

MASTER NEGATIVE NUMBER: 09296.79

Arunachalam, V.

Conservation, Genetic Erosion and Early
Warning Systems: key Issues.

In: *Proc. Technical Meeting on the Methodology
of the FAO World Information and Early
Warning Systems on Plant Genetic Resources,
Prague, Czech Republic, June 21-23, 1999.* (eds)
J. Serwinski and I. Faberova.

Prague: (1999): pp. 45-47.

Record no. E-34



Food
and
Agriculture
Organization
of
the
United
Nations

PROCEEDINGS

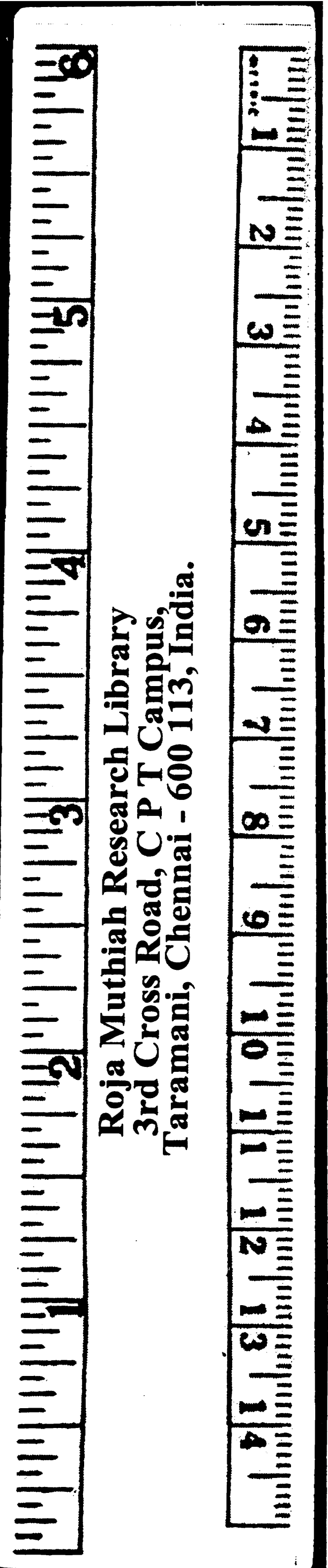
of the

Technical Meeting on the Methodology of the FAO World Information and Early Warning System on Plant Genetic Resources

Research Institute of Crop Production, Prague, Czech Republic
21 - 23 June 1999

Editors: J. Serwinski (FAO), I. Faberová (RICP)

Prague, 1999



CONSERVATION, GENETIC EROSION AND EARLY WARNING SYSTEM: KEY ISSUES

V. Arunachalam

*Centre for Research on Sustainable Agricultural and Rural Development
M.S. Swaminathan Research Foundation, Taramani Institutional Area
Chennai, Tamil Nadu, India*

Conservation of biodiversity is an activity well recognised the world over. Plant Genetic Resources (PGR) constitute an important sector of biodiversity that is crucial in attempts to feed and sustain the steadily increasing global population. Advances in the science of plant breeding from the days of rediscovery of Mendelian laws of inheritance have been instrumental in utilising PGR to develop high yielding varieties (HYVs). To a large extent, they were responsible to increase productivity and food production.

However, the rate of population increase remains higher than the rate of production increase. The hypothesis is therefore, gaining ground that conventional breeding techniques do no longer have matching potential to counter the effects of population rise. The advent of molecular techniques has provided, in this context, a new dimension to realise accelerated rates of production. For example, Tanksley and McCouch (1997) could identify molecular markers that "looked for the genes" from the wild in contrast to conventional methods that "look for the phenotypes". They reported that, when the advanced back cross method was used to examine alleles from the wild species, *Oryza rufipogon* in the genetic background of an elite chinese hybrid, two QTLs which could increase yield by approximately 17% each, were identified. However, no details were provided about the successful incorporation of the identified QTLs in a commercial cultivar.

