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BIODIVERSITY VIEWPOINT

Gap analysis for *in situ* conservation of crop genepools: implications of the *Convention on Biological Diversity*

G.B. INGRAM and J.T. WILLIAMS *Department of Forest Resources Management, University of British Columbia, Vancouver V6T 1Z4 Canada and International Fund for Agricultural Research, 1611 Kent Street, Suite 600, Arlington, VA 22209, U.S.A.*

Abstract. The needs for effective and sustainable programmes of *in situ* conservation of crop genetic resources are reviewed in terms of increased concern from a wider range of local, national and international interests notably for development of more viable crops and in shorter-term ventures in biotechnology. Gap analysis, comprised of methods to ascertain priorities for additional conservation measures, is considered in terms of the needs for expanded programmes of land management for the conservation of intra-specific variation in wild, weedy and cultivated portions of crop gene pools. Gap analysis first involves setting priorities related to long-term maintenance of genetic variation at prescribed levels of target species in response to current or projected genetic erosion. These dynamics can be described in terms of populations, spatial units, and habitat attributes and conservation measures can involve acquisition and management of networks of protected areas and broader regional management. An approach to evaluation of the effectiveness of protected area programmes is outlined in terms of representatives and control of genetic erosion. The implications of specific aspects of the *Convention on Biological Diversity* in potentially countering genetic erosion are explored.

The concept of gap analysis in conservation planning for the persistence of biological diversity across districts and regions first emerged with concerns for relatively definable communities, species and habitat attributes (Burley, 1988; Scott *et al*., 1990). Criteria for maintenance of intra-specific variation with all of the difficulties in sampling (Ingram, 1990b) has been more elusive. As concerns for the on-site or *in situ* conservation of wild relatives of crops and primitive cultivated material have increased in recent years, a notion of gap analysis for genetic variability has emerged (Millar & Libby, 1991). But the nature of the recognition of elements, indeed the targets themselves, as well as respective criteria for conservation are fundamentally different. In addition, the social and cultural process for valuation of genes and intra-specific diversity are fundamentally different to that of communities and species. While there are a plethora of reasons to be concerned about the permanent loss of communities and species, human interest in maintenance of intra-specific diversity, aside for adequate levels of fitness, is almost entirely about short and long-term potentials for utilization of potential genetic resources. We contend that, despite the rhetoric, it is necessary to sort a great deal of confusion, propose guidelines which will advance practicable projects and generate further discussion leading to more effective initiatives—often of an international nature.

In principle, there are many synergies with habitat conservation. Clearly genetic resources scientists and biodiversity conservationists should be working together at the strategy and planning level much more than they have in the recent past. Dichotomy of interests are inevitable because genetic resources scientists focus on genetic conservation rather than that of species or ecosystems. For crop genepools, the urgent task in the previous two decades was to first salvage the wide diversity represented by the primitive cultivated varieties or landscapes in farmers' fields (Williams, 1988) largely through *ex situ* means. Only in the case of forest trees was the emphasis more on *in situ* methods.

In recent years, there have been initiatives to link conservation of intra-specific variation to basis inventories of biological diversity, networks of protected areas (IUCN, 1990; Riggs, 1990; Palmberg & Esquinas-Alcazar, 1990; Cohen, Alcorn & Potter, 1991; Food and Agriculture Organization, 1991), and subsequent landscape management. The 1992 *Convention of Biological Diversity* (UNEP, 1992) is the current embodiment of the notion of comprehensive systems.

GENEPOOLS, TARGET SPECIES, DESIRED DIVERSITY AND PRIORITIES

Crop genepools range from wild species to advanced cultivars. However, for *in situ* conservation, there are two broad categories: wild populations and those cultivated or managed principally for food.

Traditional crop material is defined here as pre-20th Century varieties and 'land races' which are diverse collections of primitive types of domesticated material and related weeds. This material is sometimes called 'folk seed' (Fowler & 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 which can be used to contribute to the development of new crop varieties. There are three general categories of these biological resources which 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.

