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Utilization of plant genetic resources in crop breeding programmes

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Introduction

There are a wide variety of ways in which plant genetic resources are used in crop breeding programmes. These depend upon the problems which the breeder is trying to solve, the resources at hand to solve them, the reproductive biology of the crop, and the availability of appropriate genetic resources collections. The important fact is that all breeding programmes depend on genetic resources of one type or another to make progress in improving yield, disease or pest resistance, and product quality of the crop, forage or ornamental plants they are responsible for. This paper considers in general terms some of the important ways in which genetic resources collections are used in modern plant breeding programmes, and illustrates the general principles with an example of different uses of a very good national genetic resources collection in a breeding programme currently in its initial stages in Namibia.

First a word about the scope of the term "genetic resources," which encompasses all sources of useful plant traits or specific genes for a given crop. These can be conveniently grouped into four broad categories:

Products of other breeding programmes

Released varieties and breeding lines from past breeding programmes typically contain valuable combinations of many genes - yield potential, disease and pest resistance, quality traits, etc. - and are thus the most useful genetic resource in many cases. If a plant breeder can find the character he/she is seeking in an already adapted or elite breeding line, he/she is far ahead in comparison to using a wild relative or unadapted line as a source of the character, which may require years of selection to separate the desired character from undesired ones which will accompany it segregating generations from the original cross. This source is increasing in importance with the advent of the large International Agricultural Research Center breeding programmes which make their products freely available to any breeding programme in the world.

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Landrace varieties

Landrace varieties, those selected by farmers over long periods of time for adaptation to local growing conditions and for local preferences for taste, plant type, etc., are a very valuable source of a wide range of characters. These include tolerances of soil, climatic and biological factors which limit plant growth, plant types with different end uses, special quality traits, etc. The use of landrace varieties as sources of desired characters in a breeding programme may entail more effort, as often the landrace variety is not adapted to the environment or the type of agriculture for which the plant breeder is working, and considerable selection is required to separate the desired traits from the unadapted background. Overall however, landraces represent the greatest reservoir of useful traits of any source; hence the current effort to preserve them in the face of the rapid spread of modern varieties.

Wild relatives

Wild relatives of cultivated plants, either other species within the same genus or in allied genera, can be extremely important as sources of traits not available in the target species itself. This is most often the case for resistances to pests, diseases and viruses for which there are no resistances known in the cultivated species. Wild relatives can be extremely difficult to use in a breeding programme, however, as there are often barriers to crossability between the wild and cultivated species which can be difficult (or impossible) to overcome, and because of the fact that wild relatives contain many undesirable characteristics for agricultural plants: seed dispersal mechanisms, small seed size, an emphasis on survival rather than productivity, etc.

Products of genetic engineering

Genetic engineering technology in plant breeding will not generally be used to create new varieties directly, but to move valuable traits from one species to another, where this is impossible by conventional means. Once the transfer of the trait is made, it can be then used in breeding programmes with conventional genetic means. Thus genetic engineering technology can (theoretically) be used to create a whole new set of genetic resources, almost to order, for use by plant breeders.

Direct utilization of genetic resources materials as cultivars

There are many situations in which accessions from genetic resources collections can be used as cultivars, either directly, or with some selection for plant type, uniformity, etc., where the accession is genetically heterogeneous or heterozygous. Some of the more common of these are described below.

Early stages of a breeding programme

It can make very good sense to begin a breeding programme with local landrace varieties, or released varieties from neighboring countries. There is a high probability that such material will be adapted to local conditions, tolerant to (at least some of) the local pest and disease problems, and will have the locally desired consumer characteristics. Such a strategy also fits well with the common problem of limited resources and manpower in the early years of a breeding programme.

Low input, extensive agricultural systems

The economic value of new varieties of species for use in forestry, rangeland, erosion control, etc. may often not justify the investment required for a conventional breeding programme, particularly where productivity is mainly determined by environmental conditions rather than the potential productivity of the varieties used. Yet in such situations adapted planting material is needed for extension and development programmes. In such a case, an assessment of locally available collections, or varieties from climatically similar areas for adapted, productive species, ecotypes, strains, etc. which lend themselves to seed production (eg. which do not disperse their seed before harvest stage) may be all that is needed.