Successful plant breeding initiatives have rested broadly on vertical improvement of desired traits, common among them being grain yield. This avenue required assured and high inputs like quality seed, chemical fertilisers, irrigation and plant protection chemicals for optimal performance. The impact was therefore confined to assured rainfall areas and such farmers who could afford to provide the high inputs. Thus a large proportion of agriculture in dry and rainfed areas remained out of reach of such technological developments.

Soon it was realised that quantum improvements achieved by vertical increase were fragile in their stability when regions growing such HYVs went through vast vicissitudes of climate and rainfall over time. Continuous cultivation of HYVs led to many hazards like, for instance, genetic uniformity - prone disease and insect spread and fertiliser chemical - activated soil degradation; in turn, the productivity slipped from its high leading to concerns of sustaining desired production.

In this scenario, a significant segment of farmers, not essentially affluent, and of tribal and rural areas, in general, live away from the usual reach of institutional development initiatives. They continue to cultivate local varieties and maintain landraces as a routine at personal cost for public good. Their areas are still genetically rich; the area-specific local cultivars have a number of traits including nutritional and cooking quality, and biotic and abiotic stresses incorporated naturally in them. Such resource mines of genes have now been recognised as indispensable sources for restructuring HYVs to provide them with stability and sustainability.

However such diversity - rich areas are under continuous stress to maintain their genetic wealth. For instance, in India a large number of genetically rich rice varieties in Jeypore tract of Orissa state, rice varieties with medicinal properties, popularly called 'Njavara' in Kerala state and a wide range of millet species like Little millet

(*Panicum sumatrense*), Italian millet (*Setaria italica*), Kodo millet (*Paspalum scrobiculatum*), Common millet (*Panicum miliaceum*), Barnyard millet (*Echinochloa colona*), and Finger millet (*Eleusine coracana*) in Tamil Nadu have faded out of cultivation in their native habitats.

A number of reasons can explain the situation. For example, social and cultural uplift as a corollary of economic development has led to a rapid movement of rural population to urban areas. Continuing population pressure has promoted habitat loss which has earlier also been cited as a major reason for species extinction (Avery, 1997). External agencies exploiting farmers in low profit agriculture areas tend to rent their land for raising profit crops of their choice; to cite an example, in millet - rich areas of Kolli hills in Tamil Nadu, India, large scale commercial permeation of tapioca has taken place this way and has accelerated erosion of natural diversity and landraces of several species of millets. Further, as household income increases, the tendency to avoid physical exertion to process traditional crop produce increase proportionately too. A good example is the shift from the once preferred nutritive food from small millets to less nutritive rice by the tribal population in Kolli hills, India. One reason is the waning interest in arduous manual dehusking, polishing and processing of small millets irrespective of its nutritive value, intensified by the ready availability of rice hulling machines.

However, it is increasingly realised that sustainable food production should have to be based on horizontal trait improvement. No longer vertical trait improvement, like the dwarfing genes in wheat and rice, for example, could help to solve the problem. Gene pyramiding is increasingly attempted both by conventional and molecular methods not only to provide a broad genetic base to the new varieties but a higher degree of adaptation and plasticity. Valued genes are known to be resident in wild species, local landraces and little-explored habitats. Attempts focus on maintaining them and threats to such valuable genetic resources are sought to be forewarned.

It is then easily seen that there is a common plane of interaction between conservation and genetic erosion. Conceding that an Early Warning System (EWS) of genetic erosion is in place, we realise that such genetic resources under threat of erosion have to be conserved. At times, when *in situ* conservation is unfeasible, *ex situ* conservation has to be resorted to. In either case, gene banks have to be geared up to provide for the new in addition to the regular in-flow. We would therefore examine key issues confronting conservation, genetic erosion and EWS.

Conservation: The contours of conservation are continuously widening. Though it is advocated that genes only need conservation, it must be borne in mind that genes are carried by genotypes which are expressed as site-specific phenotypes emphasising the role of environment. Without gene expression, they cannot be located for conservation. The bugs in the concept of direct association between molecular genes (markers) and their expressed QTs, make it difficult to assume detection of genes in the 'lab' with predicted expression in the 'land' (See, for example, Arunachalam, 1998).

