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INTEGRATION OF *IN SITU* CONSERVATION OF PLANT GENETIC RESOURCES INTO LANDSCAPE AND REGIONAL PLANNING

Conservation is a social process, steeped in values and socially determined priorities and acceptable margins of risk. While the past decade has seen a progressive politicization of the use and transfer of germplasm and the natural ecosystems which support respective populations, the policy dimensions of the relationships between information, genetic conservation priorities, and subsequent requirements for protected area design and management, have barely been considered. This paper lays the basis for a theory of environmental planning for the *in situ* conservation of genetic resources.

I begin with the still largely theoretical question of the integration of conservation of wild plants with genetic resources into networks of protected areas involving a range of other concerns for habitat as well as for values and resources related to local subsistence, recreation, and heritage. My argument is that the *in situ* conservation of genetic resources is, inherently, a reflection of social concerns of germplasm and landscape-oriented interventions for the persistence of genotypes and alleles. There are, however, some crucial technical components in such programmes to minimize genetic erosion. *In situ* conservation of plant genetic resources must be based on ecogeographical surveys which correlate environmental factors to intra-specific variability. Current networks of protected areas, which support populations of genetic resources, are largely unorganized and *ad hoc* for those specific purposes and will require careful review and coordination over the coming decade if there is to be adequate conservation in terms of needs for germplasm. Such networks will necessarily overlap with and complement other operations for the conservation of biological diversity and natural areas. Special kinds of monitoring and management prescriptions are necessary.

Five functional categories of spatial zones for genetic resource conservation are considered: cores, buffers, transitions, corridors and barriers. Three examples are explored: the Sahel of west Africa, crabapple on the north coast of British Columbia, and the rich human forests of an islands off of New Guinea.

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It is with the *in situ* conservation of genetic resources that the complex linkages that are required between social values, economic policy, land management, ecology and biology become prohibitive for determination of land management prescriptions through reductionist science. The "biodiversity" paradigm (Wilson 1988) has radically transformed the formerly *ad hoc* vision of conservation of genetic variability along with the growing interest in utilization of germplasm from wild populations in the improvement of crops and livestock. The result is a set of rapidly intensifying social and economic pressures for *in situ* conservation and a lag in the necessary theory and techniques.

The status of most populations with genetic resources is still poorly known, and the development of new theory and techniques for determining conservation requirements and documentation of wild populations is necessary. A number of technical issues must be addressed before biosphere reserves and other internationally and nationally recognized protected areas can become effective for the conservation and procurement of genetic resources. Desired levels of conservation of less common genes should be determined. Acceptable levels of conservation and margins of security for loss of diversity should be set. Access to and ease of procurement of the genetic resources of wild species must be effectively regulated and in some cases expanded. Regulation and expansion of the systems of distribution (Kloppenborg and Kleinman 1988) of the germplasm taken from protected populations are inevitable.

An additional purpose of this paper is to take stock of what we know and, based on cursory evaluations of the various types of programmes, to explore ways to better integrate various concerns for a range of plant and animal populations into regional and national decision-making frameworks (WRI, IUCN and UNEP 1992). It is worthwhile to explore the possibilities, for one or two decades into the future, when new vehicles for more comprehensive conservation as the *Convention on Biological Diversity* (UNEP 1992) have been instituted. It is necessary to begin exploring typologies of *in situ* conservation as based on different factors related to particular gene pools, genetic erosion factors, sites and regions, and demands for germplasm and then to identify needs for new theory, technique, and approaches to decision-making.

We can envision a world with a growing number of programmes of surveys, evaluation, protected areas, monitoring (Dallmeier et al. 1992), and germplasm procurement for particular plant and animal species and sites of interest. *In situ* conservation of genetic resources represents a fertile cusp between conservation biology and environmental planning which has been barely explored (Ingram 1990b).

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It is necessary to develop a more dedicated set of conservation planning "tools" (Hoose 1981) as part of better identification of options for intervention in the midst of continued losses of populations and for increased access to the germplasm of the populations that remain. Perhaps more importantly, we must better situate the concerns for genetic resources within the pantheon of the conservation of biological diversity and the inevitable trade-offs and compromises of decisions over land.

By linking utilization of biological resources with funding for conservation, the *Convention on Biological Diversity*, and whatever follows, the landscape of conservation has been fundamentally transformed. However, we cannot let the various funding crumbs for reserves, which are generated from genetic resources, deter us from a more holistic vision of conservation of biological diversity and respective transitions to bioregionalism (Cheney 1989; Alexander 1990), reinhabitation, and sustainability (Redclift 1987).

IN SITU CONSERVATION OF GENETIC RESOURCES AS DRIVEN BY SOCIAL PRESSURES AND POLICY CHOICES

Why be concerned with the persistence of genotypes and alleles beyond that necessary for the actual survival of species? Maintenance of certain levels of intra-specific variation is key to a population's fitness. When we maintain as many genotypes as possible, we are, at the very least, preserving additional possibilities for utilization of adaptations, either in wild populations or as domesticates. When we maintain as many alleles as possible, we are preserving possibilities for expressions of certain traits, such as disease resistance (Browning 1991), which might otherwise be lost.

The difference between maintenance of fitness and certain levels of security for genotypes in certain environments or alleles at certain levels of occurrence can be great, in some cases, or relatively minor in others depending on the reproductive biology and genetic architecture of the species, on one hand, and the needs and pressures for conservation from a range of interest groups, regions and over various "operational scales" (Delcourt and Delcourt 1992) as related to space and time. Under their framework, the two operational scales, at least as related to the management of edges and successional mosaics which are central to *in situ* conservation of genetic resources, are the "microscale" "1 yr to 500 yr; 1 m² to 10⁶m² [100 ha]" and the "mesoscale" "500 yr to 10,000 yr; 10⁶m²[1 km²] to 10¹⁰m² [10⁴ km²]."

An additional set of conservation criteria for intra-specific variation, which

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may not be crucial to a population's continued fitness, is termed "desired diversity" (Namkoong 1983).

