ATSAF/IBPGR WORKSHOP ON CONSERVATION OF PLANT GENETIC RESOURCES Bonn, Germany, 6-9 May 1990

Genetic diversity, and crop strategies for roots and tubers



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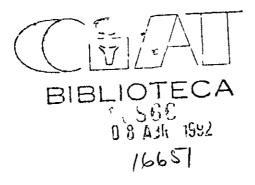
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Genetic diversity, and crop strategies for roots and tubers

Edited by Barbara Becker

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ATSAF/IBPGR BONN 1991 The Council for Tropical and Subtropical Agricultural Research (ATSAF e V) is an association of scientists of German research institutions. The activities of the Council are concentrated on the following areas

- Advice to the Federal Ministry for Economic Cooperation the Federal Ministry of Food Agriculture and Forestry etc in their policies towards the CGIAR and research institutions supported by the CGIAR as well as other international agricultural research centers developing scientifically based criteria for support to developing countries
- Coordination of German Agricultural Research by mediating and fostering contacts between scientists from various research institutions
- Participation of German Agricultural Research in International Activities by maintaining close contact with the CGIAR system and its Technical Advisory Committee (TAC) and by strengthening cooperation between German researchers and international agricultural research centers as well as national research institutions and research organizations in developing countries
- Public Relations by increasing public awareness on the importance of agricultural research for and in developing countries

The International Board for Plant Genetic Resources (IBPGR) is an autonomous international scient fic organization under the aegis of the Consultative Group on International Agricultural Research (CGIAR) IBPGR was established by the CGIAR in 1974. The basic function of iBPGR is to promote and coordinate an international network of genetic resources centres to further the collecting conservation documentation evaluation and use of plant germplasm and thereby contribute to raising the standard of living and welfare of people throughout the world Financial support for the core programme is provided by the Governments of Australia Austria Belgium Canada China. Denmark France FRG India. Italy Japan the Netherlands Norway Spain Sweden Switzerland the UK and the USA as well as the United Nations Development Programme and the World Bank.

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FOREWORD

In May 1990 a workshop was convened which brought together scientists from IBPGR and German researchers dealing with plant genetic resources The idea for this workshop had been born in September 1989 during an official visit of IBPGR's Director of Research Dr Alison McCusker to Mr Thomas Schurig then Head of the Department for Agriculture and Rural Development of the Federal Ministry for Economic Cooperation (BMZ) The objective of the workshop was to strengthen the relationship between IBPGR and German scientists by establishing research contacts and collaboration

The event was unprecedented for a couple of reasons For the first time five scientists from one single CGIAR centre had come to Germany for a research oriented workshop with German scientists Moreover since the workshop took place during the reunification process of the then still two Germanies it was the first time in ATSAF history that representatives of the former German Democratic Republic were able to take part in such a meeting whereas IBPGR has already had close links to researchers in the former German Democratic Republic for many years

After extensive preparatory discussions on the scientific focus of the meeting two distinct subjects were chosen

- crop strategies for roots and tubers (with special emphasis on cryopreservation) and
- genetic diversity (as a more general topic with specific research needs)

Both subjects play an important role in IBPGR's research programme both have special potential for collaboration between IBPGR and German scientists and institutions Furthermore both areas are highly relevant for developing conservation strategies for genetic resources of crop genepools

Each subject was given a full day of presentations discussion and working groups Professor Hans-Jorg Jacobsen kindly volunteered to chair the discussion about crop strategies for roots and tubers and Professor Gerhard Fischbeck about genetic diversity Professor Heinrich Weltzien then ATSAF Chairman commendably lead the opening session. The workshop was complemented by an excursion of the IBPGR team to two German research institutions the Max-Planck-Institute for Resistance Breeding in Cologne and the Institute for Genetics of Bonn University As intended the workshop has resulted in a number of specific proposals for collaborative research projects. These proposals are remarkable because of the number of collaborators involved who took the opportunity provided by their workshop meeting to initiate these proposals. Three research projects are presently under way as special projects.

- Refinement of Cryopreservation Techniques for Potato Cooperating partners FAL Braunschweig FRG (Dr G Mix– Wagner) DSM Braunschweig FRG (Dr H M Schumacher) University of Tubingen FRG (Dr L Schilde-Rentschler) IBPGR Rome Italy (Dr L Withers) CIP Lima Peru
- Effective Pollination Control Methods in the Regeneration of Germplasm
 Cooperating partners FAL Braunschweig FRG (Dr S Schittenhelm) ZiGuK Gatersleben FRG (Dr K Hammer) University of Halle FRG (Dr M Dorn) IBPGR Rome Italy (Dr R Rao)
- (III) Spatial and Temporal Distribution of Genetic Diversity in Wild Forage Species under Stress Conditions Cooperating partners Botanical Garden and Botanical Museum Berlin-Dahlem FRG IBPGR Rome Italy ICRISAT Sahelian Centre Niamey Niger

This publication is a joint venture of IBPGR and ATSAF just as the whole workshop and the subsequent research projects. The workshop was initiated and generously supported by BMZ. The publication of the report would not have come true without the efforts of Ms. Irmgard Berger and Ms. Gabriele König of ATSAF secretariat, who did the whole typing and layout of the report and helped with the editing. The cover has been designed and printed by IBPGR. Thanks are also due to Mr. Brammer and the printing service of the Ministry of Food. Agriculture and Forestry (BML), who printed the document at cost price.

May this report further strengthen the relationship between IBPGR and the German research community Moreover may it contribute to the enhancement of plant genetic resources research and conservation which is our common objective and which was the ultimate reason for conducting the workshop

Dr Barbara Becker ATSAF e V Liaison Officer for Agricultural Research

H-J deliaa

Dr Hans-Joachim de Haas Federal Ministry for Economic Cooperation (BMZ)

Opening Adresses

A FEW REMARKS ON THE AGRICULTURAL RESEARCH AID FOCUS

H – Joachim DE HAAS

It is my privilege and pleasure to welcome you here on behalf of the Federal Minister for Economic Cooperation Dr Jurgen Warnke who has repeatedly stressed the necessity to combine ecological and economic aspects in our common struggle against hunger and poverty in Third World countries

May I – at the same time – use this opportunity to convey to you best wishes for a successful meeting from Mr Schurig¹ who most certainly has had his impact on getting this research-oriented meeting off the ground He sincerely regrets that he is unable to attend this gathering due to an additional engagement he has to fulfil these days

During these weeks of rapid changes in Europe and between the still two Germanies in particular it certainly needs mentioning that our engagement in international agricultural research is not going to decrease and will maintain its present and fairly substantial support in the foreseeable future -- although the prospects of additional funds for our common endeavours are somewhat weak But continuing on the same level is already an achievement

I have been asked to contribute a few remarks on our targets and goals in supporting agricultural research activities

The Federal Government published its basic guidelines on development policies as early as April 1986 These guidelines refer to three major topics which need to be considered whenever support is to be granted

- ensuring sufficient food production on a national basis
- protecting and conserving natural resources
- combating poverty especially in rural areas

The second topic is of special interest to this meeting. For a considerable time the Federal Republic of Germany has clearly demonstrated the importance given to this principle. To a certain extent this can be judged from our support to IBPGR including our scientific cooperation with IBPGR and its Board of Trustees.

¹ then Head of Department for Agricultural and Rural Development Ministry for Economic Cooperation

Discussions like these had a strong influence on subsequent activities such as starting genebank projects in Ethiopia. Costa Rica and Kenya These programmes most certainly were rather effective with regard to the basic establishment of such gene conservation centres. However they are most likely less successful with regard to a liberal exchange of plant genetic materials from country to country and they are even less a success story with regard to their actual impact on national seed production programmes. Nevertheless the long-term conservation of valuable indigenous seeds is in itself a commendable achievement.

This in turn strengthens our interest in a well established and properly functioning IBPGR It is no secret that our support is going to continue as long as the present locality in Rome and close to FAO is maintained and the cooperation with FAO continues

We also know about IBPGR's keen interest in strengthening its own research activities. Since we share this interest and envisage very useful results from such an additional programme our Ministry encouraged IBPGR and ATSAF to initiate this meeting. The mere fact that so many scientists have come demonstrates the willingness of many institutes and scientists to cooperate with IBPGR in research programmes.

Of course as a development agency the Ministry is not really in a position to support what many people call basic or fundamental research activities. We have to stress that research programmes to be supported need to be close to applicability and to focus on actual problem solving

I am very confident that after two days of intensive discussions you will be able to present most valuable proposals for which we in turn will try to find the means of support. Let me conclude by saying how glad I am to find so many scientists ready to establish closer links with IBPGR May I apologize for not being able to participate in the meeting since our department in the Ministry is affected by quite a few changes which will keep me extremely busy throughout the forthcoming weeks

IBPGR s RESEARCH PROGRAMME

Alison McCUSKER

Introducing IBPGR

Although IBPGR celebrated its 15th anniversary in 1989 a formal Research Programme was commenced only in 1987 A limited amount of research – mainly on seed physiology – has been funded since the late 1970s but the range of interests and the amount of activity has expanded very significantly in the past two or three years

The name International Board for Plant Genetic Resources has been retained but whereas IBPGR came into the world as a Board of experts serviced by a secretariat provided by FAO it has since become a Centre belonging to the Consultative Group on International Agricultural Research (CGIAR) responsible to the CGIAR through a Board of Trustees and financed by the CGIAR through a trust fund administered by FAO

There are 13 Centres in the CGIAR system four have their major research focus on commodity crops a further four concentrate on agricultural improvement in particular climatic zones two others are concerned respectively with livestock and animal diseases in Africa and three including IBPGR have worldwide mandates to study fairly restricted topics

In keeping with our worldwide mandate IBPGR is a worldwide Centre In addition to the Headquarters in Rome the Centre has seven Regional Offices (in Colombia Mexico Niger Kenya India and China the other being based at Headquarters) These offices form the main channels of communication between the Centre and national genetic resources programmes Their involvement in the research aspects of the programme has been minimal to date but there are plans to strengthen it considerably from this year onwards

The Research Focus

The overall objective of IBPGR's research effort is to provide information to strengthen the scientific and technological basis of collecting conservation and description of germplasm

On the recognized spectrum of research activities basic - strategic - adaptive - applied IBPGR focuses mainly on strategic and to some

extent on adaptive research Occasionally we uncover needs for basic research which generally cannot be pursued within IBPGR s core budget In most though not all cases applied research can be done by national programmes

Currently the main aspects of research for IBPGR are genetic diversity covering a whole range of activities from the molecular biology approach to the field survey and various aspects aimed at improving conservation science and technology. Our staffing position on the research side reflects these interests. There are six Research Officers three concerned with various aspects of the study and maintenance of diversity and three responsible for the research into conservation technology and safe movement of germplasm

In attempting to develop a sound basis of scientific knowledge for germplasm conservation IBPGR has an important role to fill within the CGIAR system where several of the other Centres are coming to recognize the increasing importance of utilizing diverse genepools in their crop improvement work. Several CG Centres established Genetic Resources Units and proceeded to build up large collections of germplasm within their own programmes.

IBPGR collaborates with some of these units to undertake research that makes use of their germplasm but is not wholly within their mandates or their priorities. The CGIAR encourages Inter-Centre collaboration and IBPGR finds many opportunities in this regard

By contrast with our sister centres IBPGR does not maintain any germplasm collections at all Our function is to promote coordinate and assist germplasm conservation not to establish genebanks of our own In addition to addressing topics of widespread interest we focus much of our research effort on assisting national programmes to solve the scientific and technological problems associated with developing their genetic resources programmes

What are the key questions that need to be addressed by IBPGR? In broad terms we might sum up our task in just three questions

- What germplasm should be collected?
- How can it most effectively be conserved?
- How can it be made into an effective global resource for crop improvement?

Various members of the IBPGR staff will describe most of our activities during these two days of discussions. Let me just now focus briefly on two which they will not cover The first concerns seed storage After 15 years of concentrated activity by IBPGR and others to collect seed of traditional crop varieties threatened by the increasing use of improved varieties and wild species threatened by extensive clearing of natural vegetation to make way for farming and urban expansion the world now has a very considerable investment in stored seed. It is part of IBPGR s responsibility to ensure that research is done to protect that investment

It is not surprising then that the improvement of seed storage technology is one of the main objectives of our research. The method that IBPGR has recommended for the storage of seed – drying at 15 °C and 15 % relative humidity followed by storage at –18 °C in sealed packets – is effective but, not economical. Both the supply of electricity to maintain the recommended conditions for storage and the cost of it create serious difficulties for developing country national programmes. IBPGR is therefore giving high priority to developing regimes that we believe will enable seeds to be stored safely at higher temperatures by first reducing them to lower moisture contents. Any such regime must of course be very thoroughly tested before it could be recommended for general use. Early results look very promising and the advantages of success will be enormous.

The other area of research that I want to mention concerns proper documentation of the germplasm collected – which relies on proper identification of the material. It may seem surprising that IBPGR would be involved in plant taxonomy and we have resisted it as far as possible but no germplasm acquisition will ever become an effective global resource unless it is first listed in a catalogue under an accurate name

Our practice has been to support taxonomic work only if the naming of germplasm accessions is a serious bottleneck to their conservation and/or use of genetic resources. In that context, for example, we are currently funding a fairly substantial study in the genus Allium.

However workers wishing to identify the secondary and tertiary genepools of crop species are often impeded not only by nomenclature but also by a lack of understanding of the phylogenetic relationships between crop species and their wild relatives. This is an area of research which may seem on the face of it to be somewhat remote from the main focus of a CGIAR centre but there are still many unresolved taxonomic problems in the area of crop genetic resources and there is little interest by botanical institutions in addressing the agriculturally important taxonomic problems

IBPGR s approach to research is to identify recurring problems to seek the collaboration of experts in solving them and to transfer the results

to the sites of need The purpose of our visit to Bonn this week is to seek the collaboration of this group of German scientists together with others you may know in exploring areas of common interest in research that might help to solve some of the major problems in conserving and utilizing plant genetic resources to help feed the people of the world We suggested some particular projects for discussion but this gathering provides an ideal opportunity to explore much more widely the prospects for collaboration between us We look forward to two very fruitful days of discussion

Part I

Crop Strategies for Roots and Tubers

CROP STRATEGIES FOR ROOTS AND TUBERS POTATO – A MODEL FOR REFINEMENT YAM – A PROBLEM FOR DEVELOPMENT

Lyndsey A WITHERS

Introduction

The genetic resources of many important crop plants can be conserved by storage of their seeds at a low moisture content and at a low temperature (Seeds which survive under these conditions are termed orthodox) However there are a number of problem crops which cannot be conserved in this way. They fall into two categories the recalcitrant seed-producing and the clonally propagated crops in the case of the former, the seeds cannot tolerate drying and exposure to low temperatures in the case of the latter seed production is either absent or genetically irrelevant (e.g. due to high levels of heterozygosity). Both potato and yam are conserved as clones although not exclusively so

Until recently clones could only be conserved in the field genebank This method of genetic conservation can be unsafe because of risks of disease fire other accidents expense and management difficulties *In vitro* conservation the storage of clones in culture has been proposed as a safer alternative

In vitro Conservation

The central technologies of *in vitro* conservation relate to storage per se but this approach to conservation is a system that begins with germplasm collecting or acquisition followed by disease indexing/eradication and quarantine propagation storage and finally germplasm distribution for continued conservation or utilization (WITHERS 1989) By analogy with the seed genebank there is a need for both active and base storage *in vitro*

In vitro active storage can be carried out under conditions of slow growth in which cultures are maintained either at a reduced temperature or in the presence of growth inhibitors. Appropriate methodology is well developed for everal crops including potato and cassava. The latter has been chosen by IBPGR and CIAT as a suitable model upon which to test *in vitro* active genebank management standards and procedures (CHAVEZ et al. 1987). Slow growth does however have limitations. It is only applicable to shoot cultures and cannot on present knowledge offer safe long-term (i e base) storage Thus for the other types of culture (ranging from protoplasts to cells callus and embryos) there is a need for both short to medium and long-term storage technology and for shoots an acceptable long-term option Cryopreservation (i e storage in liquid nitrogen) promises to meet these needs (WITHERS 1987)

Research has been carried out to develop cryopreservation methods for all types of culture and most success has been achieved for cell suspensions (WITHERS & KING 1980) A widely-applicable routine procedure involves pregrowth in a modified medium cryoprotection with a mixture of compounds slow cooling rapid thawing and recovery on semi-solid medium Difficulties are experienced in achieving successful cryopreservation for large organized structures such as shoots which would on the basis of their inherently low risk of genetic instability be the system of choice for conservation. This problem hinders the wider application of cryopreservation. One means of resolution may lie in an alternative culture system such as the somatic embryo. IBPGR is currently pursuing the possibility of combining somatic embryogenesis artificial seed and cryopreservation technologies to find a new way of achieving the genetic conservation of recalcitrant seed-producing and clonally propagated crops