In the past decade, the conservation efforts for crop genepools have moved away from almost total reliance on sampling and storing cultivars to sampling the wider genepools including wild related species. To a large degree this relates to the use of such materials by plant breeders, facilitated by the newer methods of biotechnology.

Ex situ conservation is usually adequate for short-term procurement needs for germplasm, though difficulties in handling certain species and material in storage and laboratories emerge. There can be problems from dormancy, erratic germination, the need for rigorous controlled pollinations during multiplication and in maintenance of the original population structure.

The scientific conclusion is therefore, that wild species are best left in the environments where they grow naturally and only limited samples should be maintained *ex situ*, except when the species is under threat. There is a need to see that the wild relatives indeed continue to thrive, in the wild, and clearly *in situ* conservation strategies have to include this (Ingram, 1984). Additionally, such strategies should permit conservation of the widest genetic diversity including a range of characteristics not necessarily of current interest to breeders, but which might be valuable in the future.

Cultivated forms are associated with a range of environments and degrees of human intervention. They persist in a habitat continuum from near-wilderness areas to backyards, 'protected' village environments and to farmers' fields. They sustain hunter-gathering societies, shifting agriculture and intensive production in settled areas. The cultivars involved range from simple selections which are not cultivars in the sense that they require human intervention for survival (and they can revert back to the wild) to complex populations of primitive cultivars, totally reliant on the dual forces of environment and human beings for growth and survival, and many of which are recognized as landraces since they evolved by adaptation to specific areas. Certainly, not all these diverse cultivated forms have evolved as a direct result of major, directional and conscious input of farmers and for many, environment, including the farming practices, has been the chief determinant.

In situ conservation is not necessarily the most cost effective way of conserving the variability within cultivated portions of genepools unless it is so primitive it is still virtually wild as in the case of many forage and local fruit species, or other species, especially woody perennials which produce seeds which cannot be stored *ex situ*. There are often, however, some over-riding and often excessively rhetorical reasons which compel us to support some on-farm forms of conservation such as part of cultural survival and the empowerment of peasants (Altieri, 1988) as evolutionary 'gardens' (Simmond, 1962; Kuchuck 1970).

IN SITU CONSERVATION AS A RESPONSE TO GENETIC EROSION

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

> '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 has been very little monitoring, nor a funding base for these conservation activities, even where there are baselines studies.

There are a number of causal agents that fuel genetic erosion or 'genetic impoverishment' (Myers, 1988) and that have intensified over the last decade. These are principally modernization of agriculture, including mechanization and spread of uniform hybrids, and habitat destruction such as forest clearing, urbanization and flooding from dams. The rates of genetic erosion are 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 careful conservation of traditional varieties. The crop gene pools that have been most subject to losses have been primarily those that are subjects of active breeding programs (Fowler & Mooney, 1990, page 79).

The mechanisms of genetic erosion vary radically with the nature of both the populations and selection factors across landscapes and the nature of the habitat degradation. For example general habitat loss could contribute to different patterns of loss of genetic variation than habitat alteration as, for example, the invasion of alien species. Broad-scaled changed factors such as regional fragmentation, desertification and shifts from global warming all are different engines for loss. The myriad of relatively fluid cultural factors in peasant agriculture are particularly complex for modelling. *In situ* conservation measures must principally counter respective forces of genetic erosion for particular settings and target species and must be sufficiently flexible to be adapted over time. The control and management of tracts of land for conservation purposes become only a small part of a larger and ongoing process that necessarily involves continued inventorying, monitoring, and management.

MANAGEMENT OF SPATIAL UNITS

Since the network of protected areas comprises a wide range of categories of reverse depending on the degree of human use permitted in the area (IUCN, 1985) genetic resources specialists have focused on the need for 'genetic reserves' or 'gene sanctuaries' equating loosely with the 'managed nature reserve' to conserve significant species and their genetic diversity (and as conservation and development have become linked closer to buffer zones where there is continued but controlled use of resources) and on extractive reserves (equated to natural biotic area/anthropological reserves).