Ready availability of advanced breeding lines

In cases where good breeding materials are available from regional or international programmes, it may not be necessary for a country to develop its own breeding programmes, especially where resources and manpower are scarce. It may be more sensible to concentrate resources on evaluating the materials available from other organizations, to select the best adapted, most productive, etc. for direct release to farmers. This is especially true where breeding is difficult (vegetatively propagated crops, plants that are difficult to cross, etc.) and progress will be slow.

The direct use of genetic resource materials as varieties will in general be much more successful if there is a clear objective in mind, so that genetic resource materials can be effectively evaluated for their potential as new varieties. For example, the requirements of new materials for a pasture reseeding programme could be many: ease of seed production, ease of establishment, persistence, productivity, dry forage quality, etc. Different types of evaluation procedures are needed for the different attributes, so priorities need to be firmly established.

Also a knowledge of local climatic and edaphic conditions is essential, in order to know where to look for genetic resources materials that are likely to be adapted/use-

ful. Continuing the above example of planting material for a pasture reseeding programme, a knowledge of the following would be necessary to identify sources of genetic collections for testing: extremes of local soil moisture and temperature at sowing, soil toxicity or deficiency problems, rainfall pattern and season length, minimum temperatures in the cool season, etc.

It should also be noted that there are often good possibilities for reselection of introduced genetic resources materials to improve their adaptation/usefulness in local environments/agricultural systems, particularly in the case of either landrace varieties or cross pollinated species. This need not involve any complicated procedures, simply exposing the introduced genetic materials to critical factors of the environment or the agricultural system in which they are to be used, and selecting individual plants which show the best adaptation, growth, quality, etc.

Genetic resources as sources of quantitatively inherited traits in plant breeding programmes

Quantitatively inherited traits are those which are under multigenic control, such as grain yield, and hence whose inheritance is neither simple nor predictable. Improvement in such traits is usually incremental, and a continuous process in a breeding programme. Genetic resources materials of various types are regularly evaluated for potential new parents which express such traits strongly, for crossing to established varieties or parental lines. The progeny of such crosses are then evaluated in conditions in which the traits for which improvement is sought will express themselves well - i.e. in which individual plants having an enhanced level of the trait can be identified. Two common examples follow:

Improvement in product yield level

This is almost universal objective in breeding programmes, as the release of new cultivars often depends on their having an enhanced yield level. Sources of higher yield may be either high-yielding varieties or breeding lines from other breeding programmes, or varieties, landraces, or even wild relatives, which have high level of some component of high yield, such as seed size for a grain crop or growth rate for a forage crop.

Improvement in adaptation to extreme environmental conditions

In some cases an increase in the level of actual productivity may not depend as much on an increase in potential productivity, as on an increase in tolerance of environmental extremes: drought, temperature, salinity, etc. Such tolerances are often multigenic, as tolerance is required in a large number of biochemical or physiological processes for tolerance to be expressed at the whole plant level. Sources of tolerance are most likely to be found in landraces or wild relatives, which have had long periods of

evolution under the extreme conditions. Such landraces, wild relatives, etc. may in themselves not be highly productive, but contain genes which put into a highly productive genetic background will produce plants whose productivity will be maintained in extreme environmental situations.

The effective use of genetic resources materials as sources of quantitatively inherited traits requires appropriate breeding procedures for multigenic traits and effective methods for evaluation of segregating populations resulting from the crosses of these with established varieties or breeding lines. The choice of a breeding method will depend on a number of factors, including the ease and cost of measurement of the trait of interest (ie. whether or not selection can begin in early, segregating generations), and the degree of similarity of the identified source of the trait and standard varieties (ie. how much selection will be required to get an acceptable plant type). The method chosen will generally need to allow the opportunity for maximum genetic recombination to break genetic linkages between the desired trait and non-desired ones, particularly if non-cultivated or wild relatives are being used as the source of the trait. And, in general, populations of segregating plants resulting from crosses of the source to advanced lines in the breeding programme will have to be large, as the frequency of occurrence of individuals with the specific combination of the many genes involved in the expression of the trait will be small. Evaluation methods generally need to both effective and inexpensive, because of the large number on individual plants that may need to be tested.

