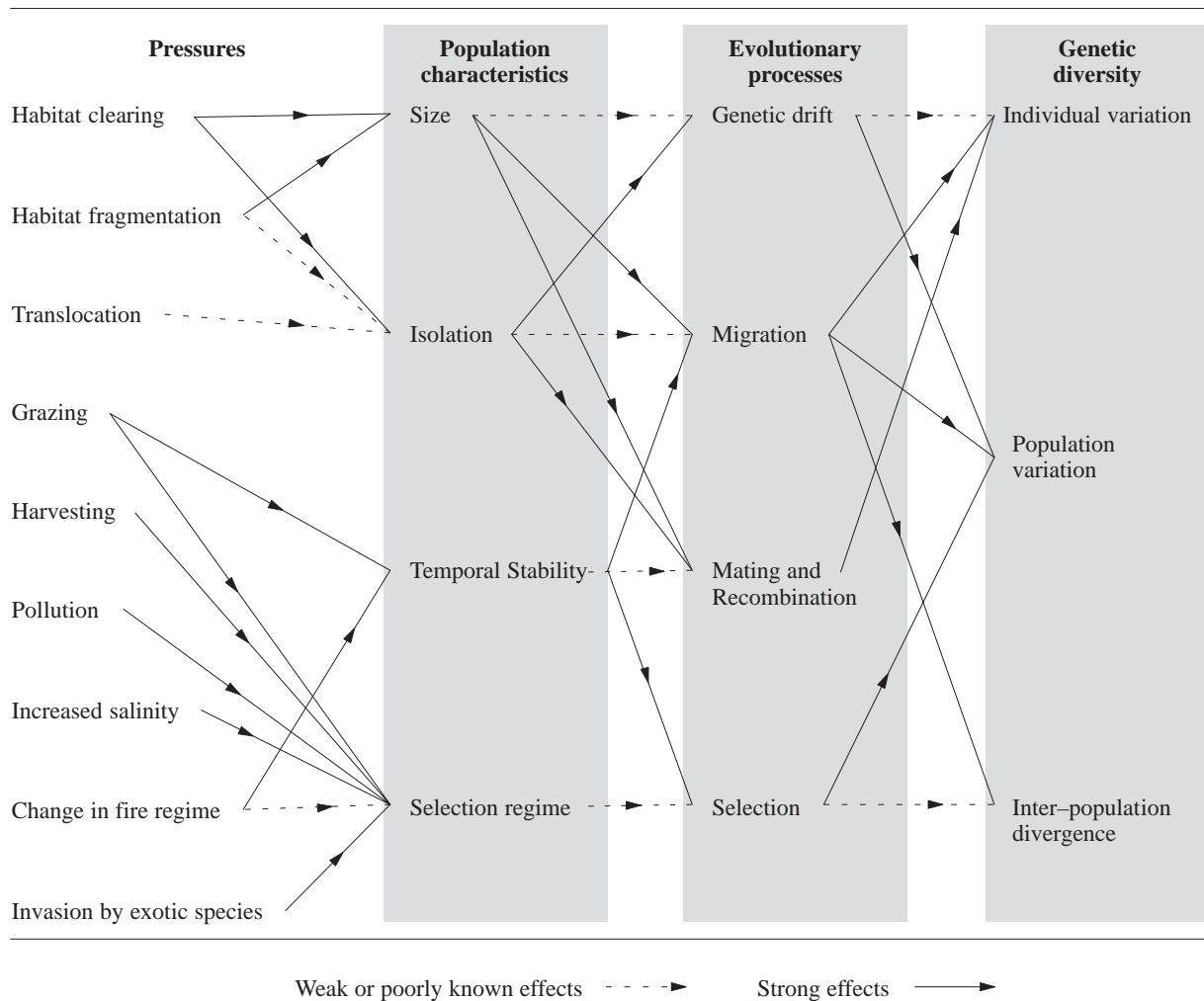
The very cryptic nature of much genetic diversity and its temporal and spatial variability is well illustrated in marked changes in the number and relative frequency of different genes for disease resistance found in individual populations of the native flax plant. Morphologically, nothing distinguishes resistant and susceptible plant types and yet, over short distances, populations range from a complete absence of resistant individuals through to ones containing many different resistance genes. Severe epidemics in such populations can reduce plant numbers substantially, as well as subtly change the frequency of different types of resistance.

## 2 Pressures at the gene level

The amount and distribution of genetic diversity within a species are determined by the interacting effects of five main evolutionary processes. These are:

1) mutation, 2) selection, 3) random genetic drift, 4) migration and 5) mating and genetic recombination. Pressures on biodiversity at the gene level are due to changes in the environment that affect these processes and, through this, influence genetic diversity.

Several such pressures were suggested in the Chatswood Report<sup>3</sup> (e.g clearing, fragmentation, pollution). Figure 1 illustrates how these, and other



**Figure 1: Relationships between pressures, evolutionary processes and biodiversity at the gene level**

Current and foreseeable pressures are unlikely to produce changes in population characteristics that will affect rates or types of mutation so this process is not addressed.

pressures, influence genetic diversity through their impacts on population characteristics and evolutionary processes. A single pressure can affect several processes and through this have an impact on different elements of genetic diversity.

Given the dynamic nature of the resource, the goal of conserving ‘appropriate’ genetic diversity is best achieved not by focusing on maintenance of the genes and genotypes that currently exist within a species, but by trying to prevent drastic alteration in the pace and direction of these evolutionary processes.

### 3 Types of indicators

#### 3.1 What sorts of indicators can be used?

Indicators of the state of the genetic environment are those parameters that are informative as to the state of evolutionary processes. Useful indicators can be drawn not just from direct measures of these processes, but also from population characteristics which are likely to affect particular processes, and from measures of diversity which reflect the action of these processes (see Figure 1). Such indicators are sometimes termed ‘surrogate’ indicators.

For example, three indicators that monitor the effects of habitat fragmentation on mating processes would

be: 1) population size, which can affect mating patterns by restricting the availability of mates, 2) mating parameters themselves such as outcrossing rate, and 3) individual genetic variation, which is directly affected by mating events (Figure 2).

Obviously these three different indicators have different information contents. Direct measurement of mating system parameters such as outcrossing rate may be the most informative at a particular point in time. However, these involve the use of sophisticated marker technologies and are expensive. Using population size as an indicator of what is happening to the mating process is appealing because it is readily measured, and so can be monitored broadly. However, in the absence of good data on how it relates directly to effects on mating, its information content is less. Heterozygosity is easier to monitor than mating itself, and has more genetic reality to it than population size, being directly influenced by mating. However, other processes such as selection influence heterozygosity and it is likely to respond more slowly to a change in mating than would a direct mating system parameter like outcrossing rate. Therefore it is likely to be less sensitive. Conversely, this slow response may be useful if it allows integration of effects over time. The choice of appropriate indicators to use is a trade-off between information content, scale of monitoring and associated costs.

