European Commission

GENETIC RESOURCES IN AGRICULTURE

A summary of the projects co-financed under Council Regulation (EC) No 1467/94

Community programme 1994–99

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PREFACE

Commissioner
Mariann Fischer Boel

During recent decades, the importance of safeguarding a broad variety of natural resources for sustainable agriculture has been acknowledged in international forums and at Community and national levels. Aside from the sustainable management of soils, water and air, the sustainable management of genetic resources is one of the preconditions for sustainable agriculture. In this context, Council Regulation (EC) No 1467/94 on the conservation, characterisation, collection and utilisation of genetic resources in agriculture was adopted in 1994 (see the link on: http://ec.europa.eu/comm/agriculture/envir/index_en.htm#genres) (1).

The driving force behind the Council regulation was the Convention on Biological Diversity (http://www.biodiv.org/welcome.aspx), one of the main outcomes of the United Nations Conference on Environment and Development (known as the 'Earth Summit') which took place in Rio de Janeiro in June 1992. The signatory parties to the Convention on Biological Diversity (which include all EU Member States and the European Commission) bound themselves to conserve their indigenous genetic resources, *in situ* and *ex situ*, to meet broad development needs. This requires the identification of *in situ* conservation sites and, in the case of existing *ex situ* collections, their consolidation and rationalisation into collections representative of available indigenous diversity and inclusive of any other diversity of potential importance to the country.

In order to meet international obligations under the Convention on Biological Diversity, one of the first steps was to define, rationalise and consolidate national collections under the Council regulation. The main objective of the regulation was therefore to coordinate and promote at Community level research on genetic resources in agriculture, in particular those species which are not competitive on the market right now but which might contain important genetic information for further breeding. Another objective was to develop data as well as quality control standards and to establish a decentralised database. Therefore, the European Commission, together with the Member States, financially supported and coordinated research on genetic resources in agriculture that are common in Europe but which are not used commercially and which are therefore threatened by extinction. This publication presents to you the outcome of these projects, one in forestry, four in animal genetic resources and 15 in plant genetic resources.

It also presents an overview of current European Union efforts to ensure the long-term conservation and sustainable use of plant and animal genetic resources in agriculture.

Commissioner for Agriculture
and Rural Development

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(1) Council Regulation (EC) No 1467/94 was adopted on 20 June 1994 (OJ L 159, 26.6.1994, pp. 1–10).

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ABBREVIATIONS

AFLP:	amplified fragment-length polymorphism
AGDB:	animal genetic databank
AGR:	animal genetic resources
BCC:	barley core collection
Bras-EDB:	European *Brassica* database
CAP:	common agricultural policy
CEC:	Commission of the European Communities
CPRO-DLO:	Centre for Plant Breeding and Reproduction Research — DLO
CSIC:	Consejo Superior de Investigaciones Científicas
DAD-IS:	domestic animal diversity information system
DED:	Dutch elm disease
DNA:	deoxyribonucleic acid
EAAP:	European Association for Animal Production
EAAP-AGDB:	European Association for Animal Production — animal genetic databank
EAAP WG-AGR:	European Association for Animal Production working group on animal genetic resources
EADB:	European *Allium* database
EBDB:	European barley database
EC:	European Community
ECDI:	European carrot/*Daucus* inventory
ECP/GR:	European cooperative programme for crop genetic resources networks
EFABIS:	European farm animal biodiversity information system
EMDB:	European maize database
EMFTS database:	European minor fruit tree species database
EU:	European Union
EU FAIR:	European Union fisheries, agriculture, agro-industry research programme (1995–98)
Euforgen:	European forest genetic resources
EUMLCC:	European Union maize landrace core collection
EUMLDB:	European Union maize landraces database
EUMLRC:	European Union maize landrace representative collection
FAO:	Food and Agriculture Organisation
Genres:	genetic resources
GEVES:	Groupe d'étude et de contrôle des variétés et des semences
HRI:	Horticultural Research International
HRIGRU:	HRI Genetic Resources Unit
IBPGR:	International Board for Plant Genetic Resources
IDBB:	International database for *Beta*
IIRB:	International Institute for Beet Research
INRA:	Institut national de la recherche agronomique
IPGRI:	International Plant Genetic Resources Institute
IPK:	Institut für Pflanzengenetik und Kulturpflanzenforschung
IRRI:	International Rice Research Institute
Nagref-GGB:	National Agricultural Research Foundation, Greek Gene Bank
NFP:	national focal points
NGO:	non-governmental organisation
NIAR:	national institutes for agrobiological resources
NMLRC:	national maize landrace representative collection
RFLP:	restriction fragment length polymorphism markers
SGQA:	Station de génétique quantitative et appliquée
Sister:	Système d'information pour le stockage, le traitement et l'évaluation des résultats
SNPs:	single-nucleotide polymorphisms
SSR:	simple sequence repeat
Syn.:	synonymous
TAGs:	triacylglycerols
TiHo:	Tierärztliche Hochschule Hannover/ Hanover School of Veterinary Medicine
UCO:	Universidad de Cordoba
UNEP:	United Nations Environment Programme
UPOV:	International Union for the Protection of New Varieties of Plants
WBN:	world *Beta* network

INTRODUCTION

Genetic resources in agriculture — a general overview

Soil, water, and genetic resources constitute the foundation upon which agriculture is based. Out of these, genetic resources are perhaps the least understood and least valued even though they are responsible for the essential and magnificent diversity in agricultural products. They depend on our care and safeguard and many of them are threatened by extinction.

When plant species were domesticated some 10 000 years ago, they still carried with them the myriad of characteristics and defences which typically make wild plants adaptable to their environment and resilient to challenges such as drought, pest and disease attack. As peoples started to migrate their plants migrated with them and underwent a selection process as they were exposed to new environments. Sometimes different species were valued for a different purpose according to the respective civilisation. Some might have used wheat in order to make bread, others might have selected spelt to produce porridge or to roast it. A tree species might have been used for timber, fuel, food or shelter.

Throughout most of history, it was the farmers and the farm families that oversaw crop evolution. They combined plants with different characteristics to obtain new varieties that suited their needs. But farmers also took advantage of natural mutations that sometimes added a valuable new trait to the crop's repertoire.

However, agricultural biodiversity is in sharp decline due to the effects of modernisation, such as concentration on a few competitive species and changes in diets. Since the beginning of agriculture, the world's farmers have developed roughly 10 000 plant species for use in food and fodder production. Today, only 150 crops feed most of the world's population, and just 12 crops provide 80 % of dietary energy from plants, with rice, wheat, maize and potato providing 60 % by themselves. It is estimated that about three quarters of the genetic diversity found in agricultural crops have been lost over the past century, and this genetic erosion continues. According to the FAO, in nearly all EU-15 Member States about 50 % of all livestock breeds are extinct or have endangered or critical status. A current example for the genetic vulnerability of modern varieties is the elm case. Mature elms have been practically wiped out in Europe by the Dutch elm disease epidemic. It is estimated that more than 90 % of mature field elms disappeared from the French countryside in the 1919 and 1972 epidemics.

Historically, plant and animal genetic resources have contributed to stabilising agroecosystems and they have provided the crucial raw material for the rise of modern, scientific plant breeding. A loss of genetic diversity of crops and breeds can lead to a higher susceptibility to diseases and stress factors, and it becomes more difficult for plants to adapt themselves to specific local growth conditions. Sustainable agriculture needs crops and breeds with a capacity to adapt themselves to local climatic and soil conditions, with variation in resistances and tolerances against pests. The future of European agriculture lies in high-quality and high value-added products and for this it needs genes with good organoleptic characteristics and optimal transformation quality. Therefore, plant and animal genetic resources remain the foundation of evolution in crops and farm animals — the natural resource that has allowed crops and farm animals to be adapted to myriad environments and uses, and which will allow them to respond to the new challenges of the next century. Therefore, there is a need to take the necessary measures and to improve our knowledge of livestock breeds and crop varieties throughout the EU in order to conserve traditional varieties and to use the potential of that diversity in a sustainable way.

General scope of the projects co-financed under Council Regulation (EC) No 1467/94

The aim of the projects was to learn more about genetic resources in agriculture, to promote their conservation, characterisation, collection and utilisation, to develop data as well as quality control standards, and to bring together national knowledge and know-how in decentralised databases. Under Council Regulation (EC) No 1467/94, 21 projects were adopted for co-financing by the European Commission — one forestry project, 16 projects on crop genetic resources (2) and four projects on animal genetic resources. Each project followed the same step-by-step progression. The detailed objectives and tasks for each step are described in Annex 1:

step 1: establishment of the work plan,
step 2: characterisation of the collections,
step 3: evaluation (secondary characterisation),
step 4: sorting of the collections,
step 5: rationalisation of the collections,
step 6: acquisition (collection) of further genetic resources.

Even if the progression was the same, it is clear that the research work and the outcome differ a lot across projects, depending on what the situation was before the project and the research approaches chosen for each project. Annex 2 provides an overview of the major objectives covered by each project.

In most of the plant projects, the material originated from collections of the project partners, gene banks or garden (orchard) material. Due to the limited evaluation capacity in some projects, a selection of the material to be characterised had to be made. In some other cases there was a lack of specimens of each accession available for characterisation. In these projects material had to be multiplied. The same goes for old material or material considered no longer viable and which needed rejuvenation.

In the first place, a database with all the relevant passport data of the accessions was created or finalised. The subsequent steps were the primary and secondary description or characterisation of the material. Primary characterisation was carried out on almost all the material available. Secondary characterisation deals with characters like disease or pest tolerance, resistance, hardiness and tolerance against abiotic growth factors like cold or salinity, and product quality (protein and sugar content, acidity, etc.). This is very useful information since one important aim of research on plant genetic resources is to produce crops that depend less on chemical products. As concerns the fight against diseases, in the project on elm genetic resources, for example, resistance against a devastating disease, the Dutch elm disease, was the main objective of the project.

Once the characterisation had been concluded, duplicates and gaps in collections were identified, with the objective of improving the coordination of collections in the Member States and to minimise duplication of effort. To this end, in some cases it was appropriate to designate part of the total collection as a 'core' or 'minimal population' that contains all relevant characters.

Apart from characterisation, molecular methods, such as DNA analysis, were applied to define genetic variability and core collections. For the rice and the maize projects, for example, genetic relations were defined and a genetic tree was elaborated. The core collections were created on the basis of these elements and of agronomic characteristics. Cryopreservation of (clonal) material was used in two projects. The collection of additional material was only encouraged if gaps were identified in the available material. This was the case for *Allium* and carrots, for example, where wild species or local breeds were collected.

Nearly all plant projects made use of ECP/GR (European cooperative programme for crop genetic resources networks) and IPGRI (International Plant Ge-

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(2) Only 15 projects are presented in this publication. The project on olives had not been finalised by the time this publication was prepared and was therefore not included.

netic Resources Institute) standards and methods, if these were available. At least 10 projects were carried out in close collaboration with ECP/GR working groups on the respective crops.

There is a growing demand for a wider choice and variety of horticultural crops and agricultural products, for which diversity in taste, colour, nutritional values and earliness/lateness of harvest is highly valued by the market. These characteristics required by consumers may be found in the various genetic resource collections. The projects mentioned in this brochure have contributed to safeguarding most of the important characteristics for further potential use. Furthermore, they have made the search for these resources, which are mainly stored in gene banks, quicker and more efficient.

Concerning animals, there is much less material available than for plants. This is because local breeds have become rare and sometimes have almost disappeared. In some cases, the genetic material is only cryoconserved in institutes (as is the case for pigs in Italy). In others, local breeds were believed to have died out, but were finally found or the herds were simply too small and inbred (pigs in Spain).

One of these four projects focused on an update and inventory of the database of farm animals; the work was carried out at Member State and EU levels. Another focused on the genotyping of 50 cattle breeds with molecular methods in order to obtain a deeper insight into breed formation and the effect of selection for milk and beef production. The other two animal projects, on pigs and rabbits, helped to build up an inventory of local breeds. In both cases, a zootechnical evaluation of different breeds was conducted. In the rabbit project, the evaluation was carried out under extensive production methods and the genetic distances between the breeds were studied. In the pig project, quality traits of pigmeat were examined.

PROJECT SUMMARIES

ANIMAL
GENETIC RESOURCES

CATTLE: TOWARDS A STRATEGY FOR THE CONSERVATION OF THE GENETIC DIVERSITY OF EUROPEAN CATTLE (3)

URL: The website is no longer operational. For further details on the project outcome please contact Dr J. A. Lenstra: J.A.Lenstra@vet.uu.nl

Project details

Start date: 1 April 1999
End date: 31 March 2002
Duration: 36 months
Project reference: Genres No CT98-118
Project total cost: EUR 1 103 794
Project EU co-financing: EUR 919 794

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Description

General information

About 8 000 years ago cattle were introduced into Europe from western Asia. Since then breeds have emerged through selection and adaptation. It has only been over the past 200 years that the identity of breeds has been formalised by the establishment of breed societies and herd books. Phenotypic breed standards were based on visible characters, particularly colour. Selection by local environments and for high production of milk or beef within the genetically isolated population has increased their genetic distinctness.