Strategies for Potato and Yam

Both potato and yam have been researched from the point of view of in vitro conservation although to different degrees of success attributable in part to differing levels of attention A large proportion (but by no means all) of this work has been carried out in the relevant CGIAR Centers CIP and IITA respectively In the case of potato virtually all of the components of an *in vitro* conservation scheme are in place including the widespread use of *in vitro* active storage by slow growth and *in vitro* exchange of germplasm (see MIX 1985 WITHERS 1989) However cryopreservation has not been developed to a level of reproducibility and wide applicability such that it could be recommended for use in a genebank

Over the last 10 – 15 years there have been a number of studies of the cryopreservation of potato shoot-tips and some notable advances made (see HENSHAW et al 1985 BENSON et al 1989 and references therein) These studies have highlighted the importance of achieving well-organized recovery and the necessity to carefully adjust culture conditions before and after cryopreservation Among the different studies there are significant variations in methodology and inconsistencies in response Nevertheless there is a substantial

foundation of work which if drawn together and combined with the advances made in recent years in the *in vitro* culture of potato and in cryopreservation in general would stand an excellent chance of success This would complete the portfolio of techniques for the *in vitro* conservation of what is both an important crop world-wide and an essential model for the application of *in vitro* conservation to other roots and tubers

Turning now to yam this can be propagated *in vitro* stored by slow growth and distributed in the form of cultures (NG & HAHN 1985) Techniques appear however to be less well developed and less widely practised than in the case of potato Cryopreservation of shoot cultures is untried that of a cell suspension of *Dioscorea deltoidea* is the only success on record for the genus (BUTENKO *et al* 1984) The development of *in vitro* conservation technologies for this crop would greatly benefit its safe conservation and wider more effective germplasm utilization

Yam is also of interest from another related point of view Conservation of germplasm does not involve a single problem and is not met by a single categorical answer. To try to apply just one approach to the conservation of a crop genepool is over-simplistic and sure to prove inadequate. There is a place for the appropriate application of *in situ* field genebank *in vitro* (both active and base) and seed conservation for a crop such as yam. Pollen storage and in due course. DNA storage should be considered also. The complementary application of these different storage technologies should in the first instance be determined on the basis of knowledge of the genepool the possibilities of seed production the need for access to the genepool at different points in time and the consequent degree of emphasis to be placed on gene versus genotype conservation. Superimposed upon this is the degree of security of the different storage modes and the level of development of the necessary technologies.

It is further suggested here that by designing a complementary conservation strategy according to knowledge of the genepool and conservation and utilization needs and assessing the fitness of current technologies to carry out that strategy we can identify the research that remains to be carried out in order to achieve safe and efficient conservation. Yam is considered to be a very suitable crop upon which to develop such a strategy in view of the balance of knowledge gained and still to be gathered and the susceptibility of its germplasm to a range of conservation technologies these factors being reinforced by the importance of yam as a subsistence crop in the developing world

For some other crops that are apparently well conserved including potato it is likely that revision of the balance of conservation technol-

ogies particularly between the storage of seeds and storage of clones would increase efficiency without hampering access to the genepool. In all cases continual revision of the balance of technologies with time would be beneficial to ensure that technological advances be incorporated and current user needs met

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FUNDAMENTAL ASPECTS OF PLANT REGENERATION

Hans-Jorg JACOBSEN

Germplasm conservation per se does not require sophisticated cell and tissue culture technology since methods of *in vitro* storage are based on the use of easily regenerable plant tissues like meristems. If however the genetic base in a given crop is limited due to extinction or loss of important material or if a certain trait (e g for a resistance or tolerance) is not available in the known accessions of a particular crop plant cell and tissue culture as well as molecular genetics may become a tool for selecting or creating new lines with the desired traits thus complementing the storage and evaluation of germplasm. The general methods for the transformation of plants nowadays are well developed. However apart from the characterization of important genes the regeneration of fertile plants from transformed or selected cell lines still remains a problem with a number of open questions.

In most if not <u>all</u> crop species *in vitro* regeneration is far from being a routine if a particular crop species can be transformed and regenerated there are always cultivars which cannot be regenerated or only with low efficiencies (generally the interesting ones) Therefore we have to consider an important genotype problem in many crops however <u>no</u> efficient *in vitro* regeneration protocol is known due to the recalcitrance of the crop

In addition with many crop species we can obtain <u>either</u> high regeneration <u>or</u> high transformation rates when using *Agrobacterium tumefaciens* as a vector for gene delivery. This implies considering alternative transformation technologies for most of the crop species. Although these alternative methods such as direct gene transfer to protoplasts or particle bombardment (to name the most promising ones) are already in use a critical point has to be made

Most attention for establishing transformation and regeneration protocols has been payed to crops relevant to the agriculture in developed countries with the exception of rice. So we lack particular expertise for crops relevant to developing countries. This requires a higher input of research efforts at the international level on plant regeneration including research aimed at a better understanding of fundamental aspects of plant biology i e plant developmental biology at the molecular level

It is clear now that the establishment of regeneration protocols based on trial-and-error approaches often is a waste of time money and.

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scientific labour since in most cases success is rather unpredictable So one has to ask how well basic research is embedded into international programmes on crop improvement and whether or not the necessity to link applied with fundamental research has been recognized A possible solution for this problem could be the cooperation of the International Agricultural Research Centers or laboratories in developing countries – where the crops and their specific problems are well known – with laboratories in industrialized countries where traditionally more research on molecular aspects of plant developmental biology is carried out

IN VITRO PROPAGATION OF YAM AND PER-SPECTIVES FOR ITS LONG-TERM CONSERVATION

Gunda MIX-WAGNER

Concerning *in vitro* preservation of plant genetic resources we are particularly interested in the root and tuber crops since storage of these species in the normal sense presents very great problems

At the Institute of Crop Science and Plant Breeding in Braunschweig we maintain an *in vitro* collection of 365 varieties and clones of potato and 40 genotypes of Jerusalem artichoke These varieties and genotypes can be stored for up to 2-3 years under minimal growth storage conditions

Recently we have begun to investigate *Dioscorea rotundata* (white yam) and *Colocasia esculenta* (cocoyam) The aim of our work is to develop a method for propagation and to test long-term storage conditions in order to create a way of maintaining collections of these species *in vitro* Up to now a number of research groups have been working with *Dioscorea* but only very few references have been published on work with *Colocasia*

In this paper I do not want to give a review of the available literature nor do I wish to give a description of the problems concerning these species instead I only wish to give a preliminary report on the first results of our work

In general the main problem working with tropical species is to get the plant material to start with We have got some tubers of *Dioscorea rotundata* from Ghana So we started the investigation of *in vitro* propagation with tuber tissue

Tuber explant cultures

Figure 1 (p 18) gives a schematic description of the procedure for taking tuber explants into culture. The tuber explants must have a piece of the outer skin. Solution A (150 mg citric acid and 150 mg ascorbic acid/l) is used to avoid oxidation/blackening of the tissue. Solution B (fungicide 5.3 g Benomyl/l and 3 handfuls of wood ashes) is added to eliminate fungi. Adding solution C (1 % Ca-hypochlorite) is the common method to sterilize the tissue.

tuber ↓ cutting the tuber explants in solution A ↓ disinfection of the tissue shaking the explants in solution B for 60 minutes ↓ surface sterilization shaking the explants in solution C for 20 minutes ↓ rinsing the explants several times in solution A ↓ planting the explants on the different media and substrates ↓ placed in culture room 16 h light 25 C temperature

Figure 1 A schematic description of the procedure for taking tuber explants into culture

The two culture media used are based on MURASHIGE & SKOOG s basal medium but half concentrated Medium 1 is supplemented with 0.01 mg/I NAA 3.5 mg/I zeatine 30 mg/I cysteine 40 mg/I adenine sulfate and 20 g/I sucrose and medium 2 with 2.0 mg/I BA and 20 g/I sucrose The media were tested as solid media supplemented with agar and as liquid media with rock wool or Perlite to support the explants

The preliminary results are summarized in Table 1 The elimination of the fungi and bacteria was much more successful when solution B in combination with solution C was used rather than solution C alone It was much easier to obtain sterile tuber material of *Colocasia* than of *Dioscorea* after the treatment Without the use of solution A to avoid blackening all yam tuber explants turned brown The cocoyam tuber explants which were kept in solution A all the time showed nearly no blackening of the tissue

Looking at the regeneration figures it is not difficult to recognize that the explants cultured on rock wool or Perlite (liquid medium) showed a much higher rate of plantlet production than on agar The Colocasia tuber explants showed a much better growth rate on medium 1 than on medium 2 For white yam it was just the other way round The explants cultured on medium 1 were able to regenerate more plantlets

<u>Table 1</u>	Preliminary	results	of	the	propagation	of	white	yam	and
	cocoyam								

	Contamination		Blackening		Plantlet Regeneration			
	Solution B + C	Solution C	Control	Solution A	solid medium	lıquid medium		
white yam	60 %	95 %	100 %	10 %	med 1 30 % med 2 3 %	40 % 5 %		
coco- yam	40 %	80 %	80 %	2 %	med 1 10 % med 2 30 %	55 % 90 %		

Next Steps

The next steps of our investigations will be the development of plants from different tissues (e.g. explants from leaves stems veins) and research on the composition of the culture media for each tissue. The aim is to get as many shoots as possible out of one explant

Perspectives for the Long-Term Storage Method

Here the aim is to make the sub-culture intervals as long as possible for the maintenance of the germplasm. The following factors have to be tested to find out the best conditions for minimal growth storage

- environmental conditions
 - * temperature
 - * day length
 - * light intensity
- culture conditions
 - * solid/liquid media
 - * addition of different compounds e g mannitol growth retardands
- plant material
 - * plantlets micro tubers

PROTOPLAST FUSION AS A TECHNIQUE IN BREEDING OF POTATO AND OTHER TUBER CROPS

Lieselotte SCHILDE-RENTSCHLER & Helga NINNEMANN

Potato

Symmetric Protoplast Fusion

In 1974 when the first successful somatic hybrids were obtained by protoplast fusion (MELCHERS *et al* 1974) the utilization of this method for breeding purposes was emphasized

The modern cultivated potato is a highly heterozygous tetraploid crop Therefore breeding is difficult and time consuming Modern potato breeding takes advantage of the possibility to breed at the diploid level To reach the tetraploid level again WENZEL in 1979 already recommended the use of protoplast fusion Protoplast fusion allows the combination of two dihaploid clones selected for different traits without the rearrangement step of meiosis This is especially important for the combination of quantitatively inherited traits

Successful somatic hybridization was reported for wild species with cultivated potato (BARSBY et al. 1984 HELGESON et al. 1988 PEHU et al. 1989) and a limited number of dihaploid breeding lines which were chosen because of their good response in cell culture (KARLSSON et al. 1988 DEIMLING et al. 1988 MASSON et al. 1989) But only recently the method of protoplast fusion is entering potato breeding programmes. The problem was to develop conditions which allow to isolate and culture protoplasts and regenerate plants for any breeding line routinely.

The purpose of our project was the development of techniques for the application of somatic hybridization of regular dihaploid breeding lines including efficient fusion methods and identification of hybrids Breeding lines of four different companies and institutions were utilized A procedure was established which allowed to obtain plant regeneration from protoplasts for almost all breeding lines tested Optimizing electrofusion conditions resulted in fusion rates for double-fusion of 10-20 % routinely (SCHILDE-RENTSCHLER & NINNEMANN 1988) For the identification of hybrids isoenzyme analysis and RFLPs of the regenerating plants were used utilizing r-DNA-probes and non-radio-active labeling with dioxigenine (SCHWEIZER & HEMLEBEN 1988) In most cases digestion with one restriction enzyme gave sufficient information to discriminate the partners (Table 1)

<u>Table 1</u> Determination of the most appropriate restriction enzyme for the identification of somatic hybrids of different breeding lines and wild species

For each clone combination the enzyme was chosen which gave typical bands for each of both partners. The r-DNAs pRZ 52 and pRZ 83 (HEMLEBEN et al. 1988) were utilized as probes. A behind the pRZ-number means that one partner can be excluded only

combination of clones	restruction enzyme (probe pRZ 52 and pRZ 83) PSTI					
	EcoRV	Dral	BamHI	Dral	Nsi	
R12		52				
1516			52			
1520		52				
1523		52		83		
1216		52				
0412		52				
0616		52	52			
0111				83		
0319		52 A		83 A		
R1V1		52		52	83	
R1V2		52		52	83	
0208				83		
0319			52			
Ngrl	52					
Nneor		52				
Nspars		52				

More than 150 hybrids including 21 different breeding lines 3 wild species and 16 combinations were identified (Table 2 p 22) This material has been propagated in vitro and a sample sent to the breeders They have been increasing the clones in the greenhouse With the tubers obtained the evaluation of agronomic traits and resistances will be carried out in the field this year

As reported for other somatic hybrids we also found segregation of chloroplasts in somatic hybrids (Table 3 p 22) In most cases analysed so far a hybrid plant is provided with the chloroplasts of only one partner. The situation for mitochondria has not yet been studied in a further project we will investigate the influence of the cytoplasmatic organells on the agronomic traits of the hybrids. <u>Table 2</u> Somatic hybrids Number of different hybrids of 19 breeding lines and two wild species time of regeneration and % of abnormal plants for the different combinations are listed. For the regenerates marked with * different feeding cultures were utilized

combination of lines	number of colonies analyzed	regeneration time (months)	number hybrids	% hybrids	% abnormal
R12*	390		21	54	50
R1V2	185	2-4	4	22	0
R1V1	167	2	0	0	
W1821*	ca 210	6	4	19	25
1520	209	4	28	13 4	50
0412	28	3	6	21 4	16 7
1523	127	2	3	24	
0111	113	2	28	24 8	04
0208	13	3	2	15 4	0
1516	116	3	30	25 9	32
0616	100	3	1	10	0
0106	113		0	0	
1216	137	2	16	11 7	12 5
N neor	13	3	9	69 2	11 1
N spars	11	6	5	45 5	0

<u>Table 3</u> Distribution of chloroplasts in somatic hybrids. In the case of R12* chloroplast–DNAs of both partners were present in the first test that of R2 in less concentration. After several cycles of propagation only chloroplast–DNA of R1 could be detected

	number of hybrids with chloroplasts of					
combination	partner a	partner b	partner a + b			
R12	0	5	1			
R1V2	3	0	1			
W1821	3	2	0			
0412	2	2	1			
Nneor	2	5	1			

Cybridization

Another area for which protoplast fusion can be used is the induction or removal of male sterility. On the one hand male sterility is wanted for potato production from true seed on the other hand it is an obstacle for breeding. It is caused by nucleus-cytoplasm interaction. Therefore fusion of one partner protoplast of which the cytoplasm was inactivated with protoplasts of the partner in which the nuclei were inactivated leads to so-called cybrids with new nucleus-cytoplasm combinations (donor-recipient technique ZELCER et al 1978) In Table 4 (IWANAGA pers communication) selected dihaploid breeding lines with specific valuable traits from CIP are listed. One of these shows good resistance to potato virus Y the other one to both potato leaf roll virus and virus Y These resistances were introduced from the wild species Solanum stoloniferum The interaction of S stoloniferum cytoplasm with S tuberosum nuclear genes leads to male sterility. These clones therefore cannot be used as pollen donor. By combination of the hybrid nucleus with different cytoplasms using the donor-recipient technique we should be able to overcome this crossing barrier

(IWANAGA personal communication)						
cross nu	mber	resistance	cytoplasm	nucleus		
V-3 2B			sto	tbr		
V-3 30		PVY PLRV	sto	tbr		

Table 4 Dihaploid breeding lines from CIP's breeding programme

Asymmetric Protoplast Fusion

The utilization of germplasm resources for breeding purposes is very limited mainly because of the drawback in breeding level which is caused by the incorporation of the complete genome of the wild species or primitive cultivar. In a future project we are trying to transfer parts of a genome only by asymmetric protoplast fusion

Other Tuber Crops

We are going to use the experience gained with potato in protoplast work for other crops one is sweet potato. As can be seen from Figure 1 (p 24) crossing barriers exist between different relatives of

sweet potato Protoplast fusion could help to overcome these barriers and make the valuable traits in the related wild species available for breeding

A-group	X-group	B-group
self-compatible	self-incompatible	self-incompatible
I triloba group triloba (AA) lacunosa (AA) ramoni (AA) trichocarpa (AA]-[I tiliacea (4x)] [I gracilis (4x)])]	I batatas group - leucantha (BB) - littoralis (BBBB) - trifida (6x) (BBBBBB) batatas (BBBBBB)

Figure 1	Sexual	compatibility	relationships	in i	Ipomoea	batatas
	section	batatas (NISH	HIYAMA I 19	982	p 267)	

Legend ____ compatible incompatible

The other crops we may be working with are the tuber bearing crops of the Andes besides potato Mainly three species exist which are important for the people in the highlands in South America Ullucus tuberosus Oxalis tuberosa Tropaeolum tuberosum Lately the germplasm which is still available is being stored in an *in vitro* genebank at San Marcos University in Lima Peru by R ESTRADA and his group We maintain a small sample of this collection in our laboratory No breeding has been carried out with these crops The Peruvian scientists are interested in using protoplast technology to increase variability since fertility is very low or nil. In preliminary experiments with Ullucus tuberosus we found that protoplast isolation and cultivation seems to be no major problem. Plant regeneration has not yet been carried out

In conclusion it can be said that in the case of potato protoplast fusion may help to utilize genetic resources more easily and to shorten the breeding process. What has been elaborated for potato should also be possible for other less developed but – on a world scale – more important crops with similar problems. If comparable effort is invested

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CRYOSTORAGE OF PLANT MATERIAL

Ursula SEITZ

In the course of work with *in vitro* cultures of plants the necessity has arisen for efficient storage methods. This is particularly obvious in the case of cell suspension cultures that typically need to be transferred to fresh media every seven to ten days or in the case of shoot-tip cultures that are used for establishing germplasm banks in order to preserve the material over long periods of time

Cryopreservation i e storage at the temperature of liquid nitrogen is regarded as being the most suitable method for these purposes. As far as we know the characteristics of plant cell cultures do not change during cryopreservation treatment. This point will be discussed on the basis of biochemical capacities.