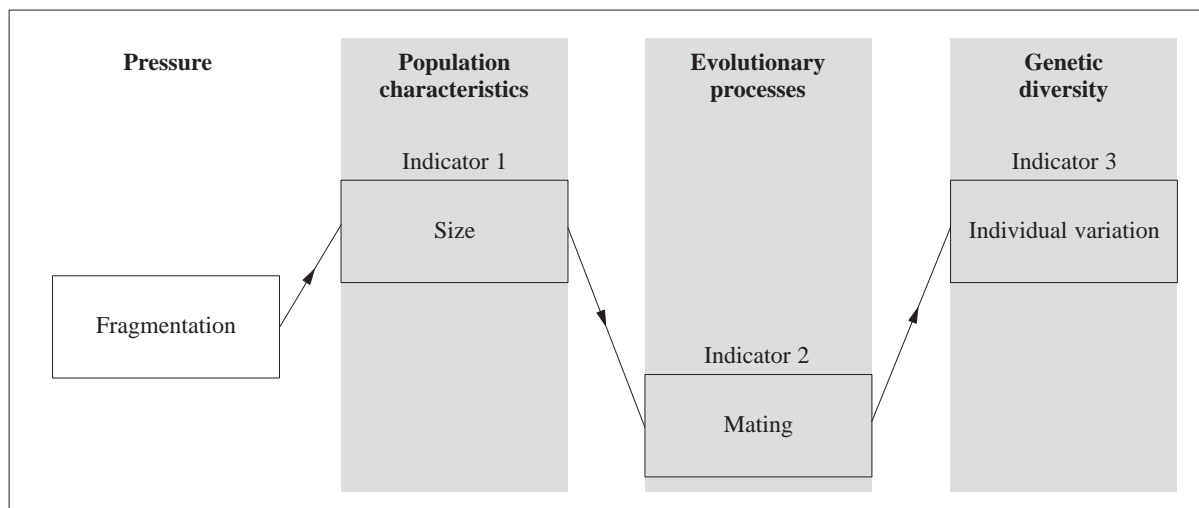


Figure 2: Possible indicators that monitor effects of habitat fragmentation on mating processes

A main research goal must be to elucidate the linkages between potential indicator sets and evolutionary processes. Currently much empirical evidence exists to test theoretical relationships between equilibrium population size, structure and mutation rates, and the amount and distribution of neutral genetic diversity. The empirical work is, however, still limited in taxonomic scope, and clearly deserves future research. Many studies relate population size to genetic diversity for higher plants, but there are relatively few for insects. Data addressing this question for quantitative genetic variation are even fewer. Information from natural populations in severely disturbed situations is also scarce.

### 3.2 Genes of particular utility

Though overall genetic diversity and its underpinning processes are the main focus of our attention, certain genes are of special interest and value in terms of either species conservation or utilisation. Such genes therefore deserve to be included among the genes sampled for SoE reporting. An example of the first interest is the histocompatibility locus complex (MHC) in mammals and birds, which shows great diversity and is linked to disease resistance and mating success. Individuals heterozygous for this complex are on average fitter. Variability within populations for this complex is highly desirable for conservation. However, exclusive attention to MHC variation alone is not justified. Variants at other neglected loci may be lost. Indeed it is possible that the strong selection operating within species on MHC variation will maintain it without specific management. Lack of MHC variation could serve as an indicator of extreme genetic poverty.

An example of the second interest is that of disease resistance genes in the wild species related to crop plants. Diversity at these genes provides a broad base for breeding programs aimed at introducing novel resistance genes into major crop species, and contributes to the species survival in nature. A second example that unites both interests is genes for resistance to *Phytophthora cinnamomi*, a pathogen that causes dieback and threatens the survival of populations of thousands of native plant species. Recently genes for resistance to *P. cinnamomi* have been found in jarrah (*Eucalyptus marginata*), an important timber species in Western Australia.

## 4 Target taxa

It is impractical to measure all, or even a subset, of the proposed indicators of genetic diversity on all taxa. As such it is necessary to choose a small suite of taxa for analysis to provide generalisations about the responses of other species with which they share genetic, biological and ecological traits (functional groups). As far as practicable, taxa chosen for analysis need to be representative of both taxonomic and biological or ecological species diversity at the bioregional level. The most appropriate reporting scale for indicators of genetic diversity will be at the level of bioregion as defined by the Interim Biogeographic Regionalisation for Australia (IBRA).

### 4.1 Criteria for choosing taxa

It is highly desirable that State of the Environment reporting on genetic diversity not be restricted to species listed as rare or threatened. Although levels of genetic diversity, and changes thereof, are of concern for these taxa, it is likely that levels of genetic diversity within such taxa will respond differently to a given range of pressures than relatively more common or widespread taxa, and thus may not be representative of, or informative about, general responses. Moreover, monitoring of changes in widespread taxa will provide a wider national perspective on the effects of broadly threatening processes like climatic change.

As far as practicable, taxa should be chosen using the following criteria:

#### 4.1.1 Biological or ecological representativeness

1. Habitat specificity—The degree to which a species occurs in a variety of habitats or is restricted to one or two specialist sites within the region.
2. Geographic range—Whether a species occurs over a wide area within a bioregion or whether it is endemic to a particular small area within the region.
3. Local population size—Whether the taxon is found in large populations somewhere within the region or is present only in small populations within the region. Clearly the size of populations is a measure with different scales for different species.

4. Life span—Whether the species is long lived or short lived. Ideally this should account for both the time to first reproduction and the average length of time over which the taxon remains reproductively active. Such detailed information is available for a limited range of taxa.
5. Reproductive strategy—Whether the species reproduces sexually or asexually.

Each of these parameters has a continuous distribution and taxa should be sampled along this continuum.

#### **4.1.2 Taxonomic representativeness**

Although the above groupings will go some way to ensuring taxonomic representativeness, in that only some taxa will be applicable to a given group, in cases where a choice is available for any of these groups, taxa should be chosen to maximise representativeness of taxonomic species diversity.

It is desirable that the following groups are represented in the suite of chosen taxa:

- Bacteria
- Fungi
- Cryptogams
- Angiosperms
- Gymnosperms
- Mammals
- Birds
- Reptiles
- Amphibia
- Fish
- Insects
- Other Arthropods
- Molluscs
- Annelids.

#### **4.1.3 Sensitivity to particular pressures**

A general monitoring of the genetic environment is the main goal for SoE reporting, and necessitates the use of a broad range of target taxa. However, when particular pressures can be identified as being significant within a region, it is useful to choose at least some target taxa that are likely to be sensitive to these. For example, while widespread species that naturally occur in large populations are likely to be affected by habitat fragmentation, species with small disjunct populations will be less so.

#### **4.1.4 Practicality of sampling and analysis**

Taxa should be chosen that are relatively inexpensive to collect (preferably non-destructively). It is anticipated that not all indicators of genetic diversity will be applicable or able to be measured for all chosen taxa. As far as possible taxa should be chosen for which as many indicators as possible are measurable, interpretable and informative.