Europe is the historic source of most dairy and beef cattle breeds. However, from the mid-part of this century, modern farming practice has focused more and more on a few highly selected breeds that require intensive management systems. Within these breeds, intense se-

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(3) This work represents the contributions of the following members of the European Cattle Genetic Diversity Consortium: J. A. Lenstra, I. J. Nijman, Utrecht University, Netherlands; K. Moazami-Goudarzi, D. Laloë, INRA, Jouy-en-Josas, France; J. L. Williams, P. Wiener, D. Burton, Roslin Institute, United Kingdom; G. Erhardt, O. Jann, C. Weimann, E.-M. Prinzenberg, Justus-Liebig-Universität, Gießen, Germany; B. Harlizius, School of Veterinary Medicine, Hanover, Germany; C. Looft, E. Kalm, Christian-Albrechts-Universität, Kiel, Germany; S. Dunner, J. Cañón, Universidad Complutense de Madrid, Spain; C. Rodellar, P. Zaragoza, I. Martin-Burriel, Veterinary Faculty, Saragossa, Spain; A. Sánchez, J. Piedrafita, Universitat Autònoma de Barcelona; P. Ajmone-Marsan, R. Negrini, E. Milanesi, Università Cattolica del Sacro Cuore, Piacenza, Italy; A. Valentini, M. C. Savarese, C. Marchitelli, Università della Tuscia, Viterbo, Italy; M. Zanotti, G. Ceriotti, Università degli Studi di Milano, Italy; F. Pilla, A. Bruzzone, D. Iamartino, Università del Molise, Campobasso, Italy; D. Bradley, D. E. MacHugh, A. R. Freeman, Trinity College, Dublin, Ireland; I. Medugorac, A. Medugorac, H. Mix, M. Förster, Ludwig-Maximilians-Universität, Munich, Germany; J. Kantanen, MTT, Jokioinen, Finland; I. Olsaker, Norwegian School of Veterinary Science, Oslo, Norway; L. E. Holm, Danish Institute of Agricultural Sciences, Tjele, Denmark; I. Miceikienė, Vilnas, Lithuanian Veterinary Academy, Lithuania; Z. Grislis, Latvia University of Agriculture, Jelgava, Latvia; H. Viinalass, Estonian Agricultural University, Tartu, Estonia; B. Danell, Swedish University of Agricultural Sciences, Uppsala, Sweden; E. Eythorsdottir, Agricultural Research Institute, Reykjavik, Iceland; G. Mommens, Dr Van Haeringen Polygen, Malle, Belgium; C. Maudet, P. Taberlet, G. Luikart, Université Joseph Fourier, Grenoble, France; A. Beja-Pereira, N. Ferrand, A. Carvalho, P. Alexandrino, Universidade do Porto, Portugal; G. Dolf, University of Berne, Switzerland; M. Felius, Rotterdam, Netherlands.

lection has reduced the genetic basis and inbreeding is now threatening productivity, e.g. by decreasing fertility and disease resistance. Conservation of genetic variation is now recognised as a crucial and international concern to preserve a basis for selection and to maintain European competitiveness in the cattle breeding sector. This can be accomplished by maintaining populations of local breeds that are considered to be important for conservation. In addition, centres for cryoconservation have been established in France, Germany and the Netherlands. However, accurate and reliable information about genetic distances within and among European breeds and about the contributions of the respective breeds to the total diversity is required for the most optimal decisions on conservation priorities. This can only be accomplished by effective cooperation at the European level.

Objectives

The objectives of the project were: (1) to provide a well-regulated access to DNA samples from the majority of the European breeds for present and future research; (2) to search for information on genetic variation and distance, based on a state-of-the art genotyping of at least 60 breeds with 30 standardised microsatellite markers and 100 amplified fragment length polymorphisms (AFLP); (3) to provide fundamental insight into the effect of intense selection on the diversity of those parts of the cattle genome that are known to be relevant for milk and beef production; and (4) to propose recommendations for conservation, both with regard to the identification of breeds that contribute most to the global diversity and with regard to the number of individuals needed to conserve the diversity that exists within these breeds.

Achievements

The project has led to the organised availability of DNA samples of several industrial and local breeds stored in the laboratories of the participants (objective 1). This has already facilitated an analysis of the Europe-wide distribution of gene variation and Y-chromosomal polymorphisms (unpublished results).

AFLP fingerprinting (objective 2) permitted the genotyping of 81 biallelic markers in 51 breeds with about 20 animals per breed. Most markers correspond to SNPs (single-nucleotide polymorphisms). We showed that by a rigorous standardisation, AFLP data from two different laboratories could be combined. The resulting data set differentiated clearly the purely taurine breeds from the Podolian breeds in Italy and Hungary, in which introgression has introduced an estimated indicine (zebu) component of 5 % to 10 %. This is most likely the result of an introduction of Podolian breeds well after the original migration of domestic cattle into Europe.

A further differentiation of the taurine breeds has been accomplished by a data set of genotypes for 30 FAO-adopted microsatellites in 64 European cattle breeds, 25 to 50 animals per breed (objective 2). Genotypes with subsets of the 30 markers were available for 58 additional breeds and yielded complementary information. Analysis by model-based clustering and Neighbour-Net graphs led to the definition of three major groups of breeds and nine breed clusters:

1. the Mediterranean breeds, consisting of the Podolian and Iberian clusters, the first with zebu introgression but both relatively close to African and zebu breeds;
2. the Alpine–French breeds with the Alpine Brown, Alpine West (Simmental-like) and French Brown clusters; and
3. the Germanic cluster with Lowland Pied (dairy black- and red-pied breeds), Baltic Red (Red Danish, etc.), British and Nordic clusters, respectively. The British breeds are relatively distinct. The Northern part of France and the Alpine regions appear to be transition zones with breeds such as Charolais and Piemontese that are intermediate between other clusters.

The relations of the clusters were interpreted as reflecting the spreading of cattle husbandry from around 6 000 BC onward via different routes. Over recent centuries, genetic isolation and selection have accentuated the molecular differentiation at the breed level, while upgrading has spread the genotypes of a few popular breeds (black-pied, Danish Red, Ayrshire, Swiss Brown, Simmental, Blonde d'Aquitaine) outside their areas of origin.

The study of the effects of selection (objective 3) allowed a detailed analysis of the variation in the milk protein genes and an analysis of the genetic variation on cattle chromosome 2 as modulated by the selection for myostatin gene variants conferring double muscling (4).

Our findings have revealed several fundamental insights into the population genetics of European cattle, as modulated by history, landscape and breeding, and led to preliminary recommendations for conservation (objective 4).

1. For several breeds, molecular data indicate or confirm their uniqueness. This is now being explored further by marker-estimated kinship analysis. However, we still need to identify molecular markers (SNPs, gene copy numbers) that correspond to the breed-specific phenotypes.
2. Furthermore, the perceived value of a breed mainly depends on its role in the local tradition and history. Therefore, we advocate that at present molecular markers are to be used with caution and only in combination with other criteria.
3. A large genetic distance from other breeds often results from a small population size and does not always indicate the genetic value of a breed. Consequently, genetic distances should not be used as the sole criterion for assessing the genetic uniqueness of a breed.

Introgression is to be considered as an integral part of the history of a breed and does not diminish the value of a breed for conservation.

Publications

European Cattle Genetic Diversity Consortium, 'Genetic diversity of European cattle', *Proceedings of the XXIXth International Congress on Animal Genetics*, Tokyo, 10–16 September 2004.

Jann, O. C., Ibeagha-Awemu, E. M., Ozbeyaz, C. et al., 'Geographic distribution of haplotype diversity at the bovine casein locus', *Genet. Sel. Evol.*, Vol. 36, 2004, pp. 243–257.

Wiener, P., Burton, D., Ajmone-Marsan, P. et al., 'Signatures of selection? Patterns of microsatellite diversity on a chromosome containing a selected locus', *Heredity*, Vol. 90, 2003, pp. 350–358.

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(4) For milk protein genes, see Jann et al., 2004. For cattle chromosome 2, see Wiener et al., 2003.

FARM ANIMALS: A PERMANENT INVENTORY OF EUROPEAN FARM ANIMAL GENETIC RESOURCES AND OF ACTIVITIES ON CHARACTERISATION, CONSERVATION AND UTILISATION OF THOSE RESOURCES.

URL: http://www.eaap.org/content/RESGEN.HTM

Project details

Start date: 1 February 1997
End date: 31 December 1998
Duration: 23 months
Project reference: Genres CT96 No 83
Project total cost: EUR 88 000
Project EU co-financing: EUR 88 000

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Description

General information

Surveys of European breeds and populations have been organised since 1982, continually updated and entered into the animal genetic databank of the European Association for Animal Production (EAAP-AGDB) which was set up in 1987 in Hanover. The storage of information in this electronic databank allowed easy characterisation of breeds according to specific factors.

Since 1991, and during the development of the global strategy of the Food and Agricultural Organisation (FAO) for the management of animal genetic resources (AGR), surveys were initiated by the FAO and the United Nations Environment Programme (UNEP), first for seven mammalian species and later for 28 mammalian and avian species. Data for the European countries were provided by the EAAP-AGDB. In April 1996, the FAO global information system (i.e. DAD-IS for domestic animal diversity information system) was made available on the Internet (http://www.fao.org/dad-is/). In May 1996, the EAAP-AGDB was also made available on the Internet via the homepage of the Hanover School of Veterinary Medicine (TiHo) (http://www.tiho-hannover.de/einricht/zucht/eaap/index.htm).

Objective

The objective of this concerted action was to regularly update a comprehensive and reliable inventory of farm animal genetic resources in Europe. Therefore, the EAAP-AGDB should be extended and linked with the FAO domestic animal diversity information system (DAD-IS).

Achievements

Due to centralised facilities and considerable efforts of the scientists, the objectives of the project were met. In 1997, the project partners decided that the EAAP-AGDB should be regularly updated and transferred to the FAO DAD-IS. The representatives of EU national focal points (NFP) for animal genetic resources have agreed to collect data following a list of descriptors, the so-called EAAP questionnaire, and to transfer them to the EAAP-AGDB on a yearly basis after they have been validated. This step implied a clear agreement between EAAP and the Veterinary University of Hanover (TiHo), in charge of the EAAP-AGDB.

Due to this concerted action of scientists of different nationalities, 10 meetings were organised between 25 April 1997 and 26 August 1998. Such meetings offered good opportunities for better coordinating the activities of the EU NFPs.

The EAAP-AGDB questionnaire for collecting data on livestock populations was revised after having received comments from national coordinators and it was then validated by the EAAP WG-AGR. A comparison was also performed between the information stored in the DAD-IS and in the EAAP-AGDB. The major difference is in the presentation of performance data, which, in the EAAP-AGDB are expressed relatively to a reference breed living under similar production conditions in the same country, as against absolute figures in the DAD-IS. More detailed information is generally asked in the EAAP-AGDB system, which in particular offers the possibility of referring to specific institutions for obtaining more precise information on specific features and which also includes information on genetic distances. It should also be mentioned that DAD-IS covers more species as compared with EAAP-AGDB and includes photographs of the different breeds. A general update of the EAAP-AGDB was launched in April 1998. The difficulties experienced in several countries have been evaluated. The task of updating was actively pursued and was completed at the end of 1998. The task of linking the EAAP-AGDB and FAO DAD-IS was pursued within the Efabis (European farm animal biodiversity information system) biotechnology project (http://www.eaap.org/content/EFABIS.HTM).

In addition, the EAAP has established a list of experts able to operate as voluntary ‘referees’ in the various areas relating to animal genetic resources. It was the aim of the project to ensure the widest possible dissemination of the results via the Internet (http://www.eaap.org/resgen.htm), as well as various channels of publication, such as scientific journals and the EAAP newsletter. This European project has also been widely publicised at several international meetings.

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PIGS: EUROPEAN GENE BANKING PROJECT FOR PIG GENETIC RESOURCES

URL project: http://www.inra.fr/DIVERS/12a.htm

Project details

Start date: 1 April 1996
End date: 31 March 2000
Duration: 48 months
Project reference: Genres CT95 No 12
Project total cost: EUR 834 100
Project EU co-financing: EUR 530 000

Coordinator

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Description

General information

Pigmeat is a major source of protein for humans. According to FAO (Food and Agricultural Organisation) statistics of 1998, pigmeat accounts for about 38 % of the world's production of meat. Variations across continents are important; the proportion ranges from about 10 % of the meat production in Africa to 53 % in Asia. Europe is also a major area of pigmeat production and consumption: over the past 10 years, about half the meat that was eaten in the EU-15 was pigmeat.

