

CHAPTER 28

IDENTIFYING AND PROTECTING THE ORIGINS OF OUR FOOD PLANTS

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Plants that are used for food present special problems in the monitoring of genetic diversity and its conservation. The diversity of food plants in existence today evolved over the past 10,000 years or so since the origins of agriculture in the Neolithic era. The progenitors of cultivated plants were wild species, which along with countless others were harvested by hunters and gatherers. The genetic diversity of crops increased greatly as the wild species were domesticated and were moved from environment to environment; cultivars adapted to specific environments and were put to different uses. Many cultivars must have been discarded even in early days, but some of them remained in certain areas and others diversified further as they were taken far from their original homes. Hence, the evolution of major crops has been a continuing process—from the wild progenitors to the products of modern plant breeding and genetic manipulation.

By contrast, other species have been used as food but have never been domesticated. Included among these are a multitude of minor fruit and forage plants that are grown in gardens. Included too are many other species that conservationists stress for their potential value in medicine, as food, or for other purposes. The intraspecific variability of such species may be rather insignificant compared with that of major cultigens and is often poorly documented. There has been less opportunity for diversification over millenia of cultivation.

There are thus three types of wild species of interest for conservation: the progenitors of cultivated plants; species used but not domesticated; and those that might be of use in the future. The distinction between these categories has been

inadequately considered both by conservationists and by international funding organizations in budgeting. It has led to the misuse of the term "genetic resources" as a justification for almost any conservation activity, and may also lead to confusion and to the unscientific planning and operation of programs. A significant exception remains the work on crop plants guided by the International Board for Plant Genetic Resources (Williams, 1984).

THE INTERNATIONAL BOARD FOR PLANT GENETIC RESOURCES PROGRAM

The International Board for Plant Genetic Resources (IBPGR) was established within the Food and Agriculture Organization because of the loss of substantial intraspecific diversity produced by domestication as fewer and fewer successful modern cultivars were grown over large areas of land. This loss was termed genetic erosion.

When IBPGR was created in 1974, the mandate given to it by the Consultative Group on International Agricultural Research (CGIAR) was to establish a global network of activities to further the collection, conservation, documentation, and use of germplasm for crop species. The network, which has been in existence for some time, is complex and includes gene banks (repositories of seeds, tubers, and other sources of genetic materials) at conservation centers and activities dealing with the collection, characterization and documentation of crop genetic resources, and training. Beginning with a handful of countries in 1974, IBPGR'S work now involves 106 countries, and the number of gene banks has grown from half a dozen in 1974 to more than 100, about 40 of which have agreed to accept responsibility for long-term maintenance of genetic resources. The more than 50 crops in the IBPGR program include cereals, legumes, vegetables, oil seeds, fruits, and a limited number of cash crops of importance to rural farmers. More recently, forage plants have been included.

Emphasis was initially placed on the collection and conservation of local cultivars of crops that had evolved in diverse environments under traditional agricultural practices; these are often known as landraces. Farming methods were also changing rapidly due to the availability of modern cultivars and agricultural techniques. The landraces have provided and continue to provide a rich resource for exploitation, but it is neither practicable to collect and conserve all of them nor is it necessary. Attempts have mainly been directed to securing representative samples from those areas with the richest diversity. These genetic resources have always been regarded by the IBPGR as a heritage of mankind to be freely available to all bona fide users.

Much of the diversity of crop plants of use in plant breeding is of cryptic expression. There are clearly limited numbers of morphological characteristics of the plant, and many of them, with the exception of those controlling such yield determinants as the number and size of ears of corn, may be agronomically irrelevant. Physiological characteristics abound, however, controlling life cycle through photoperiodicity, breeding system, and numerous responses to stress factors such as salinity, drought, and especially pests and diseases. Conserved samples are used primarily as a source of genes for broadening the genetic base of modern cultivars

and thereby counteracting the vulnerability of cultivars with too narrow a genetic base to resist new races of pests and diseases.