The cryopreservation protocol used in our investigations corresponds with the method published by WITHERS & KING (1980) it comprises the following steps preculture in media supplemented with osmotically active compounds (mannitol sucrose etc.) treatment with cryoprotective agents slow freezing storage at -196 C rapid thawing and post-thaw treatment and recovery growth Examples are presented here to show the possibilities of modifying this method and adapting it to various cell cultures. More than 20 different species have been sucessfully cryopreserved during these studies.

The preculture treatment is found to enhance freeze tolerance markedly The physiological events during this phase have not yet been investigated thoroughly but this treatment seems to induce a process which resembles stress hardening in the course of our studies we investigated the influence of several preculture additives on cell viability and freeze tolerance

The applicability of cryopreservation for storing meristems of important plant species and crop varieties will be discussed briefly on the basis of the literature published in this field

Conservation of Plant Cell Cultures with Special Characteristics

Daucus carota

Cells of an Afghan variety of *D* carota accumulate large amounts of anthocyanin The anthocyanin content of a culture which had been

frozen was compared with that of a control which had not The maximum values and the accumulation kinetics were both identical This is in complete agreement with the results published by DOUGHALL & WHITTEN (1980) who investigated the anthocyanin content in frozenthawed carrot cells for the first time

<u>Digitalis lanata</u>

Cultivated cells of *D* lanata do not synthesize cardenolides de novo but they are able to transform added cardenolides (biotransformation) A typical reaction is the 12β -hydroxylation of β -methyldigitoxin Cryopreserved and control cultures showed the same time course in β -methyldigitoxin production (SEITZ et al 1983) Moreover the final yields were also identical This was also valid after long-term storage (up to 4 years) Thus cell lines that have been selected for high productivity can be maintained in the frozen state

In this series of experiments two other plant species were investigated *Coleus blumei* (rosmarinic acid REUFF et al 1988) and *Panax* ginseng (ginsenosides SEITZ & REINHARD 1987) A summary of plant cell cultures that have been investigated after cryostorage with regard to biochemical capacities is given in Table 1. All of the frozen-thawed cultures mentioned there have been proved to retain their biochemical characteristics

Species	Natural Compound	Reference
Catharanthus roseus	indole alkaloids	Chen et al (1984)
Chenopodium rubrum	betalaines	Ziebolz & Forche (1985)
Coleus blumei	rosmarinic acid	Reuff et al (1988)
Daucus carota	anthocyanın	Dougall & Whitten (1980) Seitz et al (1985)
Dıgıtalıs lanata	cardenolides (biotransformation)	Diettrich et al (1982) Seitz et al (1983)
Dioscorea deltoidea Eschscholtzia	steroids benzophen-	Butenko et al (1984)
californica	anthridines	Ziebolz & Forche (1985)
Lavandula vera	biotin	Watanabe et al (1983)
Panax ginseng	ginsenosides	Seitz & Reinhard (1987)
Papaver bracteatum Thalictrum rugosum	chlorophylles Isoquinolin-alkaloids	Ziebolz & Forche (1985) Ziebolz & Forche (1985)

<u>Table 1</u> Freeze preservation of cell cultures with specific biochemical capacities

Cryopreservation Protocol

Many reports have shown that plant cells are only able to survive freeze-thaw processes if they have passed through a preculture treatment in a medium with enhanced osmolarity Consequently optimization of the protocol would always start at this point

Cell_Viability_during_Preculture_and_Effectiveness_of_Various Additives

Digitalis lanata cultures were used for an extensive study of this subject Digitalis cells grown in normal culture medium showed only negligible changes in their viability rates over a 3-day period As a consequence of preculture treatments the viability curves were characterized by a marked decrease during the first 24 hours. This was valid for trehalose mannitol sucrose and proline (Fig 1) and also for sorbitol (data not shown) The reduction in viability was transient in all cases where the cells were able to tolerate the treatment (trehalose mannitol sucrose melibiose) We consider this behaviour to be a consequence of stress which was then compensated for by adaptation to the enhanced molarity of the medium A more prolonged decrease in viability the production of phenolic compounds and a browning of the culture were observed in the presence of proline or sorbitol

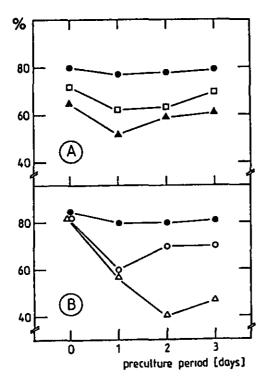


Figure 1

Viability of Digitalis lanata cells during a 3-day preculture period Concentration of preculture additives 0 3 M Fluorescein diacetate was used for viability tests

- A control sucrose •
 - mannitol 🔺
- B control trehalose • proline △

In a further series of experiments we investigated the influence of several preculture additives on the freeze tolerance of *Digitalis* cells Besides the compounds which are commonly used as preculture additives such as mannitol we directed our attention to compounds which are accumulated in plants under stress conditions such as proline. The best results were obtained when trehalose or mannitol were used (Fig 2) The post-thaw viabilities were 66 % and 53 % respectively Furthermore the cells were able to resume growth after a short lag period. This is just one more example which demonstrates the broad applicability of mannitol. Melibiose and sucrose were equally effective with *Digitalis* cultures. Neither proline nor sorbitol proved suitable for this culture even though post-thaw viability was about 40 %. In both cases the cells were not able to resume growth.

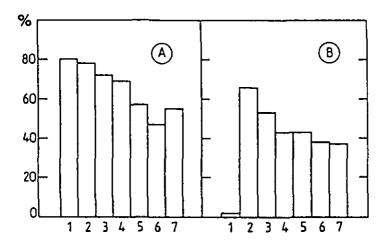


Figure 2 Viability (fluorescein diacetate) of *Digitalis lanata* cells at the end of the preculture period (A) and immediately after thawing (B) The following preculture additives (0 3 M) were used (2) trehalose (3) mannitol (4) sucrose (5) melibiose (6) proline (7) sorbitol (1) represents the control

Cryoprotectant Treatment

Without exception plant cells require chemical cryoprotection Mixtures are reported to be more suitable than single compounds DGS a mixture containing DMSO (0.5 M) glycerol (0.5 M) and sucrose (1.0 M) has been used successfully for a large number of species (WITHERS 1985) On the other hand we have found that with more than 10 different species including D lanata and P ginseng good results can be achieved with sucrose (1.0 M) as the sole cryoprotectant The replacement of DMSO by 1 2-propandiol a treatment successful with recalcitrant seeds (BOUCAUD & CAMBECEDES 1988) was investigated using two Atriplex species (PGS Table 2) PGS and DGS proved to be of equal efficacy in terms of post-thaw viability. The general applicability of this compound however should be confirmed using other plant species

<u>Table 2</u> Comparison of two cryoprotectant mixtures in freezing experiments with Atriplex litoralis and A hortensis. The percentage of viable cells was determined using fluorescein diacetate (A) at the end of preculture (B) after 1 h cryoprotection (C) immediately after thawing DGS DMSO glycerol sucrose PGS 1 2-propandiol glycerol sucrose

Species	A	B		С		
		DGS	PGS	DGS	PGS	
A litoralis	92	80	78	54	52	-
A hortensis	94	80	82	52	47	

The freezing regime storage conditions thawing and post-thaw treatments were as described previously (SEITZ & REINHARD 1987)

A list of plant species that have been cryopreserved in the form of cell cultures in our laboratory is shown in Table 3. Only those cultures are registered that are able to grow after they have passed through a freeze-thaw cycle

<u>Table 3</u> Plant suspension cultures successfully cryopreserved (Tubingen 1989)

(Chenopodiaceae) (Chenopodiaceae) (Chenopodiaceae)
(Chenopodiaceae)
(Lamiaceae)
(Apiaceae)
(Scrophulariaceae)
(Scrophulariaceae)
(Araliaceae)
(Apiaceae)

13 species from the following families

Acanthaceae Alzoaceae Apocynaceae Celastraceae Convolvulaceae Oxalidaceae Papaveraceae Sterculiaceae

Cryopreservation of Meristems and Shoot-Tips

Until now I have concentrated my interest on plant cell cultures. To give an impression of what has been done in the field of meristems. I have compiled a list of published work (Table 4)

Table 4 Cryopreservation of meristems/shoot-tips

Species	Reference	
Arachis hypogaea	BAJAJ (1979 1983)	
Beta vulgaris	BROWN (1988)	
Brassica napus	WITHERS et al (1988)	
Cicer arietinum	KARTHA & GAMBORG (1978)	
	BAJAJ (1979–1983)	
Dianthus caryophyllus	SEIBERT (1976)	
	SEIBERT & WETHERBEE (1977)	
	UEMURA & SAKAI (1980)	
	DEREUDDRE et al (1988)	
Digitalis lanata	DIETTRICH et al (1987)	
Fragaria x ananassa	KARTHA et al (1980)	
	SAKAI et al (1978)	
Malus domestica	KATANO et al (1983)	
Manıhot esculenta	KARTHA et al (1982)	
	BAJAJ (1985)	
Pisum sativum	KARTHA et al (1979)	
Rubus spectabilis	REED (1988)	
Solanum etuberosum	TOWILL (1981)	
S goniocalyx	GROUT & HENSHAW (1978)	
S tuberosum	BAJAJ (1985)	
	GROUT & HENSHAW (1978)	
	TOWILL (1983–1984)	

In many cases the regeneration of plantlets or plants has been reported but it is not always clear whether the organised growth originated directly at the meristematic part or if a callus phase was included. This is an extremely critical point for example in the case of potato since growth in the dedifferentiated state bears the risk of genetic instability. Bearing this in mind. I believe that it would be useful to investigate the cryopreservation of meristems using the following three approaches

- 1) Cataloguing Collection of all data available concerning cryopreservation of meristems (shoot-tips) Literature and unpublished work
- 2) Screening Intensive investigation of one or two important species (for example potato) with as many cultivars as possible with the aim of establishing a generally applicable protocol investigation of the regeneration potential and organised growth Avoidance of the callus phase
- 3) Plant Physiology The aim is a better understanding of freeze adaptation in nature accumulation of sugars accumulation of compatible solutes role of abscisic acid etc Such knowledge could help us to find appropriate treatments

My co-workers during this project were Eva M GÖLDNER Doris BANSPACH and Ingrid REUFF The experiments were performed at Pharmazeutisches Institut University of Tubingen Auf der Morgenstelle 8 W-7400 Tubingen FRG

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REPORT OF THE PLENARY DISCUSSION CROP STRATEGIES FOR ROOTS AND TUBERS

Results and recommendations

Lindsey A WITHERS

Clonally propagated crops including a number of roots and tubers of importance as staple foods in developing countries present serious problems in the achievement of their satisfactory genetic conservation Resolution of these problems would have significant human benefits The working group gave particular attention to potato as a relatively well-researched example in this category and to yam as a neglected one but other examples include sweet potato cassava cocoyam and taro

The genetic conservation of these crops relies heavily upon the use of the field genebank a conservation method which is expensive insecure in a number of respects and difficult to manage to adequately high standards The most serious deficiency for clonal crops is the lack of a true base storage method comparable to the low temperature storage of orthodox seeds The development of *in vitro* technologies is seen to offer many opportunities for improvement in the conservation of clones (including conservation under base storage conditions by cryopreservation in liquid nitrogen) for their safe movement in diseasefree form and in due course their genetic improvement through biotechnological approaches

In terms of the development of *in vitro* conservation technologies potato is clearly the more mature crop of the two under consideration All components of an *in vitro* conservation strategy are in place with the exception of cryopreservation. A number of research efforts carried out from the mid-1970 s yielded results that indicated the feasibility of cryopreservation for potato shoot-tip cultures but did not achieve a sufficient level of success in terms of breadth of applicability or consistency to encourage further development. Nevertheless potato remains one of the crops for which cryopreservation has appeared the most promising. The working group expressed the view that the diverse and discontinous threads of the past studies could fruitfully be pulled together to devise a programme of research that would capitalize upon the experience gained in those studies and draw upon the better knowledge that now exists in relevant areas of *in vitro* culture and cryobiology. Yam a clearly less mature crop from the point of view of its *in vitro* conservation and other aspects including knowledge of the genepool provided the working group with the opportunity to discuss some wider issues in the genetic conservation of clonal crops. Conservation targets include both genes and genotypes. For this reason seed conservation where possible has an important part to play as a means of conserving genes in their own right and as a back-up to clones. Study of the genetic diversity of the crop genepool and the extent to which seed induction is possible would reveal the scope for taking this option and the need for further research to induce seed production. For clones a balance should be struck between slow growth and (when available) cryopreservation. Among the factors to consider here are feasibility safety and accessibility.

A complementary conservation strategy that is based on a knowledge of genetic diversity and that is designed with the emphasis on needs rather than incidentally available technologies should be the objective for clonal crops. Moreover, where a distribution of sectors of the genepool of a crop e.g. potato or cassava has been based on criteria that are now out-of-date a revision along the lines suggested here would contribute to the safer more efficient genetic conservation of the crop. Tasks of routine management and safety duplication might also be eased

Of the areas of research discussed by the working group the highest level of interest and the strongest basis for collaboration in terms of experience and facilities available emerged for the refinement of cryopreservation techniques for potato Drs G MiX L SCHILDE H M SCHUMACHER and U SEITZ expressed willingness to participate in such a collaborative effort Completion thus of a package of *in vitro* conservation technologies for potato would have an immediate application for the crop itself implementation can be foreseen in national programmes and the relevant International Center (CIP) Additionally it would add to the knowledge base on cryopreservation to the benefit of other clonal crops including the neglected yam

Although one specific initiative is highlighted here it is felt that it could provide the foundation for a more extensive longer-term involvement of *in vitro* conservation technologies for problem crops with associated opportunities for collaboration with developing country scientists and for training and technology transfer

Part II

Genetic Diversity

GENETIC DIVERSITY - INTRODUCTION

Alison McCUSKER

You will recall from my brief description of the IBPGR Research Programme that genetic diversity studies constitute a substantial part of it Half the staff are working in this area although we have not yet built up a comparable level of funding in our core budget That is one reason - the main reason - why we are giving some prominence to diversity pioposals in seeking special project funding

Genetic diversity is a very crucial concept in genetic resources conservation and is very relevant to most aspects of the work of IBPGR. It is in fact exactly what the IBPGR programme is all about

Let me take you back to the three basic questions

- What germplasm should be collected?
- What is the best way to conserve it?
- How can we make it an effective global resource?