Before proceeding, we should consider the notion of the genetic resource and how this label is evolving. A population, whether wild, feral, weedy, or domesticated is, in itself, a genetic resource when it is recognized to have the potential to provide germplasm, through human intervention, to enhance a different domesticate or managed wild population. The germplasm in transfer between donor and recipient populations can be seed, sperm, eggs, or cultured material as well as DNA which is injected into living cells. A substantial portion of the species in a region might have some significance as genetic resources as human history unfolds and new technologies invariably make transfers easier. In addition, countless plant species and associated species might have potentials as new domesticates and for environmental restoration.

A species or a population is a genetic resource when it is identified but similarly aspects of the genes and associated gene pool can become part of the resource complex when they too are recognized as being valuable. What maintains genetic diversity and our highly fluid subset of genetic resources are complex ecosystems and habitat and successional mosaics across regions. When we transfer seed or even a gene, we are, in effect, transferring oddly incongruous points from one ecosystem into another. In indulging in isolated DNA, the most reduced form of the genetic transfers so far devised, it is easy to forget that there is never a clean transfer. In the case of seeds there are associated microbes, sometimes even insects, and there are numerous examples, particularly from the humid tropics, of transfers that require such mobile links as vertebrate pollinators so that the new population can be viable. In defining and conserving a genetic resource, particularly involving wild species, the seam between the genetic agent, the actual germplasm, and the context is becoming more fluid and, in terms of ownership and funding, increasingly contentious.

The groups with various interests in and uses for genetic resources are expanding rapidly. Historically, there have been plant breeders and then the actual purveyors of reproductive material such as seed houses. Today, groups of consumers have identified a stake in continued access to products such as drugs from wild populations like Taxol from the Pacific Northwest tree, *Taxus brevifolia*. Groups within production and service sectors advocated increasing access to a growing number of products. If a tiny fraction of the income generated by biotechnology from material from protected areas is actually funnelled back into conservation, we might be able to add protected area administrations and the public which enjoys these areas

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as a powerful group of indirect beneficiaries.

The proliferation of scientific, industry, and citizen groups associated with the actual genetic transfers and the subsequent experimentation and development now involves both the public and the private sectors. There are the surveyors and collectors, the technicians of the transfer and storage operations and the evaluators and the breeders. The marketing of commercial material has expanded rapidly in the last decade. Except in the maintenance of some material from recognized populations, there is no assurance that respective economic and scientific interests and priorities will be in concert.

Groups that are often neglected are subsistence and traditional users with their own interests in particular species and ecosystems. Across a region and within a community is a great range of user types, interests, and priorities and can even be at odds with the global marketplace and even the liberalism of cosmopolitan "societies" (Dasmann 1975; Ingram 1989). Between and within groups of consumers, purveyors, and subsistence communities, there are bound to be differences in valuation of particular populations and genes, conservation priorities, and acceptable levels of conservation security, risk, access and costs. This is a microcosm of the complexities of the global marketplace in the twenty-first century. As genetic resources are increasingly valued, interests will proliferate as will potential points of cooperation and conflict. The currents within this milieu have a direct bearing on what is effectively conserved *in situ*.

IDENTIFICATION AND VALUATION OF GENETIC RESOURCES

Identification procedures for genetic resources have barely been developed. In a sense, any living thing is a potential donor, though only a minute fraction of the species and populations on Earth will ever prompt such levels of monitoring and transfer. Only a minute fraction of the material transferred will be worked into general distribution as new plant varieties and breeds of animals. The following is an example of the ongoing and open-ended nature of determination of genetic resources for food crops.

"IBPGR has formulated a list of crop-collecting priorities to guide conservation activity. In general, the factors considered are the level of risk to the crop and its wild relatives; the crop's economic and social importance; the materials that need collecting; the needs of plant breeders; and the quality of present collections. The list is occasionally updated, and is made both by crop and by region, but there is nothing sacred about IBPGR's list. It is based on educated guesses. And they are probably the best guesses that can be made, even if sometimes reflecting a bias toward industrialized countries needs." (Fowler and Mooney 1990: 79).

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These species and genera in these lists include the better documented crops. If an expanded list of important potential food plants were compiled (Prescott-Allen and Prescott-Allen 1990), which included species currently only of subsistence importance as well as more distantly related populations that can only contribute genetic material to a food gene pool through laboratory means, the number of "priority crops" would be much greater.

Traditional crop material is defined here as pre-20th Century varieties and "land races" (Williams 1988) which are diverse collections of primitive types of domesticated material and related weeds. A bag of seed from one field of land races is highly diverse and this allows for some production, through the various adaptations, even in the worst years. On the other hand, the seeds of modern varieties are relatively uniform. This "primitive" material is sometimes called "folk seed" (Fowler and Mooney 1990) and the term is preferred by some as it acknowledges the important role farmers have played in selecting, breeding, and distributing crop varieties.

Wild relatives of crops are species that can be used to contribute to the development of new crop varieties. Three general categories of these biological resources correspond to genetic proximity to respective crops. Wild species that can be easily bred with a crop are, therefore, in the **primary gene pool**. Wild species that can be bred with a crop under special conditions are in the **secondary gene pool**. Wild species that can only contribute to the improvement of a crop through genetic engineering techniques are in the **tertiary gene pool**. The trend, in biotechnology, is to by-pass the genotypes of primary and secondary gene pool populations and to isolate a wide range of material in a technologically driven expansion of the tertiary gene pool. This shift does not make the more closely related wild, weedy and feral populations less valuable because it is in studying phenotypic expression, *in situ*, and relating it to laboratory evaluation of genotypes that desired expressions can be isolated. The primary and secondary gene pool populations become valuable as much as "libraries" and "*in situ*" laboratories as sources of material for transfers.

The necessary conservation measures differ greatly between traditional varieties and wild relatives of crops because populations evolve within natural ecosystems whereas land races and primitive crops are products of human practices, modified habitats, transformative social relationships and the resulting agro-ecosystems (Bedigian 1991). In terms of reproduction, crop and related wild species can be divided into two very different groups: annuals and perennials. Seeds of annuals can be conserved through cold storage. For many perennials,

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non-ecosystem-based, *ex situ* conservation is not workable because of short-lived seed, the diminishing limitations of meristem culture, and reproduction requirements which are difficult to meet in field genebanks and laboratories (Ingram 1984).