It is also well known that Europe as a whole shares a large part of the world's pig genetic diversity, since nearly 46 % of the breeds registered in the world inventory of the FAO are found in Europe. Despite the wealth in EU pig genetic diversity, for commercial purposes the European pig industry relies on a limited number of breeds, common to all countries, which are used in the framework of highly integrated breeding schemes. The evolution of improved pig populations during recent decades has brought some performances close to their biological or economic optimum, thus reducing their future importance in the breeding objectives. Consequently, traits such as meat and fat quality, reproductive fitness, mothering abilities and adaptation to extensive conditions are likely to receive more and more attention. The need to develop alternative stocks to meet a wide variety of market/production conditions is recognised. This means that it is necessary to pay more attention to 'unconventional' germplasm, such as that provided by so-called minor or local breeds. Because of their small numbers and low economic value, several local breeds may become extinct.

A rational policy of conservation of pig genetic resources is needed. Today, conservation by maintaining breeds within their production system, i.e. *in situ*, integrated with cryoconservation of gametes, embryos and somatic cells, i.e. *ex situ*, is widely advocated. Cryoconservation brings safety in the long term against the risk of genetic erosion. Material stored is used as a backup in case genetic problems or extinction occurs.

Objective

The overall objective of this project was to establish the basis of a gene bank for the conservation of

European genetic resources of pigs. Particular reliance was put on storage of frozen semen from local breeds that are exposed to serious risks of genetic erosion, if not complete extinction. More specifically, the project intended: (1) to characterise a number of local breeds in four EU countries and two neighbouring central European countries; (2) to collect data on performance/quality characteristics of each breed; (3) to evaluate genetic variability within and between breeds, using genetic markers; and (4) to collect germplasm and to apply adequate cryopreservation programmes.

Achievements

The project results provide an overview of the situation of the pig genetic resources in four major pig producing countries of the EU, namely Spain, Germany, France and Italy. They can be divided into four groups, each of which corresponds to one of the specific objectives and tasks identified in the Genres CT95 No 12 project.

First, the inventory of the pig genetic resources in Europe (primary characterisation) has offered a general idea of the local breeds that exist in the four participating countries, as well as of their management. General information as well as 'passport data' have been collected on local breeds existing in each country. Available pedigree records have also been analysed. Twenty-three breeds were initially included in the project (i.e. eight German, six French, five Italian and four Spanish). A number of breeds were discarded, while three breeds from Spain were added. In total, 24 breeds were covered, namely one Czech, seven Spanish, four German, six French, five Italian and one Polish. Their primary characterisation has been made and the relevant information has been compiled in various national, regional or global databases, which are available on the Internet through DAD-IS, the FAO information system on domestic animal diversity (http://dad.fao.org/en/home.htm).

Secondly, the evaluation of the breeds provides additional information on reproduction and production performances, as well as any specific qualification of the breeds concerned. On-farm or experimental station performance records were collected and analysed within each country. These generally confirm the lower growth and carcass performances of local breeds, which are, however, usually compensated by higher meat quality. Special attention was also given to the analysis of cross-breeding systems including local breeds, as exemplified by the German experiments showing the economic competitiveness of such systems. Possible interactions with the environment and specific farming systems were analysed (e.g. extensive vs intensive systems in France and Italy). In such a context, the Iberian pig in southern Spain offers a good example of animal and environment integration for a product of world reputation — Iberian acorn ham.

Thirdly, the evaluation of genetic diversity among European breeds (genetic distances) presents an evaluation of within and between-breed genetic variability, based on blood groups (13 systems), biochemical polymorphisms (11 systems) and DNA simple sequence repeat (18 microsatellite loci), on a subset of 19 breeds (one in the Czech Republic, three in Germany, four in Spain, six in France, five in Italy and one in Poland). The genetic distances among those 19 breeds were used to derive a diversity function allowing an estimation of the contribution of each individual breed, or any breed combination, to the overall diversity. This evaluation should thus provide useful information for establishing conservation priorities both within and among the participating countries.

Finally, *ex situ* conservation of pig genetic resources (semen collections) were operated in each country and the status of the collected germplasm at the end of the project was detailed. Overall, the stored germplasm amounts to about 25 000 doses of semen for artificial insemination, collected from 278 boars belonging to 17 breeds. The state of the art in cryopreservation techniques was also reviewed, and practical recommendations for establishing gene banks from local breeds in danger of extinction were proposed.

In addition, this EU-supported cooperation has fulfilled useful roles by either providing a stimulus for additional support by the countries through their own financial resources (e.g. Spain and Italy), or by bringing substantial complementary support to the national policies already implemented (e.g. Germany and France). The work carried out has made clear the need to develop sound conservation programmes that will integrate *ex situ* strategies, such as semen conservation, with the maintenance of local endangered breeds within economically sustainable production systems. It is hoped that these results will help the management and conservation of pig genetic resources over the whole European continent and in other countries of the world as well.

Publications

Ollivier, L., Labroue, F., Glodek, P., Gandini, G. and Delgado, J. V. (eds), *Pig genetic resources in Europe*, EAAP publication No 104, Wageningen Pers, Wageningen, Netherlands, 2001, 150 pp.

Other participants

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Animal Genetics Institute	Göttingen	Germany	P. Glodek
Veterinary Institute	Göttingen	Germany	W. Wemheuer
Istituto per la difesa e la valorizzazione del germoplasma animale (IDVGA-CNR)	Milan	Italy	G. Gandini
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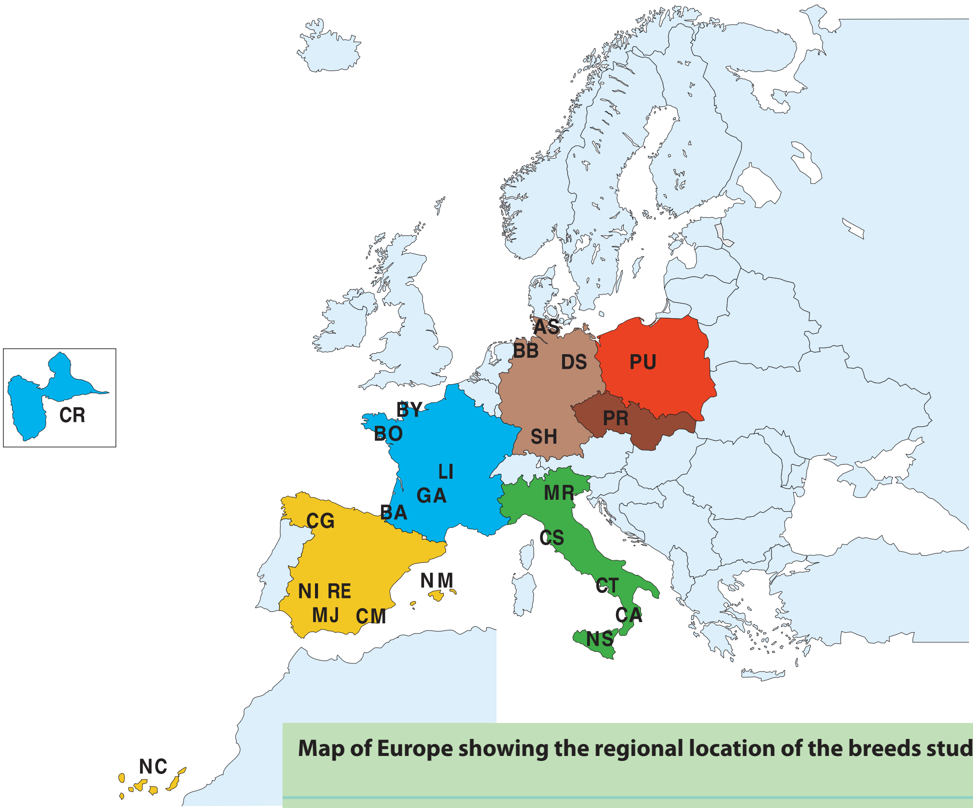

Map of Europe showing the regional location of the breeds studied in the project

France (in blue)
BA Basque
BY Bayeux
BO Blanc de l'Ouest
GA Gascon
LI Limousin
CR Créole (in the French over-sea department of Guadeloupe)

Germany (in brown)
AS Angler Sattelschwein
BB Bunte Bentheimer
DS Deutsches Sattelschwein
SH Schwäbisch-Hällisches Schwein

Czech Republic (in dark brown)
PR Presticke

Poland (in red)
PU Pulawska

Italy (in green)
CA Calabrese
CT Casertana
CS Cinta senese
MR Mora Romagnola
NS Nera Siciliana

Spain (in yellow)
CG Celta Gallego
CM Chato Murciano
MJ Manchado de Jabugo
NC Negro Canario
NI Negro Ibérico
NM Negro Mallorquín
RE Retinto

RABBITS: INVENTORY, CHARACTERISATION, EVALUATION, CONSERVATION AND UTILISATION OF EUROPEAN RABBIT GENETIC RESOURCES

URL project: http://ec.europa.eu/comm/agriculture/res/gen/60a.htm

Project details

Start date: 1 March 1996
End date: 31 October 2000
Duration: 48 + 8 months
Project reference: Genres CT95 No 60
Project total cost: EUR 586 410
Project EU co-financing: EUR 480 000

Coordinator

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Description

General information

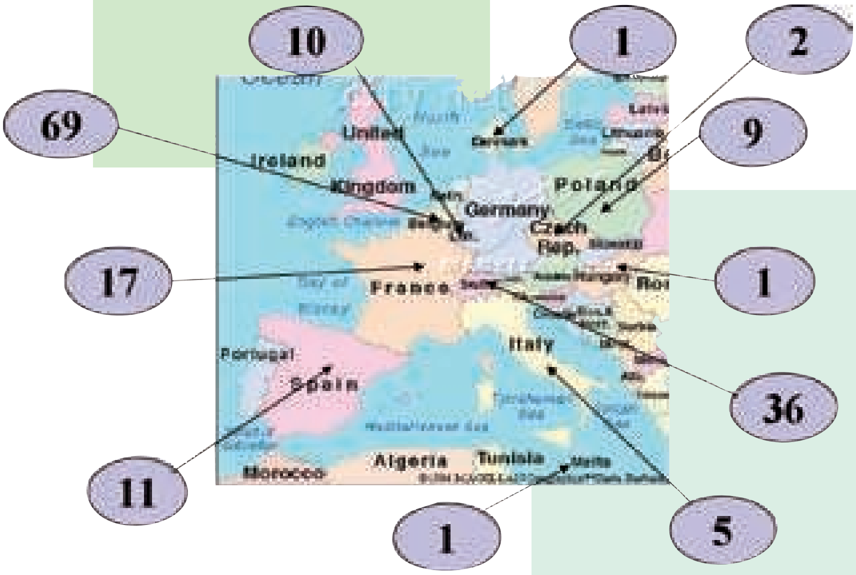
The domestic rabbit belongs to the species *Oryctolagus cuniculus* (European rabbit). It is the only domesticated mammal of western European origin. Nowadays, wild and domestic populations still coexist. The domestication of rabbits took place during the 18th and mainly the 19th centuries and the most important step in the creation of the breed occurred during the first half of the 20th century. Meanwhile, societies of breeders were created to maintain and improve these breeds. Today, national associations of breeders exist in many European countries. They are in charge of making and updating the standard book of rabbit breeds, and mounting exhibitions and competitions. They have registered more than 60 breeds in Europe. However, these breeds are rarely used for commercial production of meat, which is mainly based on specialised strains. In Europe (mainly Spain, France, and Italy), most of this production is realised using specialised breeds whose size is gradually increasing and middle-sized breeds (mainly New Zealand White, Californian) and a few heavy breeds for paternal lines. So, the role of pure breeding in meat production is very minor. Nevertheless, these unused breeds present a wide range of characteristics and constitute a unique reserve of genetic variability such as diversity of their adult size, growth, conformation, coat colour and fur type. These elements are well known but their potential diversity concerning zootechnical performances and genetic polymorphism has hardly been studied.

Objective

The general objective of this European programme, coordinated by INRA, was to promote a more comprehensive description of the rabbit breeds and to evaluate 10 of them at levels of both genetic diversity and zootechnical characteristics.

Achievements

From a questionnaire in six languages, disseminated throughout Europe by the European Association of Rabbit Breeders and the FAO national focal points, a databank has been created which includes historical, morphological, demographic and basic zootechnical information. More than 150 breeds from 11 countries have been registered (see map., *source*: INRA). This databank is available on the French FAO focal point (http://www.brg.prd.fr) and on the EAAP website (http://www.tiho-hannover.de/einricht/zucht/eaap/index.htm).



A sample of 10 of these breeds was chosen for detailed examination, namely argenté de Champagne, Belgian Hare, Chinchilla, English, Fauve de Bourgogne, Flemish Giant, French Lop, Himalayan, Thuringer, Vienna White, plus the Hungarian Giant Gigante de España breeds and a control strain from INRA.

