# Ecogeographical surveys: a review

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**Abstract**

Hodgkin, T. & Guarino, L.: Ecogeographical surveys: a review. — Bocconea 7: 21-26. 1997. — ISSN 1120-4060.

Since genetic and other kinds of diversity are not evenly distributed within taxa, ecogeographical surveys need to be undertaken so as to ensure representative sampling for germplasm collections. Such surveys permit a synthesis of of the available information on the distribution and variation within a species or related group of species. The various types of information that can be of use in an ecogeographical survey are described, as well as the ways this information can be used in developing effective strategies for the conservation and management of the wild genepools of the cultivated plants of Europe.

## Introduction

The overall geographical range of a species is frequently determined by barriers which are large, conspicuous and easily identified (e.g. mountain ranges, deserts, oceans). These can often combine in a variety of different ways to determine species distribution. However, in some cases, the barriers may be less obvious and it may be difficult to see why a species has not extended its range further. On a smaller scale, where a species is found is determined primarily by ecological factors including climate, predators, competitors and useable resources and the biological characteristics of the species in determining its response to these factors. These may result in a species which is distributed more or less continuously over a wide range or in one with a highly localized or patchy distribution.

Numerous studies at the morphological, biochemical or molecular level have demonstrated that genetic diversity is not evenly distributed within taxa, whether these be families, genera or wild or cultivated species. Founder effects and differences in the rates of mutation, genetic drift, gene flow and selection have resulted in some geographical areas being more diverse than others for a given taxon and some taxa being more diverse than others (Guarino 1992). With respect to the wild relatives of crop plants the different genepools often contain taxa with widely differing distributions and different amounts of genetic diversity. Germplasm of rare and/or narrowly endemic species may often contain unique alleles which are not present in the rest of the genepool.

The major components of an ecogeographic survey have been described (IBPGR 1985) as being the study of:
- distributions of particular species in particular regions and ecosystems;
- patterns of infra-specific diversity;
- relationships between survival and frequency of variation and associated ecological conditions.

This permits a synthesis of the available information on the distribution of and variation in a species or related group of species. The objectives to be addressed are essentially practical: the development of effective conservation strategies for the target species whether these be based on *in situ* or *ex situ* approaches (or on a combination of both).

The purpose of this presentation is to briefly describe the different types of information that can be of use in an ecogeographic survey and to discuss some of the ways in which this information can be used in the conservation of wild relatives of crop plants.

## Information on species distribution

The first source of information on the distribution of target taxa of wild relatives of crop plants is regional, national and local Floras. Increasingly such data are available in floristic databases of various kinds. These can be complemented by available reviews, taxonomic discussions and other papers on aspects of distribution or diversity. The availability of these will vary greatly depending on the importance of the related crop species and the size of the research community. Significant information can become directly available in this way (e.g. Snogerup & al. 1990) or such papers can point to sources of useful information (e.g. Hodgkin & al. 1992).

Herbaria surveys have been used as a first step in collecting primary data on species distribution in many ecogeographic surveys (e.g. Maxted 1990) and Maxted (1992) discusses the considerations involved in obtaining data from herbaria as part of an ecogeographic survey. He concludes that it is important to survey data from as many herbaria as possible in order to obtain an estimate of within-taxon variation. Data from herbaria are subject to considerable bias in that they are normally highly selected, reflecting the particular interests or opportunities of the original sample collector about which little may now be known. However the data are of value in providing an overall picture of taxon distribution as currently recorded and identifying priority areas for further study and collection.