#### **4.1.5 Existing knowledge base**

Wherever possible, preference should be given to taxa for which there is a stable taxonomy and an existing knowledge base on levels of genetic diversity.

#### **4.1.6 Amenability for laboratory rearing and captive breeding**

In some instances it may be desirable to undertake laboratory-based analyses of large numbers of specimens. Choosing taxa that are amenable to captive breeding is therefore desirable.

#### **4.1.7 Cross-regional comparability**

In order to enable cross-regional comparisons it is desirable that a deliberate decision is made to include some species that occur in a number of the regions in the analyses. This is one strong reason why rare and threatened taxa should not be chosen to the exclusion of all others.

#### **4.1.8 Bacterial diversity**

Emerging technology has led to the proposal that complete phylogenetic enumeration of species and variants is conceivable for the simplest of levels, namely bacteria. In addition, this level is the one for which least is known. Very large numbers of species

of bacteria remain to be discovered. However the extent of genetic divergence within and among them is unknown, as are their patterns of distribution. In the face of such ignorance, and given they lie at one end of the size distribution, it would be extremely risky to use members of this group alone as indicator taxa for the state of genetic biodiversity for all other levels of taxonomic diversity. The key is to sample and cover the taxonomic spectrum.

## 5 Indicators

Seven indicators are proposed that reflect both the action of the main evolutionary processes and the range of genetic diversity likely to exist within a species. These are: 1) number of sub-specific taxa, 2) population size, numbers and physical isolation, 3) environmental amplitude of populations, 4) genetic diversity at marker loci within individuals and populations, 5) quantitative genetic variation, 6) inter-population genetic structure and 7) mating. For each of these indicators, several possible alternative or complementary measures provide the relevant information. Two additional indicators that may have potential, but are difficult to use with the current knowledge base, are outlined in Appendix 1. These are population turnover and fluctuating asymmetry.

The degree to which these nine indicators meet eleven of the criteria outlined in the Chatswood Report<sup>4</sup> for an ideal indicator is scored in Appendix 2. (They all appear to be equally acceptable for an additional criterion of being either national in scope, or applicable to regional environmental issues.)

### 5.1 Indicator: Number of sub-specific taxa

#### *Description*

This indicator gives the number of distinct entities (such as subspecies; ecotypes; geographic, morphological, physiological, behavioural or chromosomal races) readily recognisable within a species.

#### *Rationale*

Sub-specific (or infraspecific) entities are a useful first approximation of genetic diversity within a species, particularly if they can be named and

described or depicted for easy recognition. They provide a possible measure of the level of genetic differentiation within a species and of the pattern of genetic differentiation throughout its range. The number of such variants occurring in an area is relatively insensitive to small changes in genetic structure. However any loss of infraspecific taxa is likely to indicate a substantial loss of genetic diversity in the species. This indicator is more useful for widely distributed species, particularly if they are rich in such variation, cover a number of biogeographic regions or habitats, and have populations with a disjunct or fragmented distribution.

#### *Analysis and interpretation*

The total number of infraspecific entities in the complete set of selected target species within the target region will provide the initial baseline data. Generally the number and therefore the genetic diversity would decline over time in areas subject to major environmental disturbance. Once the target set and area are delineated, the monitoring of change would be effective in gathering data relatively quickly and cheaply. Changes in the numbers of entities can be compared between regions based on the rate of loss and the proportion of entities lost over a specified time. Recent molecular studies have sometimes revealed discrepancies between putative subspecies boundaries and historical phylogenetically defined units. Such studies serve to caution against uncritical acceptance of this indicator of diversity. Major changes in values should trigger a deeper genetic analysis to determine whether substantial genetic erosion is under way.

#### *Monitoring design and strategy*

Infraspecific entities may consist of one or more populations unique to a geographic area, habitat type, or zone disjunct from the main species range. This includes outlier populations, island populations and ecotypes.

For each selected area or region, a change in the number of infraspecific entities for a range of target species would be monitored over time. The more species monitored, the more sensitive the indicator. If monitoring includes data on significant decline in numbers of the various entities, beyond simply noting their localised presence or extinction, sensitivity is further increased.

### ***Reporting scale***

Results can be reported from the local government levels (taxa within shires) to national levels (species with Australia-wide distribution).

### ***Outputs***

Outputs are tables and charts monitoring change in number of infraspecific units within various taxonomic groupings over time.

### ***Data sources***

Defining infraspecific entities within the target species will require information from a range of sources. Their initial recognition will be based on current taxonomic knowledge available from museums, herbaria, taxonomists and taxonomic treatments. Further subdivision of subspecific entities will rest on biogeographic, ecological, physiological, genetic or behavioural information from many sources. These include publications in books and journals, reports by government departments, research institutes and universities, and data held by individual scientists and naturalists.

### ***Links to other indicators***

This indicator links directly to species-level diversity.

### ***Supporting indicators***

Supporting indicators are:

- population size, number and physical isolation
- number, condition and extent of vegetation types
- species diversity, conservation status, economic importance and extent of knowledge.

## **5.2 Indicator: Population size, numbers and physical isolation**

### ***Description***

This set of indicators gives the numbers of individuals within each population, the number of discrete populations and their degree of physical isolation.

### ***Rationale***

In general terms, the size and number of individual populations are related to their ability to cope with both random (stochastic) fluctuations in the environment and steady (systematic) long-term

change. The frequency distribution of the sizes of individual populations is likely to reflect the way in which genetic variation is partitioned within and among populations, with small populations being at increased risk of loss of alleles, reduced heterozygosity, increased uniformity, enhanced inbreeding or possible extinction. The number of discrete populations and their degree of physical isolation are likely to reflect both the overall genetic diversity of the species, and the way in which variation is distributed. Species with widely separated, small populations in which gene-flow is limited or presently non-existent are likely to show declining levels of within-population genetic diversity even while variation at the species level remains relatively constant.

This set of indicators provide the simplest and most accessible means of obtaining a broad-scale view of the potential genetic effects of changes in the environment.

### ***Analysis and interpretation***

Map data for individual species are placed onto three-dimensional graphs to see relationship between the three parameters. Individually the three parameters, while closely linked, will show different propensity to change. Most species will fit non-linear relationships (logarithmic or asymptotic; frequently dependent on dispersal mode and efficiency) between change in the parameter and its consequence for the extent and partitioning of underlying genetic variation. As a consequence, much greater significance should be given to changes occurring against a narrow starting base (few, small, geographically isolated populations) than to changes occurring against a broad starting base (many, large, geographically widely dispersed populations). Changes in these parameters should be interpreted as early warnings of potential changes in genetic variation and structure as a consequence of increased drift, genetic erosion and reduced migration, and their impacts on genetic processes.