Eight centres of crop origin were identified by Vavilov (1951) and he assumed these to be centres of diversity. These areas were further described by Harlan (1976) and Hawkes. Some scientists now believe there are twelve centres of diversity (Fowler and Mooney 1990). Crops have dispersed from these areas to create secondary centres of diversity.

There is not necessarily a perfect fit between centres of origin and centres of species and intra-specific diversity for wild relatives of crops. For both mango, *Mangifera* spp., and citrus, involving *Citrus* spp. and related genera, the centres of domestication were further west toward India while the centre of species diversity extends from Burma through peninsular Malaysia to Sumatra and Borneo. The implications of the location of the centres of diversity are that the great majority of crop genetic resources are in the tropics and in countries with relatively ineffective programs of protected area planning and management.

Recent work on the structure of crop populations (Zimmerer and Douches 1991) and on wild relatives of crops describes a fine mosaic of genotypic variation. This genetic diversity is difficult to capture and maintain even in networks of protected areas and comprehensive genebank collections (Brush 1991). For long-term breeding needs, there is a wider range of plant characteristics that is not of current interest to breeders.

How will each interest group deal with the open-ended nature of setting priorities for surveying, conservation and evaluation? We can be assured of haphazard responses from the global marketplace of products and information. There will inevitably be the accelerating "generushes" related to particular traits, species, and entire commodity groups: searching for drought-resistance genotypes in times of climatic shifts or rapid screening of a large number of wild relatives for a gene which is resistant to a blight or epidemic. The implications for land management are that a growing number of populations will be considered worthwhile for new protected areas, expansions of current reserves, and intensified monitoring and management.

Significant differences between the genetic resources of food crops and other groups, such as plant species with value as forage, medicinals, or in environmental restoration and the wild relatives of livestock. The implications for identification and valuation of wild, weedy, and feral populations are that delineation of a target group for research and conservation is the result of the knowledge base related to taxonomy

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and the perceived short and long-term demand for improved or introduced types. In these non-crop groups, the knowledge, political and capital bases are far more modest.

ECOGEOGRAPHICAL SURVEYS OF GENETIC RESOURCES: LINKAGES BETWEEN TAXONOMIC AND INVENTORY DATA AND PRIORITIES IN CONSERVATION PLANNING

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The core of any *in situ* conservation effort is actually the long-term programme of inventory and monitoring. Initial inventories of populations involving collection of field data related to phenotypic expression and biophysical and spatial factors can be termed "ecogeographic surveys" (Ingram 1990a). The sub-text of an ecogeographic survey is the "second-guessing" of crucial relationships between two things. First, there is the ascertaining of the pattern of genetic variability which only occurs when site and laboratory data are correlated. Secondly, a survey explores possible correlations between life histories and landscape trajectories (Hansen et al. 1992) which are particularly vulnerable to disruption from particular segments of cause-effect linkages within the disturbances matrices (Forman and Godron 1986) to ascertain the cumulative impacts of genetic erosion. Vulnerability in this context relates to either habitat loss or habitat alterations which could eventually have a significant impact on the frequencies of certain alleles across landscape units and regions.

These surveys involve subsequent evaluation of sampled material in laboratories and field genebanks through techniques, such as electrophoresis. Material is often "grown out" in controlled conditions and some sense emerges of the overall genetic variation across distributions of each species.

It is usually necessary to record ecogeographic and cultural data at scales involving the site and the habitat isolate to the landscape and the regional meta-population. Site information for each sample is necessary as is more contextual information, such as biogeography which relates to patterns of gene flow. The types of ecological information of relevance will vary with ecosystem structure and respective successional and phenotypic factors. Some information will be spatial and some will be descriptive and biophysical. Usually a host of social use factors and related selection pressures exists. There might already be some differentiation between phenotypes, and possibly genotypes, along the lines of the units within the cultural landscape (Rapoport 1992). Information on the presence and extent of introduced species is crucial.

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Two divergent formats and approaches to ecogeographical surveying have emerged: for an entire species, genus, or gene pool across entire distributions or regions and multi-gene pool surveys for particular biotic districts and regions (Ingram 1990a). The single gene pool surveys have tended to be reductionist and autecological in emphasis whereas the multi-gene pool surveys have often been more biogeographical in outlook.

The design of a survey programme involves a number of structural decisions as related to:

1. the taxonomic scope of the gene pool(s) as related to the target species;
2. the spatial scope in terms of realms, regions, bioregions (WRI, IUCN and UNEP 1992), political boundaries and districts;
3. the minimum number of samples to be taken and the criteria for sampling;
4. the minimum size of the samples to be taken; and
5. the extent of the data collection and subsequent documentation.

Corollaries exist between the number of samples and sampling sizes and the "where and how much" discussions for planning protected areas.

Of the surveys that have been undertaken over the last decade, there still is a tremendous problem with documentation in terms of the availability of the site information taken for each sample. In many of the *ex situ* settings to which sampled germplasm is deposited, there is very little motivation (or resources) to maintain the kinds of data bases that would allow for intensive use of ecogeographic data in genetic evaluation. This is one of the sleeping problems that will emerge as the *Convention on Biological Diversity* and other accords on access, distribution and profit sharing of genetic resources are instituted.

In considering the needs for ecogeographic surveying and the subsequent linkages to programmes of *in situ* conservation, it is necessary to first ascertain the political and administrative interests, and the prioritization of related questions for particular gene pools. The following are examples of some of the variables of these surveys.

THE SAHEL SURVEY AND THE *PENNISETUM* GENE POOL

The 1984 African famine intensified the concern in crop breeding for drought resistance at a time when there was also increased interest in expansion and sustainability of agriculture in semi-arid regions. Pearl millet, *Pennisetum* spp., a west African crop was the subject of research and sampling of germplasm. The surveying was organized by the International Board for Plant Genetic Resources

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of the Consultative Group on International Agricultural Research and the Food and Agricultural Organization of the United Nations and the cooperating institutes were Sahelian, U.S.(USDA), Indian, and French. There were also similar efforts for crops such as sorghum and okra in the Sahel. It became evident that a large portion of the variability within the primary gene pool was still in the area of origin: the northern and central band of the Sahel extending from Senegal to Chad. There was particular concern for location rural landscapes with relatively low human densities and with high probabilities of introgression across land use-related ecotones involving wild and weedy material and land races (Benz et al. 1990).