There are problems in each of these three areas that can only be resolved by increasing our understanding of genetic diversity which is relevant to deciding

- how much material should be collected
- where and when it should be collected and
- how to plan the collecting programme so as to <u>supplement</u> rather than <u>duplicate</u> what has been collected before

A knowlege of the diversity of germplasm is also important for developing good management practices in genebanks - to determine for example

- how many of the accessions are in fact duplicates or nearly identical genetically
- whether gradual loss of viability of seeds is resulting in random loss of variation or selective loss i.e. whether there are selection pressures at work in the genebank eroding the variation we have so diligently collected
- how best to sample seeds from an accession for regeneration or distribution to users or
- how to ensure that in vitro conservation techniques are effective for long-term conservation

The measurement of genetic diversity is therefore a very important matter for IBPGR Many advances in basic research in this field have been made by the research community in recent years and there is a clear advantage for IBPGR to follow these developments closely and to ensure that new methods are improved and adapted for application in the genetic resources management context

Genetic diversity is a topic which creates an interface between two well-established fields of study namely genetics and ecology

I suppose you are aware that *in situ* conservation of genetic resources (or of biodiversity more generally) has recently received widespread attention by scientists and the general public IBPGR has not been involved directly in *in situ* conservation but in 1988 we signed a Memorandum of Understanding with the World Conservation Union IUCN agreeing on cooperation to further all matters of mutual interest to the two organizations in areas such as

- ensuring the compatibility of our programmes
- exchanging information and scientific data
- developing joint activities or
- working together on field activities as appropriate

It is in the area of genetic diversity studies that we believe there is much common ground between *ex situ* and *in situ* conservation and therefore between IBPGR and IUCN For example the same type of information about the distribution of genetic diversity in the field is necessary to plan collecting strategies and to select *in situ* conservation reserves. Moreover, the problems of conserving diversity and the effects which management practices might have on reducing it over time are probably just as great in the field as they are in the genebank and a thorough understanding of them is necessary to ensure long-term conservation by either method

Our present intention in IBPGR is not to become involved with in situ conservation directly but to aim for stronger collaboration with in situ conservation programmes to ensure a fully integrated approach to the conservation of crop genepools

Genetic diversity research as relevant to germplasm conservation involves some fairly new and important concepts and it is timely therefore for us to base a full day of our discussions on this topic

GENETIC VARIATION IN CROP SPECIES AND THEIR WILD RELATIVES A VIEWPOINT FOR THEIR CONSERVATION

Daniel G DEBOUCK

Introduction

The mandate of the International Board for Plant Genetic Resources (IBPGR) is to conserve the genetic diversity of useful crop species for present and future uses of plant breeders and agronomists (ANONY-MOUS 1988) Being a centre of the Consultative Group on International Agricultural Research (CGIAR) its activities of research are related to germplasm collection characterization evaluation conservation and distribution as particular problems arise or as particular needs are expressed by the other CG centres for their commodity crops by national programmes worldwide and by the scientific community in plant genetic resources (PGR) in general I shall deal with some aspects of the raw material we are working with that is the genetic variation in crop species and their wild relatives dealing successively with some characteristics of genetic variation stressing on the interest of wild relatives of crops as part of this genetic variation suggesting eventually what could be an approach to conserve the genetic variation in order to fulfil IBPGR s mandate. I will also enlist some of the areas of research where collaborative work might be particularly fruitful as it will appear evident that only strong collaborative work can cope with such a huge task

Characteristics of Genetic Variation

It would be vain to give a short definition of genetic variation in crop species as there might be as many definitions or interpretations of that phenomenon as living organisms we can observe around us. There are however some attributes of genetic variation I shall illustrate with some examples as they orient our current activities for conservation. Genetic diversity soon appears as unique indivisible dynamic and of unpredictable value

Uniqueness is perhaps best illustrated by genes of disease resistance in cereals where a stable resistance is often the result of a long builtup process of unique genes (CAUDERON et al 1973 DINOOR 1975 MOSEMAN et al 1984 PLUCKNETT et al 1987) and as observed by HARLAN (1978) a single gene can make the difference once you have found it As methods of easier gene transfer exist or will arise soon (protoplast fusion genetic engineering) gene identification and availability will turn out to be the crucial questions. This is the reason why germplasm collections *ex situ* or *in situ* which are well-studied and maintained and variable enough are so important.

I shall illustrate the fact that genetic variation in crop species is indivisible and dynamic by the following examples. It is often difficult to draw the line between the wild relatives and the crop species with accuracy most of our tree species can still be viewed as wild plants with a modified fruit. The same statement is also valid for several herbaceous crops where the difference between the wild and the cultivated just depends on a couple of genes the translation of which into the phenotype has a very spectacular effect (GEPTS & DEBOUCK in press) Perhaps another illustration is found in the wild-weed-crop complex (HARLAN 1975) where a continuous gene flow between the wild and cultivated forms occurs which consequently leads to the genetic enrichment of both the wild and the cultivated materials (Table 1) This flow however is rare today (but of high significance for the future evolution of the crop and thus worth conserving and also in order to understand past events) as crops often are no longer in biological contact with their wild progenitors

Table 1	Reports of	the presence of the	wild-weed-crop complex
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Crop species	Place	Reference
Chickpea	Karahbace Turkey	VAN DER MAESEN (1973)
Chili peppers	Central America	PICKERSGILL (1971)
Common bean	Junin Cuzco Peru	DEBOUCK et al (1989)
Lima bean	Cajamarca Peru	DEBOUCK et al (1987)
Maize	Huehuetenango Guatemala	WILKES (1977)
Potato	Potosi Bolivia	HAWKES (1977)
Rice	India and Thailand	OKA & CHANG (1961)

It seems very difficult to predict what will be the economic value of a very ordinary trait – and its genetic basis – over long periods of time Let us illustrate this observation with a few examples

 H S GENTRY curious about plant evolution collected wild beans in Mexico in the 1960s (GENTRY 1969) SCHOONHOVEN and coworkers observed that only the wild beans were resistant to bean weevils but the cultivated beans were not (SCHOONHOVEN et al 1983) This resistance is due to the presence of a particular seed protein variant (OSBORN 1988) unevenly distributed in the wild bean populations (OSBORN et al 1986) and not necessary for their survival (DEBOUCK 1989)

- Gossypium thurberi TOD is a wild cotton distributed in Arizona Sonora and western Chihuahua (ANONYMOUS 1968) It has no lint however it gave lint strength to the upland cotton (HARLAN 1976)
- Lycopersicon hirsutum a wild tomato from Ecuador and Peru has greenish fruits (RICK 1979) however it brings higher contents of B-carotenes into the cultivated tomato and thus more colourful fruits (LATERROT 1989)

Again with tomatoes RICK (1976) mentions the case of transgressive variation where progenies of interspecific crosses outyielded expectations in comparison to the normal behaviour of the parents But this possibility has been little exploited so far

Interest in the Wild Relatives of Crops

As sources of agronomical characters in addition to the previous examples some reviews on this subject have been made (HARLAN 1976 HAWKES 1977) and one can see that there is practically none of the important crops where wild germplasm has not been used during the last sixty years (GOODMAN et al 1987) Some legume species have been left out but even there breeding approaches are changing (HARMSEN et al 1987) Breeders are thus progressively looking for interesting genes beyond the primary genepool that is the cultigen and its immediate wild relative(s) (HARLAN & DE WET 1971) This has been particularly true so far for the cultivated species of Poaceae (e.g. Triticale CAUDERON 1981) and Solanaceae (PATERSON et al 1988) but will probably be extended to other plant families As the lifespan of a plant variety is expected to be shorter and as integrated pest management procedules are to be extended due to increasing costs because of pollution one could reasonably expect an increasing use of alien germplasm in the next decades (PRESCOTT-ALLEN & PRES-COTT-ALLEN 1983 WILKES 1984)

As tools to understand evolutionary problems in crop species This is perhaps a less frequent use of the wild relatives of crop species by which we try to answer the following questions

- How did that particular crop arise?
- What is the amount of genetic diversity present in the crop versus in the whole plant species?
- Has the crop gained/lost additional genetic diversity during the course of the domestication process?

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- How have the genepools evolved and which are the consequences for future breeding?

A recent example of this use has been given with *Phaseolus* beans where the origin of each cultigen has been established Until recently only four cultigens were usually referred to in literature (LEON 1987) but lately a fifth cultigen has been reported (DEBOUCK *et al* 1990) With the use of biochemical markers it has been possible to give a comprehensive explanation for apparently divergent data compiled from morphology and archaeology showing that genetic variation present in the cultivars is organized in genepools

 for the common bean 	DEBOUCK & TOHME (1989)
- for the lima bean	GEPTS et al (1986) DEBOUCK et al (1989)
	MAQUET et al (1990)
 for the tepary bean 	DEBOUCK (1989)
	SCHINKEL & GEPTS (1988)
 for P polyanthus bean 	DEBOUCK et al (1990)
	SCHMIT & DEBOUCK (in press)

Similar findings have also been reported for rice (SECOND 1986)

These studies also allowed to improve our knowledge about the fraction of genetic diversity that has or has not been included during the domestication process A good appraisal of that balance – also known as founder effect (LADIZINSKY 1985) – is of definite importance when deciding about which part of genetic diversity should be collected/conserved particularly as far as the wild germplasm is concerned

<u>Table 2</u> Quantitative estimation of the founder effect in *Phaseolus* beans by the number of variants in seed proteins

Sp	ecies	Zone	Wild/	Cult	Reference
P P	vulgarıs vulgarıs	Mesoamerica Andes	16 13	2 7	GEPTS et al (1986) DEBOUCK & TOHME (1989)
P	lunatus	Mesoamerica	7	2	MAQUET et al (1990)
P P	lunatus acutifolius	Andes Mesoamerica	5 25	4 2	MAQUET et al (1990) SCHINKEL & GEPTS (1988)
P	polyanthus	Mesoamerica	25 6	4	DEBOUCK et al (1990)

Similar observations about a reduction of variability during domestication have been done in other crops (chili peppers PICKERSGILL 1971 rice ENDO & MORISHIMA 1983 tomato RICK 1983) Out of the four conclusions reached by GOODMAN (1988) about the origin of maize three involved a certain kind of founder effect But it is certainly too early to conclude about a general applicability of this concept to most of our crops and much more detailed studies are needed (BROWN 1978) As there are still many evolutionary problems unsolved even for some of the most common crops (e g maize peanut) one could expect an increasing use of their wild relatives since they can be used as geographical markers (GEPTS 1990)

These studies - and many others particularly with the help of isozymes (wild barley NEVO et al 1979 wild bean KOENIG & GEPTS 1989 wild oat HAMRICK & ALLARD 1972 wild tomato RICK & FOBES 1975) also showed that the genetic variation is not uniformly distributed in a crop species spatially speaking that is some alleles are only regionally distributed. It is tempting to think also about an uneven distribution of the alleles in time that is a variation from one year to another in certain populations according to their size as it is influenced by stresses (drought etc.) but evidence is still scarce. One can note that the evidences accumulated so far give rather a qualitative picture than a complete quantitative one of the allele distribution over the whole range of distribution of the wild relative of a crop species and its derived cultigen and on a reduced number of them too (HAMRICK et al 1979) A last point worth commenting is the likely influence of breeding systems and their variation on the genetic structure of natural populations (ALLARD 1975 BROWN 1978 HAMRICK et al 1979) an accurate knowledge of which seems to be a prerequisite for adequate regeneration and in situ conservation as well

Towards a Strategy for Conservation

Once we have considered these attributes of the genetic diversity of crop species we must conclude that we cannot separate the cultigen(s) from their wild relative(s) and that we have to consider them together in a broader conservation strategy

Some sort of germplasm exploration for using the PGR has been practised perhaps before the beginnings of agriculture during the plant gathering phase (REED 1977) But germplasm exploration for conservation (and this aspect is usually secondary to the utilization of germplasm) has been carried out on a large scale only during the course of this century This was due to an increasing awareness of the benefit of using more plant species and varieties (HARLAN 1984 SMITH 1986) and of the narrow genetic basis of plant varieties (ANONYMOUS 1972 HARLAN 1975) VAVILOV and his team launched a very broad programme – some seventy expeditions and 400 research institutes – for the collection and study of PGR (HAWKES 1990) and this task was the starting point of hundreds of explorations around the world IBPGR recently helped in the collection of 170 000 additional samples for more than 130 species (PLUCKNETT et al 1987) principally focused on the land races and old varieties progressively wiped out by modern cultivars However it seems that the crop genetic diversity will perhaps never be completely collected and that the ex situ conservation will not be that kind of total food insurance contemplated at the beginning

Faced with increasing genetic erosion and pressures on natural resources (MYERS 1983) several ways of conserving diversity in plant organisms have now to be considered. Although some kind of achievements can already be claimed for securing the land races of the most important crops (PLUCKNETT et al. 1987) – but could it stand the comparison with VAVILOV s enterprise? – for the wild relatives there is still a long way ahead of us that could be oriented at

- defining the primary and secondary genepools of the different crops
- establishing the patterns of genetic diversity by defining the potential distribution of the target species by herbarium surveys
 - * the actual distribution of the species by field explorations
 - * through genetic studies the frequence and distribution of alleles
 - * the dynamics of genetic diversity e.g. introgressive hybridization
- assessing risks of genetic erosion at population level

Once that information has been centralized for the different crop species it then becomes possible to design a synthetic approach of conservation linking the most traditional methods of *ex situ* and *in situ* conservation for efficiency reasons as they present complementary advantages (PRESCOTT-ALLEN & PRESCOTT-ALLEN 1983) the need for a co-evolution and for access being particularly relevant

Table 3 Characteristics/advantages of conservation methods

ın sıtu

ex situ

Access and use in breeding
Direct costs
Orthodox seeds
Annual and short lived perennials
High level of exchange
Safe exchange
Regeneration costs low

It progressively becomes evident that *in situ* conservation should be considered through ecosystems conservation including as much living organisms as possible in order to allow the continuity of the evolutionary processes and also to have cost effective entities particularly over long periods of time (FRANKEL & SOULE 1981) The latter aspect concerns monitoring as from now onwards the conservation approach will not only be a synthetic one but also a dialectic one with periodical revisions of the germplasm status of the different target species and flexible responses When needed rescue collections could be organized where appropriate relativitions could be planned

Conclusions

In order to be meaningful conservation methods should address a large fraction of the genetic variation present in crop species certainly beyond the primary genepool. For crops other than the most common ones in the Poaceae and the Solanaceae the definition of genepools is still to be completed.

In order to have some impact conservation methods should be flexible highranking first information about genetic erosion at the population level But together with the compilation of that information there is still a lot of basic information to gather about plant species distribution plant ecology and biology breeding systems etc with the help of ecogeographical surveys wherever necessary

In order to be useful to plant breeders conservation methods should primarily deal with all alleles known for a particular crop. In this area there is still a large task ahead particularly in screening large populations of the wild relatives with the help of biochemical markers. Some of these markers have proven to be useful, but there are still important methodological problems to be solved for a better and true assessment of the genetic diversity present in a crop species. Without the latter information, it is not sure that any conservation effort will really fulfil its purpose.

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POTENTIAL AND LIMITATIONS OF CURRENT METHODOLOGIES FOR INVESTIGATING GENETIC DIVERSITY

Toby HODGKIN

The collection characterization storage and improved utilization of plant genetic diversity are central to IBPGR's operations. Currently three areas of research in genetic diversity of particular concern to IBPGR can be identified.

- the way in which the biological ecological and environmental factors interact to produce the observed distribution of variation for target taxa
- the characters that can be used to describe genetically determined variation
- the procedures used to analyse the data and the statistics that most efficiently describe the observed genetic diversity

This paper is concerned with the kinds of characters that can be used to provide the raw data for genetic diversity studies and the advantages and disadvantages associated with their use

Four major types of characters which have been used in genetic diversity studies can be distinguished

- morphological characters and disease or pest resistances under the control of major genes – qualitative characters
- morphological characters (often of direct agronomic importance and relating to yield) controlled by polygenes – quantitative characters
- biochemical markers particularly seed proteins and isozymes which can be identified using some form of electrophoresis
- molecular genetic markers which identify variation at the DNA sequence level

Qualitative characters

The description of visible variation using easily detectable and simply inherited characters is or should be the starting point of any investigation of genetic diversity Such characters have been routinely included in IBPGR's Descriptor Lists and provide essential information on the material under study Most of the classic studies of variation by VAVILOV and his colleagues (e.g. SINSKAIA 1928 BARULINA 1930) relied heavily on such characters and these still provide valuable descriptive information on patterns of variation in the species studied An example of the value of such data is the study by QUALSET (1975) of the correlation between resistance to barley yellow dwarf virus (BYDV) disease and major morphological characters in barley BYDV resistance was found to occur most frequently in Ethiopian land races with white or purple grain colour short rachilla hair and long glume awn incidentally QUALSET was also aware of the importance of including environmental data in his studies and identified geographic location (Ethiopia) and elevation as major features affecting frequency of BYDV resistance. This kind of information is of immense practical value in determining collection and utilization strategies.