Characterisation of genetic diversity within and between breeds involving six laboratories was also realised. This was performed by using different sets of genetic markers: mitochondrial DNA, microsatellites (28 loci), protein polymorphism, analysed either at the level of genes products (25 different loci) or at the molecular level (k-caseins), immunoglobulin and MHC genes. The analysis indicated strong genetic differentiation between breeds together with some structuring within the breeds. These domestic breeds showed an allelic diversity dramatically lower than that of the wild populations taken as a whole; no significant reduction was observed when compared with the wild populations from which they originated, with the notable exception for the immunoglobulin loci.

In addition, zootechnical evaluation was performed on five experimental farms with a common control strain on three of these. Reproductive performance was generally low for all breeds except fertility in breeds of small size. Preliminary results revealed a large diversity with respect to growth carcass and meat quality traits and original features for some breeds, with potential economic interest.

Finally, a cryobank was constituted, aiming at the conservation of well-characterised animals rather than endangered resources. This cryobank has collected about 15 000 frozen embryos and 360 semen straws from eight breeds.

This European programme was the first opportunity to approach the evaluation and conservation of rabbit genetic resources in such an extensive way. Moreover, its results allows all European partners to exploit the great genetic variability of this species to improve rabbit production, diversifying both its products and its conditions of production, in order to increase its contribution to the diversification of European agriculture.

Other participants

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PROJECT SUMMARIES

PLANT GENETIC RESOURCES

ALLIUM: PROTECTING FUTURE EUROPEAN COMMUNITY CROPS: A PROGRAMME TO CONSERVE, CHARACTERISE, EVALUATE AND COLLECT ALLIUM CROPS AND WILD SPECIES

URL: http://www.hri.ac.uk (for more detailed information please contact Dr David Astley, see below)

Project details

Start date: 1 March 1996
End date: 28 February 2000
Duration: 48 months
Project reference: Genres CT95 No 20
Project total cost: EUR 948 192
Project EU co-financing: EUR 530 000

Coordinator

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Description

General information

This project dealt with the gene pools of five crops, namely onion, shallot, leek, garlic and chive, which are important commercially, for nutrition and health and in local cultures throughout the EU. They are relevant at all levels of production including local communities and garden cultivation. All these crops show variations within Europe. In addition, some EU countries are important for wild taxa: Mediterranean countries for the wild relatives of leek; Nordic countries for chive (*Allium schoenoprasum* L.). The wild material was collected specifically for the evaluation work. These *Allium* crops are at risk since they are not competitive in the market today. And since wild taxa are under-represented in gene bank collections, there is a need to collect material so that it is available for use.

Before the project, collections had been established by national programmes. But a proportion of seed propagated material (onion, leek and chive) required regeneration in order to be available for characterisation and utilisation. Vegetatively propagated material (garlic, shallot and wild taxa) was maintained generally *in vivo* with all the associated costs, management and quarantine problems. Two EU centres, the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) and the University of Cordoba (UCO), had developed routines for disease elimination and *in vitro* maintenance. The Nordic Gene Bank had been responsible for the collection of traditional shallots (*Allium cepa* L.) in Nordic countries. Although minimal descriptors had been published by the International Plant Genetic Resources Institute (IPGRI) for crop groups (onion, shallot, leek and garlic), only a few accessions had been characterised and even fewer data included in the European *Allium* database (EADB). Characterisation data were required to identify gaps in collections, particularly for landrace material. Only the Centre for Genetic Resources, in the Netherlands, had made significant advances in the rationalisation of their collections of commercial accessions. In contrast, the representation of wild taxa in collections was seriously deficient, particularly for those taxa occurring naturally in the EU, such as the close relatives of leek in the *Allium* section and wild chive in Nordic countries.

Objective

The general objective of this project was to support applied and pure research in both the public and private sectors with access to characterised and well-documented, high-quality genetic resources collections for five *Allium* crops and related wild species. The specific objectives were to coordinate the genetic resources centres for *Allium* in the EU using the established European *Allium* database (EADB) at Warwick HRI, Wellesbourne.

Achievements

After agreeing a minimum list of descriptors and a common format for data exchange, passport data were collected, transferred and incorporated in the EADB by Warwick HRI Genetic Resources Unit (HRIGRU). It totals around 8 400 accessions and is available as a downloadable file from the HRIGRU website (http://www.hri.ac.uk); for more detailed information please contact Dr David Astley, project coordinator. The project partners have been involved in the continued development of the European cooperative programme *Allium* working group to develop an updated version of the *Allium* descriptors list.

- **Seed propagated material (onion, leek and chive)**

  The total number of accessions which were characterised in order to set up defined minimum descriptors for the seed propagated crops were: 532 for onion, 168 for leek/leek relatives, 4 for *A. fistulosum* and 36 for chives. In addition, 325 accessions of onion have been scored for bulb characteristics over three years by HRIGRU in association with a commercial onion breeder. The total numbers of accessions for which seeds have been regenerated were as follows: 307 for onion, 44 for leek, 22 for *A. ampeloprasum*, two for *A. tuberosum*, 4 for *A. fistulosum* and 36 for chives. All aspects of the regeneration and long-term storage process have met the international standards laid down by the IPGRI/FAO Seed Storage Committee.

  Preliminary core collections for leek and onion were defined using different criteria. The leek preliminary core was defined by wild/cultivated status, crop type, umbrella variety designation and country of origin. The breakdown for the onion gene pool was based on crop type, day-length adaptation, varietal group and provenance. A similar breakdown was used for the onion gene pool based on crop type, day-length adaptation, varietal group and provenance. For onion, no wild taxa were included in the core. The partners agreed a working protocol that gave target figures for the preliminary cores of 48 accessions for leek and 268 for onion.

  The responsibility for the collection of genetic resources in the project lay with the Greek Gene Bank and the Nordic Gene Bank. The Greek Gene Bank was extremely productive with a total of 217 accessions of wild *Allium* taxa being collected. Some of this material was utilised directly in the evaluation work. The ecogeographic survey has detailed the areas of Greece covered during the collection missions and information was collected on the status of the wild populations. The Nordic Gene Bank was successful in collecting landrace and wild chives in Scandinavia to fill gaps in the European collections.

  The evaluation work on leek and wild taxa for characters of horticultural importance was also successful. The screening work for pest and disease resistance in the cultivated and wild *A. ampeloprasum* complex provided interesting results in relation to resistance against white tip disease (*Phytophthora porri*), rust (*Puccinia porri*) and thrips (*Thrips tabaci*). Screening of the wild taxa for male fertility showed that most species produced flowers and that pollen viability proved to be high in most instances. In Denmark, trials were carried out screening onion germplasm for resistance to downy mildew. Although no significant resistance was found in those onion accessions which were screened, there was a detectable variance in the level of infection between accessions.

  The results and conclusions of the rationalisation trials were based on the remarks of onion and leek experts in consultation with the project partners. The results for the onion trial showed that for the various groups putative duplicates could be identified along with obvious mistakes and misnamed accessions.

- **Vegetatively propagated material (garlic, shallot and wild taxa)**

  The crop-specific characterisation descriptors for garlic and shallot were reviewed by the project partners and revised in consultation with the European cooperative programme for genetic

resources networks (ECP/GR) garlic and shallot group. The revised descriptors were used to characterise 17 accessions of shallots (*Allium cepa* var. *ascalonicum*). The overall activities of the partners involved in the characterisation of garlic have been considerable, leading to the definition of a garlic core collection of the 50 most important accessions extracted from a total of 285 accessions characterised within the project.

The work of producing disease-free *in vitro* material of vegetative accessions encompassed the following elements: the elimination of virus through thermotherapy and/or meristem culture techniques, the regeneration of plants from culture, the confirmation of successful eradication of virus using routine ELISA serological tests, the micropropagation of virus-negative plant material and the maintenance of this material *in vitro* as a virus-free *in vitro* gene bank. IPK and UCO have been successful in applying meristem culture in order to obtain virus-free *in vitro* plants, including virus-free plants from 94 accessions in IPK and from 70 accessions in UCO.

- **Additional output**

The outputs for each of the tasks defined have been met and in some cases exceeded significantly. However, the influence of the project reaches much wider than the specific achievements of the individual participants. Links with EU FAIR projects have been made, and additional *Allium* contacts in the EU and associated countries that will benefit any further developments for projects in EU plant genetic resources programmes have been developed. In addition, the project partners have had significant input into the revision of the IPGRI *Allium* descriptors and the work plan of the ECP/GR *Allium* working group and the new ECP/GR vegetables network.

Other participants

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Centre for Genetic Resources, The Netherlands	Wageningen	Netherlands	I. Boukema
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Dirección General de Investigación Agraria	Cordoba	Spain	F. Mansilla

The partners would like to record the very positive input of Teresa Kotlinska, Plant Genetic Resources Laboratory, Research Institute of Vegetable Crops, Skierniewice, Poland, who attended project meetings funded by the European cooperative programme and was active in all aspects of our work.

AVENA: EVALUATION AND ENHANCEMENT OF *AVENA* LANDRACE COLLECTIONS FOR EXTENSIFICATION OF THE GENETIC BASIS OF *AVENA* FOR QUALITY AND RESISTANCE BREEDING

URL project: http://www.fal.de/bgrc/eu99106

Project details

Start date: 1 January 2000
End date: 31 December 2004
Duration: 60 months
Project reference: Genres CT99 No 106
Project total cost: EUR 460 632
Project EU co-financing: EUR 415 273

Coordinator

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Description

General information

Oats are more nutritious in some respects than other EU-grown cereals and are an intrinsically low input cereal crop. The oil, protein and beta-glucan content of oat grains are unique in composition and quality amongst the cereal grains. Also, oats are among the least demanding of cereals in regard to suitable soil type for growing. Nutrient requirements are less than those for wheat or corn. Thus, oats can grow well in the less favoured agricultural areas of the Union.

Cultivated oats (*Avena sativa* L. and *Avena byzantina* C. Koch) rank fifth among cereals in term of world production. Although during the 18th and 19th centuries the oat cultivars planted were heterogeneous mixtures of mostly homozygous genotypes (oats is an annual self-pollinated crop), breeders in the 20th century started to practise mass selection and later pedigree selection, leading to the development of pure lines. Thus, most modern oat cultivars are highly homozygous and very uniform in appearance. Given modern breeding approaches, it is of great importance to preserve, conserve and characterise the plant material that can provide useful genes in the genetic pool of cultivated oats. Cultivated *A. sativa* and *A. byzantina* landraces are considered an excellent source of germplasm donors for classical breeding, since transferring genes from diploid and tetraploid *Avena* species to hexaploid oats by conventional breeding is very difficult. Furthermore, a large number of modern cultivars have been derived from individual plant selections from landraces or from crosses involving these selections. It is estimated that more than 100 cultivars have been derived worldwide from the Red Rustproof landrace.

Objective

The overall aims of the project were to record, characterise and evaluate the oat landraces present in the European gene banks. Characterisation of the landraces included primary descriptors (morphological highly heritable traits), secondary descriptors (resistance screenings to three major diseases — crown rust, stem rust and powdery mildew — and protein content) and molecular markers (AFLPs).

Achievements

The activities of the project were divided into seven tasks, which were accomplished by the five partners. The oat landraces present in the partners' collections, along with the landraces contributed by other gene banks, reached a total number of 1 053 entries, representing germplasm from at least 22 European countries, which were evaluated. All entries were included in an inventory database and a website (http://www.fal.de/bgrc/eu99106) and an information platform was set up (task 1). Seed quantities needed by all partners were estimated and multiplication plots were established by each partner (task 2). All entries were distributed and planted during three different growing seasons by all partners and primary descriptors were set and recorded (task 3). For comparison reasons, 10 established cultivars (two from each partner) were also included in the evaluation fields. Thirty-two primary descriptors (as published by the ECP/GR *Avena* working group IBPGR. IPGRI 1985 (http://www.ipgri.cgiar.org/publications/pubfile+.asp?ID_PUB=146) were used for analysis. The hierarchical clustering method using Ward's minimum variance method was used for constructing dendrograms showing the relationships among the entries. Reactions to naturally occurring infestations of diseases were also recorded (powdery mildew, crown rust and Barley Yellow Dwarf Virus). The secondary descriptors (task 4) included screenings for disease resistance to artificial inoculations with crown rust (*Puccinia coronata* f.sp. *avenae*), stem rust (*Puccinia graminis* f.sp. *avenae*) and powdery mildew (*Blumaria graminis* f.sp. *avenae*). A very small percentage of the entries tested (0.05 %, 0.01 % and 0.004 %, respectively) proved to be immune, very resistant or resistant to the abovementioned diseases. However, more entries proved to be resistant to naturally occurring outbreaks of these diseases. Protein content of the entries, which was also used as a secondary descriptor, ranged from 9.84 % to 18.87 % with a mean of 14.04 %.

The landraces were further characterised using molecular markers (task 5). Amplified fragment length polymorphism (AFLP) was the method used since it is a reliable and replicable method, generating a large number of polymorphic bands. An AFLP protocol for *Avena* was established during the first year of the project and the most informative pair of primers was chosen. All reactions were run in an automated genetic analyser. Comparisons between runs and scorings of polymorphic bands were done automatically using suitable software. The binary data obtained was used to calculate the genetic similarities and dendrograms were constructed revealing the relationships among the entries.