Genetic resources as sources of simply inherited traits in plant breeding programmes

Simply inherited traits are, as the name implies, governed by one or a few genes, and are therefore often more easily and completely transferred from source to new variety than are multigenic traits. In fact, more effort is often spent in the search for a source of a desired trait, such as resistance to a new race of a disease, than is required to transfer the trait to otherwise good, accepted cultivars. Genetic resources collections are regularly used in such searches, with the search progressing from released varieties, to landraces, and finally to wild relatives if the trait is not found in the cultivated types. Examples of simply inherited traits commonly sought in genetic resources collections include:

Resistance to plant diseases, especially fungal diseases

The problem often involves the appearance of a new race of a common disease, following a mutation in the pathogen which overcomes existing host plant resistance. The breeder is thus forced to find a source of resistance to the new race and to transfer it to his/her varieties and breeding lines as quickly as possible. Repetitions of this cycle result in a series of genes for virulence in the pathogen, matched by a series of genes for resistance in the host - the so called 'gene for gene' theory of virulence

and resistance. But as mutations do not occur in higher plants at the same rate as they occur in pathogens, the breeder is forced to search in genetic resource materials in the hope that sometime in past history a gene evolved for resistance to an earlier race of the pathogen which is also effective against the new race.

Mechanisms for resistance to insect attack

Effective resistance to insect attack often involves the cumulative effect of several different mechanisms, which deter, delay, tolerate, etc, insect attack, feeding, reproduction, etc. These individual mechanisms are often simply inherited, even if the cumulative phenomena of resistance is not. Thus if a plant breeder or entomologist can identify the individual components of resistance, these can be transferred piecemeal to varieties lacking sufficient resistance. Fortunately such resistance mechanisms have often evolved in response to more than one pest (glandular hairs on the leaf surface may discourage feeding by many insects, for example), so that the frequency of occurrence of resistance mechanisms in genetic resources collections is often greater than is the frequency of resistances to specific races of a pathogen.

Utility and quality traits

This is a broad category of what are often single gene mutants that singly or in combination result in changes in the phenotype of a plant carrying them that may greatly increase its utility or quality. Common examples include flower and leaf colour in ornamental plants, seed coat colour and pattern in many seed crops, and mutants causing changes in seed protein or carbohydrate composition such as the sugary and high lysine genes in maize. These traits are the result of past mutations, which may be present only in low frequencies in genetic resources materials, as they may be detrimental in natural conditions, for example dwarf stature among tall individuals.

Simply inherited traits are relatively easy to transfer from their source to breeding lines or varieties. Because these traits are controlled by one or a few genes, they tend to appear in complete, recognizable form or not at all, so those individuals carrying them are easy to detect in segregating populations. Utility and quality traits - colour, texture, size, etc. - can often be detected visually. Detecting the presence of a specific gene for disease resistance may require inoculation of segregating populations with the specific race of the disease for which it provides resistance, but insect resistance mechanisms can be detected directly in many cases by, for example, microscopic examination.

Because of this easy detection of simply inherited traits, segregating populations from crosses can be smaller and several special breeding methods designed to accelerate the process of transfer of the trait can be effectively used. Among these are back-crossing, in which segregates which contain the desired trait are crossed each generation to the original variety to which the trait is being transferred, producing a plant virtually identical to the original, but containing the new trait, in 4 to 6 generations. This procedure is often used in the case of resistance to specific races of a disease.

Methods which involve a rapid advance of the segregating lines to homozygosity, such as the single seed descent method are also often used, in which case the evaluation for the presence of the desired trait is done only once, on genetically homozygous lines which will not segregate further.

Genetic resources as sources of new ideas in plant improvement

Genetic resources collections typically contain novel phenotypes, which are usually present in low frequencies and which are sometimes non-competitive or unproductive, such as a dwarf or very early flowering plant among tall, vigorous, later flowering ones. Such phenotypes however, can stimulate plant scientists to form and test hypotheses about the function of the traits that distinguish them, and to adapt these traits to novel agricultural uses. It could be argued that the science of genetics began in just such a way: as Gregor Mendel became intrigued by the different ratios of various flower colours in the pea plants in the monastery garden.