### ***Monitoring design and strategy***

Information for these parameters should be collected at regular intervals from the appropriate organisations and agencies working on designated species. For less vagile species (plants and some animals), area measurements of habitat patch sizes will provide a reasonable basis on which to estimate population size. In some of these cases, measuring the extent and rate

of vegetation fragmentation will monitor change in status; in other cases, monitoring may be possible through existing tagging programs. All other situations will require direct field measurements.

### ***Reporting scale***

The reporting scale is from local government areas to the IBRA regional scale (and sometimes to the continental scale).

### ***Outputs***

Outputs are tables, maps, graphs and advice based on empirical data for planners, policy makers, recovery team coordinators etc.

### ***Data sources***

Data sources are maps of vegetation types and remotely sensed imagery held by State and Territory conservation agencies, departments of land, ERIN and COSSA; distribution data held in databases and on collection labels of State, Territory and Commonwealth herbaria, museums and other biological collections; data on individual species held by the Biodiversity Group of Environment Australia; and individual researchers in State, Territory and Commonwealth institutions.

### ***Links to other indicators***

The indicator is linked to ecosystem indicators such as vegetation cover.

### ***Supporting indicators***

There are no supporting indicators for this set of indicators.

## **5.3 Indicator: Environmental amplitude of populations**

### ***Description***

This indicator is a measure of the extent to which a species maintains occupancy of the full range of habitats in which it naturally occurs, including those habitats where the species is on record as having occurred.

### ***Rationale***

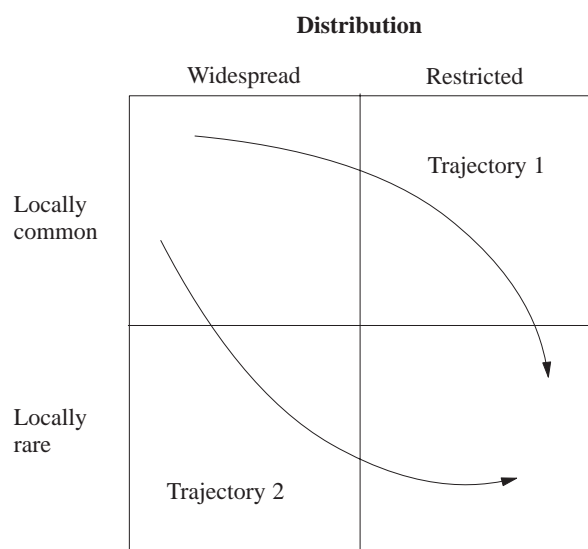
Virtually all species naturally occur in a range of habitats. In many cases, such habitats differ from one another by specific sets of physical environmental conditions (e.g. low oxygen tensions, higher salinity, heavy metal presence, changed pH, different temperatures or insolation levels) to which individual populations of a species may have adapted over many years. Maintaining the species' ability to occupy or colonise the full extent of its range is one mechanism whereby underlying, highly adaptive, genetic variation may be conserved.

### ***Analysis and interpretation***

Two analytical approaches are available. The first of these uses broad assessments of patterns of distribution ('distribution approach'). The second approach ('physiological approach') is a much more precise instrument focusing on the detailed distribution of individual species.

For the 'distribution approach' classify the distribution of designated species into four categories of: 1) widespread, locally common; 2) widespread, locally rare; 3) restricted, locally common; 4) restricted, locally rare (Figure 3). Movement of species between categories along trajectories 1 and 2 on Figure 3 have different genetic implications. Trajectory 1 implies a changing distribution of the species, with increasing restriction to particularly favourable or protected environments. This is potentially indicative of initial losses of genetic variation associated with the species' ability to exist in more marginal habitats. Trajectory 2 implies overall reductions in population sizes, with initial losses in genetic variation at the individual population level (through bottleneck effects and random genetic drift); at first this may not be accompanied by loss of variation in the species as a whole. In both cases, though, movement of species from widespread, locally common towards restricted, locally rare should be regarded as a 'flag' for further assessment.

For the 'physiological approach' tabulate the number of populations occurring in each distinctly recognisable environment and determine the rate of loss of populations of each ecotype. A significant differential in the different rates of loss is indicative of changing ecological amplitude of the species in question. Another option is to measure variation in stress resistance, as the genes that control such tolerances may mediate responses to climate change.



**Figure 3: Possible distributional trajectories of species through time**

### *Monitoring design and strategy*

The distributional approach has the potential to assess relatively rapidly a very wide range of species on an IBRA region or continental scale. Monitoring will require estimates of numbers of populations and of the relative density or numbers of individuals within populations. For the physiological approach it will be necessary to identify and measure relevant characters of the physical environment in the field at the local level with aggregation of data to IBRA region level.

### *Reporting scale*

There are two approaches to reporting:

- ‘distribution approach’—IBRA region to continental scale
- ‘physiological approach’—local government areas combined at IBRA regional level.

### *Outputs*

Outputs are tables, diagrams and advice based on historical and current empirical data for planners and local and regional recovery teams.

### *Data sources*

For the ‘distribution approach’, sources are distribution data held in databases and on collection labels of State, Territory and Commonwealth herbaria, museums and other biological collections, data on individual species held by the Biodiversity Group of Environment Australia, and individual researchers in State, Territory and Commonwealth institutions. For the ‘physiological approach’, high-resolution distributional data from the above sources are overlaid with appropriate high-resolution climatic, terrain and geological mapping data. In many instances, the relevant selective character(s) will have to be identified and measured directly in the field.

### *Links to other indicators*

The ‘distributional approach’ has linkages to both species- and ecosystem-level indicators.

### *Supporting indicators*

Supporting indicators are ecosystem-level indicators (e.g. vegetation-type data).

## **5.4 Indicator: Genetic diversity at marker loci within individuals and populations**

### *Description*

This indicator measures genetic diversity as close as is feasible to the deoxyribonucleic acid (DNA) level, by screening for differences among the many variants of genes. A steadily expanding range of techniques provides the tools for detecting differences for various kinds of DNA sequence variation. Levels of variation can differ between cytoplasmic and nuclear markers, between protein and DNA sequences etc. However, the trend is for the same kind of changes over time to occur for different kinds of markers in response to environmental pressures such as bottlenecks in population size.

### *Rationale*

It is likely that biodiversity at the gene level cannot be adequately assessed by monitoring only at higher levels (species and community biodiversity). It is essential therefore that gene diversity itself be monitored, and that structured sampling takes account of this need for ‘ground-truthing’ of the

generalisations that emerge from monitoring at higher levels.

Similarly, it is not known whether measures of population size and number alone monitor gene diversity sufficiently well. The advantages of measures based directly on marker genes are that they are precisely defined in a genetic sense; they can be summed and their statistical sampling errors can be specified. This makes them ideal statistics for comparison with other studies and data from other countries.

### ***Analysis and interpretation***

The interpretation of marker gene polymorphism itself has seen a long history of controversy. They are, at the least, measures of the ‘ancestry’ of individuals and populations, of the outcomes of evolutionary processes such as migration, breeding system, bottlenecks of population size etc. It is also possible that some fraction of the variation is directly or indirectly responding to selection pressures. The direct determination of which variants are of adaptive significance requires considerable research effort.