The Sahel is a vast region and, to use time and resources effectively for surveying populations in wild and weedy crop gene pools, a range of other species in crop and forage gene pools of global significance was identified. Various sites across a range of ecological zones, countries, regions, and districts were visited (Ingram 1985, 1986b; Ingram et al. 1987) with a vision of a long-term effort to inventory and monitor a range of traditional crops and wild species of importance for food and fodder (Ingram 1986a).

Much of the Sahel is flat and homogeneous with environmental variation largely microscaled. Areas with steeper gradients, such as mountains and marshlands, are of interest particularly in light of the archaeological evidence of patterns of settlement and land use in the region (Munson 1976) an extensive multi-gene pool survey was undertaken in the Air Mountains of north Niger (Ingram 1990a) a mountain range which, because of the patterns of rain capture, has maintained Sahelian ecosystems as the Sahara moved southward. But even with only modest grazing pressures, there were extensive areas with dessication and destruction of woodland and savanna vegetation (Ingram 1985; Ingram et al. 1987). In such settings of rapid genetic erosion, human responses, such as recently innovated irrigated gardens, become the cultural refugia for formerly riparian and seasonal wetland vegetation.

The resources required to carry out such a research programme across a region are formidable. The required political cooperation is daunting especially in wartime. Sampling of viable seed is problematic under the best of conditions and almost impossible in times of drought. The collection of site-data (Ingram et al. 1987) is difficult except for the highly trained especially in extreme heat and in 14 hour field days. Local institutes were highly skeptical of such ambitious approaches. But without such accelerated efforts, sampling and monitoring will not be sufficiently ahead of losses to inform conservation planning.

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THE CRABAPPLE GENE POOL ON THE NORTHERN COAST OF BRITISH COLUMBIA

Burnaby Island, *Skwa-ikungwa-i*, is part of the Gwaii Haanas National Park Reserve on the Queen Charlotte Islands, *Haida Gwaii*, and before 1989 was under considerable pressure for conventional clearcut logging. A survey of the island's biological diversity was initiated in the mid-1980s which included concerns for species of traditional significance and genetic resources (Ingram 1989). One species with relatively well-recognized genetic resources, and with some significance to European breeding programmes for apple, *Malus* spp., is crabapple, *Pyrus fusca*, which was traditionally called *k'anlha* by the Skidegate Haida (Turner and Levine 1971).

The north Pacific coast of North America is relatively depauperate, biologically, because the glacial withdrawal has occurred within the last 10,000 years. However, the islands are remarkable in terms of their rugged landforms (Swanson et al. 1988), the complex biogeoclimatic zonation, ancient coniferous forests (Pojar and Broadhead 1984), and some oddly disjunctive occurrences of plant species (Roemer and Ogilvie 1983).

Four terrestrial, biogeoclimatic zones have been identified in the Burnaby Island area: coastal western hemlock zone, *CWHg*, the superhumid coastal cedars-pine-hemlock zone, *CCPH*, (Pojar and Annas 1980), mountain hemlock zone, *MH*, and alpine tundra. Within these zones are a number of associations (Lewis 1982). Over 90% of Burnaby Island is dominated by coniferous forest. A number of physiognomic types in the Burnaby Island area: saltmarsh; beach strands; Sitka spruce forest near shores; alluvial meadow forest; deciduous, red alder woodland; alpine; various association of western hemlock, Sitka spruce and red cedar; topogenous bogs, fens and marshes; and forests of yellow cedar and mountain hemlock at higher elevations.

The crabapple extends widely across a number of biophysical gradients although it is usually associated with more geomorphic as well as successional ecotones in the following zones. The crabapple extends from the upper edges of saltmarshes to various lowland forest types (British Columbia Ministry of Forests 1988) including: *Q1* - mixed old growth - moss association, *Tsuga heterophylla* - *Thuja plicata* - *Picea sitchensis* - *Vaccinium* spp. - *Rhytidiadelphus loreum* comprised of climax lowland forest, dominated by western hemlock, red cedar and Sitka spruce; *Q4* - alluvium Sitka spruce - moss association - *Picea sitchensis* - *Tsuga heterophylla*

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-- *Rhytidadelphus loreus* - *Plagiomnium insigne*; Q7 - pine - yellow cedar scrub, *Pinus contorta* - *Chamaecyparis nootkatensis* - *Carex* spp. - *Sphagnum* spp., a complex of shrub and bog associations which extend into the mountain hemlock biogeoclimatic zone; and Q9 - lowland, colluvial association, *Picea sitchensis* - *Alnus rubra* - *Huperzia selago* - *Pogonatum alpinum* an "erosional disclimax" (Lewis 1982) and the colluvial phase of CWHg-Q1.

The Haida population in the Burnaby Island area was concentrated along a shallow channel with extensive saltmarshes called *K'iit*. The most historically complete and site-specific description of the Haida villages are provided by Swanton (1905a,b) who noted one town occupied before 1870: *£a'nadágAña* translating to "Bad-talk-town." Virtually all of the crabapple trees in the area were "owned" and managed by well-ascribed, matrilineal family groups (Turner and Levine 1971). Therefore, given the extensive modification of lowland areas, as related to Haida settlements, and traditional patterns of utilization, these "wild" populations can be considered forms of cultural artifacts. With the removal of the pressures for clearcut logging, several years ago, the threats to these populations are from tourism, introduced black-tailed deer, *Odocoileus hemionus*, and further disintegration of the cultural landscapes which were largely abandoned after the recurring small pox epidemics and resettlement efforts of the late nineteenth century.

The Pacific crabapple is slow-growing and occurs in relatively low population densities especially in terms of the trees of the Pacific northwest. This species, however, is remarkable in its range of occurrences and the respective biogeoclimatic sub-zones and ecotones. Global warming could shift altitudinal zonation, on this highly complex island landscape, at such a rapid rate that regeneration declines below viable levels of resilience. In the shorter term, the introduced deer have no predators and their populations continue to increase to levels where all low lying deciduous vegetation is continuously browsed. A more extensive survey of the impacts of introduced deer should include monitoring for crabapple regeneration and mortality from browsing.