The categories for biodiversity protection were designed for just that purpose—to perpetuate ecosystems. They can serve for continuation of wild relatives which are to be left in the wild, providing there is sufficient *in situ* monitoring rather than focused *in situ* species conservation (Wilkes, 1991).

A number of authors have proposed genetic resource management units (GRMUs) as specific area designations. Although developed by foresters (Riggs, 1982; Krugman, 1984; Ledig, 1988) we propose its modification for the *in situ* conservation of wild relatives. The main objective would be to progressively impose genetic management to maintain natural genepools, to regenerate them if necessary with the right species compositions and population structures and to monitor subsequent intervention for relatively high levels or distinct elements of genetic diversity.

Developing GRMUs would not involve a network separate from the IUCN categories. In many cases, they would overlap and would avoid the daunting task of trying to inventory all the reserves to meet crop genetic resources requirements. Only a small percentage would be needed and agreements could easily be developed between international organizations for this.

The design of the GRMU designations would be based not only on the priority species, but on the most effective reserve size. In some cases, numerous small reserves would be needed, but in other, fewer larger ones depending on the geographical distributions of variation and breeding systems. Some areas could be considered 'definite' where ecogeographical survey has been used as a basis, others 'temporary' until screening of variation has been carried out. This is a new concept in *in situ* conservation: to designate areas on a temporary basis; but, they could be few and justified on the basis of priority and value. The GMRU should also be designed with a buffer to avoid unwanted geneflow from outside and usually there has to be a degree of active buffer management.

METHODOLOGIES AND POLITICAL DIMENSIONS OF GAP ANALYSIS

Burley (1988) stressed the use of gap analysis in establishing short-term and longer-term conservation priorities. In fact, this is unconsciously used and is a stepwise process, which entails comparing and analysing many different sets of information (Scott *et al.*, 1990). In the case of genetic resources, surveys which relate genetic material to spatial, ecological and social conditions are necessary (Ingram, 1990b). Gap analysis for genetic resources is based, primarily, on an ecogeographic survey with information of the status of habitat protection across districts, regions and between regions.

The recognition of GRMUs enables some important reserve areas to be established to cover ecosystems not accorded high priority for conservation of sensitive or spectacular species and ecosystems. For crop genetic resources, there is a strong justification for *in situ* conservation in ecotones particularly for wild populations in more disturbed and open forest mosaics dominated by second-growth forest. In many cases, areas of maximum species diversity may not be those areas that are automatically priorities for GRMUs of crop genepools.

IDENTIFICATION OF GAPS IN NETWORKS OF PROTECTED HABITAT FOR *IN SITU* CONSERVATION OF GENETIC RESOURCES

> 'Merely designating areas or establishing laws does not guarantee the protection of biological and genetic diversity' (Schonewald-Cox & Stohlgren, 1988).

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 in order to avert losses of rarer genes and other potential genetic resources. There are three general levels of effectiveness of *in situ* conservation of crop genetic resources which are described below.

Level I in situ conservation of crop genetic resources represents largely unplanned coverage through ecosystem conservation. When protected areas which have been designed or planned without recognition of the occurence of plant species with genetic resources include these species, it cannot be assumed that there will be adequate coverage within the boundaries of the reserve to maintain viable populations over the long-term. 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 where narrow amplitudes of ecological requirements are involved.

Level II in situ conservation of crop genetic resources requires the planning and design of protected areas with use of lists of species with genetic resources and respective distribution data. The implications of principles of biogeography and conservation biology must be considered for these species. The scale is often district-wide (Ingram, 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 *Level II* conservation.

Level III in situ conservation of crop genetic resources involves on-going monitoring, management and procurement for particular levels of conservation for specific 'functional population units' (Solbrig, 1991, page 18). 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.