Identification of duplicates is based on combined results from the field evaluation (primary descriptors), the disease screenings and protein content (secondary descriptors) and the molecular data (AFLPs) (task 6). Landraces within the same cluster indicating com-

Other participants

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Institut national de la recherche agronomique (INRA)	Clermont-Ferrand	France	J. Koenig
Nordic Gene Bank (NGB)	Alnarp	Sweden	L. Bondo F. Ottoson M. Veteläinen J. Weibull

mon background can be considered mixtures of similar genotypes.

Dissemination of the project results is accomplished through publications, presentations in national and international conferences and the establishment of a website. Field results, along with photos of the landraces, the dendrograms (from field and molecular data), disease resistance and protein content from all entries are available at the website address.

Publications

Germeier, C. U., Frese, L. and Katsiotis, A., 'The European *Avena* database (EADB) — Towards an expert system for *Avena* genetic resources', *Proceedings of the seventh International Oat Conference*, 17–22 July 2004, Helsinki, Finland, p. 143.

Katsiotis, A., Drossou, A. and Bladenopoulos, K., 'Genetic diversity of *Avena* landraces accessed by AFLPs', *Proceedings of the seventh International Oat Conference*, 17–22 July 2004, Helsinki, Finland, p. 40.

Koenig, J., Germeier, C. U., Frese, L. et al., 'Characterization of European oat landraces for agronomical, morphological and quality data: assessment of genetic diversity and link with geographical origin', *Proceedings of the seventh International Oat Conference*, 17–22 July 2004, Helsinki, Finland, p. 39.

Veteläinen, M., Germeier, C., Katsiotis, A. et al., 'European *Avena* landraces as sources for genetic base-broadening, quality and resistance breeding', *Proceedings of the Eucarpia cereal section meeting 'From biodiversity to genetics: breeding strategies for small grain cereals in the third millennium'*, 21–25 November 2002, Salsomaggiore, Italy, pp. 18–21.

BARLEY: EVALUATION AND CONSERVATION OF BARLEY GENETIC RESOURCES TO IMPROVE THEIR ACCESSIBILITY TO BREEDERS IN EUROPE

URL: http://barley.ipk-gatersleben.de/

Project details

Start date: 1 April 1999
End date: 30 September 2002
Duration: 36 months + 6 months prolongation
Project reference: Genres CT98 No 104
Project total cost: EUR 1 040 314
Project EU co-financing: EUR 823 000

Coordinator

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Description

General information

Barley is grown in the European Union on more than 11 000 000 ha, which is about 2.5 % of the cultivated area, and accounts for some 2 % of the total value of crop production.

Barley genetic resources collections in Europe comprise about 160 000 accessions, among them 80 000 in the 'previous' 15 EU Member States. The use of genetic resources existing in national gene banks on a European level requires easy access to information about the accessions for all users in EU countries, such as breeders, farmers and scientists. Existing information has to be complemented by important data, such as disease resistance or tolerance to abiotic stresses. Indeed, genetic resistance against biotic stresses is, among other traits, a decisive factor for the productive value of a cultivar. The development of disease and pest resistance is important in order to reduce chemical plant protection in this crop. In addition, tolerance to abiotic stresses is important to stabilise the yields of this crop.

Therefore, this EU-funded project was launched involving gene banks, research institutions, breeding firms and one NGO. The participation of an additional seven partners from six 'previous' non-EU member countries in evaluation activities and project meetings was co-funded by the European cooperative programme on crop genetic resources networks (ECP/GR).

Objective

This project was complementary to activities performed within the ECP/GR. It was coordinated by the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK). Its aim was to evaluate several hundred to several thousand barley accessions for resistance to various pathogens and pests such as fungi, viruses or aphids, and for tolerance to environmental stresses such as drought, cold, heavy metals, salinity or acidity. Therefore, agreed evaluation methods were used (see the project website). Accessions to be evaluated were selected from the international barley core collection (BCC) and from the partners' gene banks. As part of the project, the ECP/GR European barley database (EBDB) was to be updated and extended in its func-

tionality to include characterisation/evaluation data resulting from the project. Other activities included: identification of duplicates; provision of information on gaps and unique accessions; identification of needs for urgent multiplication and characterisation; provision of promising material to interested breeders, some of whom have already participated in the project.

Achievements

The material was mainly multiplied for evaluation purposes within the project. While 8 299 barley accessions were multiplied instead of the 6 120 foreseen ones, the multiplication of wild barley species proved to be more difficult. Only 137 out of 530 foreseen accessions were successfully multiplied. Most wild accessions originated from the Near East, the centre of origin of the cultivated species. This material possesses, therefore, interesting traits such as disease resistance or drought tolerance. In total, the project partners characterised 30 000 accessions for a range of morphological traits. The choice of descriptors was left to the individual multipliers of the germplasm.

The European data in the EBDB was extended from 90 000 to 156 000 accessions. Several database fields were further standardised and the database is hosted on a Linux-based web server (http://barley.ipk-gatersleben.de/) at IPK. By standardisation and combination of data sets from different contributors it was possible to obtain some interesting results. As an example, promising hot spots for leaf rust resistance in *H. vulgare* subsp. *spontaneum* were located in Israel.

An important task at the beginning was the standardisation of evaluation methods for biotic and abiotic stress factors.

Concerning biotic stresses, the emphasis of these evaluations was placed on field experiments (58 033 observations, see table), but glasshouse observations were also made (11 200). The accessions with good results for resistance were selected and their results were tested for confirmation, in another year and other sites with more repetitions at each site. In many cases modern breeding lines have shown a better combination of resistances than most gene bank material. No accession was found in any of the tests that showed a significantly lower infection and better performance than the resistant standards. However, a series of accessions with lower infection than the

Table

Biotic stresses	*Number of observations*
Fungal diseases	
Puccinia hordei (rust)	10 798
Pyrenophora teres (net blotch)	7 223
Blumeria graminis (powdery mildew)	12 227
Rhynchosporium secalis (scald)	10 146
Pyrenophora graminea (barley stripe)	2 204
Virus diseases	
Barley yellow dwarf virus (BYDV)	1 233
Barley yellow mosaic virus 1 and/or 2 (BaYMV)	5 060
Barley mild mosaic virus (BaMMV)	184
Aphids	
Rhopalosiphum padi	2 232
Sitobion avenae and *Metopolophium dirhodum*	2 232

susceptible standard was found. These accessions can be considered as resistant in a broad, qualitative sense. The majority of the tested material contained low to moderate resistance. In addition, spring and winter barley showed rather different resistance distribution frequencies for the four major fungal diseases.

Regarding the abiotic stresses, a number of accessions have been found to be tolerant. The abiotic stress factors that were observed are the following: cold, drought, salinity, heavy metals and soil acidity. The screened accessions showed a large variation for frost tolerance, and few of them could be considered frost tolerant. Drought-tolerant accessions were found but most of them showed a rather low level of productivity in non-stress environments. Major differences were also recorded due to the variation in tolerance against heavy metals and soil acidity. The effect of salt on the germination of material from the Israeli/British *spontaneum* collection was observed and potential sources of salt tolerance were also found in this material.

In conclusion, access to barley germplasm for increased utilisation by breeders has been provided and some partners even wish to continue the project on a free cooperative basis. Furthermore, 50 000 accessions have been identified with various degrees of duplication. The further steering and implementation of actions after this project have been handed back to the ECP/GR working group on barley.

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Barbier, A., Steyer, S. and Habekuß, A., 'Evaluation of the barley genetic resources for virus resistances (BYDV, BaMMV, BaYMV)', in: Marè, C., Faccioli P. and Stanca A. M. (eds), *From biodiversity to genomics: breeding strategies for small grain cereals in the third millennium, Proceedings of the Eucarpia cereal section meeting*, 21–25 November 2002, Salsomaggiore, Italy, 2003, pp. 48–50.

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BETA: EVALUATION AND ENHANCEMENT OF *BETA* COLLECTIONS FOR EXTENSIFICATION OF AGRICULTURAL PRODUCTION

URL: http://www.fal.de/bgrc/eu9542/default.htm

Project details

Start date: 1 June 1996
End date: 28 Feburary 2002
Duration: 60 + 9 months
Project reference: Genres CT95 No 42
Project total cost: EUR 848 109
Project EU co-financing: EUR 550 000

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Description

General information

Europe is the major source of wild species of the genus *Beta* and its cultivated forms such as the leaf beet, garden beet, fodder beet and sugar beet cultivar group. Sugar beet has become one of the most important cash crops in Europe and the world. Since modern sugar beet hybrid varieties were all derived from a single source population, the Silesian beet, the breeding gene pool is considered to be narrow. Until the mid-1980s, sugar beet breeding mainly focused on the improvement of yield and sugar quality as well as seed quality, resulting in a considerable increase in productivity. The progressive industrialisation of agricultural production, economic constraints and the wide use of agrochemicals have contributed to a narrow system of crop rotation and to a concentration of crop production in specific areas.

Consequently, the stability of sugar beet production is increasingly affected by the spread of pests and diseases such as the cyst nematode in the 1960s (*Heterodera schachtii*) in 'old' production areas close to sugar factories, Rhizomania in the 1980s, and more recently Rhizoctonia disease. Since the 1980s, it has been clear that sugar beet production would not be competitive any more without new resistant varieties. Increasingly, resistance has become an important breeding objective to secure sugar beet production in Europe.

Objective

The overall aim of this project was to enable the evaluation of agronomically important characters in stored material. By enabling all partners to work together, this project allowed for the first time the generation of comparable data and the identification of individual accessions resistant to pests, diseases and tolerant to drought stress.

In accordance with the work programme set out for Council Regulation (EC) No 1467/94 the project was divided into three main tasks: (1) improvement of conservation; (2) evaluation for utilisation; and (3) rationalisation of collections.

Achievements

The project has been organised following the step-by-step progression suggested by the work programme of Council Regulation (EC) No 1467/94 (Annex 2).

Since a similar project had been submitted to the Commission of the European Communities (CEC) in September 1990, a project plan and network of potential project partners (step 1) existed already in 1991. The descriptor list for *Beta* (CPRO-DLO/IPGRI, 1995) was published by an international group of *Beta* experts and an online accessible taxonomic key to species of the genus *Beta* started functioning in the year 2001.

The collection had been taxonomically classified to a large extent before the project started and had partly been characterised (mostly data on growth habit and annuality) (step 2). A common database for data exchange of passport, characterisation and evaluation data had already become operational in 1989. The database served during the project as a central management tool in particular for the acquisition of germplasm and the import and export of the characterisation and evaluation data. The passport data were used to develop a draft *Beta* core collection of 805 accessions, a maximum of 700 were used for screening for disease resistance and drought tolerance.

Timely seed production was a prerequisite for the evaluation work which was performed in step 3. Project partners multiplied a total of 937 accessions and recorded 16 397 characterisation data either during seed production or during the comparison of probable duplicates in the field. The information was published in the International database for Beta (IDBB) and is accessible online (http://www.ecpgr.cgiar.org/databases/Crops/beta_intl.htm). Depending on the individual project partners' task, between 410 and 700 accessions were evaluated. In total 5 248 new evaluation data calculated from single plant tests or replicated trials were gathered and compiled. Resistance to beet mild yellow virus, beet yellow virus, beet necrotic yellow vein virus, *Aphanomyces cochlioides*, *Pythium ultimum*, *Cercospora beticola*, *Erysiphe betae* and tolerance to drought have been detected. The evaluation data were imported into the IDBB and were made available to interested parties.

The possibility of combined searches for passport and evaluation data allows the sorting of the collection (step 4). Since the IDBB can be searched online, all information gathered during the lifetime of the project, as well as the accessions, are freely available to any user. A search for duplicates in the European *Beta* holding was concluded with the goal to rationalise the European *Beta* holding. In theory, the identification of duplicates can reduce the amount of redundant germplasm in collections and minimise the duplication of effort expended in seed regeneration, characterisation and documentation. Furthermore, a streamlined European collection would help avoid the evaluation of redundant material and thus facilitate access to useful variation in large collections. After identifying probable duplicates through the analysis of the IDBB, genetic similarity was investigated using field morphological comparisons and molecular markers.

The results confirmed only 12 pairs of accessions which could reliably be considered as duplicates — the identification of duplicates allowed the European *Beta* holdings to be rationalised (step 5).

Also, a draft core collection was constructed according to a branching method. This allowed the identification of those branches of the *Beta* diversity tree which contained useful variation. For each individual disease trait, as well as for drought stress tolerance, it was possible to associate 'resistant' or 'tolerant' accessions with a taxon and country of origin. In order to improve access to useful traits, users can search for detailed data on individual accessions which can easily be ordered from gene banks. And if a breeder is searching for additional variation to broaden the genetic base of a trait within a specific breeding gene pool, he or she can screen accessions belonging to the branch (subpath) of the diversity tree, where a specific trait has been discovered previously. Detailed knowledge on the taxonomic and geographical structure of useful genetic diversity is the major and most specific output of the Genres CT95 No 42 project and great progress has been made compared to the 1990s. Resistant accessions are already used in follow-up research projects, partly funded by the European Community, with the objective of broadening the genetic

base for the breeding of sugar beet. Indeed, the discovery of resistant germplasm has created new options for the breeding of resistance and the genetic improvement of today's hybrid varieties.