A MULTI-GENE POOL RECONNAISSANCE OF FERGUSSON ISLAND, PAPUA NEW GUINEA

Linking the concerns for genetic resources and their conservation *in situ* as part of larger programmes for preservation of primary rain forest has been poorly explored. This survey of the forests of an island in southeastern New Guinea, with high levels of biological richness, was an effort to develop effective inventory and planning

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practices (Ingram 1989, 1991). A number of wild species in the following gene pools were identified including banana, *Musa* spp.; sugar cane, *Saccharum* spp.; mango, *Mangifera* spp.; taro, *Colocasia* spp.; and citrus including *Microcitrus* spp., *Citrus* sp., *Monanthocitrus* sp., and *Wenzelia* spp. These were considered as part of a list of "focal species" (Ingram 1989) to guide the choice and design of protected areas and the relationships with subsequent management.

In such a setting, with so little inventory data and only tentative taxonomic identifications possible, the focus shifts to strategic areas of species richness and types of mosaics that might be sufficiently diverse to support a wide range of genotypes. But even for forest species, it is difficult to generalize about such mosaics. If a specimen of a target species is found, it is still very difficult to generalize about respective distributions, life history, and ecology. The few samples that are found can be subjects to extensive laboratory scrutiny if there are the facilities for genetic analysis. But such evaluations usually require a large number of samples and individuals and few of these are possible in the low densities usually occurring in primary rain forest.

A survey such as this is almost more of an object lesson in the conservation of the biodiversity of humid forests. Initial inventory data are non-existent, weak, or suspect. Occurrences are at such low densities as to make any extrapolation on ecological relationships questionable. Few herbarium samples are available for the training of collectors and surveyors and few taxonomists who can find the time to identify specimens at the species level. Even if species are successfully identified, and this usually requires flowering in the case of perennials, the technical possibilities for sampling and *ex situ* conservation are limited without extensive evaluation. If material is successfully "grown out," most likely through meristem culture, the species might well require other aspects of its ecosystem for reproduction. At the same time logging companies are clamouring to remove as much marketable timber as possible and the numbers of swidden farmers continue to grow.

PROTECTED AREAS AND LAND MANAGEMENT IN RESPONSE TO GENETIC EROSION

In referring to the erosion of crop gene pools, the Keystone International Dialogue (1991) noted,

"Loss continues today at a rapid rate. As we do not know how much total diversity once existed, it is impossible to quantify the losses."

Unfortunately, there is currently very little monitoring, nor a funding base for these

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activities, even where baseline studies exist. A number of causal agents fuel genetic erosion or "genetic impoverishment" (Myers 1988), and these have intensified over the last decade. The rates of genetic erosion tend to be the greatest in areas with the most fertile and most easily mechanized agricultural lands and near urban centres and markets. It is in impoverished and marginal areas, such as mountainous uplands, where traditional varieties are still grown and are sufficiently relied upon to allow for conservation of traditional varieties. The crop gene pools that have had the most losses have been primarily those that are subjects of active breeding programs (Fowler and Mooney 1990).

With strategies for *in situ* conservation of genetic resources (Ingram 1987, FAO 1991), across a site or region, measures do not function to maintain an aspect of human experience of wildland but rather to preclude and counter largely cumulative impacts (Dickert and Tuttle 1985). These measures can usually be labeled as either land acquisition or management but can involve a complex set of human activities which, while idealizing the maintenance or reconstruction of relatively "intact" ecosystems, often appear as uncoordinated and *ad hoc*. Genetic erosion is often so rapid and pervasive that the key to conservation programmes is simply in responding to particular cause-effect linkages. Such a reactive approach is fundamentally incomplete from a bioregional or "reinhabitation" perspective but might suffice to maintain acceptable levels of intra-specific variation while freeing up energy for a broader vision of regional environmental management.

An initial framework for understanding genetic erosion in wild, weedy and feral populations can emphasize models of fragmentation and extinction at finer scales (Merriam and Wegner 1992). However, in considering intra-specific variation, some contradictory management objectives can emerge in contrast to for maintenance of fitness. Maintenance of higher levels of genetic variability, such as frequency of rarer alleles or even persistence of a phenotype which might reflect a genotype, require protection of populations across gradients of active selection. Additional reservoirs, with population sizes sufficiently large to support alleles for which there is currently little selection, are also necessary. This gradient / reservoir dynamic can underly nearly any genetic conservation intervention and requires the integration of concepts of landscape ecology including ecotones, matrices and successional mosaics (Forman and Moore 1992) with laboratory analyses subsequent to surveying and linkages with the (limited) options for land management.

EFFECTIVENESS OF CONSERVATION OF GENETIC RESOURCES

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The conservation of genetic resources and the on-site maintenance of particularly valuable populations has been an integral part of most cultures since the shift from gathering to agriculture. However, the pressures for loss of intra-specific variability and the stakes in utilization of germplasm for economic purposes have greatly increased. This decade will see a great proliferation of objectives and approaches for *in situ* conservation as a result of the increasing numbers of species recognized as genetic resources, increasing possibilities for successful transfers of alleles, and intensifying genetic erosion compounded by human population growth, forest clearing and agricultural expansion, and climate change (di Castri and Hansen 1992).

In this context, the following review of the types of *in situ* conservation programmes is more historical and in the past tense. Virtually all of the current programmes are only partially effective and are bound to be integrated into more comprehensive regional programmes for biodiversity.

As noted by Schonewald-Cox and Stohlgren (1988),

"Merely designating areas or establishing laws does not guarantee the protection of biological and genetic diversity."

Virtually all protected areas and landscapes have some populations of some species of economic importance which are more or less adequately protected at least in the short-term. However, in virtually all protected areas, substantially increased monitoring and management programmes will be necessary to avert losses of rarer genes and other potential genetic resources. Three general levels of *in situ* conservation of genetic resources described below.

Random *in situ* conservation of genetic resources is largely unplanned coverage through ecosystem conservation. When protected areas that have been designed or planned without recognition of the occurrence of genetic resource species include such populations, adequate coverage within reserve boundaries for maintenance of viable populations cannot be assumed. The scale for ecosystem conservation is often at the regional level and is often too broad to consider an array of species and finely scaled distribution data. Consequently, the extent of actual conservation is modest especially narrow amplitudes of ecological requirements for particular species exist.