Since we are using a very tiny sample to indicate trends on a much broader base, in interpretation we need to ask whether changes in indicator values are restricted to those examples, or some peculiar features of the species or population or class of genes or sampling strategy.

Comparative interpretations have also been the subject of much controversy. The supposed lack of correlation between ‘neutral’ marker variation and variation in ecologically significant characters has received much attention, as have contrasts between estimates in different species, or on the same suite of markers in two different species, or between two different kinds of marker genes. Meta-analyses have, however, shown worthwhile overall trends in, for example, the effect of population size on ‘allelic richness’ (K) or gene diversity index ( $H_e$ ).

### ***Monitoring design and strategy***

It is clearly impossible to census many populations from a large number of species of the biota in all major biomes for their genetic variants. Therefore this indicator should be monitored in a very limited, structured sample of species and populations from a representative set of biomes.

Type studies should ensure that examples of each of the full range of genetic techniques are employed on a reasonable sample of genes.

Various summary measures for allozymes and restructured fragment length polymers (RFLPs) that contribute to this indicator are:

1.  $K$  = ‘allelic richness’ or observed number of alleles in a sample (standardised for sample size)
2.  $H_o$  = observed heterozygosity of an individual
3.  $H_e$  = gene diversity index, or probability that two random copies of a genetic locus will differ.

Both kinds of statistics ( $K$  and  $H_e$ ) of allelic diversity are needed.  $K$  is the more sensitive, and measures the basic raw material for evolution, yet is more susceptible to sampling effects, and to alleles occurring at low frequency.  $H_e$  is bounded and converges with sample size.  $H_o$  is also a very useful indicator of processes such as the mating system, or as a predictor of fitness. To interpret the data and sum over taxa etc., an estimate of the proportion of the loci screened that were polymorphic ( $P$ ) within the total species sample is needed.

In the case of microsatellite loci and DNA sequences, more powerful measures are available that incorporate the degree of phylogenetic similarity among the allelic variants at a locus.

### ***Reporting scale***

Reporting is on a variety of species at all scales.

### ***Outputs***

Outputs would be a table of species- or population-specific estimates with averages at various levels of the sampling hierarchy and attached sampling errors. Multivariate analyses of such tables would be helpful in indicating major significant trends, or weights for suites of loci.

### ***Data sources***

A considerable body of allozyme data now exists for a haphazard sample of higher animal and plant species of Australia. In addition, molecular data are beginning to accumulate. This published and unpublished information needs to be assembled and codified. From this, a set of species for detailed monitoring could be defined. The existence of prior data will affect species chosen for further monitoring. These data could also provide baselines for assessing

the significance of future changes in measure values. A good deal of data will have to be generated anew.

### ***Links to other indicators***

The estimates link naturally to measures of population divergence. Population size and total species abundance are indirect estimates of diversity usually on a log scale. They also link closely with indicators of evolutionary processes because such processes determine their values and their variation. (Alternatively, indicators of the processes are indirect indicators of genetic variation.)

It may be that the major pressures that are likely to alter the values significantly, or the major responses, would be evident from indicators at higher levels. However, as mentioned, this reasonable claim requires 'ground-truthing'.

### ***Supporting indicators***

A supporting indicator is population size distribution.

## **5.5 Indicator: Quantitative genetic variation**

### ***Description***

The variance among individuals in measurable or countable characters can reflect genetic variation in a plurality of contributing loci. The characters can be relatively simple ones such as lengths of bones, internodes, number of abdominal bristles etc., or more difficult physiological traits such as ribonucleic acid (RNA)/DNA ratios frequently used in fisheries.

### ***Rationale***

A major limitation to monitoring genetic variation within and between populations close to the DNA level is the expense and effort such work entails. Variance of metric characters is often more readily scorable than any underlying genetic variation. Also, characteristics such as growth rate and reproductive output are relevant to management. Changes in characters such as survivorship and fecundity are often the most serious manifestations of inbreeding depression.

### ***Analysis and interpretation***

Comparison over time of phenotypic variation in a single character in the same population will show one or other of the following results: no change, decrease or increase. If variation in the character is entirely due to chance, then there is no important information to be gained from the comparison over time. If variation is predominantly due to environmental influences (e.g. highly plastic characters in plants such as plant weight), then change in variation would be an indicator of change in the environment of the population. Either an increase or a decrease may signal an adverse alteration of the available habitat. If variation was partly due to genetic factors, then interpretation is more complex: variation may have changed because of environmental alterations, because of erosion of genetic variation in a small population due to chance losses of genotypes, or (in a fitness-related characteristic) because of selection, whether natural or artificial. Also, a result showing no change in variation may mean that the environmental variation has increased but the genetic variation has decreased, both of which are thought to be likely if heterozygosity decreases.

Interpretation is simpler when the same result (increase, decrease, no change) is found in a suite of characteristics, preferably supported by other indicators, such as population size. The distinction between random and selective loss of genetic variation is apparent in several ways. First, if  $V_A$  (additive genetic variance within populations) have decreased for all phenotypic characters, serious random loss seems most likely. If  $V_A$  has decreased in some characters, then it may be prudent to give the same interpretation because of the large sampling errors associated with variance estimates. However, reduction in  $V_A$  for particular characters may be due to selection. For this reason, it is important to estimate  $V_A$  for two groups of characters—those that are particularly likely to be subject to selection, such as seed set, and those unlikely to be subject to selection, such as bristle number.

Fitness characters often have lower  $V_A$  than other characters. However, appreciable levels of additive variance in fitness traits often accompany non-equilibrium situations, when the population is not at the optimum value for these characters. This will often apply in the conservation of a species that has inadequate reproduction or survival in its current environment.

### ***Monitoring design and strategy***

The two measures of quantitative genetic variation are:

1. Total phenotypic variance within populations ( $V_P$ ). This indicator is readily measured and has intuitive appeal, but it cannot be strongly recommended.
2. Additive genetic variance of metric characters within populations ( $V_A$ ). The distinction of this indicator ( $V_A$ ) from the total phenotypic variance ( $V_P$ ) is that for  $V_A$ , it is necessary to identify the portion of the variance that is heritable and due to additive interactions between genes. This measure is of fundamental importance in evolutionary biology as it reflects the ability of a lineage to respond to selection and therefore adapt to changing environmental conditions.

Neither of these measures is directly comparable between different populations of the same species, so the same populations must be monitored at each time of SoE reporting. Large numbers of individuals (e.g. at least 50) must be scored. A mix of characters should be scored; some of which should be obviously associated with fitness.

Unlike  $V_P$ , to determine  $V_A$  requires the scoring of related individuals: partial family data must be obtained. Various types of family structure can be used, as long as the basic mode of inheritance is known (e.g. whether the species is haplo-diploid, such as bees or some algae), and the exact relationship between the sampled individuals is known (eg. full-sib, parent-offspring etc.). The traits must be measured in individuals of the same age, unless the traits are stable with age. The advent of genetic parentage determination may expand the data sets available for this work.