Literature is abound listing a vast variety of natural and generated variability fit for conservation. Yet it may be mentioned that apart from accessions identified on exploration, novel genetic stocks

resulting from innovative research (like cytogenetically ameliorated stocks, e.g., translocations carrying rust resistance, thermo- and photo-genetic male sterility), and genotypes carrying special genes [like the var. *Macchakanta* of rice that has high resistance to cyclone effects, probably because of robust roots, supple but strong stem, identified recently in an Indian participatory plant breeding program, varieties that grow well under famine conditions e.g., *ye-eh* (*Cordaeuxia edulis*) identified in Ethiopia (Worede and Mekbib, 1993) and varieties that are resistant to adverse conditions like deep water rices] add to the list.

In the process of maintaining PGR in gene banks, a silent erosion is continuously operating. Due to low sample sizes used in grow-out nurseries, genes are lost due to genetic drift, heterozygous stocks, particularly of cross-pollinated species, lose their genetic identity due to segregation, inadequate isolation between growing stocks entail cross-pollination and chromosomal changes are frequent in cryopreserved tissue cultures, to mention a few. In addition, duplicates add to the pressure on gene bank as they cannot be identified at the time of collection. Molecular differentiation of PGR includes the risk of adding duplicates, in general. (Arunachalam, 1998). Thus we are confronted with erosion of genes and erosion of space in gene banks. Relevant issues that need a specific emphasis are the following:

- How often regeneration is needed? How to identify duplicates - on a single trait or multiple traits? If so, can we zero in on a minimal set of traits so that decisions across gene banks remain compatible?
- How to select between *in situ*, *ex situ* or other forms of conservation? To ensure safety against loss, do we need more than one mode of conservation?
- Intellectual property rights and the restriction they place on free exchange of PGR, would necessitate multiple copies of PGR across global gene banks. How to contain such duplication at manageable levels?

In essence, the main problem is to strike an optimal balance between **Including the excluded** and **Excluding the included** in conservation endeavours.

Genetic Erosion: There are two major aspects of genetic erosion. The first is a development of a warning system to alert when PGR is threatened. The second is the development of mechanisms to conserve such PGR as are rescued. Thus conservation and genetic erosion concerns are closely linked and deserve concurrent attention.

Natural PGR is an important source of threat with endangered wild species, local community landraces including genetic stocks that express their superior traits in specific environments. This is an area that has been recognised. It is said that, of the 10,000 varieties of wheat which were in use in China during 1949, only 1,000 remained in 1970. In U.S.A., 95% of cabbage, 91% of field maize, 94% of pea, 86% of apple and 81% of tomato varieties of last century have been lost. Andean countries have lost potential sources of proteins and vitamins while losing their indigenous crops and their wild relatives. At the same time, logical arguments are advanced indicating that concerns on genetic erosion need not be overexpressed or overstressed. For example, out of 250,000 plant species known to mankind, 30,000 are edible, 7,000 used for food, 120 cultivated today and only 9 provide more than 75% (and 3 more than 50%) of human food [Information Bulletin issued during 2nd International Crop Science Congress, New Delhi, India, 1996]. From a small fraction of pre-breeding material, breeders continue to develop HYVs (Anishetty *et.al.*, 1996). Reasons like gradual breaking of close linkages and forming of new epistatic gene combinations were emphasised. The yield advances made in 6-rowed barley in U.S.A. when traced back to their breeding history,

were found to have come from two or three putative ancestors only (Rasmusson and Phillips, 1997). It was argued 'that epistasis is more important than commonly viewed in extending the phenotype range for traits of interest'.

Introgression of genetic diversity from unimproved collections widened the genetic gap between elite gene pools and unimproved ones with each breeding cycle (Martin *et.al.*, 1991). Further, many species have little potential for direct use, many others are sufficiently similar to cause concern on their loss. Intensive search can, in some cases, locate other species with similar attributes (Collins and Qualset, 1999).