A large number of examples of productive uses of novel phenotypes and traits in plant breeding can be cited; a few examples follow. In virtually all cases, however, a considerable amount of breeding work has been required to transfer the trait of interest into usable plant varieties.

Dwarfing genes, which reduce stem internode length

These have been used to reduce lodging, permit mechanical harvesting, and allow higher plant populations in many cereal and seed legume crops; to produce more compact and attractive flowering plants, to increase the leaf to stem ratio, and thereby the nutritional value, of forage crops, and to reduce the difficulty and cost of harvest in tree fruit and oil crops.

Variations in inflorescence morphology, colour, etc.

Many new varieties of ornamental plants are based on novel inflorescence morphological characters found in genetic resources collections; multiple layers of petals, ruffled petals, variegated colours in petals, pigment synthesis mutants which produced novel flower and bract colours, etc.

Defective microsporogenesis

Heritable genetic defects in microsporogenesis which result in non-functional pollen have been found in many species. The male-sterility which these mutants cause is the basis of a very large hybrid seed industry for dozens of cereal, vegetable, ornamental and oilseed crops.

Novel plant types, inflorescences, etc. are often simply inherited, and can therefore be manipulated relatively easily in a breeding programme. The task is often to place

the novel trait in a genetic background in which it is useful, i.e. to combine ruffled petals with a large petal size so the ruffling is striking, or to put the male-sterile trait into a breeding line which combines well with a range of other parental lines.

Traits which govern novel plant types are also often recessive, making their transfer a bit slower, as the trait is discernible only in plants homozygous for the trait.

Utilization of the Namibian pearl millet germplasm collection

During April and May of 1991, a major collection of pearl millet (or mahangu) was made in the three northern districts of Namibia. It was joint project of the Ministry of Agriculture, the SADCC/ICRISAT Sorghum and Millet Improvement Program, and the Genetic Resources Unit of ICRISAT Center, India. Each sample collected was shared equally among the three institutions; The Ministry's set is currently in the cold store at the Mahanene Research Station, awaiting transfer to the Namibian National Genetic Resources Center, once its storage facilities are completed; the SADCC/ICRISAT Program's set has been multiplied for use in initiating a Pearl Millet breeding programme in Namibia, and the ICRISAT Center's share has been placed in long-term cold storage in the ICRISAT genebank.

The collection is one of the most intensive ever made of the crop, totaling 1000 individual accessions, or approximately one accession for every 150 hectares cultivated to pearl millet in Namibia. It was also done before there has been any significant replacement of the traditional landrace varieties by modern varieties. It therefore represents an extremely valuable resource for future use. Initial observations of the collection during seed multiplication in Zimbabwe during the winter season of 1991, suggest that it is an excellent source of a number of useful traits: plant vigour, tillering ability, panicle size, and especially grain quality, in the form of round, white, hard grains, which could have potential for commercial milling.

The collection will form the basis of a pearl millet breeding programme which has been initiated by the Division of Agricultural Research of the Ministry of Agriculture, with the assistance of the SADCC/ICRISAT Sorghum and Millet Improvement Program. Plans are to use the collection to meet both the short term objective of making new varieties available to Namibian farmers for testing within the next 3 years, and the longer term objective of building a genetic base for the breeding programme over the next 10 - 20 years. The following paragraphs describe the specific plans for the use of the collection, according to the general types of utilization described in the previous sections of this paper.

Direct utilization as varieties

The obvious immediate use of the Namibian germplasm collection is as a source of varieties for immediate use by Namibian farmers. Approximately three-quarters of the collection will be evaluated in replicated trials this coming season at two locations in Namibia and one in Zimbabwe to select those individual accessions which have the greatest potential for use as varieties. This evaluation will include a number of characteristics: vigour, tillering ability, uniformity, maturity, panicle size, grain yield, grain size and grain colour. Final choices will include samples of a range of phenotypes, to offer farmers a selection of plant and panicle types, maturities, etc.