Along with the general level of conservation for a species is what has sometimes been referred to as 'desired diversity' (Namkoong, 1983). In both natural and well-protected populations, there is a constant flux of gene frequencies with some alleles becoming rare or disappearing. In protected areas, the natural and human-induced declines of populations can cause the narrowing of the base of variation and subsequent loss of potentially valuable genetic resources. In order to maintain rare alleles or possible adaptive complexes associated with certain environments and selection factors, additional requirements for larger and sometimes additional populations must be set.

With species which do not involve a concern for maintenance of potential genetic resources, *level I* conservation is often adequate and *level II* is needed for the long term. For *in situ* conservation for crop genetic resources, both traditional varieties and wild species, *level II* is always necessary to assure capture of desirable minimum percentages of alleles and *level III* is necessary for long-term security as well as procurement for extended programmes of plant breeding.

The extent of representative of networks of protected areas is a persistent question. In terms of the best monitored internationally recognized protected areas (Ingram & Williams, 1984; Ingram, 1990a), only a very small portion of the 300 biosphere reserves which are part of UNESCO's Man and the Biosphere

Programme are in centres of crop origin and indeed in the regions of high species diversity, such as the humid tropics. Well over 20% of the biosphere reserves have populations of the relatives of the major crops (World Conservation Monitoring Centre, 1992, page 549). However, interest in many of these would fall into the realm of 'data gathering' and *in situ* monitoring as proposed by Wilkes (1991) as part of wider ecogeographical research.

The biosphere reserve concept is based around the idea of a set of land use zones with one or more central protected areas surrounded by well-managed, primarily wildland areas and then surrounded by a heavily modified 'transition' zone. By monitoring these transitions from natural baselines to human-modified ecosystem, important data for environmental management can be generated. Over the last decade, the role of biosphere reserves for the conservation of biodiversity has increased.

A major part of the data gathering as part of *in situ* monitoring will have to include systematic documentation of the crop varieties, landraces and other primitive cultivated material in either the transition areas or in the buffer zones of biosphere reserves or within World Heritage Sites. There has been only cursory reporting of agricultural activities within and on the edge of biosphere reserves and World Heritage Sites. Guidelines for the most relevant data types are urgently needed.

IN SITU CONSERVATION IN AGRO-ECOSYSTEMS

Apart from a number of well-known examples (e.g. wheat and barley in Israel), all of the current farm crop conservation programs have been initiated by small institutes and NGOs. These programmes tend to emphasize research, education, technical advice, and credit schemes that support traditional farming systems.

In order to implement medium-term programs in developing countries with the dual mandate of monitoring genetic resources in agro-ecosystems and supporting farmer-driven development, national institutes and NGSs require major questions about the effectiveness of virtually all of the *in situ* on farm-conservation programmes for crops. At the local level, there are overlapping, unprioritized and jumbled objectives. Many farmer organizations are more concerned with producing their own seed than with conservation of genetic diversity.

It is not at all clear how conservation of local and traditional agroecosystems can fit into the GRMU categories due to the lack of long-term security to sustain the practices. The element these programmes have in common is a living connection to the past. The case for their continuation is as a teaching and information tool (Wilkes, 1991). When scientific standards are set and work externally evaluated, a limited number of such areas could become GRMUs.

Two myths are apparent in this context. The first is that all landraces are valuable and they do not change. It is thought that somehow they represent something that evolved directionally with time and human culture therefore all three are progressively related. This is not the case. Landraces as seen and sampled represent a particular genetic mix at that time after long periods of continuing changes in gene frequencies. The second myth is that many peasant farmers actually breed from such mixes, whereas the selection criteria are simply aspects of the agro-ecological environment and few such farmers actually use the landraces in breeding.

Nonetheless, perpetuation of dynamically evolving landraces probably represent the best sources for enhanced use in many marginal habitats and for many minor traditional crops, for which genetic resources conservation programmes are unlikely to be funded internationally.