In addition, within this crop-specific sector, the project has promoted collaboration and task-sharing between different and complementary institutions (gene banks from Germany and Greece, public research institutions from Italy and the United Kingdom, and private companies from Germany, Italy, Sweden and the Netherlands) at the Community level. But it has also brought together at the international level via collaboration of the project partners, organisations such as the International Institute for Beet Research (IIRB), the ECP/GR working group on *Beta* and the world *Beta* network (WBN). The project has furthermore contributed to the preservation and exploitation of genetic resources of one of the few genera of worldwide importance which are native to the European region, thus supporting the European Community to fulfil international obligations arising from the Convention on Biodiversity (5).

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(5) The Convention on Biodiversity was approved by the European Community on 21 December 1993.

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Asher, M. J. C., Luterbacher, M. C. and Frese, L., 'Wild *Beta* species as a source of resistance to sugar-beet pests and diseases', *International Sugar Journal*, Vol. 103, 2001, pp. 447–451.

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BRASSICA: COLLECTIONS FOR BROADENING AGRICULTURAL USE INCLUDING CHARACTERISING AND UTILISING GENETIC VARIATION IN *BRASSICA CARINATA* FOR ITS EXPLOITATION AS AN OILSEED CROP

URL: http://www.cgn.wur.nl/pgr/collections/brasedb/

Project details

Start date: 1 January 2000
End date: 31 December 2003
Duration: 48 months
Project reference: Genres CT99 Nos 109–112
Project total cost: EUR 1 654 991
Project EU co-financing: EUR 935 818

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Description

General information

The project was a fusion of two separate proposals Genres No 109 '*Brassica* collections for broadening agricultural use' and Genres No 112 'Characterising and utilising genetic variation in *Brassica carinata* for its exploitation as an oilseed crop'. From the 16 partners, 11 conserved collections of the four *Brassica* species (*B. carinata*, *B. napus*, *B. oleracea* and *B. rapa*), two use *Brassica* in their research and three were plant breeding institutions of which one partner coordinated nine breeding companies. Data concerning the majority of accessions in these collections were already included in the existing European *Brassica* database (Bras-EDB), managed by the CGN, the coordinator of the project. These collections constituted about 70 % of the total accessions held in Europe, including eastern Europe, Turkey and Russia. However, the data on the database were mostly limited to passport data. Only part of these collections had been characterised for minimal descriptors and only very limited material of these collections had been evaluated for important characters like resistance to various pests, disease and environmental stress and quality properties, like glucosinates and TAGs (triacylglycerols). In addition, major parts of the collections needed regeneration.

Objective

The project aimed to conserve, document, characterise, evaluate and rationalise European collections of four important *Brassica* species and to contribute to a better knowledge of the genetic resources of these important *Brassica* species and improve utilisation of the gene pools in Europe by plant breeders and growers. The project deals with the following *Brassica* species: *B. oleracea* (cole crops, e.g. kales, cabbages, cauliflower, broccoli, kohlrabi, couve tronchuda, Brussels sprouts); *B. rapa* (turnip and turnip rapeseed); *B. napus* (rapeseed or colza and swedes); *B. carinata* (Abyssinian mustard).

Achievements

The Bras-EDB was updated twice during the four-year project period. This database focuses on passport data

Table: Overview of the evaluations conducted

Property	**Number of properties**	***Brassica* species**
Pest and diseases	11	All four *Brassica* species
Quality	4	*B. Napus, B. rapa,* *B. carinata*
Salt tolerance	1	*B. oleracea*
Agronomic evaluation	2	*B. carinata*

of collections of the genus *Brassica* maintained in European countries. The version 2001 of the Bras-EDB included 32 collections in 22 countries. This version contains 19 110 accessions of both cultivated and wild material. The 2004 version was extended with a few new collections and further updated and improved with addresses in line with the FAO/IPGRI multi-crop passport descriptors. The database contains passport data of about 19 600 accessions and includes 36 collections of 22 countries. The 2004 version of the Bras-EDB has been made online searchable on the Internet (http://www.cgn.wur.nl/pgr/collections/brasedb/).

The project was divided into four subgroups, each of which had its own core collection developed. The size of the four core collections is as follows: 395 accessions of *B. oleracea*, 100 accessions of *B. rapa*, 150 accessions of *B. napus*, 80 accessions of *B. carinata*. The project has given much emphasis on regeneration, characterisation and evaluation of germplasm included in the core collections. Evaluation for 18 different properties has been carried out. All accessions selected for the four core collections are tagged in the Bras-EDB. The subgroups agreed upon sets of minimum descriptors for each of the four *Brassica* species. The cores and parts of the collections were characterised for these descriptors. In total, the project characterised over 1 250 accessions. A large part of the *B. carinata* collection was characterised using DNA fingerprinting. The project regenerated some 889 accessions covering all four *Brassica* species.

More than 4 800 samples were evaluated for a range of properties (see table). Results of these evaluation experiments will be linked to the Bras-EDB. The different evaluations resulted in the detection of accessions with interesting properties for further breeding. Partial resistance was found in *B. oleracea* accessions against *Plasmodiophora brassicae* (clubroot), *Xanthomonas* and *Mycosphearella*. In *B. napus* resistance or partial resistance against stem flea beetles, stem weevils and field slugs were detected. Differences for qualitative and quantitative composition of glucosinolates were found in *B. rapa*, where the quantitative characters were highly dependent on the growth stage. Differences in seed storage components were found in *B. napus* as well as in *B. carinata*.

The system of safety duplication of *Brassica* collections in Europe has been greatly improved compared with the situation at the beginning of the project in 2000. The majority of the gene banks have now safety duplicated their *Brassica* collections in another place.

All subgroups identified gaps in the respective four *Brassica* species. For *B. oleracea*, gaps in the European collections were found in the Balkan region, north Africa and the Middle East for cultivated material and at the Adriatic coasts and northern part of the Ionic and Aegean Seas for wild material. For *B rapa*, there is insufficient wild material available. Suggestions were made to collect this in the Baltic States, because almost no cultivated *rapa* is grown there. For *B. napus* there is very limited material from China available in European collections.

This information can be seen as a guideline for the future to fill the gaps in the existing *Brassica* collections.

In addition, the results of the project were disseminated by means of a workshop, publications and presentations and the Internet (see above). The project has brought together European scientists actively involved in the conservation and utilisation of plant genetic resources of the most important *Brassica* species as well as private breeding companies, universities and institutes. This guarantees the future use of the *Brassica* material in the production of new varieties for the benefit of European agriculture.

The enormous improvement of the Bras-EDB, with an addition of more than 6 500 accessions, allows opti-

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mal access of the European *Brassica* collections to all potential users. This specific crop database is unique in the world and can be used by researchers and plant breeders for selecting *Brassica* germplasm. The linkage of the evaluation and characterisation results of this Genres project makes the Bras-EDB even more useful for future research.

Publications

Boukema, I. W., Bas, N., Thomas, G. et al., 'Evaluation, characterisation and regeneration of *Brassica oleracea* germplasm collections in the EU Genres CT99 109–112 project "Brassica, including *B. carinata*"', *Cruciferae newsletter*, Vol. 25, 2004, pp. 107–108.

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CARROT: THE FUTURE OF THE EUROPEAN CARROT — A PROGRAMME TO CONSERVE, CHARACTERISE, EVALUATE AND COLLECT CARROT AND WILD RELATIVES

URL: http://www.hri.ac.uk (for more detailed information please contact Dr David Astley, see below)

Project details

Start date: 1 January 2000
End date: 31 December 2003
Duration: 48 months
Project reference: Genres CT99 No 105
Project total cost: EUR 799 283
Project EU co-financing: EUR 584 533

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Description

General information

The carrot, *Daucus carota*, is an important commercial vegetable. The genus *Daucus* is native to Europe and hence a responsibility of EU countries under the Convention on Biological Diversity. Wild taxa can be conserved *in situ* and *ex situ* and they are being used increasingly in research and breeding. There are some populations threatened in the wild, e.g. by overgrazing, and *ex situ* conservation is a valuable way of ensuring the material is conserved.

Before this project, there had been no coordinated effort in Europe, or indeed elsewhere, to conserve, document and make available the genetic resources of carrot and related wild taxa. Some institutes and gene banks in the EU maintain collections of carrot and *Daucus* taxa, but there had been no attempt to compare the contents of these collections or coordinate their management. It is important to ensure the efficient management of genetic resources collections, to reduce duplication of effort between gene banks and to offer well-documented high-quality material to users. In addition, there is great pressure from governments and the public to reduce pesticide chemicals in the environment, leading to an urgent need to develop alternative methods of crop protection. The development of resistant or tolerant cultivars reduces the volume of pesticides used in the production of a crop, thus improving the environment and reducing production costs.

Objective

The project dealt with the gene pool of carrot and its wild relatives, aiming to coordinate work in European collections through five main areas of activity: (1) the conservation and documentation of European collections; (2) characterisation for minimal descriptors; (3) evaluation for important horticultural characters, such as pest and disease resistance and chemical composition; (4) sorting and rationalisation of the collections; and (5) collection of germplasm to fill the gaps in the collections.

Achievements

The main result of the project is the establishment of the European carrot/*Daucus* inventory (ECDI). This

ECDI database contains passport information for 5 317 *Daucus*/carrot accessions from 18 institutions across Europe (data from seven of the project partners are included in the ECDI). The European cooperative programme for genetic resources networks (ECP/GR) multicrop passport descriptors were used as the basis for the ECDI with the addition of three descriptors taken from the International Plant Genetic Resources Institute (IPGRI) descriptors for carrot. All the information is available on the Genres carrot project information pages on the Warwick HRI Genetic Resources Unit website (http://www.hri.ac.uk); for more detailed information please contact Dr David Astley, project coordinator). The site provides details of the project partners, the objectives and milestones and a link to the ECDI database.

The project characterisation data, also available on the site, were recorded based on a minimum set of descriptors taken from the IPGRI descriptor list for wild and cultivated carrots (1998) and the International Union for the Protection of New Varieties of Plants (UPOV) guidelines for the conduct of tests for distinctness–uniformity–stability carrot (1990). A total of 1 045 accessions have been characterised over the four years of the project. In addition, many of the partners also captured digital images of the material, which are maintained by individual partners. The images are particularly useful to demonstrate the variation found in traditional cultivated material for such traits as root colour. Up to 347 biennial accessions have been regenerated during the period of the project, using best local practice, with the seeds being conserved under long-term storage conditions.

Molecular markers have proved their efficiency for the identification of duplicate accessions in genetic resources collections. The partners decided to evaluate the use of molecular markers for the identification of carrot accession duplicates using, as a model analysis, 25 presumed duplicates of Jaune du Doubs from a number of European collections. Based on these results, a protocol for the identification of carrot duplicates was produced.

Data for specific horticultural traits have also been collected relating to accessions: the insect pest (carrot root fly, 60 accessions), root fungi (cavity spot, Sclerotinia soft rot (*Sclerotinia*), Crater rot (*Rhizoctonia*) and Liquorice rot (*Mycocentrospora*), 63 accessions), foliar fungi (*Alternaria*, 426 accessions). A number of accessions were detected which expressed a stronger resistance than the standard. These accessions are of interest for carrot breeders as potential genetic resources of resistance alleles. The selected resistant cultivars are directly available to breeders. These represent an important source for new alleles associated with a resistance usable in an introgression breeding programme or research. Quality characters were also evaluated from about 250 accessions for a number of characters including the root content of carotenoids, sugar and nitrate. Large differences between accessions were found for all characters. A number of accessions evaluated in different seasons evidenced genotype x environment interaction for nitrate, carotene and sugar content. Some germplasm accessions showed useful characters for their particular stability across environment or suitability for production in specific conditions, with more favourable traits than commercial standards.

In addition, preliminary work has been carried out to develop a core collection for the carrot/*Daucus* gene pool but more research is required in this area. A collecting mission to Crete, an area for which no *Daucus* or carrot collections existed in the European carrot/*Daucus* inventory or other international collection databases, was also realised. The mission was very successful, collecting a total of 60 *Daucus* samples, the majority being wild *Daucus* species from throughout the island, plus obtaining seed of the last remaining carrot landrace on Crete.

Thereby this project, having promoted the coordination within the EU for carrot/*Daucus* genetic resource programmes, has minimised the duplication of scientific and administrative efforts, and maximised the availability of genetic resources and associated information within the Community.

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The partners would like to record the very positive input of Teresa Kotlinska, Plant Genetic Resources Laboratory, Research Institute of Vegetable Crops, Skierniewice, Poland, who attended project meetings funded by the European cooperative programme and was active in all aspects of our work.