But novel genes that are generated by innovative approaches including molecular interventions and those that are specific like, for instance, self-incompatible and partially incompatible edible oil types of *Brassica campestris* var. *brown sarson* in India are also becoming unavailable and warrant attention.

It has further been argued (Avery, 1997) that habitat loss is the most important for species extinction. The oft-emphasised farmer-participatory organic farming would be low yielding and labour-intensive as observed in some case studies. Though it may be environment-friendly and technologically benign, it leads to the use of large natural areas that would, otherwise, harbour valuable PGR. On the other hand, HYVs not only tripled major food crop yields but saved valuable land area. For instance, globally HYVs crop the same 6 million sq. miles of land today as was in 1960 but feed 80% more people a diet with more than twice as many grain-equivalent calories. These results are, at the most, dampeners of over-reaction to the phenomenon of genetic erosion. At the same time, we need to be vigilant and develop an early warning system of genetic erosion before precious PGR is irretrievably lost. A balanced approach is the need of the hour.

In this context, bioindicators can be of some advantage as an EWS. Vast literature is available on indicators for various phenomena; for example, some tree species are cited as indicators of air pollution (Agrawal and Tiwari, 1997), tiger beetles as indicators of forest degradation (Rodriguez *et.al.*, 1998) and necrosis in *Pinus* species as indicators of uranium mining (Sanger, 1995). Evidence is available in old Indian tribal literature on indicator plant species. For instance, a perusal of old tribal songs of India, *Khana Bachana* in oriya language reveals that a good growth of sal (*Shorea robusta*) would indicate good mango production, good growth of bamboo would indicate poor seed fill and high chaff in rice, good growth of *sabai* grass (*Eulaliopsis binata*) would indicate less soil erosion, good growth of finger millet (*Eleusine coracana*) would indicate good yield of niger and the like. Such indications may not be decisive but may be useful indicator information to take note of. A lot remains open to strengthen this area and make it really worthwhile.

Reverting to the constraints on gene bank space outlined earlier, it would be useful to scale-up the concept of FGB. Field Gene Banks (FBG) are basically *in situ* on farm centres of conservation. Landraces and location-specific PGR, usually identified on a participatory plane with the local farmers are conserved in FGBs. They are periodically grown in their native habitats for seed renewal. They serve as effectively decentralised and highly cost-effective arms of a community gene bank (CGB). By partaking the load of conservation and maintenance, FGBs can reduce the pressure of space, regeneration and maintenance on the CGB considerably. They can be strategically located at natural resource centres of PGR. Those FGBs which are situated at good elevations are likely to have cooler and conducive climates. No expensive infrastructure would be needed then to set up FGBs. The FGBs would ensure *in situ* on farm maintenance of landraces and preservation of cultural and cropping practices under which PGR acquired their distinctive traits. The communities in natural resource areas would be stake-holders in

the FGBs. They can then provide active support not only to prevent genetic erosion in those areas but add new genetic stocks as and when they discover them.