Selected accessions will put through one cycle of improvement, using S_1 progeny testing. In this procedure, 200-300 plants will be self-pollinated during the dry season (under irrigation); the progeny of the best 150 or so of these will be evaluated in a replicated trial in the following rainy season, on the basis of the same criteria by which the parent accession was selected. From this evaluation 10-20 similar, uniform progenies with a good grain yield and grain characteristics will be selected and remnant S_1 seed of these recombined by hand pollination during the following dry season to form a variety for testing the next rainy season. Such a variety should be much more uniform and have a 10-20% yield advantage over its parent accession, while retaining the good characteristics for which the parent accession was selected.

This is a very rapid and efficient procedure; it requires only three seasons (one and a half years with two seasons per year) to produce a variety for testing, and does not involve complicated breeding procedures, only the ability to conduct good evaluation trials. Even a small programme should be able to produce 5 - 10 varieties for testing each year by this procedure. Because such varieties are based on local landraces, they should not have serious problems of adaptation, acceptance by consumers, etc. The improvement in uniformity makes it possible to accurately describe them for purposes of variety release and seed production and seed certification, which is often impossible for the parent landrace because of a high degree of heterogeneity.

Utilization as sources of simply inherited traits

The entire germplasm collection is far too large to grow out regularly in search of good sources of specific traits. The alternative of limiting the search to a small subset is also not satisfactory as this means that many good sources may never be used. One solution to this dilemma is the formation of trait-specific gene pools, which bring together into a single population a large number of individual plants which all have a common trait - for example bristled panicles - but which differ for many other characters: maturity, height, panicle size, etc. Selection can then be done in this bristled population for many different phenotypes - all with bristled panicles - to meet varying requirements of different environments or agricultural systems.

During the seed multiplication of the Namibian germplasm collection 2500 single, self-pollinated plants were selected on the basis of plant and panicle type. The progeny of these plants will be grown during the 1991/92 season to select either whole

progenies or single plants from them to recombine to form a series of trait-specific gene pools to be used as described above. The plans are to form the following pools:

- *an early maturity, high tillering pool
- *an intermediate maturity an height pool
- *a late maturity, tall, thick stemmed pool
- *a bristled panicle pool
- *a large panicle (diameter and/or length) pool
- *a reduced height pool

Not all of the particular distinguishing phenotypes of the pools are necessarily simply inherited traits (eg. panicle size) but can be handled as such using a gene pool approach, in the sense that they can be fixed in the pool before selection for other characters is begun.

It will not be possible or necessary to exploit all of these gene pools immediately or simultaneously. Once the selected plants or progenies are recombined for several generations, a large seed lot of the pool (up to 100 kg) can be put into the cold store and samples taken whenever and by whomever is interested in the particular phenotype of the pool. Such a sample will allow anyone access to the broad range of the genetic variability in the original germplasm collection, without the need to grow out the entire collection.

Utilization as sources of quantitatively inherited traits

Experience with breeding materials introduced from other regional and international programmes indicates that these materials have a range of valuable traits for use in Namibia, but may lack the basic adaptation of the Namibian germplasm to the environmental conditions in which millet is grown in Namibia. This strong adaptation, plus the exceptional vigour, large panicle size, etc. of many of the Namibian accessions, make them a valuable resource for cross breeding with introduced varieties, to produce a strong genetic base for future breeding programmes.

A subset of 50 of what were considered the best accessions at the time collection was being made was selected as parents for crossing to a set of 12 varieties and germplasm lines from other SADCC countries. These in turn had been selected on the basis of their appearance in breeding nurseries at Mahanene in 1990/91. Crosses between the two sets of materials were made during the winter season of 1991 in Zimbabwe, by putting bulk pollen from the regional varieties on single plants of the Namibian landrace accessions. This generated approximately 1000 F₁ progenies for evaluation in Namibia. This is far too many to manage at one time; F₁ populations from selected crosses, including those between the landraces and the variety Okashana 1, will be planted at Mahanene during 1991/92 and the rest placed in the cold store for future use.

Superior plants from the F₁ progenies will be self-pollinated and may either be advanced by pedigree selection, for use in making synthetic varieties, or be back-crossed to the introduced variety parent, to increase its vigour, panicle size, etc. One

specific objective of the crossing programme is to produce a white and, hopefully, a harder seeded version of the variety Okashana 1 (which has a gray seed colour and a soft endosperm) by transferring both of these traits from a Namibian germplasm source, through repeated backcrossing of segregates with the desired seed type to Okashana 1.