### ***Reporting scale***

Reporting is on a range of species at all scales.

### ***Outputs***

Output would be an assessment of changes in genetic variation that forms the basis of adaptive evolution within individual populations in a variety of species.

### ***Data sources***

In some cases these characters can be measured on museum specimens, but much field work will have to be done on each species. A limited number of studies of variation in natural populations have been published and these populations may serve as samples for new measurements.

### ***Links to other indicators***

This indicator shares data with fluctuating asymmetry (see Appendix 1). Data on the relationship between quantitative genetic variation and heterozygosity for marker loci do not show a straightforward, consistent trend across all species and populations. However, in many situations a loose positive association has been found, consistent with the underlying relationship of both variables to population size and ancestry.

### ***Supporting indicators***

This indicator requires support from ecological indicators to allow interpretation. Random processes erode additive variance ( $V_A$ ) in small or fragmented populations at the same rate as they do for gene diversity, so that comparison of these indicators should allow validation.

## **5.6 Indicator: Inter-population genetic structure**

### ***Description***

This indicator describes the nature and distribution of genetic variation between populations within a species. This includes spatial and evolutionary patterns of genetic variation between populations.

### ***Rationale***

Partitioning of genetic variation between populations is an appropriate measure of genetic diversity above the population level within a species. This may be used as a descriptor of the process that generates and maintains genetic diversity. This variation may be indicative of current or future adaptation and any overall loss would indicate a significant loss of genetic diversity.

Additionally, the variation is a useful indicator of the genetic distinctiveness of the populations and their evolutionary relationships.

Phylogenetic analysis of patterns of genetic variation among populations combined with information on

geographical distribution can allow the distinction between naturally disjunct populations from those fragmented due to human intervention. It can also provide a baseline for measuring the impact of land clearing and fragmentation on genetic diversity within a species that already has a disjunct population system.

### ***Analysis and interpretation***

Two approaches to measuring interpopulation genetic structure are 1) marker-based techniques and 2) quantitative measures.

**1. Marker-based approaches:** Using appropriate genetic markers, differences between the populations of a species can be expressed in terms of a genetic distance or variance statistic. A measure of genetic partitioning within a species can then be obtained by averaging all pairwise genetic distances between populations. The same approach is applicable to the variance statistics. Loss of a population or major change in the genetic structure of any given population will be reflected in the average distance and variance measures.

Genetic distance measures can also be used to reconstruct phylogenies. Such a reconstruction identifies the populations that make the greatest contribution to a species' overall genetic variation. Loss of a population or major change in the genetic structure of any given population will be reflected in tree length and tree topology.

**2. Quantitative measures:** When the monitoring work shows that the variation between the populations is wholly or largely genetic, the phenotypic variation can be used as a genetic distance measure along with other measures.

### ***Monitoring design and strategy***

As with Indicator 5.4 it is not possible to investigate inter-population genetic differences in a large number of species in all biomes. This indicator should be monitored in a very limited number of carefully selected target species.

**1. Marker-based measures:** An appropriate range of genetic markers covering a suitable sample of genes should be employed for each target species. Marker choice should be based on their suitability for analysing spatial distribution of genetic variation and evolutionary relationships between populations.

Various statistical measures provide suitable estimates for this indicator. Genetic distance and variance statistics (Nei's  $D$ ,  $F_{ST}$  etc.) are valid measures of the partitioning of genetic variation within species and have suitable approaches for both diploid and haploid systems. Measures such as Crozier's 'genetic diversity' or Faith's 'phylogenetic diversity' provide ways of incorporating phylogeny into biodiversity estimation. These have been used in the context of optimising wildlife reserve design for maximum preservation of biodiversity. They can also be used for the interpretation of changes in time.

The initial analysis of interpopulation variation will identify the populations that:

1. contribute most to the species' overall genetic diversity
2. have been genetically isolated for the longest and least periods of time (this is not always directly linked to geographical proximity)
3. are the most taxonomically (phylogenetically) distinct
4. are part of a cline in morphological variation or whose phenotypic distinctiveness does not have a genetic component.

These data will allow managers to prioritise those populations that should be maintained to maximise genetic and taxonomic diversity within a species.

**2. Quantitative measures:** Quantitative variation ( $V_P$ ,  $V_A$ , above) can be partitioned into within- and between-population components. Determining whether variation between two populations has a genetic component requires the bringing of a sample of individuals from each population into a common environment. This is done either by raising juveniles together in controlled conditions, called a common garden, or by reciprocal transplant experiments that compare individuals from resident and introduced alien populations. Phenotypic differences that remain after the groups are raised in the same environment signal the action of genetic factors as contributing to population divergence. Large numbers of individuals must be studied (at least 50 from each population), so this work is most frequently done in plants using seed, but can also be done in animals.

### ***Reporting scale***

Results can be reported from the local government levels (taxa—species within shires) to national levels (species with Australia-wide distribution).

### ***Outputs***

Outputs are tables of average genetic distances and variance statistics, and phylogenetic tree topology and length.

### ***Data sources***

A relatively large body of allozyme data is available for higher animals and vascular plants of Australia. Data are also available for other molecular markers such as mitochondrial DNA (mtDNA) in animals. These data need to be assembled and used to assist in the selection of target species for monitoring and used as baseline information following the first phase of monitoring.

Museum and herbarium repositories can provide information on the patterns of distribution of populations and the range of phenotypic variation between populations. This information can be used to implement sampling strategies for collection of new data that will be necessary for most species.

### ***Links to other indicators***

Measure 1 can use the same data as general measures of Indicator 5.1. Measure 2 utilises the same data as Indicator 5.2.

### ***Supporting indicators***

Supporting indicators are number, condition and extent of vegetation types; and species diversity, conservation status, economic importance and extent of knowledge.

## **5.7 Indicator: Mating**

### ***Description***

This indicator measures the amount and pattern of mating within populations of target taxa. This includes the relative amount of outcrossing, inbreeding and asexual reproduction.

### ***Rationale***

Mating is the main process that determines how genes are recombined and transmitted from one generation to another. It is the primary determinant of how genetic variation is partitioned among individuals within and between families. Changes in patterns of mating can have significant effects on individual fitness and population viability if the degree of relatedness among parents either increases (inbreeding depression) or decreases (outbreeding depression). Mating events can respond more rapidly to population changes than indicators of genetic diversity per se. This indicator is more useful for plants than for animals.

### ***Analysis and interpretation***

Comparisons of all measures for this indicator will be species- and population-specific. For example, seed set in one year can be compared with seed set for another year for a given population. A significant difference between these measures from two times reflects a change in mating events. The definition of significant is difficult. Literature values can be used to provide some concept of the expected variance about parameter means.

Simultaneous data collection to allow calculation of several types of measurements—for example, outcrossing rate and population size—in a subset of target taxa and populations will provide information on the validity and usefulness of the less direct measures.