In the search for technically superior procedures the importance of this simple and directly useful information should not be neglected. However it does not lend itself to any very formal analysis of genetic diversity in many species variation for many of the known marker genes may be absent over much of the material and the numbers of characters that can be studied is often extremely limited. Genotype constitution is seldom known since most of the characters are controlled by dominant genes and heterozygote frequencies are unknown. Moreover, different genes may have the same morphological effect and hence be phenotypically indistinguishable. Many of the known marker genes have a pronounced effect on vegetative growth and reproductive capacity which restricts their use in large-scale studies of diversity.

Quantitatively inherited characters

For crop species and to a lesser extent their wild relatives the characters of most concern in breeding programmes are those which affect yield quality and performance. These are usually determined by polygenes and have to be analysed using quantitative genetic procedures They are therefore quite unsuited to formal analyses of genetic diversity in so far as individual alleles cannot be identified or their effects measured Nevertheless because of their agricultural importance there have been a large number of studies of variation using such characters. With the increased availability of multivariate analysis procedures a number of studies which seek to describe the variation of many characters in large numbers of accessions have been conducted For example SPAGNOLETTI-ZEULI & QUALSET (1987) measured eight characters in 3000 accessions of durum wheat and ERSKINE et al (1989) measured nine characters in 1 370 accessions of lentil In most cases geographic distribution of variation has been of particular concern although PEETERS (1988) has investigated the amount of diversity present in different countries for eight characters in barley (Hordeum vulgare) and a number of workers have explored the correlation between environmental variables such as altitude and climate and yield characters

The information that such studies provide on diversity within populations is usually limited or absent (although JARADAT 1989 provides data on this) In fact most are not designed to give this information and the complex nature of the variates measured and the influence of the environment on their expression do not favour such an approach However such studies provide data on total variation in a crop or species for characters of direct interest to plant breeders and can provide information on the importance of major environmental variables such as altitude in determining character expression

Biochemical characters

Prior to the development of procedures for examining variation at the DNA level HUBBY & LEWONTIN (1966) noted that isozymes best fulfilled the criteria for population genetic studies. The facts that their expression is normally unaffected by environment, that they are simply inherited with codominant expression, that individual alleles can easily be detected and methods for their assay are now quick and economical make them almost ideal markers of inter- and intrapopulation variation. Compared with morphological gene markers larger numbers of loci can be surveyed, although it should be remembered that some enzymes seem inherently more variable than others and that this may be reflected in the results obtained.

Partly because of their nutritional importance seed storage proteins have also been the subject of a considerable number of investigations of genetic diversity (GEPTS 1990) In general higher levels of diversity are detected for seed storage proteins than isozymes. This is not surprising the techniques used for analysis of seed protein diversity (SDS-PAGE) differ somewhat from those used for isozyme electrophoresis and detect different causes of polymorphism and seed storage proteins are encoded by small multigene families. Generally, however the advantages and disadvantages of investigating genetic diversity using seed storage proteins are similar to those for isozymes and the two can be considered together.

Isozyme surveys have provided data on levels of genetic heterozygosity in target taxa and on outcrossing rates. They have been used to demonstrate the adaptive nature of isozyme variation for example through the association of particular alleles or allele combinations with environmental factors and viability differences. Thus NEVO et al. (1988) described variation at 47 isozyme loci in *Triticum dicoccoides*. at Tabighe Israel and suggested that the distribution of alleles was structured according to aridity of the microsite tested. On a larger scale WEEDEN *et al.* (1988) surveyed 59 isozyme loci and morphological genes in 237 accessions of *Pisum sativum* from 17 countries. He found high diversity levels considering the self-pollinated nature of the crop noted that coloured flower accessions contained most of the allozyme diversity and postulated that additional as yet uncollected variation probably existed in Turkey.

Clonally propagated crops and species and perennials with a long generation time present particular problems for diversity analysis. The standard procedures for estimation of genetically determined variation may not be available. Progenies for analysis of inheritance may be difficult or impossible to obtain. While the significance of isozyme band patterns should normally be confirmed by inheritance studies in yam phenotypic isozyme patterns have been used to provide preliminary data on the amount of variation present in different areas and cultivated groups and to assess the differences between different cultivated groups (HAMON 1988)

Despite obvious advantages some problems in the use of isozyme or protein variation should be noted First from a practical point of view the significance of allozyme diversity is not always clear Direct relationships between morphological characters and allozymes have only rarely if ever been determined. It has been suggested that while isozymes are largely controlled by structural genes (DARMEVAL *et al* 1987) variation in agronomic characters is controlled by regulatory genes. The relevance of isozyme variation to useful diversity is therefore not yet established. On the other hand, they do not fully reflect variation at the DNA level since only some base changes will result in amino acid changes of a type causing a change in mobility during electrophoresis.

Molecular genetic markers

DNA sequence variation detected by molecular biological methods has been used to examine variation in single copy genes multigene families and organelle genomes (CLEGG 1990) Relatively few studies of variation in populations have yet been done using molecular techniques but their potential is frequently noted (e g BERNATZKY & TANKSLEY 1989) By comparison with isozyme studies much larger numbers of markers are available which can assay any component of the genome and detect any mutational change (e g in maize more than 800 markers have so far been mapped) The major disadvantages for genetic diversity analysis are that the assays are still relatively slow and expensive and hence limited to rather small numbers. Most procedures still rely on the use of radioactive chemicals which also restricts the widespread adoption of the techniques

RFLP maps based on polymorphism in single copy sequences have now been produced for maize tomato lettuce *Brassica* spp rice potato and soybean and are being developed for many other crops Their use in diversity studies however has so far been limited GEPTS & CLEGG (1989) surveyed 53 cultivated and 25 wild lines of pearl millet for polymorphism associated with the *Adh1* locus and found high levels of polymorphism in both wild and cultivated materials

To date the majority of surveys of plant molecular diversity have used the nuclear encoded ribosomal RNA gene family which is arranged in tandemly repeated blocks that occur at one or more chromosomal locations. In practice the differences in DNA banding pattern for these genes which have been observed between plants or taxa require careful analysis because observed heterogeneity can have a number of causes (e.g. SAGHAI-MAROOF et al. 1984) Generally however the results have shown that variation is present and that this approach has potential in more extensive diversity analyses

Much popular interest has been shown in the development of DNA fingerprints for use in the analysis of the human genome (JEFFREYS et al 1985) These fingerprints which result from variation in dispersed arrays of short tandem repeats have now been found in rice and other plant species (DALLAS 1988 ROGSTAD et al 1989) The genetic significance of pattern variation and similarity will require detailed analysis (LEWIN 1989 UITTERLINDEN et al 1989) but the technique may offer possibilities for analysis of clonally propagated material particularly where precise identification of duplicates in collections is required in fact IBPGR is already funding a visiting scientist to work in the pilot *in vitro* genebank project for cassava at CIAT and investigate the potential of DNA fingerprinting for characterisation and assessment of genetic stability in the material

IBPGR has already funded some research projects which involve the use of molecular genetic techniques The major focus of these projects has been the improved determination of species relationships by organelle genome analysis and data on intraspecific diversity in organelle DNA has been limited Other studies have detected intraspecific variation in cpDNA in some species (NEALE et al 1988 BANKS & BIRKY 1985) although GEPTS & CLEGG (1989) found none in pearl millet Analysis of variation at the DNA level has considerable theoretical attraction and will provide a versatile new set of techniques for investigating plant genetics. However, the expensive complex and cumbersome procedures suggest that its most appropriate use at least in the near future will be to answer specific questions and not to conduct large surveys of variation

<u>Table 1</u> Advan charad		of the above mentioned
Character	Advantages	Disadvantages
Simply inherited morphological markers	 obvious expression simple inheritance easy and quick to record 	 small number little variation heterozygotes often undetected can effect vegetative growth and reproductive ability
Quantitatively inherited characters of agronomic significance	 obvious expression easy to record large amount of variation direct value in utilization 	 genetic analysis complex confounded by environ- mental effects intrapopulation variation usually ignored interaction with growth and reproduction
Biochemical markers	 individual alleles detected simple inheritance easily and quickly assayed environmental effects not common 	 only protein coding genes assayed only variants causing mobility changes de- tected limited number of loci available relevance to useful variation uncertain
Molecular markers	 individual alleles detected simple inheritance no environmental effects can detect changes throughout the genome 	 expensive and complex only small numbers can be assayed relevance to useful variation unknown

Table 1 Advantages and disadvantages of the above mentioned

Conclusions

IBPGR is concerned to ensure that the techniques used to investigate genetic variation will provide improved germplasm collecting characterisation conservation and utilization procedures. It is unlikely that any one technique will be entirely satisfactory in this respect. Improved measures of diversity based on molecular genetic or protein polymorphism may not adequately reflect morphological variation and at present molecular genetic techniques cannot be deployed on the scale required for the effective analysis of species diversity. However, a number of possibilities for the use of molecular genetic techniques exist such as the use of DNA fingerprinting in identifying duplicates, the investigation of genetic similarity in clonally propagated crops and the study of species relationships

More generally research to extend the amount of information available from molecular genetic analyses is urgently needed as are studies which will provide fully comparable data on diversity using the different techniques available. The most effective increase in the information needed to develop collection or conservation strategies will come from the combination of a variety of different techniques for describing diversity and no one technique should be regarded as replacing the others or making them obsolete

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PROBLEMS AND METHODOLOGIES FOR MANAGE-MENT AND RETENTION OF GENETIC DIVERSITY IN GERMPLASM COLLECTIONS

V Ramanatha RAO

The following discussion is basically aimed at problems and methods of conservation of seeds with a view to preserve as far as possible the genetic structure of conserved accessions/populations. In this type of static conservation the genotype or allele frequencies undergo some changes but loss of genes or alleles is minimized and contamination is avoided (FRANKEL & SOULE 1981)

The genetic diversity in a collection is eroded mainly due to the loss of seed quality in storage and loss of variation during regeneration

Loss of Seed Quality in Storage

The quality of seeds conserved is lost mainly due to the loss of viability the loss of vigour resulting in changes in development and yield and genetic effects on storability

These factors are largely influenced by storage conditions regeneration techniques applied and pre-harvest processing The differential survival of genotypes (ALLARD 1970) has been highlighted in the past however there is little precise evidence for this phenomenon. It is generally believed that standard practices such as regenerating material when the viability drops by 5 to 10 % of the original germina-tion level will counter most of these effects. This underlines the importance of monitoring viability during storage.

Loss of Variation during Regeneration

Regeneration of germplasm is an important area of genetic resources activity because conservation of the genetic structure of an accession as well as the retention of variation within an accession largely depend on this process. The discussion that follows is largely drawn from the report of Prof E L BREESE (1989) whom IBPGR engaged as a consultant to review and evaluate the literature on regeneration. One has to consider two major factors which influence the genetic structure of the conserved material during regeneration. The frequency of regeneration and the regeneration methods Both the frequency of regeneration and the regeneration methods may be crop-specific and will be difficult to generalize The frequency with which genebanks regenerate their material depends on the initial sample size the actual usage (demand to provide seed) and the length of seed viability

It is necessary to remember that however careful one is during regeneration further bottle-necking of material is inevitable A bottle-neck is an observable drop in the size of a population. So the frequency of regeneration should be kept to a bare minimum. Good conditions of long-term storage protect viability and therefore would considerably help in reducing the frequency of regeneration. Generally one regeneration immediately after collecting or release from quarantine will not be enough. However, it is very essential that the initial seed increase should be as great as possible so that future regenerations can be reduced.

Regeneration Methods

Integrity of an accession as reflected by the change in its genetic structure is affected by gene mutation outcrossing genetic drift genetic shift and contamination

The need in genetic resources is conserving adapted genotypes minimizing further evolutionary change (static conservation) until the desirable genes can be manipulated in developing better crop plants for the present and future in regeneration the important considerations are the following

In self-pollinating species the genetic and genotypic composition of the population is to be preserved. Major limiting factors in preserving the genetic structure could be the population size and absence of selection during regeneration. In the case of outcrossing species, it is important to maintain the heterozygous/homozygous balance. Here we need to have information on the life cycle reproductive biology and breeding system of the crop species under consideration. However, presently such information is seriously lacking for most crops and there is an urgent need to work on these aspects.

Regeneration tactics are basically influenced by collection strategies A major problem is that the initial sample may include alleles with frequencies less than 0.05 Each regeneration would increase the bottle-necking process and the risk of losing such rare alleles is very high The level of outbreeding would greatly influence the tactics to be employed These could be

- avoiding contamination by alien pollen or seed through isolation and seed handling techniques
- minimizing drift or shift by manipulating the population size and by avoiding natural selection or
- pollination control (selfing/sibbing or securing random mating)

The genetic diversity of conserved material must be preserved during regeneration activity and this is more complex and difficult in the case of cross-pollinated crops than in inbreeders (PORCEDDU & JENKINS 1982)

Major Problems and Counteracting Measures

Mutations

The natural mutation rate though very small is an important consideration especially in ageing seeds and in the case of seeds with less than 80 % germination

One way to counter these effects is by regenerating material before there is serious loss in viability Direction of mutations mutation rate etc are thought to influence the differential survival of genotypes in heterogenous collections. However, there is no precise evidence and such effects have not been quantified. More information through research on this aspect would help in planning better regeneration strategies.

Pollen Adulteration

Even a moderate flow of foreign pollen can cause significant changes in the genetic structure of accessions. Hence isolation techniques become a significant consideration during regeneration. Isolation depends on methods of pollination and reproductive biology of the crop Isolation can be obtained by spatial/temporal barriers or natural/artificial barriers or hand crossing and bagging

When dealing with a large number of accessions regeneration in isolation is impractical though there is a rapid decrease in the rate of pollen contamination over distance. Nevertheless in most crops less than 5 % cross pollination can occur over long distances depending on season location crop species direction of wind and species of vector and their preferences (RICHARDS 1986) Tall growing crops with islands of material being regenerated can act as an effective barrier Use of linen cloth or paper bags can further improve it However all these should be considered on a species basis and would also depend on the effects of screening/bagging on the quality of seed

Most of the pollination control methods currently followed in regeneration of many crop species are based on intuition rather than experimental evidence information on the extent of outcrossing effectiveness (including cost effectiveness) of different methods of isolation and their effect on seed yield and quality will considerably help in evolving suitable regeneration methods

Population Size and Genetic Drift

The sample size at collecting has a direct bearing on the number of plants to be grown for regeneration. An accession would rarely come from a single plant. In this case, a small number of plants would satisfy the requirements for regeneration, and the total number would mainly depend on the quantity of seed required. However, the number of plants sampled at collecting generally would be larger, thus contributing to the heterogeneity of the accession and hence requiring the growing of a greater number of plants to retain the variation during regeneration.

In small populations such as is the case with many of the genebank accessions to be regenerated random loss of alleles (genetic drift) can be very significant. Effective population size (N) depends on the number of individuals contributing equally to the next generation. Then the expected proportion of variation in a random mating population after t generations is equal to

$$(1 - \frac{1}{2N})^{t}$$

There will be about 1-2 % loss per generation with population size ranging from 25 to 50 Rare alleles are lost faster alleles with higher frequencies are preserved with greater confidence. If one foresees more than 5 regenerations during the period of conservation of an accession N_e should then be much larger than 50. It is also important to use constant population size over generations

 N_e is generally smaller than the actual population size (N) since not all the plants grown contribute to seed production due to chance or uncontrolled variation in the environment or genetic differences between plants. The relationship between N and N due to these factors has been studied theoretically (CROW & KIMURA 1970) and in model situations (BRAY 1983 GALE & LAWRENCE 1984). However, experimental evidence is lacking and additional research would be required to get more information on these aspects. If the differences between N and N_e are solely due to chance and/or environment then

$$N_e = (4N - 2) / (2 + V_{(k)})$$

where $V_{(k)}$ = variance in genetic contribution due to differences in fecundity and k = number of alleles

If the differences in fecundity are heritable then the formula becomes

$$N_e = 4N / [2 + (1 + 3h^2) V_{(k)}]$$

where $h^2 = heritability$

Based on the above calculations the following methods may be used while regenerating outcrossing species

- 1) Pair crossing with maximum control over generations
 - a) <u>Pair crossing families kept distinct</u> (variations chain crossing cyclical mating) This appears to be the most effective method since it eliminates differences due to chance environment and to some extent differences due to genetic constitution

 $N_e = (4N - 2) / 2$ if N = 50 then $N_e = 99$

b) Mixing equal amounts of seed from each pair

 $N = (4N - 2) / (2 + 2) = N - \frac{1}{2}$ if N = 50 then N_e = 495

- Controlled polycross hand crossing random females with mixed pollen
 - a) Maternal lines held as distinct subsets

N = (4N - 2) / (2 + 1) = (4N - 2) / 3 since V_(k) is almost 1 if N = 50 then N = 66

b) Equal amounts of seeds from maternal lines are bulked and maintained in a common container

 $N \leq N$ if N = 50 then N_0 is about 50 or less

3) Polycross with natural pollination equal quantities of seed pooled from each genotype/population

 $N = (4N_mN_t) / (N_m + N_t)$ if N = 50 ie $N_m = N_t = 25$ then N = 50

assuming pollen comes from an equal number of plants (male)

4) Bulk-harvested naturally pollinated polycross

N may be close to N/2 if N = 50 then N_a << 50

Some of the problems with the above methods are

- Few attempts have been made to investigate the effects of variation in gametic contributions on effective population size. This needs further investigation.
- Variation in plant size and/or fecundity can potentially have significant effects on genetic drift by reducing N. Usually this is countered by increasing the number of plants (N) well above the minimum required. However, quantifying the effects will considerably help to keep the numbers to the minimum necessary, thereby reducing cost of regeneration.
- The calculations involved in arriving at effective population size assume that the reproductive differences are due to random environmental variables. In practical situations this is very unlikely especially so in the case of wild populations and heterogeneous land races. Additional complications may arise due to level of ploidy
- The methods of regeneration described above are labour intensive and costly but there is no way around it. This emphasizes the need for greater funding.