An idea for a new use for pearl millet

The collection contains a number of accessions with excellent seed quality - round, white, medium to large seeds, with a relatively hard, corneous endosperm for pearl millet. Such a grain type has the potential to be commercially milled to produce a near-white meal, which could be either substituted for maize meal, or blended with it, without a loss of the characteristic white colour of the maize meal. Preliminary studies by the SADCC/ICRISAT Food Technology Program have indicated that flour made from a dehulled white Namibian millet can also be blended with wheat flour to a level of 30% to make bread, without a detectable change in either loaf colour or loaf volume.

Maize presently represents 38% and wheat 22% of cereal consumption in Namibia (SADCC Food Security Quarterly Bulletin, 30 June, 1991). The share of both of these cereals is likely to increase as the population becomes more urbanized and fewer housewives have the time or inclination to prepare their own millet flour, but will rely to an increasing extent on either commercially available maize meal or wheat bread. The country is not self sufficient in the production of either maize or wheat, and the prospects for increasing production of both are limited. (Wheat can be grown only under irrigation in Namibia, and the climate in all but perhaps Caprivi is very marginal for maize - production levels will fluctuate greatly from year to year under dryland conditions). While Namibia may be able to afford to import maize from neighboring countries, as in the past, it is not at all certain that these countries will continue to have exportable surpluses in the future.

Pearl millet, in contrast to both maize and wheat, is well adapted to northern Namibia and it should be possible to greatly expand production. In order for millet to compete with or to supplement maize and wheat flour, however, two conditions will have to be met: the millet will have to be in the form of meal or flour, not as unprocessed grain, and production cost per ton of grain will have to be either equal to or lower than those of maize and wheat. Meeting the second condition will depend on a number of unknowns, but it is almost certain that grain yields would have to be raised substantially for production costs to compete with those of domestically produced or imported maize. The technology to meet the first condition appears to exist, provided that the milling industry has access to uniform supplies of grain of the proper type - round, large, white grains with a relatively hard endosperm.

The possibility of meeting both conditions for millet to compete with maize clearly depends on the availability of new varieties with a higher yield potential and the required grain quality characteristics. The basic germplasm to meet this requirement is available: the Namibian millet collection for the grain quality requirement and the

SADCC White grain Composite, for the high yielding phenotype suitable for higher input systems of production. The breeding programme is therefore proposing to create a new Namibian White Grain Composite, by recombining selected S₁ progenies from both sources, to provide a genetic base for producing varieties which can compete with maize and wheat in the national economy in the future.

Thus there are a variety of potentially very productive ways in which the Namibian pearl millet germplasm collection can be used in future breeding programmes to produce new varieties for Namibian farmers. Hopefully the resources, human and material, will be available to exploit the collection to the fullest.

Some guidelines for Plans of Action of National Plant Genetic Resources Centres

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1. Introduction

The SADCC Regional Gene Bank for Plant Genetic Resources (SRGB) is an autonomous regional scientific organization under the aegis of the Southern African Development Coordination Conference (SADCC). SRGB, which was established by SADCC in 1988, is governed by a Board which is made up of a Chairman and ten members representing each SADCC member country. SRGB is stationed in Zambia, at Chalimbana Research Station, 20 km east of Lusaka. SRGB was set up as a network activity to promote and coordinate a regional network of Plant Genetic Resources Centres (NPGRCs). The activities of the network are the collection, conservation, documentation, evaluation and utilization of regional plant germplasm. The first formative years were devoted largely to laying the groundwork for efficient management and administration, purchasing equipment and supplies needed for effective future operations, rehabilitating SRGB's temporary accommodation at Chalimbana and planning the construction and development of the permanent institutional complex.

With all regionally and internationally recruited staff now in place, it is time to initiate Plant Genetic Resources (PGR) activities in all the SADCC states. Before this can be done, however, national strategies and plans of action should be developed.

For practical and scientific reasons, it is necessary to have a good working definition of the kind of plant material to be preserved in a PGR conservation programme. The following five categories of plant material are usually distinguished:

- i) Genebank material (germplasm, genetic resource material);
- ii) Plant breeding material;
- iii) Plant introduction material;
- iv) Plant production material;
- v) Food or industrial plant products.

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