Over the last 20 years or more there has been extensive collecting of plant germplasm in Europe and more recently this has tended to focus on the wild relatives of crop plants. Much of this has been carried out by individual specialists or groups with interest in studying the distribution and diversity of specific taxa or with an interest in broadening the genetic basis of specific crops. The need to collate this information has often been recognised and in a number of cases this has been coordinated through a variety of mechanisms of which the crop working groups of the IBPGR ECP/GR programme are a highly developed example. One of the first activities of such groups has frequently been the development of a crop database listing the germplasm holdings of gene banks in Europe and *inter alia* holding information on wild relatives of crop plants. Currently it is estimated that there are some 22 European crop databases (Bettancourt pers. com.) holding at least passport (origin) data on germplasm holdings. These include databases on *Dactylis, Pisum,* and *Brassica* ($n$ = 9 spp.) as well as on *Allium, Beta, Prunus* and a number of forage grasses and legumes. Where coordinated databases on existing genebank holdings of wild relatives do not exist it may be possible to identify individual collections with relatively significant holdings of wild crop relatives through IBPGR ECP/GR Directories of Germplasm Collections.

As with herbarium surveys, data from genebank may not be a particularly reliable indicator of the actual distribution of wild relatives. Much depends on the source of the material and the objectives of the original collectors of the germplasm and the genebank now holding it. The information available on *Brassica* species in Europe with $n$ = 9 is extremely complete (Gómez-Campo 1990 and Gustafsson in this volume) representing the results of an extremely detailed survey of a set of -related wild taxa. However information available for other species may be much more variable and it may be difficult to determine how complete it is. Hodgkin & al. (1992) surveyed current holdings of wild *Triticum* and *Aegilops* species and found that there were approximately 27,000 accessions in the world's genebanks, mostly originating from the Middle East or Europe. However, while precise origin data was available for only 78% of accessions ecological data was available for less than 20 % of accessions. Interestingly, much less information was obtained from a parallel herbarium survey of wheat relatives, reflecting no doubt the interest of plant breeders in obtaining such material for crop improvement programmes. In contrast, Maxted (pers. comm.) found less than 20 accessions of wild relatives of *Vicia, Pisum, Lathyrus, Lens* and *Cicer* from the southem states of the CIS in his recent ecogeographic survey of these taxa in this region although he was able to develop a herbarium database of several hundred records. This work demonstrated the need for conservation activities involving these species in the target area and the herbarium survey provided information on the areas to be visited in collecting trips.

Direct survey data are usually less available although often such data have been collected as part of long term survey work by interested individuals, Browicz (Perret, pers. comm.) has carried out a detailed study of the distribution of wild *Prunus* spp. in Greece which has yet to be published. This provides a fairly precise evaluation of the occurrence of individual species together with an assessment of their rarity and would provide an invaluable source of information for those concerned with conserving this genus.

## The distribution of genetic diversity

Within species, studies of genetic diversity have seldom been undertaken as part of a systematic ecogeographic survey of the distribution and variation of a species or group of species (although that described by Gustafsson may represent an exception in this respect). Much more commonly population geneticists have tried to identify the distribution and extent of genetic diversity in individual populations of a target species. In some cases, where extensive work has been undertaken, a more or less complete sample of the species has been included in such studies. Part of the reason for this is historical in that complete and representative collections have had to be developed before such work could be undertaken. It also reflects the different interests of those involved in the work.

Data on genetic diversity may come from a study of morphological and physiological characters which may be inherited as simple Mendelian characters or may require quantitative genetic studies to determine their inheritance. Such studies are not uncommon in the case of wild relatives of crop plants where the interest is often on characters such as disease resistance or on stress or yield related characters. Extensive evaluation of wild *Triticum* and *Aegilops* species has been carried out with a view to identifying particular characters of interest in breeding programmes. Such studies tend to favour wild relatives which can be crossed with the desired crop types and may not reflect the total variation to be found in the wild genepool. However, they are concerned with phenotypic (non-neutral?) characters and may be of considerable importance in developing practical conservation programmes.

Much more information is available from biochemical studies involving isozymes or seed proteins. A number of classical studies of diversity in wild relatives of crop plants have been carried out including those on *Triticum dicoccoides* (Nevo & al. 1988) and by Weeden (1988) on *Pisum* genotypes from Europe and the Middle East.

These studies can be extremely informative in identifying areas of high genetic diversity, identifying the range of variation that may exist in wild relatives, establishing new collecting priorites and indicating populations which should have priority in any *in situ* conservation programme.