Natural Selection and Genetic Shift

Natural selection depends on total fitness of individual genotypes It operates through differential survival and fecundity both of which may result in gene loss or change in gene frequencies. So it is necessary to choose environments and cultural practices to reduce selection pressure during regeneration. It is important to identify the major causes of differential survival and of G x E interactions which contribute to differential fecundity and to counter them. Selection pressures may vary due to changes or differences between the original and new habitats. However, the suggestion that the accessions need to be regenerated close to the areas of their collection, though ideal is usually impractical. So due importance has to be given to ensure conditions that will improve survival (temperature water requirements etc.) improve reproduction (photoperiod sensitivity thermo sensitivity etc.) and provide special conditions (protection against biotic and abiotic stresses pollinators)

Seed dormancy ageing and germination can affect an individual plant s contribution to seed production. Therefore, these factors also have to be considered during regeneration. Similar consideration has to be given to competitiveness plant density and vernalization requirements. Optimal cultural conditions are required to produce high quality seed, a prerequisite for medium- and long-term conservation. Much research needs to be carried out to find out about these conditions for most crop species. When we consider their wild relatives almost nothing is known.

Inbreeding Species

Most of the previous discussion centered around cross-pollinating crop species The majority of inbreeding species show genetic variation in floral morphology and mechanisms governing the degree of outbreeding which may be under the control of a small number of genes and highly influenced by the environment These do not show marked inbreeding depression and could be maintained as subsets of inbred lines or as bulk populations

Conclusions

In most genebanks very little consideration is given to the factors that have been discussed so far when planning for the regeneration of material. In the past IBPGR has stressed the monitoring of viability to determine <u>when</u> the material should be regenerated. However, much less attention has been paid to <u>how</u> it should be done. When we turned our attention to this matter recently we found that information about genetic diversity and breeding systems of accessions, which would be necessary to provide guidelines on regeneration is sadly lacking.

Much of the material collected 10-15 years ago when IBPGR began its activity is now becoming due for regeneration and therefore it is essential that research be undertaken and guidelines developed Otherwise we run the risk that genetic erosion will be just as serious in the regeneration plots as it is in the field/nature

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CHARACTERIZATION OF GENETIC DIVERSITY WITHIN CORE COLLECTIONS BY RESTRICTION FRAGMENT LENGTH POLYMORPHISMS (RFLPs)

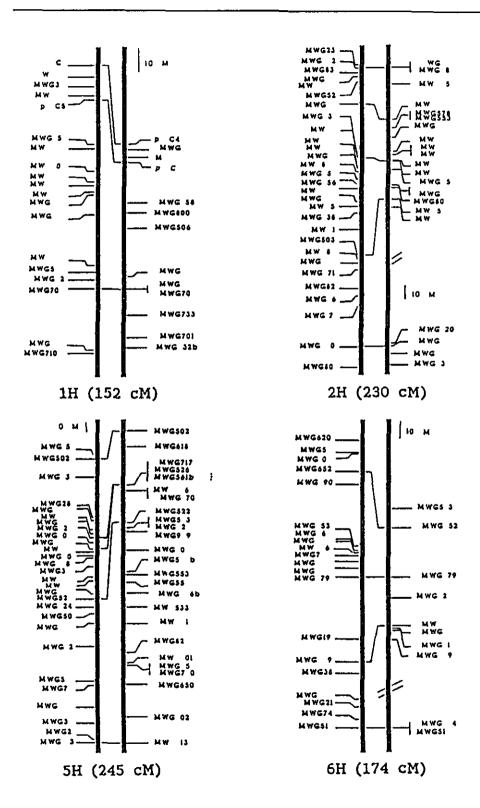
Gerhard FISCHBECK

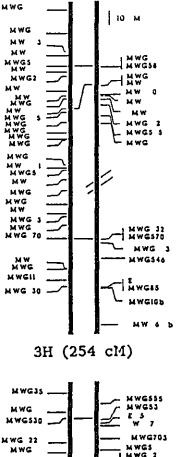
Better use of genetic diversity stored in germplasm collections of cultivated plants can only be made if a proper level of evaluation of the accessions is reached. Keeping in mind the huge number of accessions already stored in existing collections of some of the more important crop species such a requirement can only be met if a rational way of partitioning the work can be developed and followed. To this end the concept of core collections was introduced by BROWN (1988). In essence a core collection should be extracted from the total number of available accessions in such a way that the limited number of core accessions reaches a representative level of genetic diversity compared to the total number of accessions

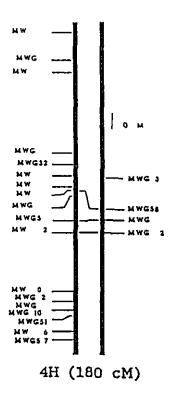
Based upon the results of several years of cooperation within the European Genetic Resources Programme which has been carried out under IBPGR guidance with special attention to barley a working group has been established and given the mandate to outline a programme for the establishment of a Barley Core Collection (BCC) The draft proposal of this programme envisages to extract a set of accessions which does not exceed 2 000 of the estimated total of about 100 000 barley accessions maintained in genetic resources collections around the world. It is intended to discuss the proposal with the international community of barley workers during the barley genetics congress to be held in 1991 in Helsingør with the intention to finalize the programme and put it into action

During the last decade a significant part of molecular genetics research with cultivated plants has been devoted to develop genetic markers based upon the polymorphism obtained from cloned DNA probes upon hybridization with DNA extracted from different genotypes and the treatment with a set of restriction enzymes (JAHOOR *et al* 1990 BERNATZKY & TANKSLEY 1986 HELENTJARIS 1987)

With the support of the Federal Ministry for Research and Technology (BMFT) a cooperative effort is being made by the Institute for Botany (Prof HERRMANN) Munich the Institute for Resistance Genetics (Prof WENZEL) Grunbach and the Department for Plant Production and Plant Breeding (Prof FISCHBECK) Freising-Weihenstephan to establish a set of RFLP markers for the barley genome The result of these efforts is shown in Figure 1 (p 70/71 – replacing the preliminary table







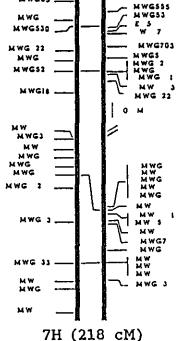


Figure 1

RFLP map of the barley genome For each chromosome the DH-derived map is shown on the right the F_2/F_3 -derived map on the left bar Chromosomes are oriented with the short arm on top The positions of common references are marked by lines between the bars and gaps are indicated by inclined lines Vertically oriented dotted lines mark regions of distorted segregation

(GRANER JAHOOR et al 1991 p 253)

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presented at the workshop) The marker set mainly consists of single copy and low copy DNA clones The 251 clones listed in Figure 1 have been assigned to specific chromosomes of the barley genome by hybridisation with a set of wheat – barley addition lines The mapping of genetic linkages between the markers located on the same chromosome is based upon segregation data obtained from the F_2 population of two barley crosses

Most likely the polymorphisms which can be detected with such a set of probes will not be randomly distributed but will indicate genetic similarities as well as genetic diversity if applied e g to a set of barley cultivars. Therefore it may be helpful to select for a maximum degree of genetic diversity between prospective crossing parents even before linkage relationships with economically important characters are established which eventually will also include quantitative trait linked loci (QTL)

Within the near future it should be possible to select a set of 28 probes which are not closely linked but located on the same arm of each of the seven barley chromosomes and which are known to reveal restriction fragment polymorphism between commercial barley cultivars. It certainly would be extremely informative to use such a set of markers not only to determine but also to quantify the genetic diversity which will be present in the future barley core collection since such data may provide sufficient information to develop a characterization system for genetic diversity in barley.

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CHANGING PRIORITIES IN CONSERVATION OBJECTIVES OF GENETIC RESOURCES

Hans-Rolf GREGORIUS

General Deliberations

This short communication is not intended to be a representative report and evaluation of changes in the objectives of conservation of genetic resources but will rather try to make a short and concise statement on why such changes are required and in which direction they could proceed For this purpose it is helpful to start with brief definitions of some basic terms in the sense in which they will be used in the following

The object of conservation the genetic resource consists of biological material which is either known to or for a given reason can be expected to contain either specific genetic information or a defined range of variants of such information. In most cases the latter range is defined quantitatively but it may also include qualitative characterizations. Hence the declaration as genetic resource of a given collection of biological material is dependent on the presence of genetic characteristics that might be of either a highly specific or an extensively variable nature. In this respect conservation thus designates an activity that is directed towards the preservation of genetic material falling into either of the above categories of genetic variation.

Sometimes the term gene conservation is applied in the general sense of conservation of genetic resources. This is unfortunate in cases where for example a distinction has to be made between vegetatively and generatively maintained resources. While in the first case the genotype is the unit of conservation in the second case the intermission of sexual processes imply recombination which leaves genes as the only possible units of conservation. In this situation it might be advisable to distinguish between genotype and gene conservation.

Turning to the present topic even though the precise objectives of conservation are quite numerous they can nevertheless be summarized under the following three categories

- Preservation of the potential for the realization of desired trait expressions (breeding products particular physiological adaptations etc.)
- Preservation of adaptability of populations races or species (latent genetic potential resistance and tolerance factors etc.)

- Preservation of unrecognized variation (population species and ecosystem protection)

These objectives are intimately related to the two major methods of conservation static and dynamic

Static conservation (obviation or minimization of micro- and macroevolutionary processes) is particularly relevant in emergency situations where comparatively small or genetically highly specialized (uniform) collections are to be rescued from acute or predictable danger of extinction. This includes genetic variants which can be expected to be of only temporary significance in production populations (resistance nutritional quality etc.) For purposes other than those arising from immediate need this method of conservation has been criticized on various grounds. For example losses during the conservation or intermittent and final regeneration phases of the statically conserved genetic resource may result in undesirably altered genetic compositions Among the most frequently cited causes are the accumulation of deleterious mutations or the evolution of adaptations to in vitro or ex situ conditions rather than to the relevant in vivo or in situ conditions These are strong arguments suggesting that statically conserved resources should again be exposed as soon as possible to the vagaries of evolutionary adaptation in order to avoid detachment of their genetic base from changing environmental demands

In contrast dynamic conservation explicitly allows for evolutionary processes and can therefore help to prevent most of the above problems Obviously dynamic conservation (*in* or *ex situ*) of a genetic resource requires protection of the resource population and in this way it also contributes to species protection. Yet population protection cannot be achieved without inclusion of the supporting environment which thus necessitates ecosystem protection. Two of the most basic measures determining the success of population protection are

- securing the (species-specific) demographic characteristics (habitat requirements population density subpopulation structure age class structure timing of sexual maturity etc.) required for survival and reproduction and
- providing the genetic variation required for adaptation and preservation of adaptability

Consequently population protection and dynamic conservation of genetic resources have in common the objectives of securing the conditions for survival and reproduction and preserving the adaptability of populations Moreover genetic factors are likely to affect a considerable portion of the variation in demographic characteristics within species which further emphasizes the interdependence of protection and conservation The insight that the persistence of a genetic resource is most effectively warranted by methods of dynamic conservation and that this in turn decisively depends on the possibility of population and ecosystem protection has only just started to attract attention in conservation philosophies and practice Remarkably this coincides with a period of increased awareness of ecological problems

Specific Concerns of Dynamic Conservation of Genetic Resources

There are however demands on dynamic conservation beyond those on population protection. These demands are mostly concerned with the necessity of maintaining genetic variation in excess of that required for the preservation of adaptability. As a rule such an excess constitutes a genetic load in the sense that the population fitness would increase after subtraction of individuals (and their successful gametes) carrying the excess genetic types. Endangerment of resource persistence could be the consequence of an overly high genetic load. Nevertheless under most systems of reproduction one may expect the genetic variants causing excessive load to be eliminated as a consequence of their selective disadvantage. This however leaves the conservationist with the dilemma that dynamic conservation runs counter to her/his conservation efforts. Therefore

a major concern of dynamic conservation of genetic resources consists in specification of the conditions under which genetic variation existing in excess of that required for adaptation and constituting a genetic load can be maintained without endangering the adaptability of the resource population

As a rule the maintenance of genetic diversity requires sufficient environmental heterogeneity to allow for the evolution of differential adaptations. However, a distinction has to be made between spatial and temporal environmental heterogeneity since in combination with restricted gene flow the first offers the opportunity for the evolution of local adaptations with positive effects on the overall population fitness while the second implies adaptive lags that may lead to critical reductions in population fitness. Thus a reduction of genetic load without loss of genetic diversity can be achieved by decreasing the temporal and increasing the spatially effective environmental heterogeneity. Herewith spatially effective refers to that part of the local environmental variation that cannot be levelled out by migration or gene flow Random mating or unrestricted and undirected migration for example would effectively homogenize spatial environmental heterogeneity to a large extent. Moreover, equalization of the spatial representation of the effective environmental heterogeneity may additionally increase the genetic diversity by increasing the genetic evenness

Another major factor that determines the success of a conservation measure is the size of the resource population Again any recommendation must proceed from the principles of population protection and must thus account for the basic demographic requirements for survival and reproduction of the species considered. As far as the genetics of the resource are concerned a central problem is frequently seen in the selective forces that might reduce the genetic variation in the resource. However, as was shown above, these forces may either be desirable in that they indicate advantageous adaptive evolution, or they may be controlled by an appropriate apportionment of spatial and temporal environmental heterogeneity. Thus, the crucial factor consists in the amount of genetic drift taking place among selectively equivalent (neutral) genetic variants as a consequence of limited population size.

Consequently from a genetic point of view

the size of a resource population should be determined by the amount of genetic variation the loss of which by drift (at selectively neutral gene loci) is tolerable over a specified number of generations

Specification of the number of generations and the tolerable loss of variation are chiefly governed by practical reasoning. The measurement of the amount of genetic variation should not be based on specific properties of genetic structures. Heterozygosity for example is an inappropriate measure since depending on the mating system realized heterozygosity may vary almost independently of the numbers and frequencies of alleles at a gene locus. More appropriate are measures of genetic diversity or differentiation.

In summary since purely static conservation is efficiently applicable to a quite limited (though important) scope of objectives only dynamic conservation should be given considerably more room than it presently occupies in the field of conservation of genetic resources Moreover both the objectives and methods of conservation should be more explicitly oriented towards the preservation of adaptability which necessarily entails measures of population species and ecosystem protection

TAXONOMY OF CULTIVATED PLANTS - SOME EXPERIENCES FROM THE GATERSLEBEN GENEBANK

Karl HAMMER

The tasks of taxonomy with respect to cultivated plants were recently characterized as follows (HANELT 1988)

- to describe the often enormous variability by various methods and techniques in order to enable researchers of genetic resources to communicate on the representatives of this variability
- to relate this variability to ecological and geographical parameters
- to analyse and to explain the relationships between cultivated and closely related wild taxa in a (phylo)genetic context and
- to contribute to the understanding of the complex interactions between evolution and domestication (see HAMMER 1984) of cultivated plants and development and history of man

Characterization of the variability and the evaluation of evolutionary relationships as the two main contributions of taxonomy to the research of genetic resources are highly relevant to problems of applied botany mainly to the management of plant genetic resources in genebanks and to breeding aims (HANELT 1988)

HARLAN & De WET (1971) proposed a rational classification of cultivated plants which is rather useful for genebanks because it explains the genepool concept and presents an informal classification scheme on the infraspecific level. The primary genepool is equivalent to the biological species. Within this category <u>two</u> subspecies occur subspecies A which includes the cultivated races and subspecies B which comprises the spontaneous (wild and weedy) races (Fig. 1).