Ecosystem-level *in situ* conservation of genetic resources requires the planning and design of protected areas with use of lists of species with genetic resources and respective distribution data. Implications of principles of biogeography and conservation biology must be considered. The scale is often district-wide (Ingram

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1989) where more specific decisions of about species and sites can be made. Many of the "genetic reserves" (Jain 1975) involve this level of conservation. Management for particular species and associated successional phases is usually necessary. Species that are monitored and managed under programmes of ecosystem coverage can also have ecosystem-level conservation.

Allelic-level *in situ* conservation of genetic resources involves on-going monitoring, management and procurement for particular levels of conservation for specific "functional population units" (Solbrig 1991). The scale of such planning and management is site-specific. For this level of conservation to be attained, population viability thresholds must be set with prescriptions for maintenance of intra-specific variation and rarer alleles. Natural and well-protected populations, have constant flux of gene frequencies with some of these alleles becoming rare or disappearing. In protected areas, the natural and human-induced dwindling of populations can cause the narrowing of the base of variation and subsequent loss of potentially valuable genetic resources. To maintain rarer alleles or possible adaptive complexes associated with certain environments and selection factors, additional requirements for larger and sometimes additional populations must be determined. It is only at this level of genetic conservation that management to maintain levels of desired diversity can be set.

With species that do not involve a concern for maintenance of potential genetic resources, random *in situ* conservation is often adequate and ecosystem-level *in situ* conservation is needed for the long-term. For *in situ* conservation for crop genetic resources, both traditional varieties and wild species, ecosystem-level *in situ* conservation is always necessary to assure capture of desirable minimum percentages of alleles, and allelic-level *in situ* conservation is necessary for long-term security and germplasm procurement.

Concerns for genetic resources have begun to be worked into broader national park management. However, rarely are there complete lists of plant species and distribution maps even in developed countries. Management is too often oriented to other ecological concerns or for the management of recreation. Biosphere reserves will play an increasingly key role in the conservation and utilization of wild relatives of crops because of institutional potentials for monitoring and international exchange of information (Ingram 1990b). The concept has not been effectively utilized for traditional crops. The network is very new (Batisse 1982; Verhnes 1989), and most biosphere reserves are still poorly inventoried with only a small portion of the total number of species with potentials for providing genetic material having been

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identified.

The biosphere reserve concept is based around the vision of a set of land use zones with one or more "core" protected areas surrounded by well-managed, primarily wildland areas and then surrounded by a heavily modified "transition" zones. By monitoring these transitions from natural baselines to human-modified ecosystems, important data for environmental management can be generated. Over the last decade, the role of biosphere reserves for the conservation of biodiversity has increased (Unesco 1984). Unfortunately, the management requirements for particular populations with genetic resources have rarely been related to the central concepts of cores, buffers, and transitional areas, although great potential exists (Gregg 1991). Until recently, traditional agriculture was largely suppressed within core areas even where indigenous species were involved.

Extensive debates on the viability of *in situ* conservation of traditional crops have taken place (Altieri 1988; Brush 1988; Brush 1991; Wilkes 1991). Almost all of the current "in farm" crop conservation programs have been initiated by small institutes and non-governmental organizations. In Ethiopia, the Seeds of Survival program is working with the Plant Genetic Resources Centre in Addis Ababa to re-introduce traditional varieties and landraces to farmers. During droughts, farmers were forced to eat their stocks of seeds. The new response has been to make extensive collections *ex situ*, re-introduce land races where there is interest, establish research plots, monitoring productivity, and establish training and support programs for farmers.

The traditional agroforestry system practiced on Fergusson Island, Papua New Guinea serves as an example of *in situ* conservation of traditional varieties of crops within a particularly biodiversity-rich setting (Flavelle 1991). Because of low human populations, mountainous terrain, and distance to market, cash crop ventures have so far been unsuccessful. The system revolves around yams cultivation, principally of *Dioscorea esculenta* and *D. alata*. These crops are the basis of the subsistence economy, but it is their cultural importance that might ultimately prevent them from being replaced by introduced food crop species.

Yams seeds are inherited through the matrilineage; they are exchanged as gifts at funeral feasts and other occasions; they are the focus of magic ritual and myths. Other tubers that farmers have grown for generations but which hold less status than yams include: sweet potato, *Ipomea* sp., *Colocasia esculenta*, and manihot, *Manihot esculenta*. Prominent food trees in the system include mango, *Mangifera* sp., *Citrus* sp., *Szigium* sp., *Carica* sp., banana, *Musa* sp., and *Arctocarpus* sp., and *Ficus* sp.,

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Cocos nucifera, and sago, *Metroxylon* sp. Every time that a community opposes intrusion of the cash economy and especially such environmentally degrading activities as some forms of logging, it is a form of *in situ* conservation. Such approaches might not be permanent but the record of such traditional conservation measures suggests that they can often be more effective over the longer-term than the measures of an unstable government.

One of the most impressive examples of *in situ* conservation of crops in an internationally monitored protected area is that of Niger's Aïr and Ténéré National Nature Reserve. However, in recent years order has declined (Newby and Wilson 1993). A range of traditional and contemporary garden types are persisting as well as primitive, traditional and more recent crop material for the gene pools of sorghum, *Sorghum* spp., pearl millet, *Pennisetum* spp., barley, *Hordeum* sp., and wheat, *Triticum* sp. A number of key agroforestry gene pools are also being protected including *Acacia* spp.; a close wild relative to cultivated olive, *Olea* sp.; and the important African fruit tree, *Ziziphus* spp. The area is at an ecological crossroad in terms of material and farming practices from North Africa and the Sahel. But, regardless of the support from maintenance of these gardens within the framework of protected area management, progressive desertification, due largely to climatic change, could destroy prospects for long-term *in situ* conservation.

People with a history of living in and off the forest have knowledge about the location and natural history of wild populations of crops, their near relatives, and their sustainable management. Local people have a central role in surveying and monitoring wild populations (Ingram 1990c). The persistence of local knowledge and sustainable traditional forest-use practices over generations require intact and yet evolving cultural systems. Today, most such cultural systems are under assault or are being more subtly undermined by market forces.