But in a world where population increases are going to stretch the world's ability to feed itself to the full, emphasis on channelling scarce agricultural research resources towards creating new technology for marginal, low productivity lands is questionable. One strategy is to address the return to society as a whole, raise productivity on the robust lands and remove agriculture from fragile lands. Economic development provides the means of dealing with environmental and sustainability issues.

However, in the framework of unstable government and policies, some limited agro-ecological conservation could be justifiable in the short-term. For instant the traditional agro-forestry system practiced on Fergusson Island, Papua New Guinea serves as an example of *in situ* conservation of traditional varieties or 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 the growing of yams, principally *Dioscorea esculenta* and *D. alata.* Yams are the basis of the subsistence economy, but it is their cultural importance that may ultimately prevent them from being replaced by introduced food crop species. For example, yam seeds are inherited through matrilineage; they are exchanged as gifts at funeral feasts and other occasions; they are the focus of magic ritual and myths.

Are such locally and culturally based approaches secure forms of conservation? But then are some government-coordinated systems of protected areas not even more vulnerable? Such local approaches may not be permanent but the record of such traditional conservation measures suggests that they may be effective into the medium-term as continued sources of germplasm.

IMPERATIVES FOR PROGRAME DEVELOPMENT

Many crop scientists would suggest that the gap analysis leading to *in situ* conservation units proposed above is too detailed and not necessary. We would argue it is needed to urgently bridge the gap between the conservation of biodiversity and the interests of crop enhancers in relation to the availability of conserved segments of genepools and for cross-referencing databases. It would apply for conservation interests on genepools of crops, forestry, medicinal plants, reserve area, non-timber forest products and others and hence avoid the development of diverse terminologies.

A number of key actions now need initiation.

(1) Designation of priority species/genepools.
(2) Development of management practices.
(3) Adequate training of those involved at the reserve level.
(4) Foraging specific linkages between protected areas and national genetic resources programmes.

It is beyond the scope of this paper to discuss these except to point out that they are not new ideas. They have simply been ignored, in terms of real prospects, by international organizations to the present (Williams, 1992, Hawkes, in press).

CONCLUSIONS; IMPLICATIONS OF THE *CONVENTION ON BIOLOGICAL DIVERSITY* ON THE DEVELOPMENT OF FRAMEWORKS OF GAP ANALYSIS

The concept of an international convention and conservation of biological diversity and related 'genetically coded functions' (Vogel, in press), particularly as this relates to transfers of genetic material and the funding conservation, has been extremely contentious. The version that went before the 1992 United Nations Conference on Environment and Development (UNEP, 1992) represented a compromise that very much left it to nation states to determine their own approaches to setting priorities and linking of biological resources from natural areas to programmes of habitat conservation. In this context, which is foreseeable for the next decade as the Convention is ratified and implemented, the nature of gap analysis turns decided towards social priorities both for genetic resources and land management.

Articles 6 and 8 of the Convention talk of integration of concerns for biological resources into conservation planning and for the development of systems of protected areas of which some of the criteria should be for intraspecific variation. Articles 15 and 16 talk of access to germplasm and also information that is central to gap analysis. Unless we know what we 'have' in an ecosystem, and this nearly always requires some *ex situ* evaluation and indefinite storage, it is near impossible to determine credible priorities for additional conservation across spatial units and additional protected areas and for regional management. Unfortunately, Article 17 embodies only a weak commitment to exchange of information.

While gap analysis for *in situ* conservation of wild and cultivated genetic resources is a highly technical exercise, issues of priorities and potential user groups will become increasingly prominent. If it was not the case before, the politics will overshadow the badly needed science. More *ad hoc* international and national arrangements to assure unfettered scientific evaluations for better gap analysis will be necessary if the Convention is to have any impact in slowing genetic erosion and the associated loss of species and degradation of ecosystems.

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