Molecular genetic techniques are increasingly being used in studies of genetic diversity. Although these techniques are often regarded as expensive and require a greater level of technical sophistication than isozyme techniques, they have considerable potential in work on issues concerning the conservation of wild crop relatives. Hodgkin & Debouck (1991) have recently reviewed the possibilities in this area.

The major drawback to their use in genetic diversity studies of any scale concerns the relatively small number of samples that can be tested in any investigation and this aspect is currently the subject of a European community initiative. Studies of genetic diversity have supported the view that genetic diversity is structured in space and time and that breeding system and life form have a particular influence on the amount of diversity in a species. Schoen and Brown (1991) have suggested that infraspecific variation in population genetic diversity is strongly correlated with breeding system in plants and that in self-pollinators the amount of variation in populations may differ considerably among populations. This suggests that it is particular important in such species to identify local 'hot-spots' of variation which may be of great significance in the effective conservation of diversity.

General studies of the genetic variation in wild relatives of crop plants which occur in Europe are rather limited although more data is becoming avalable.

However, the value of such studies is now clearly established for a number of crops such as tomato (Miller & Tanksley 1990), *Phaseolus* (Gepts 1992) and *Pennisetum* (Tostain 1992).

These studies have clearly documented the amount of variation that can exist in the wild relatives of a crop and have indicated which species and what populations are likely to contain variation of particular importance for conservation.

Thus, Miller and Tanksley (1990) found that almost 75 % of the unique RFLP restriction fragments in their study of diversity in *Lycopersicon* came from three wild selfincompatible species while cultivated *L. esculentum* contributed only 5 %. Molecular and biochemical markers have established that there exists a small (possibly original) relic population of wild *Phaseolus* which has subsequently diverged into Middle American and Andean groups in which separate domestication has occurred (Gepts 1992).

The studies on *Pennisetum* have provided clear evidence that wild millet diversity is structured into geographical groups and that it is necessary to conserve populations from many different sites.

## Conservation Strategies

The ecogeographic survey, in the wider sense that is used here so as to include the collation of available information on the extent and distribution of genetic diversity, provides the basic planning tool required to develop an effective strategy to conserve and manage the genetic diversity of the wild genepools of the cultivated plants of Europe. The collection and colllation of the required information requires a multidisciplinary approach involving, among others, taxonomy, biogeography, ecology, population genetics and statistics. It is also an iterative process in which information on species distribution and ecology is used to guide collecting and studies on diversity which in their turn can point the way to further studies on ecology, distribution and population dynamics.

It is not possible to conserve all populations of a species of interest either by *in situ* or *ex situ* methods and some selection of populations and techniques will be necessary. Much will depend on the individual species, its immediate importance for plant breeding, the amount and distribution of diversity within it and its own distribution characteristics. One way of approaching these issues is to seek to identify those populations which would enable us to conserve significant amounts of the total variation of a species with a minimum of repetition.

Generally, we can recognize four classes of allele distribution:

— common, widely distributed
— common, locally distributed
— rare, widely distributed
— rare, locally distributed.

The conservation of the first class (common, widely distributed) should present no problems and that of the last two classes will depend ultimately on the resources that we are prepared provide and hence population sizes that we are prepared to conserve. The conservation of alleles which are locally common but not widely distributed is likely to be most dependent on choices made by conservationists. Their maintenance may largely depend on the identification of populations adapted to specific environments i.e. with significant numbers of adaptive alleles. In crop plants the identification of such populations or groups has been by way of hierarchical structuring of diversity todistinguish the major agroecological and phenological types present in a crop. Such an approach would need to be complemented by one which permitted the location of populations with particularly high levels of variation, particularly for self-pollinated species.

Ecogeographic surveying will also enable effective complementary conservation strategies to be developed. A knowledge of the overall distribution of a species and of the ecological and genetic aspects of variation can be used to identify populations which are suited for *ex situ* or *in situ* conservation.

There are good arguments for preferring *in situ* conservation for most wild relatives of crops and for emphasizing *ex situ* conservation where populations are particularly threatened or where an immediate use of the germplasm is foreseen.

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