CUCUMIS MELO (MELON): MANAGEMENT, CONSERVATION AND VALORISATION OF GENETIC RESOURCES OF *CUCUMIS MELO* AND WILD RELATIVES

URL: http://www.eelm.csic.es/PM/index.htm

Project details

Start date: 1 January 2000
End date: 31 December 2002
Duration: 36 months
Project reference: Genres CT99 No 108
Project total cost: EUR 261 439
Project EU co-financing: EUR 180 000

Coordinator

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Description

General information

Melons are widely cultivated in warm climates all around the world. A total of 2 502 000 tonnes were harvested in 1996 in Europe, mainly in the Mediterranean countries. Among these, Spain has the highest melon production (943 000 tonnes in 1996). In Spain, Portugal and Turkey, melon hybrids are grown not only for national consumption but also for export to the countries of central and northern Europe. Gallia, Amarillo or Charentais types are grown mostly for export to Germany, France and the United Kingdom, these being the most important melon markets in Europe. The environmental conditions in the countries of southern Europe are very good for growing melons. In some areas, the different species have become highly diversified. In fact, the International Plant Genetic Resources Institute (IPGRI) considered the Iberian Peninsula as an important secondary centre of melon diversity. This variety of plant genetic resources provides the material for growers to improve their crops in response to biotic or abiotic stress and for breeders to draw on in their breeding programmes. However, in recent times, melon growers have abandoned traditional varieties in favour of modern types and the collection of seeds held in melon gene banks around the world are somewhat threatened because of inadequate conditions. It is assumed that since the beginning of the century a significant percentage of melon genetic diversity has been lost. Furthermore, there is still insufficient knowledge about the intraspecific variability in *C. melo* for many characters related to fruit quality and disease resistance. Melon collections in Europe contain mainly landraces and cultivars of *C. melo* and some related wild species. Although there exist important germplasm collections in different countries, little information is available on their horticultural features. Since their evaluation costs much time, effort and money, they are unfortunately still undervalued and of little use.

Objective

This project aimed to improve the conservation, characterisation, collection and utilisation of genetic resources of melons in Europe. Furthermore, collaboration and work coordination among the different partners were to be promoted. It concentrated on five main topics: (1) design and test a database and inventory; (2) characterisation of the collections; (3) evaluation and utilisation; (4) sorting and rationalisation of the collections; and (5) acquisition of genetic resources.

Achievements

The areas in Turkey which were prospected by the University of Çukurova were the south-east, eastern and central Anatolian, Thrace, Aegean and Marmara

regions. In all those areas, old melon varieties and landraces which are at risk were collected. It is assumed that an important reduction of the risk of genetic erosion in Turkey has been achieved.

Initially, an inventory of 1 762 melon accessions including wild relatives was established relating to 20 passport data. They all belong to five European collections. The Turkish partners added 176 new melon accessions. And, finally, a total of 149 duplicates have been found among the different melon collections.

The evaluation of a total of 397 melon accessions has been carried out on the basis of a list previously established regarding 18 descriptors and 16 relevant characters for fruit quality which are of interest in melon breeding (Abak, 2001, López-Sesé et al., 2002, 2003). Those accessions have also been regenerated by partners. In addition, Estación Experimental 'La Mayora' (CSIC) and Centro de Investigación y Tecnología Agroalimentaria de Aragón have evaluated their assigned accessions under artificial conditions of infection against *Sphaerotheca fuliginea* races 1 and 2, *Fusarium oxyosporum* f.sp. *melonis* races 0.1 and 2, watermelon mosaic virus, papaya ringspot virus, zucchini yellows mosaic virus, cucurbit yellows stunting disorder virus and cucumber mosaic virus (Díaz et al., 2003, Alvarez et al., 2005). Due to its economical importance and interest and the non-availability of resistance in melons, 138 melon accessions coming from different origins and 14 wild relatives have also been evaluated against cucumber vein yellowing virus (Marco et al., 2003, Montoro et al., 2004).

A framework of a melon database (Excel® file) to accommodate all passport, first characterisation and evaluation data for those accessions has been established. A core collection composed of 186 melon accessions and wild relatives has been established, too (Gómez-Guillamón et al., 2004). This collection will be maintained in long-term storage in the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) situated in Gatersleben. Free exchange according to international rules will be possible for the partners of the project and it should also be extended to other institutions interested in this European project.

Other participants

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Publications

Abak, K., 'Melons from Turkey: main types and their characteristics', *Proceedings of the 23rd Geisenheim meeting*, 2001, pp. 12–14.

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EGGPLANT: GENETIC RESOURCES NETWORK — MANAGEMENT CONSERVATION AND VALORISATION OF GENETIC RESOURCES OF EGGPLANTS (*SOLANUM* SPECIES) — EGGNET

URL project: http://www.bgard.science.ru.nl/eggnet/eggnet01.html

Project details

Start date: 1 January 2000
End date: 31 March 2005
Duration: 63 months
Project reference: Genres CT98 No 113
Project total cost: EUR 497 301
Project EU co-financing: EUR 429 987

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Description

General information

Eggplants (in the broad sense) encompass several species of *Solanum* that are grown as gastronomically interesting and nutritionally valuable vegetables or dessert fruits. Many wild species related to eggplants are also used as food or medicinal plants. The best-known eggplant species is *Solanum melongena* (aubergine or brinjal eggplant, of Asian origin), but other species, very popular in their native countries, can contribute to the diversification of European food, such as the African *S. aethiopicum* (scarlet eggplant) and *S. macrocarpon* (Gboma eggplant), which are fruit and/or leaf vegetables; the American *S. muricatum* (used as a dessert fruit as well as a vegetable) and *S. quitoense aff.* (which produce pleasantly fragrant fruits). Furthermore, many wild *Solanum* species are rich sources of different kinds of steroidal alkaloids and saponins, which have an increasing interest for pharmaceutical uses. The aubergine seed market is important in the Mediterranean basin (Spain, Italy and Turkey are important producers) and in most Asian countries where this vegetable is very popular (China and India being the top producers with respectively 16 million and 8 million tonnes of fruits produced annually).

The initial motivation for applying to the Resgen programme was born (1) from the urgent need to save the precious and endangered Birmingham *Solanaceae* collection (which contained mostly eggplants and eggplant wild relatives, 1 446 accessions and (2) from the wish of some core scientists to strengthen their collaboration which had started at the time of the EU ESIN project (European *Solanaceae* information network 1993–96). Eggnet (the eggplant network) included nine partners and two private companies as subcontractors (Vilmorin and Rijk Zwaan) from seven countries (Germany, Greece, Spain, France, Italy, the Netherlands and the United Kingdom). Though eggplant has a modest importance in Europe, this part of the world has an exceptional collection of genetic resources representing the genetic diversity of this species and about half of its wild relatives.

Objectives

The overall objectives of the Eggnet project were (1) the inventory of the germplasm and the creation of

the Eggnet database; (2) to save, regenerate and identify (when necessary) the accessions handled by the project; to carry out (3) primary and (4) secondary characterisation; (5) to rationalise the European collections and to promote their utilisation; and (6) to coordinate efficiently the project.

Achievements

Objective 1: Database
The Eggnet database (http://www.bgard.science.ru.nl/WWW-IPGRI/eggplant.htm) is one of the more advanced crop databases in Europe, integrating passport data with primary and secondary characterisation data, and multiple criteria searching. It is the core of the ECP/GR eggplant central crop database, which is already hosted on the IPGRI/ECP-GR website. The Eggnet database contains passport data for 4 715 accessions of several cultivated species of eggplant and their wild relatives.

Objective 2: Regeneration
Eggnet partners have handled 3 149 accessions and have obtained seeds out of 1 138 (plus 199 still in progress). The endangered Birmingham collection has represented 72 % of the accessions handled by Eggnet over five years. When not already duplicated in some partners collections, the Birmingham accessions have been sown (often several times, when germination failed) and about half of them (666) have been saved, i.e. produced freshly regenerated seeds.

Objective 3: Primary characterisation
All the materials regenerated have been described when regenerated (or the year after), and the morphological description is most often completed by photographs and herbarium specimens.

Objective 4: Secondary characterisation
Secondary characterisation has been handled in two ways.

First, it concerned traits that needed centralised planning and concerned mostly wild material. As many as 97 accessions were tested for day-length sensitivity (versus a duty of 80 accessions), 95 were tested for graft affinity with eggplant (versus a duty of 48 accessions), 615 accessions were tested towards *Verticillium* (versus a duty of 372 accessions) and 564 accessions were tested towards nematodes *Meloidogyne incognita* (versus a duty of 316 accessions).

Second, it concerned (i) fruit quality traits which could be measured at the same time as regeneration, and (ii) parthenocarpic aptitude and cross-compatibility experiments (this, only for *S. muricatum*). The commitments were overdone for froth index (396 versus a duty of 260), refractometric index (224 versus 220) and ratio sugar/acids (183 versus 180). They were almost fulfilled for culinary interest (114 versus 120), parthenocarpic aptitude (178 versus 220) and interspecific cross-compatibility (42 versus 60). And, last, some traits which are not indicated in the technical annex were measured for fruit flavour (184 accessions), flesh browning (373 accessions) and fruit pH (141 accessions).

Secondary characterisation data have been entered into the database, except those concerning graft affinity, *Verticillium* and nematode resistance trials, which deserve first scientific publications.

Objective 5: Utilisation
Special attention was paid to the avoidance of any useless duplicate effort (for regeneration and characterisation) and the duplicates between partners collections have been 'chased' at the time of the planning of the annual regeneration and secondary characterisation. Though there are some gaps in the genetic diversity available in Eggnet partners' collections (in particular for about half of the wild species related to *S. melongena*, which have never been collected), these gaps cannot be filled for the time being. Partners' collections were rationalised and the duplicates within and between the partners' collections were detected. They were not suppressed, because they concern mostly wild material which is very erratic in its seed production and seed germination, and this duplication must be considered as a kind of safety duplication. Core collections are potentially designable for the wishes of any end-user, thanks to the multiple search criteria available in the database. The concept

of 'virtual core collection' is very flexible, and allows any end-user to extract from the database the core collection he would like to have access to — from the seed availability information and any combination of passport and primary characterisation data. The material held by Eggnet partners, regenerated during Eggnet or not, is available on request, given that enough seeds are available.

Objective 6: Coordination

Eggnet was coordinated by a coordination board (three partners) who met 19 times over the five years of the project, either for planning tasks or for preparing or concluding the full meetings. The Eggnet project has been the catalyst of the initiation in 2001 of the ECP/GR *Solanaceae* working group. The Eggnet main coordinator is also the coordinator of the ECP/GR *Solanaceae* working group. Two ECP/GR *Solanaceae* working group meetings have been held concomitantly with Eggnet full meetings (2001 and 2004).

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Publications

Daunay, M. C., Jullian, E. and Dauphin, F., 'Management of eggplant and pepper genetic resources in Europe: networks are emerging', *Proceedings of XIth Eucarpia meeting on genetics and breeding of capsicum and eggplant*, 9–13 April 2001, Antalya, Turkey, 2001a, pp. 1–5.