IBPGR's emphasis began to shift away from the collection of landraces as its work progressed and as plant breeding techniques advanced, and to include the wider gene pools of the crops such as the wild progenitors and close relatives. The materials conserved embrace an evolutionary spectrum of the past 10,000 years and include obsolete and fairly recent cultivars, but breeders' lines rarely need conservation; their diversity is already present elsewhere. This point, which is not widely understood, has led pressure groups to urge the conservation of breeders' lines, which except in a few cases is not justified. In any case, germplasm for major staple crops is available from the International Centres of the CGIAR, the parent body of IBPGR, and from several national agricultural research organizations.

For most of the major crops, germplasm collections provide opportunities for continued introduction of genes with conventional or sophisticated breeding techniques. For many minor crops that have not greatly diversified following domestication, collections may contain cultivars that may be introduced as crops to other countries without further breeding. Hence, the collections of the major crops, e.g., rice, wheat, millet, and groundnut, will be large, whereas those of the minor ones, e.g., okra, many tropical fruits, and forage crops, will be relatively small. As the value of such minor crops becomes appreciated, however, there is likely to be a need for a more diverse germplasm base.

The IBPGR budget is small (a little over U.S. \$5 million per year); hence, it does not provide long-term institutional or program maintenance support but, rather, serves as a stimulus or catalyst to work done by national or international organizations. Some of its funds are used to carry out urgent work and to fill gaps in the collection. Linked with the IBPGR program are all crop genetic resources activities in the world, many collections of which were initiated and supported by IBPGR. IBPGR coordinates rather than directs these activities in which all participants are equal partners.

To date, IBPGR has organized more than 500 collecting missions in scores of countries. Germplasm has been acquired in accordance with established priorities (IBPGR, 1981; Williams, 1982) and conserved in long-term storage in 40 centers around the world. All major crops have now been placed in designated gene banks. The IBPGR is currently reviewing the financial support it gives to such gene banks and to centers that are actively involved in ensuring that genetic resources are available for use in crop improvement programs.

CROP ORIGINS AND GERMPLASM USE

Over the past few decades, a great deal of information has been accumulated on the origin and evolution of cultivated species. In general, the wild species tend to have limited patterns of distribution. Although Vavilov (1951) laid the basis for further work in defining centers of origin and centers of diversity based on observed botanical variation, the nuclear centers of the origin of agriculture have

been confused with the areas of evolution and diversity of crop plants (Hawkes, 1983). Harlan (1951) identified smaller microcenters that are rich in diversity and not necessarily near civilization nor confined to plains or mountains—features strongly associated with the Vavilovian centers—usually in the areas that would be regarded as broader centers of diversity.

There are therefore different definitions of the regions that comprise centers—from Vavilov's to those of Zhukovsky (1975). Whatever the definitions, it is still clear that there are areas where crop plant diversity is great and others where it is slight. The centers of diversity of several crops coincide and comprise limited numbers of regions in contrast to the 13 centers proposed by Vavilov. Crop germplasm is by no means obtained solely from developing countries; centers also cover areas of the developed world. Examples of crops that originated in the developed world include the adzuki bean (*Vigna angularis*) in Japan, oats (*Avena sativa*) and rye (*Secale cereale*) in northern Europe, and the sunflower (*Helianthus annuus*) in the United States. Many old landraces of the developed world are extremely valuable resources being fed back, through breeding, to Third-World agriculture.

In view of the apparent confusion surrounding the definition of the regions of diversity, it is pertinent to question how the material can best be identified and preserved. Over the past decade IBPGR's strategy has been to mobilize scientific information from hundreds of the world's best breeders and crop botanists. Scientists who have grown, used, and evaluated germplasm know far more about its variability than collectors who can only observe phenotypes. This strategy has been highly successful in ensuring the preservation of intraspecific diversity in a very limited time and is still implemented.

For the wider gene pools, where species and species relationships are the principal interest, taxonomy plays a major role in the conservation of genetic resources work, especially experimental taxonomy designed among other things to clarify genomic relationships. But information on the origins and evolution of crop gene pools is obtained not only from taxonomy but also from a synthesis of disciplines, including archaeology, linguistics, ecology, and molecular biology.