### ***Monitoring design and strategy***

Information on mating events can come from several parameters measured at the population level:

1. Outcrossing rate and paternity analysis are direct measures of mating events. They require progeny array samples from several mothers and the use of genetic marker techniques.
2. The fixation index reflects deviation from expected heterozygosity under random mating. It requires samples from multiple individuals and the use of genetic marker techniques.
3. Fecundity and progeny fitness—mating affects fecundity through the availability of compatible gametes, inbreeding or outbreeding depression. Therefore, measures of such parameters as seed set or clutch size are reflections of mating. These require quantitative data on reproductive output and/or progeny fitness.

4. Pollinator abundance affects the probability of male gamete dispersal. This parameter requires data on abundance of pollinators.
5. Population size and sex ratios have an impact on mating pattern through changes in mate availability. These parameters require quantitative data on reproductive population size and the relative abundance of males and females.
6. Density of reproductive individuals affects the probability of male gamete dispersal either directly, or indirectly through influence on vectors (e.g. may change pollinator movement behaviour).

Target taxa should include species with differing mating systems that might be expected to react differently to the same stress—for example, wind-pollinated, self-incompatible plants compared with insect- or bird-pollinated self-compatible plants. Monitoring would be at the population level. The temporal monitoring period can be shorter than for diversity indicators as response times of mating system parameters and their measures are likely to be less.

### ***Reporting scale***

The temporal reporting scale can be shorter than for genetic diversity measures due to the responsiveness of mating system measures to population changes.

### ***Outputs***

Outputs will be estimates of mating system measures which can be compared within populations between reporting periods.

### ***Data sources***

Information for these measures will come from three different sources. Measures 1 and 2 require genetic marker-based information, measures 3 and 4 require quantitative field based survey information, and measures 5 and 6 require some field-based information, but could in part be approximated from vegetation or land use maps, remote sensing etc. All data will have to be derived anew.

### ***Links to other indicators***

Data from measures 1 and 2 can also be used to generate genetic diversity indicator measures and

structure. Data from measures 3 to 6 also provide information on population demography.

### ***Supporting indicators***

Supporting indicators are individual-level genetic diversity measures—specifically  $H_0$ —and population size and isolation.

## **6 Indicator interpretation**

Three points require attention in the interpretation of changes in values for different indicators. The first issue is the need to understand the ways in which evolutionary processes cause changes in the various indicators. Figure 1 depicts how several processes can affect indicators and their measures. Second, the amount of change in an indicator that would signify a ‘significant’ negative or positive change in genetic diversity is unclear. How many alleles are enough? How much inbreeding can be tolerated before populations become inviable? This second point is the issue of baselines, or reference points. The third issue is determining how to interpret multiple indicators, particularly when they appear to give conflicting results.

### **6.1 Baselines**

In the simplest form for SoE reporting, values of measures taken at the beginning of the reporting period ( $T_0$  values) can serve as baselines against which future changes can be measured ( $T_{+1...}$  values). The limiting assumptions that go with this approach are that the current state of genetic diversity and the current dynamics of evolutionary processes are desirable. Both of these assumptions are necessary but unlikely to be true.

A second approach is to use data from studies that are already to hand to provide general baselines for different indicators for the different groups of target taxa. For example, the large amount of allozyme data available on both plant and animal species allows some expectations for the values of such measures of genetic diversity as heterozygosity or allelic richness within populations. The advantage of this approach is that the significance of a deviation from these expectations can be appraised quantitatively relative to the variance associated with these expectations. However, the approach is limited to target taxa for which sufficient studies have already been conducted and there are large gaps. For example the many

studies for some groups of vascular plants and vertebrates (e.g. trees and mammals) contrast with the scarce information for insects, non-vascular plants, fungi or bacteria.

A third approach is to limit target taxa to those for which it is still possible to gather information from relatively undisturbed populations. These populations can be monitored as baselines (controls) while disturbed populations can be monitored simultaneously to check effects of ongoing pressures. This approach is appealing as it also establishes baselines for expected temporal variation in indicator measures which are generally unavailable.

## 6.2 Conflicting trends among different indicators

In most situations several indicators will be monitored, often with several measures for each indicator. The interpretation of the joint behaviour of different indicators and their measures is a matter of interest and potential conflict. When all measures and indicators are performing in the same fashion, interpretation is simplified. Indeed, the joint response of a range of indicators lends credibility to any observed trend. However, at other times some indicators show changes from one monitoring period to the next while others may not. Even more difficult is when some indicators show trends in one direction, while others show movements in another.

When different indicators of the same evolutionary process apparently conflict, the indicator that more directly reflects that process is the more reliable one. For example, a change in outcrossing rate is a more direct sign of a change in mating than is a change in heterozygosity. Differences in the response of different indicators to a single stress may reflect the different effects that this stress has on different processes. One example is when allelic richness declines as population size is reduced, but

heterozygosity is unaffected. This would suggest that the change in population size has increased the amount of random genetic drift in the population, but it has had little effect on mating.

It may also be that the same measure of an indicator shows different trends when measured on different marker genes or quantitative traits. Rather than being a problem, careful choice of marker genes or traits affected by different evolutionary processes allows these contrasts to uncover differential effects of the same stress on different processes. Indeed, comparative analysis of markers thought to be under strong selection with those unaffected may be the only way to examine genetic responses to stress through selection.

## 7 Research

The main areas for further research to support implementation of genetic indicators for SoE reporting relate to:

1. elucidating linkages between different indicator groups (see Figure 1). For example, what is the relationship between population size and genetic variation for arthropods? This ‘ground-truthing’ of genetic inference based on indirect indicators that are easier to implement is crucial if these indicators are to be widely adopted.
2. understanding how different groups of organisms are historically structured (connected or fragmented) and how various pressures affect these functional groups.
3. providing baseline data on genetic diversity for groups of species for which this information is currently missing (e.g. arthropods, fungi, bacteria).

This requires a substantial research effort. However, without such information, the monitoring of the state of Australia’s genetic environment is open to misleading conclusions.

## End notes

1. A more inclusive concept is as follows: Genetic diversity 'consists of differences between individuals and species in the presence of particular DNA sequences, or (differences in) their location in the genome. Its building blocks thus include: diversity encoded by specific genes that some organisms possess but others lack; differences in sequences that regulate gene expression; differences in other noncoding sequences; diversity arising from differing copies of homologous or related DNA sequences (e.g. allelic variation); and diversity due to translocation of a sequence from one chromosomal site to another (e.g. position effect)' (Frankel, Brown & Burdon 1995, *The conservation of plant biodiversity*, Cambridge University Press.  
p. 10). The genome comprises both nuclear and cytoplasmic components.
2. Namkoong, G., Boyle, T., Gregorius, H.R., Joly, H., Savolainen, O., Wickneswari, R. and Young, A. 1996, Testing criteria and indicators for assessing the sustainability of forest management: Genetic criteria and indicators, Center for International Forestry Research Working Paper No. 10.
3. Department of the Environment, Sport and Territories 1996, *Proceedings of a workshop on Key Environmental Indicators of Biodiversity in State of the Environment Reporting*, 4–6 June 1996, Chatswood, Sydney. Pressures on genetic diversity are listed in Table 1a on page 15.
4. Department of the Environment, Sport and Territories 1996, *Proceedings of a workshop on Key Environmental Indicators of Biodiversity in State of the Environment Reporting*, 4–6 June 1996, Chatswood, Sydney. Selection criteria for environmental indicators on page 44.