Provincial park and nature reserve designations capture only a tiny portion of the wild gene pool of crops. In Amazonia, extractive reserves, designed to be compatible with needs of local people, conserve fragments of forest and the wild gene pools of Brazil-nut, *Bertholletia excelsa*, rubber, *Hevea* spp., cacao and other important crops (Smith and Schultes 1990). Local control and management of extractive reserves are necessary, but are inadequate for sufficient conservation of adequate levels of rarer but, nonetheless, potentially valuable, alleles. Local people need incentives to maintain wild populations and to minimize growing reliance on production of cash crops.

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GENERAL PRINCIPLES FOR *IN SITU* CONSERVATION

It would be highly disadvantageous, at this phase in the development of conservation biology and landscape ecology, to generalize about the nature of the requirements for *in situ* conservation of genetic resources as part of broader regional programmes for the conservation of biological diversity. Many of us are familiar with the almost farsical misreading and misuse of the numbers 50/500 in early discussions on population viability (Frankel and Soulé 1981). However, it is definitely possible to say that requirements for genetic resources will be "different" than other kinds conservation measures if only because the uses and socially related standards for more altruistic and recreationally oriented programmes of protected areas are rooted in separate human needs. However, if we really can construct a bioregional ethic and aesthetic, it should have a place for appreciation of maintenance of a comprehensive set of habitats, edges, gradients and respective selection factors across regions.

It is also possible to describe the following trends in requirements for *in situ* conservation, in terms of land management, as they emerge from ecogeographical surveys and subsequent and ongoing evaluation.

1. If we are dealing with a gene pool with extremely high significance to the economies of particular regions, it is worthwhile to conserve even the rarer alleles. In order to maintain these alleles, larger and more numerous populations are usually necessary than that simply to maintain fitness.
2. In terms of the small number of populations that are wild and feral relatives of livestock, virtually all of the current alleles, even the ones expressed in ways which are currently deleterious to respective populations, are worth maintaining. To assure the persistence of these alleles, culling practices must be seriously reviewed, and many population sizes must be effectively increased through combined *in situ* / *ex situ* strategies.
3. Landscape diversity is "good" but only to a point. Every set of species in particular regions has amplitudes that allow a wide range of populations and habitat and successional isolates and sufficiently large populations to maintain rarer alleles as well as sufficient resilience. We cannot assume that, across a region or landscape unit and for a suite of genetic resources, a that a median position will be possible. This problem manifests in decisions over management of mosaics. Some populations, genotypes and rarer alleles are

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invariably better protected than others and this reflects priorities, the state of the (spatial) biogeographic and ecological knowledge, and the nature of larger gaps in environmental data bases.

4. As concerns for germplasm increase and requirements for conservation are refined, concerns will grow for an expanding set of elements of respective ecosystems, such as mobile links (Nabhan and Norman 1992) and keystone mutualists.
5. Virtually all *in situ* conservation requires interventions and management prescriptions at multiple scales, in terms of time and space, and this, in turn, requires linked strategies corresponding to sites, habitat isolates, landscape units, districts, and regions.
6. In planning and management of landscapes five functional categories for strategies of *in situ* conservation are recognized:
 - a. natural cores,
 - b. natural and culturally modified buffers,
 - c. transitional areas of cultural landscapes involving gradients of modern and traditional, social and technological impacts,
 - d. corridors for gene flow, and
 - e. barriers for the control of gene flow and the invasion of species.
7. *Ex situ* conservation and evaluation is necessary for any sustained protection of the genetic variability population, *in situ*, but might not necessarily be geared to the central questions for land management. Consequently, virtually all *ex situ* programmes need to be reviewed and expanded because there is elaboration on land management questions for particular populations, species, sites and regions.
8. Virtually all *in situ* conservation involves conservation of cultural landscapes either as artifacts and anomalous isolates or as part of traditional human communities under threat. Therefore, every intervention for *in situ* conservation has economic, social, and cultural impacts which can either support or undermine such communities. These communities often have the only expertise for the necessary fine-scaled management. The pattern of their

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adaptations to changing land-use patterns and resource availability, which are partially influenced by *in situ* interventions, has a direct bearing on options for regional strategies (Nabhan et al. 1991). Essential to effective *in situ* conservation of genetic resources must be viable forms of co-management, which require directing of the global economic benefits of genetic resources back to local operations (Dasmann 1991, WRI, IUCN and UNEP 1992).

9. Because of the dual of nature traditional and global interests in maintenance of genetic resources and the dynamics of co-management that are emerging in most networks of protected areas, it is necessary to observe the principle of multiple and sometimes conflicting, sets of management objectives for particular sites and populations. Effective *in situ* conservation of these resources is as much about building social, political, and administrative frameworks to resolve these contradictions and respective conflicts as is the design of reserve boundaries.

GUIDELINES FOR MONITORING, HYPOTHESIS TESTING, AND ADAPTIVE MANAGEMENT

Genetic resources are, by their nature, dynamic, fleeting, and unpredictable. Their requirements, as we are coming to perceive them, are profoundly humbling to the environmental planner and land manager. We will require vastly increased "protection" in the coming decades, but this must be based as much on various "inquiring systems" as networks of protected areas. It is with genetic resources that perhaps we can say that our networks of reserves are only as effective as our knowledge bases or at least our abilities to translate the second-guessing of our ignorance into prudent decision-making. Reductionist science does not give us much help and we are left to relate our correlations of ecogeographic data to laboratory evaluations and then to a myriad of possible cause-effect linkages. How do we begin this open-ended and daunting enterprise for a particular region, park, reserve network or gene pool? The following are some key principles.

1. Concepts of genetic diversity, as they relate to definitions of genetic resources and risk of loss, need to be expanded and clarified within broadly oriented research programmes on biological diversity (Solbrig 1991).
2. It is necessary to clarify relationships between selection factors, ecologically

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and geographically related variation and both priorities for conservation and crop breeding, this should be for particular plant groups as related to life histories, reproduction and environmental heterogeneity. Literature review and a field research phases must follow.