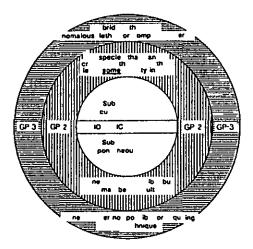


Figure 1

Classification of cultivated plants Schematic diagram from HARLAN & DE WET (1971)

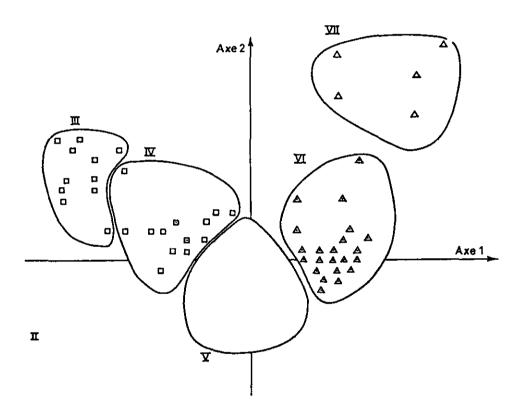
- GP-1 = primary genepool
- GP-2 = secondary genepool
- GP-3 = tertiary genepool

This simple classification prevents to a certain extent taxonomic studies on the infraspecific level. The *Papaver somniferum* example (Table 1) shows that there are <u>three</u> subspecies which are geographically and/or evolutionary based (HAMMER 1981). As it has to be expected there is a growing artificiality in the lower levels of infraspecific classification. For the distinction of botanical varieties e.g. seed- and flower colours are used. At least for the seed colours a certain domestication trend can be pointed out. As for *Papaver somniferum* for many other crops as well infraspecific systems have been elaborated at Gatersleben (see HAMMER 1981). By using these systems for classification genebank material can be well characterized and divided into morphologically defined lines. This procedure is considered necessary to prevent losses during the reproduction of genebank material ex situ

<u>Table 1</u> System of classifying *Papaver* somniferum proposed by DANERT (1958) modified by HAMMER (1981) see also HANELT & HAMMER (1987)

species level	Pp mit	ml		
ssp level	ssp m lf m		ssp g i m BASL	Bap ig m (DC) CORB
oonvar level	convar m l fe m	oonvar 1 1 Idii HAMMER	conver thm le l HAMMER	convar <i>ie i ie</i> DANERT s. L
	indehisoent capsules	dehisoent capsules	indehiscent capsules	dehiscent cepsules
vär level <u>3eeds</u> white, yelowish, or pink	ver somnii m er ndid m VESS ar oseoi m VESS ver p iii m ALEF ar ma o p m COSS ar pspy i m DANERT ar ola m DANERT	Br di oca p m ALEF ar b p m m VESS. Var g i e m VESS ar ili m DANERT Br h ili ALEF ar pictifi m DANERT Br t m DANERT	var ib s VESS ar bio nd m VESS var hoda ih m VESS. var ig um DANERT var ga m igi m DANERT var aplat m VESS. var limb lio m DANERT	veri m (ROTHAL) HAMMER Ver pim DANERT eri im DANERT veri igid m DANERT verm i m DANERT verh pi ihm DANERT erp II im DANERT
<u>eeds</u> light gray light blue, or dark blue	var h egee m ALEF var o e / ROTHM. var oculetum DANERT var ig m HAYNE ar se e m DANERT ar bg ise m VESS	Broot stim DANERT Brpilldm ROTHM. VBrmdrii Sa VESS Brq ssandm ALEF VBrpilthm DANERT VBrbiot m VESS.	varmi dim DANERT arli VESS varhi im DANERT varbidim VESS. varsigili im DANERT arbo isum DANERT	verie c mium DANERT verge se (ROTHM) DANERT verpedetm DANERT vert dibm DANERT vergeittm DANERT verpitm DANERT

The elaboration of morphological classifications can also be done by using statistical methods e.g. principal component analyses (Fig 2) in this way the Cuban material of *Phaseolus lunatus* was classified (ESQUIVEL et al. 1990) and the original taxonomic treatment of this crop by MACKIE (1943) could be supplemented. Our findings are supported by evolutionary conclusions concerning the infraspecific groups



A I

Figure 2 Result of the principal component analysis for Phaseolus lunatus from Cuba (from ESQUIVEL et al 1990)

1	=	wild
II -	=	weedy
Ш	=	Potato
IV	=	Potato - Sieva

V = Sieva VI = Sieva - Big Lima VII = Big Lima 79

Knowledge about the breeding system is important for the reproduction ex situ in the genus Secale anther length turned out to be an important indicator of the breeding system (HAMMER et al 1987 HAMMER 1990) and allows a number of phylogenetic conclusions (Fig 3) These conclusions are the basis for the classification on the specific and infraspecific levels

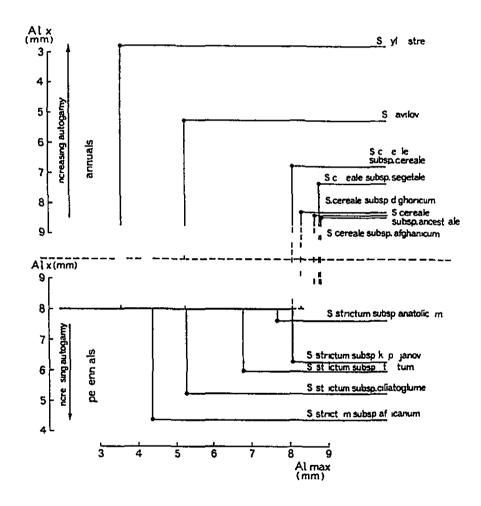


Figure 3 Phenogram constructed on the basis of anther characters for demonstrating evolutionary trends in Secale (after HAMMER 1990) Perennial and annual races are separated Delimita-tion of races according to HAMMER et al (1987)

Al max = maximum anther length Al \bar{x} = mean anther length Though taxonomy is principally based on morphology other scientific fields have to be considered too and evaluated with respect to their usefulness for taxonomic conclusions. Usually these conclusions can be drawn in cases in which it is possible to show evolutionary tendencies. Within the genus *Aegilops* this could be demonstrated by using disease resistances against several pathogens (Table 2). The most primitive species *A speltoides* showed as a rule the highest resistance levels. Also a geographical tendency could be demonstrated (HAMMER 1987).

Table 2 Disease resistances in the genus Aegilops (HAMMER 1987)

						5		b	-	S	00	
		Tilleria Ca ies	Usthago r Itici	Ersiphe 9 amini:	Mayerola destructa	Puccinta econd	Puccinia striitor	Schlaphis Graminus	Puccinia Caminic	Pseudoc herpor be cos	Septoria nodorum	Genome
		28	32	र्ध्व के	Å, o	భి లై	d 3	9.6	9,0	8 4 8 4	ર્કે ટે	ů
Ae	mutica	100	71	100	0	0	33	-	0	0	0	M۲
Ae	speltoides	84	90	78	52	91	83	67	81	6	2	S
Ae	longissima	100	29	96	50	23	23	75	6	0	0	S'
Аө	searsii		36	-		67	35	-	0	0	_	S
Ae	bicornis	86	0	83	40	8	0	0	0	33	0	S⁵
Að	peregrina	75	100	91	67	74	33	67	0	20	0	US
Aø	kotschyl	50	29	100	0	13	20	0	0	20	0	US
Ae	umbellulata	100	79	83	83	84	29	14	0	0	13	U ⁸
Ae	biuncialis	100	86	100	0	50	50	0	0	11	0	UM ^b
Ae	columnarıs	100	86	89	50	60	22	0	0	11	0	UM°
Ae	neglecta	100	93	96	67	100	82	0	14	0	22	UM ¹
Aθ	geniculata	82	50	92	100	29	52	8	4	6	0	UM
Aө	comosa	100	57	50	33	57	100	0	0	0	0	M
Аө	uniaristata	100	93	0	_	0	75	-	25	0	50	М
Ae	crassa	100	79	13	100	0	0	100	0	5	0	DM °
Ae	ventricosa	90	86	75	100	0	46	0	0	29	0	DM
Ae	juvenalıs	100	100	67		0	0	-	0	0	0	DM ° U
Ae	tauschii	41	67	27	-	8	8	-	12	2	0	Ð
Ae	cylindrica	100	43	54	100	35	0	0	0	0	15	CD
Ae	markgrafıı	83	29	71	50	71	80	100	60	0	0	С
Ae	triuncialis	100	64	87	57	55	35	0	0	20	4	UC
Aeg	gilops spp	84	70	66	60	40	33	18	14	6	4	

¹ after KRIVČENKO et al (1983)

5 see VALKOUN et al (1985)

² after NIELSEN (1985)

⁶ see GROLL et al (1985)

³ combined from GILL et al (1985) and VALKOUN et al (1985) ⁷ see FRAUENSTEIN & HAMMER (1985)
 ⁸ see KIMBER & ABU BAKER (1981)

⁴ after GILL et al (1985)

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BCV 1 = beet cryptic virus 1	BCV 2 = b	eet cryp	tic virus
Aaterial	BCV 1	BCV 2	Number of tests
Beta vulgaris var rapacea (fodder beet)		
Altenburger Tonnen	+	+	1
Criewener Gelbe	+	+	2
Polyrouge	+	+	3
Rote Walze	+	+	4
Unikum	+	+	2
Žlta	-	-	1
Beta vulgaris var vulgarıs (red beet)			
Boliver Kogel	_	+	3
Boldurdy	-	+	2
Bordo	-	-	1
Carotine	-	-	1
Nina 4	-	-	1
Plattrunde Rote Feinlaubige	+	+	3
Podsi	-	+	3
Queen	-	+	2
Redpack	-	+	2
Renora	-	+	3
Rote Kugel	-	+	8 ^{\$}
Rubia	-	+	3
Ruddigore	-	+	3
Trianon	-	+	2
K 5899 Soviet Union	+	+	3
K 6871 Soviet Union	-	+	2
K 7157 Italy	-	+	2
K 7168 Italy	+	+	2
Beta 155 Soviet Union	+	+	3
Beta vulgarıs var cıcla (chard)			
Fudanso	+	-	4 \$
Gruner Schnitt	-	-	1
Lucullus	+	-	7\$
K 6596 Soviet Union	-	+	3
K 6911 Italy	+	-	2
K 7156 Iraq	+	+	3
K 7187 Iraq	+	+	2
K 7289 Italy	-	+	3

<u>Table 3</u> Occurrence of beet cryptic virus (BCV) in different beet races (from HAMMER *et al* 1990)

- leaf material from 5 to 10 different plants in mixture for each test

- * material was tested also by ISEM-D
- material from collecting missions

The differential occurrence of certain viruses can reflect evolutionary pathways too as in beets (HAMMER *et al* 1990) The results show that the genepools of chard and red beet have developed quite independently from each other (Table 3) important parts of the taxonomic classification of beets (HAMMER 1986) could be supported in this way

This example already leads to the molecular level New methods in this field should be evaluated with respect to their usefulness for taxonomic purposes. Within the genus *Hordeum* the fast and simple squash dot hybridization technique was used to determine redundancy differences in highly repeated DNA probes (JUNGHANS & HAMMER 1990). A large number of *Hordeum* races was screened using six different barley-specific highly repeated DNA probes (Table 4). Closely related races of *Hordeum vulgare* are characterized by a homogenous and high redundancy of repeated DNA tested. As a consequence, the races of the *Hordeum vulgare* complex should be considered as a single species. In contrast, wild barley species show different redundancies at a lower level. Therefore, this method is useful to elucidate phylogenetic tendencies especially on the species level.

<u>Table 4</u>	Redund	ancy	an	d dist	ribution	of	gen	iome-s	pecific	hrDNA
								some	other	cereals
	(after	JUN	GHA	NS & F	IAMMER	19	190)			

4	=	100 % of H	vulgare	3	=	75 % of H	vulgare
2	=	50 % of H	vulgare	1	=	25 % of H	vulgare

					pBHV28	pBHV107	pHB40 pHB96	•
Cultivated b	parley :	and closely re	elate	ed wild races				
H vulgare (convar	deficiens	var	deficiens	4	4	4	4
	convar	distichon	var	medicum	4	4	4	4
			var	nutans	4	4	4	4
t i	convar	intermedium	var	harlanı	4	4	4	4
l l	convar	labile	var	steudelıı-				
				nigripallidum	4	4	4	4
(convar	vulgare	var	coelste	4	4	4	4
		-	var	densum	4	4	4	4
			var	dundarbeyi	4	4	4	4
			var	himalayense	4	4	4	4
			var	horsfordianun	n 4	4	4	4

		pBHV28	pBHV107	pH840 pH896	
н	vulgare convar vulgare var hybernum "E	irfa 4	4	4	4
	var hybernum	4	4	4	4
	var subparallelu		4	4	4
н	agriocrithon var agriocrithon	4	4	4	4
	var dawoense	4	4	4	4
	var paradoxon	4	4	4	4
H	• • • •	4	4	4	4
Н	spontaneum x H vulgare convar distichon	4	4	4 4	4
н	spontaneum var bactrianum	4	4 4	4	4
	var ischnatherum	4	4	4	4
	var spontaneum	4	4	4	4
	var transcaspicum	-	4	•	-
W	ild barleys				
н	brachyantherum 2x	2	3	2	3
	6x	3	4	3	1
	bogdanıı	1	2	3	3
н	brevisubulatum subsp brevisubulatum	1	3	2	1
	subsp turkestanicum	2	3	2	1
	subsp violaceum	1	2	3	1
Н	bulbosum subsp bulbosum	2	4	4	2
	subsp nodosum	2	3	2	2
Н	capense	2	3	4	2
	chilansa	1	3	1	2
Н	cordobense	1	2	1	2
Н	euclaston	1	1	2	3
Н	flexuosum		-	3	2
	Intercedens	1	1	1	3
	jubatum	2	3	2	2
	lechleri	2	3	3	1
Н	marinum subsp gussoneanum	3	4	3	3
	subsp marinum	3	4	3	3
Н	murinum subsp leporinum	3	3	2	2
	subsp murinum	2	3	2	3
н	parodu subsp parodu	2	3	3	3
	subsp santacrucense	1	1	1	2
н	procerum subsp procerum	2	2	2	2
	subsp setifolium	1	1	1	3
	pubiflorum	2	2	-	-
	pusillum	1	1	2	1
	roshevitzii	2	3	2	2
н	secalınum	Z	3	-	3
0	ther species				
A	vena sativa	1	0-1	1	0-1
	ecale cereale Petka	0	0-1	-	-
T	riticum aestivum Chinese Spring	0	0	0-1	0

Modern methods should be included into taxonomic approaches in cultivated plants. But their usefulness has to be tested with respect to the plant group the taxonomic level within this group and other items of the plants under investigation. This is a well-known fact from the work with morphological characters.

For the taxonomy of wild species the specific level is most important whereas in cultivated species the infraspecific level plays an important role However in this plant group as well the specific level is still an object of taxonomy Nearly 5 000 species are cultivated (excluding ornamentals) on a world-wide scale (SCHULTZE-MOTEL 1986) To supplement and update this global list and as a useful tool for germplasm collecting area-specific checklists have been used (Table 5) (see also BAIK et al 1986 HAMMER et al 1988 ESQUIVEL et al 1989 and HAMMER et al 1990) The large amount of newly detected plants under cultivation in these regions stresses the actual importance of taxonomic investigations also on the species level

Area	Number of cultivated species	Number of collecting missions
Cuba	819	4
South Italy	520	10
Korea	515	5
Libya	279	3

<u>Table 5</u> Checklist of cultivated plants for areas

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GENETIC VARIATION IN CROP SPECIES AND THEIR WILD RELATIVES

Daniel G DEBOUCK - Report of Working Group A

Participants

B BECKER D G DEBOUCK E DETTWEILER H-R GREGORIUS K HAMMER A McCUSKER G MIX-WAGNER H-P MÜLLER

The working group expressed its interest in seeing more studies carried out on the patterns of plant genetic diversity in space and time particularly in view of the balance of diversity present inside natural populations and between them The group recommended that the following biological and genetic aspects should deserve further in-depth study through projects on plants of mutual interest

- the differential seed production between individuals giving opportunity for certain cytoplasmic information to become dominant in a population (extension of studies carried out on Vicia monitoring in the wild for other selected crop species and refinement of appropriate molecular markers)
- the differences in maturity in the gametophytes during the course of a season especially for certain tree species and their possible consequences for the diversity in the next generation (particularly in view of a sampling done for germplasm purposes at different times)
- the causes of those differences (stresses competition inside population consequences of indiv dual physiological reactions etc.)