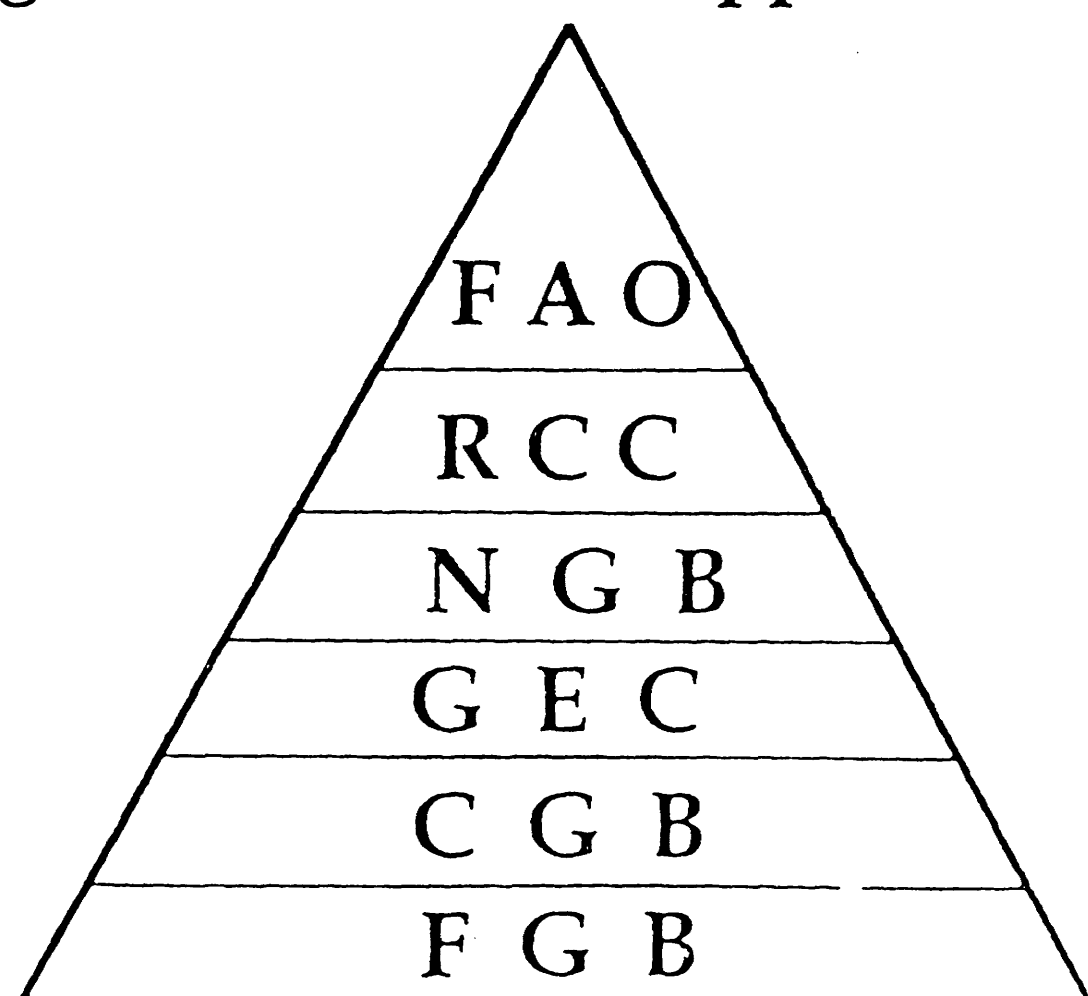
Several FGBs can be linked to a CGB taking into account factors like distance, communicability, conservation space and the like. One or more CGBs can be linked to a Genetic Enhancement Centre (GEC). The main function of a GEC is to utilise the landraces and the location-specific PGR in developing cultivars catering to the needs of a community. Participatory Plant Breeding is a good option in this context to involve the farming community in a participatory mode to blend the farmer and formal (scientific) skill. The material in GEC would be periodically evaluated and utilised in specific plant improvement programmes. GECs can also undertake genetic enhancement based on specific molecular techniques, if adequate funding is available. The successful case histories of *Hevea* and sugarcane employing 'portable (molecular) laboratories' provide encouraging evidence (Lenaud and Lebot, 1997).

The World Information and EWS (WIEWS) developed by FAO is an important user-friendly software organising information on global PGR in a format enabling easy data flow and retrieval. The major input to WIEWS comes from Government reports to national PGR programmes and FAO. This is a welcome beginning but the system of information in-flow has possible handicaps. For example, information from various reporting agencies across countries can be highly heterogeneous and the quality of data may be variable. When a national PGR programme is under fund stress, there can even be discontinuity of data flow. It would therefore be reassuring to conceive of a feasible networking under FAO for successful operation of WIEWS.