For some of the major crops, e.g., wheat and maize, there are still gaps in our knowledge, but in many other cases, the progenitors are well known. Although the ancestor of the faba bean (*Vicia faba*) has not been equivocally identified, several closely related species have frequently been found, the most recent during an IBPGR mission to Syria in 1986. Truly wild forms of cassava are not definitely known either, although Brazilian workers supported by IBPGR may have found one in 1986.

When a theory of origin has been postulated but not verified by taxonomic work, it may not be clear what germplasm should be collected and where. The cowpea (*Vigna unguiculata*) is a good example; taxonomically its ancestral home has been variously proposed as Ethiopia or central/southern Africa. IBPGR examined all herbarium specimens of this species in 1986 and found that the progenitor of the cowpea occurs in every country of sub-Saharan Africa. Thus until experimental work on freshly collected material is complete, we will not know the patterns of variation or where to collect samples. Meanwhile, collection of material

will be ad hoc and provide useful allelic diversity but not necessarily from the ancestral area of domestication.

In other cases, such as that of citrus crops (*Citrus* spp.), existing classifications are substantially untested in the field. IBPGR has put emphasis on relatives of the lime, lemon, and orange and will be organizing fieldwork to this end—not knowing whether the taxonomy works or not. Obviously, the field strategy may have to be modified to fit new knowledge and adapted as necessary. The collection and conservation work will no doubt greatly add to information on the origins, evolution, and distribution of *Citrus* gene pools. This has already proved true for beans of the genus *Phaseolus* (G. Deboucq, IBPGR/Centro Internacional de Agricultura Tropical, Colombia, personal communication, 1986), coles (*Brassica*) (wild gene pool of the Mediterranean), perennial soya bean (*Glycine*) (IBPGR collaborative work in Australia; A.H.D. Brown, Commonwealth Scientific and Industrial Research Organization, Australia, personal communication, 1986), African eggplants (*Solanum* spp.) (Lester et al., 1986), and cucurbits (Cucurbitaceae) (L. Merrick, University of California, Davis, personal communication, 1986). Numerous other crops will be worked on in a similar way.

Harlan and de Wet (1971) defined primary, secondary, and tertiary gene pools on the basis of the degree to which closely and distantly related species can be cross-bred. Hitherto a gene-pool approach has been taken in defining IBPGR work. This has obviously been the best strategy, because wild progenitors and their related species have increasingly been shown to be valuable sources of genes for crop improvement. Others, such as wheat, are used for transferring entire chromosomes or parts of chromosomes. Both somatic hybridization and conventional crossing are likely to be more successful among closely related species, but embryo rescue techniques are already commonly used where the parents are less closely related, e.g., in wide crosses between wheat or barley and related wild grasses.

Many advances will continue to come from breeding closely related plant species, but where breeding is far advanced, even species of the tertiary gene pool are useful. IBPGR has recognized this for two groups: first, wild grasses of the tribe Triticeae, which includes wheat, barley, rye, forages, and dozens of species in more than 20 genera distributed throughout the world, and second, the East Asian-Pacific-Australian species of soya bean of the tertiary gene pool. In other cases, the wider gene pool has been used very little; hence, conservation priorities have been imprecisely defined. Wild plants related to maize in the genus *Tripasacum* are unlikely to be used in maize breeding before the next century.

EVALUATION OF THE RESOURCES

Integral to crop genetic conservation, but a step subsequent to collection, is description and evaluation of germplasm. Although this activity lags behind, it is an ongoing, long-term process. In autumn 1985, IBPGR held a small strategy workshop to look at the collections and study how they could be used more effectively. It has initiated, in particular, research and development to see how best to work on subsets of large collections, thereby accelerating work. Physiological or otherwise cryptic variation must be thoroughly assessed during this process.