In case these causes involve any climatic factors the group was interested in measuring the variation from one year to another Perhaps in parallel to those studies to be carried out in natural populations the group suggested similar studies be carried out on samples of populations of the same plant material in order to better control the genetical drift during management practices in germplasm collections *ex situ*

Finally particular interest was expressed by one participant to see more work carried out on the Asian genepool of the genus Vitis for both purposes of germplasm conservation and enhancement

POTENTIAL AND LIMITATIONS OF CURRENT METHODOLOGIES FOR INVESTIGATING GENETIC DIVERSITY

Toby HODGKIN - Report of Working Group B

Participants

A -W ALFERMANN G FISCHBECK T HODGKIN H -J JACOBSEN G KAHL L SCHILDE-RENTSCHLER U SEITZ

The working group agreed to concentrate its discussions on the potential application of molecular genetic techniques in the study of plant genetic diversity

The direct practical experience of two participants of the workshop G KAHL and G FISCHBECK in relevant molecular genetic research was noted as was the experience of a number of other German scientists in this area

The working group identified a number of important objectives for genetic diversity research using molecular genetic techniques

- evaluating the potential of techniques such as DNA finger-printing in the identification of duplicate accessions in genebanks
- comparing genetic diversity analyses using molecular genetic markers with results obtained using morphological or biochemical data
- evaluating the potential of molecular genetic markers in screening germplasm collections for desirable characters such as disease resistance
- describing variation in land races at the molecular genetic level as an aid to the production of crop varieties suited to sustainable agriculture
- developing molecular genetic techniques more suited to use in developing countries (e.g. avoiding the use of radiolabelled probes) and the provision of training for personnel from developing countries

The working group was convinced that there were immediate opportunities for work using molecular genetic techniques in barley chickpea lentil and yam and that at a later date work on minor Andean tubers would also be valuable. Although there are a number of crop-specific objectives it is likely that suitably planned research projects would deal with a large number of the objectives listed above.

PROBLEMS AND METHODOLOGIES FOR MANAGE-MENT AND RETENTION OF GENETIC DIVERSITY IN GERMPLASM COLLECTIONS

V Ramanatha RAO - Report of Working Group C

Participants

Chr LEHMANN U von POSCHINGER-CAMPHAUSEN VR RAO S SCHITTENHELM

The working group considered the problems as discussed during the presentation of V R RAO on regenerating seed of germplasm. The major issues identified by the group were

- effect of mutation rate and direction of mutation
- isolation requirements/methods
- pollination control methods
- relationship between actual population size and effective population size
- effect of the variation in gametic contribution on effective population size
- estimation of genetic erosion in gene banks over regenerations
- crossing techniques for regeneration of germplasm
- reproductive biology and breeding systems

After careful consideration of interests of both IBPGR and German scientists the following items were identified that could be developed into projects to provide information necessary to develop appropriate strategies to regenerate outbreeding crops

Effective pollination control methods in the regeneration of germplasm

This includes identifying cost effective methods to promote random outcrossing in crosspollinated crops with emphasis on identifying the most effective pollinator. Insect behaviour during pollination breeding and multiplication patterns will also be studied. Another important issue is the effect of screening/cages/bags on seed quality. Different population sizes will be included to determine the most appropriate number of plants to be grown and the most adequate pollination control methods to be used. This work is essentially viewed as a joint effort between FAL (Braunschweig) and ZiGuK (Gatersleben) iBPGR will help in planning the project and in disseminating the results which are expected to be widely applicable in genebanks in both developing and developed countries

Comparative studies on the efficiency and cost effectiveness of crossing techniques in the regeneration of allogamous crop germ-plasm

Various available crossing techniques e.g. pair crossing polycross etc. will be tested using different population sizes. These tests will provide information needed for regeneration of allogamous species. Markers (enzymic molecular) could be used to clearly follow the contribution of individuals to genetic variability in the next generation. Such research could be expanded to provide opportunities for collaboration with various interested national programmes.

SPECIFIC PROJECT PROPOSALS ANNEX 1

At a two-day workshop discussions were held between scientists representing the Federal Republic of Germany the German Democratic Republic and IBPGR to explore areas of common interest in research on genetic resources of crop genepools. In particular discussions focused on crop consurvation strategies for roots and tubers and on genetic diversity studies.

A list of six potential collaborative projects was compiled during the workshop Two of three projects proposed by IBPGR were identified as being of particular interest for further development and short-term implementation 1) Refinement of Cryopreservation Techniques for Potato and 2) Spatial and Temporal Distribution of Genetic Diversity in Wild Forage Species under Stress Conditions

Refinement of Cryopreservation Techniques for Potato

IBPGR regards the refinement of cryopreservation technologies as a most important step in conserving the germplasm of root and tuber crops in this context potato is being considered as the most promising species

Success in freezing potato cultures in liquid nitrogen and subsequently thawing and re-establishing them has already been achieved in several laboratories. Since it has not yet been possible to achieve success with sufficient frequency to permit the use of cryopreservation as an appropriate technology for germplasm conservation, the project should contribute to developing this technology towards a more reliable routine method.

L A WITHERS IBPGR has agreed to participate in the planning and coordination of the project A number of German scientists are also interested in research collaboration. Technical support access to *in vitro* culture- and cryopreservation equipment and access to appropriate germplasm would be necessary.

Spatial and Temporal Distribution of Genetic Diversity in Wild Forage Species under Stress Conditions

The aim of this project would be to develop and apply methods for sampling the genetic diversity of selected Sahelian forage species growing over a wide area but possibly separated into distinct genepools isolated from each other by space and/or flowering time. This investigation would serve as the basis for designing appropriate germplasm collection and conservation methods for plant populations growing under stress conditions and flowering in response to intermittent rainfall rather than in a regular seasonal pattern.

Target species will be chosen according to their importance in local agricultural systems and practices their potential use in environment rehabilitation and their suitability as models for wider application

It is envisaged that the project would engage a German post-doctoral fellow who would have the major responsibility for the day-to-day scientific programme and an IBPGR Research Associate preferably recruited from a country in the region. These two persons would constitute the survey team and would both be based at Niamey Niger.

IBPGR s input to the supervision of the project would be made by the Research Officer (Wild Species) based in Rome and the Coordinator for West Africa based in Niamey

A third project Effective Pollination Control Methods in the Regeneration of Cross-Pollinated Crops was regarded as being of particular scientific importance at this time its results would be widely applicable to the multiplication and regeneration of genebank material in developing and developed countries

This project would most logically be jointly carried out by the Institute of Crop Science and Plant Breeding at the FAL in Braunschweig and the Institute of Genetics and Crop Plant Research (ZiGuK) at Gatersleben Although there is no justification for IBPGR s formal involvement in the project administration IBPGR would be prepared in assisting with the project design and in disseminating the experiences and results this includes the eventual transfer of the methodology to genebanks in developing countries

Another three projects which are however not ready for immediate implementation were identified as being of great interest to both German scientists and IBPGR

- Molecular genetic diversity in barley land races from South-West Asia
- The development of a strategy for the conservation of genetic diversity in West African yams
- Comparative studies on efficiency and cost effectiveness of crossing techniques in the regeneration of allogamous crop germplasm

WORKSHOP PROGRAMME

Sunday 6 May 1990

20 00 h Dinner at Bonner Stuben Wilhelmstrasse 22 Bonn

Monday 7 May 1990

Opening Session

(Chairperson H WELTZIEN)

- 8 30 h Opening Remarks (H WELTZIEN)
- 8 40 h A Few Remarks on the Agricultural Research Aid Focus (H -J DE HAAS)
- 8 50 h The Plant Genetic Resources Approach of the Federal Republic of Germany (G MIX-WAGNER as a substitute for M DAMBROTH)
 - Programme Presentation (H WELTZIEN)
- 9 00 h IBPGR s Research Programme (A McCUSKER)
- 9 20 h Presentation of Participants (H WELTZIEN)
- 11 00 h Coffee Break

Part I Crop Strategies for Roots and Tubers (Chairperson H -- J JACOBSEN)

- 11 20 h Crop Strategies for Roots and Tubers Potato a Model for Refinement Yam – a Problem for Development (L A WITHERS)
- 11 50 h Discussion
- 12 30 h Lunch
- 14 00 h Contributions by German Scientists (presentations 15 min discussions 5 min)
 - Fundamental Aspects of Plant Regeneration (H -J JACOBSEN)

ANNEX 2

	 In Vitro Propagation of Yam and Perspectives for its Long-Term Conservation (G MIX-WAGNER) Protoplast Fusion as a Technique in Breeding of Potato and Other Tuber Crops (L SCHILDE- RENTSCHLER) Cryostorage of Plant Material (U SEITZ)
15 30 h	Coffee Break
15 50 h	Plenary Discussion Crop Strategies for Roots and Tubers (L A WITHERS)
20 00 h	Dinner at MAREDO Wesselstrasse 5 Bonn

Tuesday 8 May 1990

Part II Genetic Diversity

(Chairperson G FISCHBECK)

- 8 30 h Introduction (A McCUSKER)
- 8 40 h Introduction (G FISCHBECK)
- 8 50 h Genetic Variation in Crop Species and Their Wild Relatives A Viewpoint for Their Conservation (D G DEBOUCK)
- 9 05 h Potential and Limitations of Current Methodologies for Investigating Genetic Diversity (T HODGKIN)
- 9 20 h Problems and Methodologies for Management and Retention of Genetic Diversity in Germplasm Collections (V R RAO)
- 9 35 h Discussion
- 11 00 h Coffee Break
- 11 20 h Contributions by German Scientists (presentations 15 min discussions 5 min)
 - Characterization of Genetic Diversity within Core Collections by Restriction Fragment Length Polymorphisms (RFLP) (G FISCHBECK)
 - Changing Priorities in Conservation Objectives of Genetic Resources (H –R GREGORIUS)
 - Taxonomy of Cultivated Plants Some Experiences from the Gatersleben Genebank (K HAMMER)

- 12 30 h Lunch
- 14 00 h Work ng Groups
 - A Genetic Variation in Crop Species and Their Wild Relatives (D G DEBOUCK)
 - B Potential and Limitations of Current Methodologies for Investigating Genetic Diversity (T HODGKIN)
 - C Problems and Methodologies for Management and Retention of Genetic Diversity in Germplasm Collections (V R RAO)
- 16 00 h Coffee Break
- 16 30 h Results and Recommendations of the Working Groups
- 17 30 h Closing Remarks (G FISCHBECK)

Wednesday 9 May 1990

Excursions of the IBPGR Scientists

- 7 30 h Visit to the Max-Planck-Institute for Resistance Breeding Cologne
- 14 00 h Visit to the Institute for Genetics University of Bonn

LIST OF PARTICIPANTS

ANNEX 3

Prof Dr A Wilhelm	Institut fur Entwicklungs- und
ALFERMANN	Molekularbiologie der Pflanzen
	Universitat Dusseldorf Universitatsstr 1 Geb 26 13 D-W 4000 Dusseldorf 1

Arbeitsgemeinschaft Tropische und Subtropische Agrarforschung e V (ATSAF) Hans-Bockler-Str 5 D-W 5300 Bonn 3

Dr Daniel G DEBOUCK

Dr Barbara

BECKER

International Board for Plant Genetic Resources (IBPGR) Via delle Sette Chiese 142 I – 00145 Rome

Dr Erika DETTWEILER Bundesforschungsanstalt fur Rebenzuchtung Geilweilerhof D-W 6741 Siebeldingen

Prof Dr Gerhard FISCHBECK Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung Technische Universitat Munchen-Weihenstephan D-W 8050 Freising 12

Prof Dr Hans-Rolf GREGORIUS	Abteilung fur Forstgenetik und Forstpflanzenzuchtung Universitat Gottingen Busgenweg 2 D-W 3400 Gottingen
Dr Hans-Joachim de HAAS	Bundesministerium fur Wirtschaft- liche Zusammenarbeit (BMZ) – Referat 223 – Karl-Marx-Straße 4–6 D–W 5300 Bonn 1
Dr Karl HAMMER	Zentralinstitut fur Genetik und Kulturpflanzenzuchtung (ZiGuK) Corrensstr 3 D-O 4325 Gatersleben
Dr Toby HODGKIN	International Board for Plant Genetic Resources (IBPGR) Via delle Sette Chiese 142 I – 00145 Rome
Prof Dr Hans-Jorg JACOBSEN	Lehrgebiet Molekulare Genetik FB Biologie Universitat Hannover Herrenhauserstr 2 D-W 3000 Hannover 1
Prof Dr Gunter KAHL	Fachbereich 16 – Biologie Universitat Frankfurt Siesmayerstr 70 Postfach 11 19 32 D-W 6000 Frankfurt / Main 11

Zentralinstitut für Genetik und Kulturpflanzenzuchtung (ZiGuK) Corrensstr 3 D-0 4325 Gatersleben

International Board for Plant Genetic Resources (IBPGR) Via delle Sette Chiese 142 I - 00145 Rome

Dr Gunda Institut fur Pflanzenbau und Pflanzenzuchtung Bundesforschungsanstalt fur Landwirtschaft (FAL) **Bundesallee 50** D-W 3300 Braunschweig

Prof Dr Hermann-P MOLLER

Institut für Genetik Abt Biochemische Genetik Universitat Bonn Kirschallee 1 D-W 5300 Bonn 1

Dr Ulrich von **POSCHINGER-CAMPHAUSEN** Arbeitsgemeinschaft Tropische und Subtropische Agrarforschung e V (ATSAF) Hans-Bockler-Str 5 D-W 5300 Bonn 3

Dr V Ramanatha	International Board for Plant
RAO	Genetic Resources (IBPGR)
	Via delle Sette Chiese 142
	I – 00145 Rome

Dr Alison

McCUSKER

Dr Christian

LEHMANN

MIX-WAGNER

Dr Lieselotte SCHILDE-RENTSCHLER	Medizinisch-Naturwissenschaftliches Forschungszentrum (MNF) Universitat Tubingen Ob dem Himmelreich 7 D-W 7400 Tubingen
Dr Siegfried SCHITTENHELM	Institut fur Pflanzenbau und Pflanzenzuchtung Bundesforschungsanstalt fur Landwirtschaft (FAL) Bundesallee 50 D-W 3300 Braunschweig
Dr H Martin SCHUMACHER	Deutsche Sammlung von Mikro- organismen und Zellkulturen GmbH (DMS) Mascheroder Weg 1b D-W 3300 Braunschweig
Dr Ursula SEITZ	Gottlieb-Olpp-Str 20 D-W 7400 Tubingen
Prof Dr Heinrich C WELTZIEN	Institut fur Pflanzenkrankheiten Universitat Bonn Nußallee 9 D-W 5300 Bonn 1
Dr Lyndsey A WITHERS	International Board for Plant Genetic Resources (IBPGR) Via delle Sette Chiese 142 I – 00145 Rome

LIST OF ACRONYMS

ANNEX 4

- ATSAF Arbeitsgemeinschaft Tropische und Subtropische Agrarforschung e V (Council for Tropical and Subtropical Agricultural Research) Bonn Federal Republic of Germany
- BML Bundesministerium für Ernahrung Landwirtschaft und Forsten (Federal Ministry of Food Agriculture and Forestry) Bonn Federal Republic of Germany
- BMZ Bundesministerium für Wirtschaftliche Zusammenarbeit (Federal Ministry for Economic Cooperation) Bonn Federal Republic of Germany
- CGIAR Consultative Group on International Agricultural Research Washington D C USA
- CIAT Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture) Cali Colombia
- CIP Centro Internacional de la Papa (International Potato Center) Lima Peru
- DSM Deutsche Sammlung von Mikroorganismen und Zelikulturen GmbH (German Collection of Microorganisms and Cell Cultures) Braunschweig Federal Republic of Germany
- FAL Bundesforschungsanstalt fur Landwirtschaft (Federal Research Centre for Agriculture) Braunschweig-Volkenrode Federal Republic of Germany
- FAO Food and Agriculture Organization of the United Nations Rome Italy
- IBPGR International Board for Plant Genetic Resources Rome Italy
- ICRISAT International Crops Research Institute for the Semi-Arid Tropics Hyderabad India
- IITA International Institute of Tropical Agriculture Ibadan Nigeria
- IUCN The World Conservation Union Geneva Switzerland
- ZIGuK Zentralinstitut fur Genetik und Kulturpflanzenzuchtung (Institute of Genetics and Crop Plant Research) Gatersleben then German Democratic Republic