3. The pool of methodologies for surveying wild species with genetic diversity is still remarkably undeveloped (Ingram 1990a), and various approaches must be tested and evaluated. Major revisions between surveying phases are inevitable.
4. Documentation practices for collection of germplasm and respective site and regional data, involving both biophysical and cultural factors, are currently poor and highly variable. Even though every species, population, and context is unique, there needs to be some standardization for particular plant and population types, ecosystem and landscape types, and types of genetic erosion.
5. Given the extreme importance of a wide range of information, a distribution system for survey and collection data on genetic resources must be developed by and for larger regional land management and genetic resource institutes. An *in situ* conservation strategy is in no small part structured by the nature of these information systems.
6. Linkages and methodologies for *ex situ* evaluation and the "growing out" of material from wild populations must be reconsidered in the light of expanding pools of information on respective ecosystems and selection factors. This is particularly important to expanded use of germplasm from humid tropical ecosystems which might thrive only with complex sets of conditions. The nature of evaluations and the extent of their implications for *in situ* conservation interventions will change with the extent of sampling and evaluation techniques and the subsequent information base.
7. In the design of new protected areas as well as in management plans for cores and buffers, models are necessary to account for population viability, prescribed levels of conservation of rarer genes, and selection factors across successional mosaics. Such models are best computerized and have spatial aspects that could be integrated into conservation planning through geographic

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information systems.

8. The theories of domestication for many crop groups and gene pools have gone through paradigm shifts that have direct bearings on priorities for conservation of traditional varieties and primitive and weedy populations. *In situ* or in-farm conservation components of larger gene pool conservation and screening strategies should reflect careful review of hypotheses of crop evolution and genetic erosion.

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FRAMEWORKS FOR INTEGRATION OF CONCERNS FOR GENETIC RESOURCES INTO PLANNING FOR CONSERVATION OF BIOLOGICAL DIVERSITY

The previous principles were applied for the species and scales in the three examples. A framework can be based on the principle of the relatively *ad hoc* and scattered nature of necessary for cores, buffers, transitional areas, corridors, and barriers. These functions can be integrated through relatively subtle manipulation of landscape mosaics providing that human activity can be sufficiently constrained and that regional and global shifts are not too rapid and extreme.

With the Sahel Survey and surveying for the *Pennisetum* gene pool, the precise nature of the cumulative impacts of genetic erosion, as they derive from desertification and human pressures, become the key set of research questions for successful networks of genetic reserves and other managed areas. If for example, the recent shifts in loss of vegetation are less permanent and involve shorter cycles (Malo and Nicholson 1990), reserves might be smaller as connectivity and the management of populations across ecotones are more viable. But if we are looking at much longer-term changes in the region's biogeography, a few large preserves, primarily the Air Mountains reserves, are possible. Management would have to focus on these few large areas and be highly site-specific in steep, complex areas with mosaics of small landscape units. The scale of the strategies and the organization of the interventions would differ radically depending on the model for "desertification" which is accepted.

Some corollaries with the cultural diversity of the Sahel also exist. If we accept that plant domestication involved small, scattered points with selection factors from pastoralism, such cultural landscapes, indeed cultural interfaces, are of crucial importance for *in situ* conservation. If we assume a more pastoral, northern Sahel and a largely dry-land farming central and southern Sahel, maintenance of gradients of land use within these zones might be more important. Again the scales of strategies

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and interventions, and the nature of their organization across national boundaries, vary radically with species and regional landscapes.

With the crabapple gene pool in the example from the northern coast of British Columbia, populations are "protected" within the context of the South Moresby National Park Reserve but will only be viable as genetic resources, over a range of landscapes and with viable populations, if specific management plans are prescribed. Threats from climate change can only be countered at international levels.

The more immediate threats from deer, which invaded only in the 1950s and whose numbers continue to climb, require fencing. A fenced area becomes a kind of fragment or restoration-zone isolate. A range of trade-offs exists between a larger number of small-fenced sites and a smaller number of large-fenced areas. However, the reality of fencing in such steep terrain is that the technical constraints of construction and maintenance are as crucial to the survival of any regenerating populations as the fine points of capture of gradients of biophysical factors.

Trampling from tourism, in synergy with browsing, could prove to have a similarly lethal effect on shore populations of crabapple. *In situ* conservation measures might best be organized around design programmes involving trails and signs in order to keep people away from key or vulnerable populations and points within the mosaic.

In the multi-gene pool reconnaissance of Fergusson Island, Papua New Guinea, it is highly debatable if information on the location of certain individuals of genetic resource species should provide the basis for choice of protected areas even after years of field work. Inventorying and conservation can best focus on the stability-related refugia for species associated with primary rain forest and areas of more tightly situated and high contrast edges for other species. Individual trees must be identified and marked and certain buffers should be related to the spatial patterns of reproduction of particular species.

The best way to minimize risk is to slow the cutting of primary forest and to diminish maximum block size while increasing the minimum dimensions of forest fragments. An alternative might be to alter logging practices, as related to timber removal or road engineering, to lessen overall fragmentation and other impacts. To integrate timber harvesting into cultural mosaics of swidden and gathering, the control of invasions of alien grasses is necessary.

CONCLUSIONS

The integration of concerns for the *in situ* conservation of genetic resources will

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require some of the most complex conservation frameworks for choice and compromise in regional planning, landscape design, and land management. Inevitably heightening conflicts will occur between different interest and user groups as related to germplasm and sites. Such integration must allow for a wide range of objectives and acceptable levels of conservation security and access to germplasm and must function to resolve respective conflicts to acquire and manage natural and culturally modified territory. Management will necessarily be co-management with parallel concerns related to the interests of both global biotechnology and traditional users.

The core of a regional programme for the *in situ* conservation of genetic resources is a long-term inventory, research, and monitoring effort that in turn informs adaptive management. As well as ascertaining initial conservation requirements, such research must allow for hypothesis testing on an indefinite basis as related to particular species, populations, sites, and landscape units.

The face of *in situ* conservation at regional levels will be dominated by a range of overlapping concerns for a growing multitude of species and sites with dynamic aggregations of functional spatial units such as cores, buffers, transitions, corridors, and barriers. These functions will be implemented through designs and prescriptions which are mainly conceived and expressed between the scales of 1:1,000 to 1:50,000. In addition, these functions will need to be supported by a range of economic, administrative, and political policies that elaborate on broader frameworks of the conservation of biological diversity and channelling the benefits of biotechnology back to the sources of germplasm.

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