A 5-tier system appears to be feasible. FGBs would function at the grassroot level, as explained earlier. They will be linked to community gene bank (CGB) which will coordinate between a few FGBs located around it. A few CGBs will be linked to a GEC which will coordinate their work. GECs will be connected to National Gene Banks (NGB) and in turn to Regional Coordination Centre (RCC) and finally to the apex body, FAO (Fig. 1). Obviously RCCs will account for the NGBs of a few countries in a global region. It is suggested that this networking be decentralised with specific functions delineated across the component units ensuring a degree of autonomy. Sub-networks can be set up between NGB and (GEC, CGB, FGB) as needed. The total programme would be executed and monitored through coordinators at RCC level and appropriate staff in other levels. The whole network would be programme-based and operated on participatory fund support between FAO and participating countries. As genetic erosion covers a vast horizon, an extensive network is needed to take adequate precautionary steps. Such a set-up will account for all the needs of an effective minimisation, if not prevention, of genetic erosion.

Fig.1

Suggested Five-tier Support for WIEWS



C: Regional coordination centre; NGB: National Gene bank; GEC: Genetic enhancement centre; CGB: Community gene bank; FGB: Field gene bank

References

- Agrawal, S. and Tiwari, S.L. 1997. Susceptibility level of a few plants on the basis of air pollution tolerance index. *Indian Forester*, 123: 319-322.
- Anishetty, N.M., Cooper, H.D., Kermali, I.R. and Spillane, C. 1996. Harnessing plant genetic resources for sustainable agriculture. Draft paper of a satellite symposium on Agrobiodiversity, conservation and use. 2nd International Crop Science Congress, New Delhi, India.
- Arunachalam, V. 1998. Genetic erosion in plant genetic resources and early warning system: A diagnosis dilating genetic conservation. FAO invited paper. Published in Internet April 1998, 19 pp. [For retrieval, <<http://apps.fao.org:8080/wiews.new>> select "Early Warnings" and then "Thematic papers on Genetic Erosion, etc.,"]
- Avery, D.T. 1997. Saving nature's legacy through better farming. *Issues in Science and Technology*, Fall 1997: 59-64.
- Gollin, D. and Smale, M. 1999. Valuing genetic diversity: crop plants and agro-ecosystems. Chapter 13, pp.237-265 In: *Biodiversity in Agroecosystems*, eds. W.W. Collins and C.O. Qualset. CRC Press, London.
- Lenaud, C. and Lebot, V. 1997. *Molecular techniques for increased use of genetic resources*. pp. 92-97. In: *Molecular Genetic Techniques for Plant Genetic Resources* (eds.) Ayad, W.G., Hodgkin, T., Jaradat, A. and Rao, V.R. IPGRI, Rome, Italy.
- Martin, J.M., Blake, T.K. and Hockett, E.A. 1991. Diversity among North American spring barley cultivars based on coefficients of parentage. *Crop Science*, 31: 1131-1137.
- Rasmusson, D.C. and Phillips, R.L. 1997. Plant breeding progress and genetic diversity from *de novo* variation and elevated epistasis. *Crop Science*, 37: 303-310.
- Rodriguez, J.P., Pearson, D.L. and Barrera, R.R. 1998. A test for the adequacy of bioindicator taxa: are tiger beetles (*Coleoptera: Cicindelidae*) appropriate indicators for monitoring the degradation of tropical forests in Venezuela? *Biological conservation*, 83: 69-76.
- Sanger, H. 1995. Flora and vegetation on dumps of uranium mining in the southern part of the former GDR. *Acta Societatis Botanicorum Poloniae*, 64: 409-418.
- Tanksley, S.D. and McCouch, S.R. 1997. Seed banks and molecular maps: Unlocking genetic potential from the wild. *Science* 277: 1063-1066.
- Worede, M. and Mekbib, H. 1993. Linking genetic resource conservation to farmers in Ethiopia pp.78-84. In: *Cultivating knowledge: Genetic diversity, farmer experimentation and crop research* (eds.) W. de Boef, K. Amanor, K. Wellard and A. Bebbington. London: Intermediate Technology Publications.