By contrast, other conservation programs lack this user-driven input. It seems to me that scientists must develop aesthetic, moral, and evolutionary arguments for wider conservation practices that are not based on whims of individuals but, rather, are geared to perceived needs such as environmental stabilization and rational land-use planning. Only when studies on biological diversity provide data for these arguments can a clear rationale be presented. It is evident that the environmental data bases needed by my community of scientists are only just being developed. Interestingly, when speaking about wild relatives of crops, a well-known crop botanist recently said that identification of environments was more important than proceeding from past taxonomy and searching large areas with often poor chances of success (G.Ladizinsky, Hebrew University of Jerusalem, Israel, personal communication, 1986).

SCIENTIFIC SUPPORT FOR GENETIC RESOURCES WORK

Conservationists outside the field of crop genetic resources frequently base their plea for conservation of wild species on spurious evidence and unrecognized needs resulting from a lack of adequately trained scientific manpower. The work in crop genetic resources has been successful because of its user orientation, and in fact has been solely directed to this end. There is a clear lesson here for the wider conservation movement and also a reminder of the need to identify gaps in scientific knowledge.

The success of IBPGR would not have been possible without the work of botanists, geneticists, and scientists in related disciplines. Nonetheless, there has been insufficient scientific research pertinent to the conservation of crop genetic resources. This has been partly due to lack of funding and partly to the fact that strategic research is often not as attractive to the academic community as basic research. Accordingly, IBPGR has had to shift its program to accommodate strategic problem-solving research, much of it of an interdisciplinary nature.

Areas of research where such problems exist are:

- the elucidation of patterns of genetic variation using such disciplines as taxonomy, ecology, cytogenetics, molecular biology, and population genetics; and
- the understanding of genetic stability in conservation systems, again as interdisciplinary work involving genetics, tissue culture, molecular biology, and seed physiology.

IBPGR has initiated relevant research that not only will provide practical solutions to specific problems but also will add to scientific knowledge. Traditional disciplines such as taxonomy and cytogenetics have to keep up with exciting new developments in, for instance, molecular biology. One recent development is the proposal that DNA is in a state of flux. Exchange of genetic material between organelles and nuclei may be possible, while bacterial infection and tissue culture, for instance, may induce new genomic changes in response to changed environments (Hohn and Dennis, 1985).

On the whole, conservation biologists have not fully considered the technologies necessary for scientific and practicable solutions and need a synthesis of data from numerous disciplines. One recent initiative, that is supported in part by the government of the United Kingdom and draws on a wide range of expertise, is the International Legume Database Information Service (ILDIS). IBPGR has been associated with this service from its inception and views positively the mobilization of scientists within several institutions. Yet the provision of checklists of taxa continent by continent draws heavily on traditional taxonomy. This venture and the Missouri TROPICOS system and the BIOSIS (BioSciences Information Service) Taxonomic Reference File are to be applauded.

EX SITU AND IN SITU PRESERVATION

Because of their nature, most crop genetic resources are conserved *ex situ*. Many crop relatives are annuals or weeds associated with disturbed agricultural environments, and most do not lend themselves to *in situ* conservation. Landraces cannot be conserved by growing them in primitive agricultural conditions; it is neither practical nor can it be justified morally. There are exceptions to what can be conserved *in situ*, especially perennial species associated with complex ecosystems such as tropical rain forests, e.g., cocoa, oil palm, relatives of *Citrus*, and some root crops. To encourage *in situ* conservation where it is relevant and to rationalize further collecting work, IBPGR has recently been developing its expertise in the ecogeographic sampling and monitoring of genetic resources. But the opportunities for *in situ* conservation are limited and should not be overemphasized.

In addition, preservation of species diversity by ecosystem maintenance is not always relevant to the conservation of crop genetic resources. Allelic diversity is rarely considered by ecosystem conservationists, yet it is needed for utilization by crop botanists (Frankel and Soulé, 1981; Ingram and Williams, 1984).

The interface between ecosystem conservation and the special needs to conserve crop genetic resources has been discussed by Ingram and Williams (1984). Many of the scientific points have not yet been addressed by the wider conservation movement and merit further attention if scientific objectivity is to prevail over emotive generalization.

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