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## Appendix 1: Additional indicators

### **Indicator: Population turnover**

#### *Description*

This indicator measures the rate per unit time (rapidity) at which an existing local population dies out and a new population becomes established, averaged over populations.

#### *Rationale*

This indicator measures the temporal dynamics of extinction and colonisation. It aims to account for situations where the total number of populations may remain more or less constant but the rate of turnover changes, becoming either substantially more or less rapid. Increased population turnover indicates a shift in the frequency distribution of population age towards younger age classes. Depending on the normal cause of local extinction, such a change could signal changes in the genetic structure and overall diversity found within a species. For example, in interacting metapopulations involving a host species and a parasite, pathogen or predator, a declining host turnover rate may well reflect an uncoupling of this interaction and the loss of the temporally and spatially fluctuating selective environment associated with it. This should result in reduced genetic variation both within and among populations.<sup>1</sup>

#### *Analysis and interpretation*

Since turnover rates themselves are only assessable over time, determining changes in turnover rates with time is a long and difficult process. This makes the analysis and interpretation of population turnover a complex task. Given this, population turnover is probably most useful as an indicator in situations where undisturbed ecosystems can be monitored as baselines, while disturbed ecosystems are monitored simultaneously to assess impacts of environmental change on turnover rate and the effects on genetic diversity.

#### *Monitoring design and strategy*

Estimation of turnover rates is only possible through repeated field assessment of the presence or absence of existing populations plus surveys of potential but currently unoccupied sites. As a consequence, assessments of presence and absence should be

carried out at local government level with appropriate aggregation up to IBRA regional level. Because new populations may become established at the same site of previously existing populations that have recently become extinct, the rate of population turnover is likely to be heavily dependent on the generation time of the species in question and the frequency of assessment. Frequency of monitoring will therefore have to be determined in light of the identity of the designated species.

#### *Outputs*

Outputs for this indicator are data on frequency of population turnover.

#### *Data sources*

Data sources are direct field assessments for most species. For some rare or endangered species, baseline data may be available in Rare or Threatened Australian Plants (ROTAP) and other appropriate databases.

#### *Reporting scale*

The reporting scale is from local government to the IBRA region. The temporal reporting scale for this indicator is highly dependent on the longevity of the species under consideration, but is generally likely to be longer than for other indicators.

#### *Link to other indicators*

This indicator links functionally with genetic diversity at marker loci and inter-population genetic structure through its effects on gene flow.

#### *Supporting indicators*

Supporting indicators are species diversity indicators at the local scale where population extinctions may be recorded as reduced species diversity.

### **Indicator: Fluctuating asymmetry of phenotypic characteristics**

#### *Description*

Fluctuating asymmetry (FA) is defined as random differences between the repeated units in normally symmetrical organisms (e.g. left and right sides of bilaterally symmetrical organisms, radial structures in

radially symmetrical organisms). This indicator is derived from variables that can be measured in repeated, identical units of a single individual (e.g. left and right foot-length, width of each petal in a flower). Fluctuating asymmetry is distinguished from other forms of asymmetry (directional asymmetry or antisymmetry) when there is no tendency for any one unit to be consistently more asymmetric than another.

### ***Rationale***

A number of studies have shown that FA increases when individuals are under stress either from genetic alterations such as inbreeding or low heterozygosity, or from environmental stresses such as pollutants. Thus, measurement of FA serves as a generalised early-warning indicator that a population is under stress, including genetic stress.

### ***Analysis and interpretation***

There is a variety of ways in which the variation between the repeated measures can be summarised to give an estimate of FA. Fluctuating asymmetry provides an early warning of populations subject to stress. Under some circumstances, changes in levels of FA may indicate subsequent changes in fitness-related parameters (e.g. survival fecundity).

### ***Monitoring design and strategy***

Repeated structures must be measured on each of 30 or more individuals from a population. Any repeated structure can be useful, so they can be chosen for ease of measurement on the material available. The degree of FA within a population can then be compared between SoE reporting periods.

### ***Reporting scale***

The reporting scale is population-based monitoring. The ease of measuring asymmetry suggests it as a

useful indicator for monitoring stress at the continental scale, and across a broad range of target taxa. Its main drawback is the difficulty of isolating which of many possible environmental and genetic stresses link with the observed changes in the indicator. However, in situations where effects of well-identified stresses are being monitored, FA could prove to be a very useful indicator.

### ***Outputs***

Outputs are changes in FA over time for particular populations.

### ***Data sources***

If appropriate species and characteristics are chosen, museum specimens can be used. Otherwise new collections will be required.

### ***Links to other indicators***

Under some circumstances this indicator may be directly linked to changes in genetic diversity (heterozygosity).

### ***Supporting indicators***

Supporting indicators are estimates of genetic diversity, indicators of environmental pollution. This indicator shares data with Indicator 5.5: Quantitative variation.

## **Note**

1. Burdon, J.J. 1996, 'The dynamics of disease in natural plant populations', in *Frontiers of population ecology*, eds. R.B. Floyd, A.W. Sheppard & P.J. DeBarro, CSIRO Publications, Melbourne, pp. 291–300.

## Appendix 2: Scores of proposed indicators of biodiversity at the gene level against ideal indicator criteria outlined in the Chatswood Report

Criteria	Indicators							8) Population turnover	9) Fluctuating asymmetry
	1) Number of sub-specific taxa	2) Population size, number and isolation	3) Environmental amplitude	4) Genetic diversity —marker loci	5) Quantitative variation	6) Inter-population genetic structure	7) Mating		
<i>Theoretical properties as an indicator</i>									
Reflects valued aspect of the environment	++	++	+	+	+	+	?	?	–
Scientifically credible	+	+	++	++	++	++	+	?	?
Robust indicator of change	+	+	+	++	+	++	+	?	?
Warns of problems early	–	++	++	0	–	–	+	+	+
Renders progress evident	+	++	++	+	0	+	+	–	?
Aggregative	+	–	–	+	–	–	–	–	–
<i>Practical issues of implementation</i>									
Can be monitored regularly	++	++	++	++	+	++	++	+	+
Easily understood	++	++	+	–	–	–	+	+	–
Cost-effective	+	++	+	?	–	?	?	–	+
Relevant to policy and management	++	++	++	+	+	+	+	+	–
Involves the community	+	+	–	–	–	–	+	–	–
<b>Additional Indicators</b>									
Code : ++ = Good + = Fair – = Poor ? = Unknown or open to question									