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ELM: CONSERVATION, CHARACTERISATION, COLLECTION AND UTILISATION OF GENETIC RESOURCES OF EUROPEAN ELMS

URL: www.cemagref.fr/Informations/Actualites/elm/

Project details

Start date: 1 January 1997
End date: 31 December 2001
Duration: 60 months
Project reference: Genres CT96 No 78
Project total cost: EUR 864 000
Project EU co-financing: EUR 600 000

Coordinator

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Description

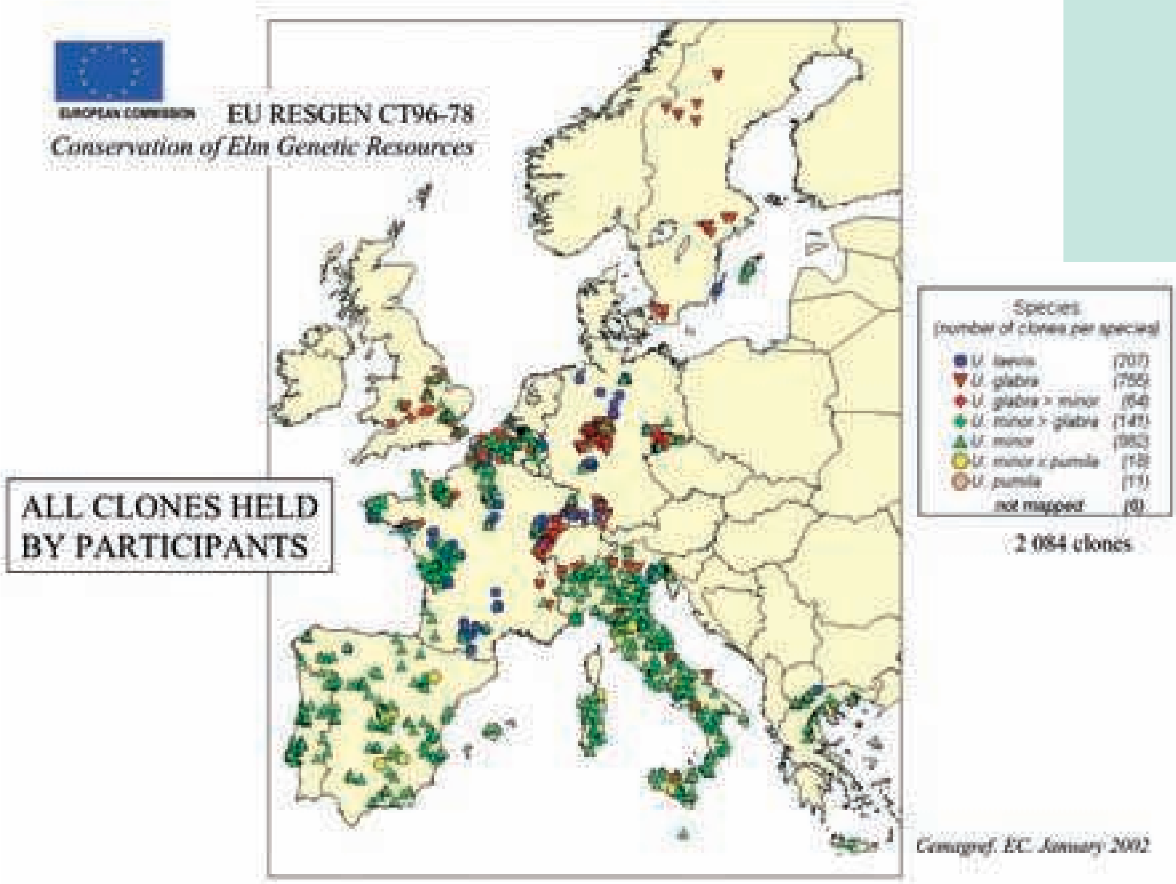
General information

The elm is an important landscape tree, yielding timber which used to be of considerable value. But, for several years, its genetic resources have been endangered. As a matter of fact, the two Dutch elm disease (DED) pandemics that spread across Europe during the last century have caused a dramatic mortality in the elm population, and the disease is still a great threat for each individual elm tree. It has caused the death of most of the adult field elms (*Ulmus minor* Mill. *sensu latissimo*). It is even estimated that more than 90 % of mature *Ulmus minor* disappeared from the French countryside in the 1919 and 1972 epidemics. Now DED is causing the death of many Wych elm trees (*U. glabra* Huds.). The third elm species native to Europe, the European white elm (*U. laevis* Pall.), is less attractive to the elm bark beetle (*Scolytus* sp.) which spreads the spores of the fungus causing the disease (*Ophiostoma novo-ulmi Brasier*). It is therefore less damaged by DED, but is still endangered because of the disappearance of the riparian ecosystem in which it thrives.

However, the statement that elms are an endangered species needs to be scrutinised and the situation of each elm species must be considered separately. Factors of importance in elm gene conservation must be discussed before practical recommendations for the implementation of elm gene conservation can be made. In 1996, a project was proposed to extend the elm genetic resource conservation programme to the whole of Europe. The proposal was accepted by the European Commission in 1997 and the 'Conservation of elm genetic resources' project (Genres CT96 No 78) grouped together 15 partners in nine EU countries engaged on a five-year programme partially financed by the EU.

Objective

The project aimed at a better evaluation of the existing collections and the long-term conservation of the threatened biodiversity within elms. Through characterisation with molecular markers and consistent registration in a common database, these collections were to be rationalised. Their conservation was to be opti-



mised in a frame of European molecular markers adapted to the geographic partitioning of the genetic variation; conservation methods associated with cryopreservation and sustainable field clonal banks (low hedges are unattractive to the vector of DED). Evaluation consisted of clonal screening for low susceptibility to DED and good landscaping traits. The results of the projects were expected to be useful for amenity planting, afforestation and the reconstruction of hedges.

Achievements

The project complemented the Euforgen strategy (European forest genetic resources programme carried out by IPGRI). Additionally, it provided coordinated actions in nine partner States representing the geographical range of the EU, from Germany to Portugal and from Sweden to Greece. It was based on an existing core of *Ulmus* in *ex situ* collections in several countries and complemented with material originating from other EU countries where conservation actions had not yet begun. The project was built on a diverse group of scientists experienced in elm research (pathologists, taxonomists, forest geneticists, etc.), each of whom provided expertise and tested the methodologies in the different fields.

The elaboration of a database (passport data and characterisation available) on all the clones in the partners' collections was finished in the earlier years of the project. In 2002, the database held 2 084 elm clones (1 023 *Ulmus minor*, 819 *U. glabra*, 207 *U. laevis* and 36 other species). The database gives information about the origins, including the habitats, of the clones.

The project also conducted a molecular characterisation of the different elm clones of the three European elm species. Knowledge of the geographical partitioning of the genetic variability provided a logical base for the definition of an efficient conservation strategy. Therefore 963 samples were analysed for chloroplast DNA and 535 clones for nuclear characterisation. Other benefits of this characterisation were the uniform (in one laboratory) procession of the material, the clarification of elm taxonomy, the provision of guidelines for cryopreservation, the availability of tools for the monitoring of hybridisation and the provision of aid for the selection of *in situ* conservation stands.

In addition, the clones were screened for resistance to the insect vector and fungus in order to find material for use in breeding programmes for elms. A strong variability in bud burst period and an interesting variability in susceptibility to DED were found within the European native elms; some of the less susceptible clones found in this project are certainly of interest for dynamic genetic conservation, breeding and also for

the prudent reconstruction of hedges in the countryside. Knowledge on the attractiveness of elms to bark beetles was also improved, indicating that the variability for this factor is probably low between clones belonging to the same species. However, first results of chemical analysis of the young 'bark' terpenes components suggest an interesting direction for further research in the behaviour of the bark beetle and the screening for less attractive elm clones.

A core collection was then established using the criteria taxonomy, habitat, molecular markers and geographical partitioning of diversity, valuable traits and hybrids. Therefore 850 clones were selected (455 clones are pure *U. minor*, 210 *U. glabra*, 82 *U. laevis*, 3 *u. pumila* and the others hybrids between them), passport data sorted and technical guidelines for fields banks defined.

In addition, the protection and long-term conservation of a major portion of the genetic diversity within the elm collections of participating countries have been enhanced through duplication, exchanges and conservation of material in different sites and using different methods. Over 850 clones were planted in the participants' field clonal banks and 444 native elm clones were cryopreserved. Due to these activities, the protection and long-term conservation of the genetic diversity available in the elm collections of the participating countries have been enhanced. Also, thanks to cooperation, efficiency was increased and costs reduced. Public awareness has been raised regarding the situation, risks and perspectives for elm resources in Europe, and the genetic conservation activities carried out at national and European levels have been made known to the general public. Professional foresters, arborologists and conservationists were informed of the scope and progress of the project and the results were diffused at the second International Elm Conference held in Spain in May 2003. Scientific papers on elm genetic diversity, pathology and conservation were published as well as a number of other articles.

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Publications

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GRAPEVINE: EUROPEAN NETWORK FOR GRAPEVINE GENETIC RESOURCES CONSERVATION AND CHARACTERISATION

URL: http://www.genres.de/eccdb/vitis

Project details

Start date: 1 March 1997
End date: 30 September 2002
Duration: 65 months
Project reference: Genres CT96 No 81
Project total cost: EUR 676 126
Project EU co-financing: EUR 567 500

Coordinator

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Description

General information

Worldwide, grape producers and consumers are concentrating more and more on a few well-known varieties such as Chardonnay, Cabernet Sauvignon, Merlot and Syrah, moving away from traditional varieties. Therefore, this project focuses mainly on indigenous and long-neglected varieties.

Recent scientific investigations have discovered that the high-quality varieties Chardonnay and Syrah, whose area under cultivation is continually increasing, descended from grape varieties which have been abandoned by viticulture and which are rarely cultivated. In the case of Chardonnay, the parentage could only be discovered since Gouais Blanc (*syn. Heunisch weiss*), one of the parents, has survived in grapevine collections. The survival of these neglected varieties will enable researchers to investigate their apparently good combining ability. Work still remains to be done to provide a genetic explanation of the high-quality characteristics of the offspring. At least it has been demonstrated that the conservation of grapevine genetic resources for today and for the future is of extreme importance.

Objectives

The objectives of the project were: (1) the establishment of a European *Vitis* database; (2) the selection of appropriate primary and secondary descriptors for (3) morphological description and the evaluation of agronomic traits of mainly old and long-neglected grapevine varieties; and (4) the utilisation of SSR-marker analysis for variety recognition.

Achievements

The European *Vitis* database established within the scope of the project is the inventory of the grapevine accessions existing in 13 European wine-growing countries. For that purpose the project partners agreed on a common format for the passport descriptors for the European *Vitis* database, following also the FAO/IPGRI multi-crop passport descriptor guidelines (IPGRI, 1997). Grapevine collection lists were gathered from 18 partners and about 27 000 accessions were compiled. Each of the 27 000 accessions was characterised by 12 passport descriptors such as the accession name, the holding institute, the accession number and pedigree.

About 95 % of the varieties in the world grapevine collections are true to type. The errors, due to synonyms, homonyms and about 5 % misnamed varieties, are propagated through material exchange. Wrong variety designations have an impact on research, grapevine breeding, the rationalisation of collections and the preservation of genetic resources. Hence the checking of the true to typeness of the varieties in grapevine collections is indispensable. The efforts carried out within Genres No 81 have been an important step in that direction. There has also been considerable activity aimed at determining the identity of varieties in grapevine collections by means of primary and secondary descriptors, photographs and bibliography, isoenzymes and microsatellites.

For primary descriptor recording during the project, 33 ampelographic, 21 ampelometric and 14 secondary descriptors of the OIV descriptor list (OIV, 1983) were selected and slightly modified (e.g. the time of observation, expression stages or example varieties). Some newly created descriptors were added. The primary and secondary descriptors of the Genres No 81 project were published as the 'Primary descriptor list for grapevine cultivars and species (*Vitis* L.) (Anon., 2002) and the 'Secondary descriptor list for grapevine cultivars and species (*Vitis* L.) (Anon., 2002)'. The Genres No 81 project partners also agreed on the compilation of a 'primary descriptor priority list', comprising 14 primary descriptors as the first priority. The list will be useful for rapid characterisation of varieties discovered *in situ*. The chosen descriptors allow strong discrimination between varieties, and most of them are easy to score.

The description focused mainly on indigenous and long-neglected varieties. Within the scope of the project, for the first time, 54 primary descriptors of 802 varieties and 14 secondary descriptors of more than 432 varieties have been recorded according to a common code and with two repetitions per cultivar. All the descriptor data gathered during the five years of the project were made available via the Internet (http://www.genres.de/eccdb/vitis).

For the illustration of the rare and endangered grapevine varieties described, photographs were taken of different anatomical parts of the plant (shoot tips, leaves and clusters). In addition pictures are a useful supplement for variety distinction and identification and can help winegrowers and breeders who are interested in cluster and berry shape and size. Around 1 700 photographs of approximately 500 varieties were added to the corresponding accessions of the EU *Vitis* database, for an example see the figure above.

Because microsatellites turned out to be extremely efficient and useful for grapevine variety differentiation and identification, the partners of the Genres No 81 project agreed that the project was an excellent platform to utilise already developed SSR markers for the implementation of a universally accessible SSR-marker database for variety identification purposes. The most informative markers, VVS2, VVMD5, VVMD7, VVMD27, VrZAG62 and VrZAG79, were selected. Three circular tests were carried out, where 8 to 11 partners worked with identical DNA, which was distributed either through shipment of DNA or through shipment of woody material.

As a result, the activities carried out within Genres No 81 are acknowledged at an international level and have gained a good reputation. This is demonstrated by the frequent use of the European *Vitis* database, up to 200 times per month. There has furthermore been a considerable increase in the safeguarding, description and evaluation of old and rare grapevine varieties. The discussion about descriptor recording and descriptor definition, practical ampelography in grapevine collections, enhanced the objectivity of descriptor recording. Through the integration of SSR-marker analysis in Genres No 81, the work done in this field was stimulated, intensified and advanced. The comparison of findings, which was an effective control, finally led to improved protocols and reliable data. The idea of using example varieties turned out to be effective for differentiation and identification purposes and will also help to make research findings comparable with each other.

Publications

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MAIZE: IMPLEMENTATION OF THE EUROPEAN NETWORK FOR EVALUATION, CONSERVATION AND UTILISATION OF EUROPEAN MAIZE LANDRACES GENETIC RESOURCES

URL: http://www.montpellier.inra.fr/gap/resgen88/default.htm

Project details

Start date: 1 January 1997
End date: 31 March 2002
Duration: 63 months
Project reference: Genres CT96 No 88
Project total cost: EUR 961 182
Project EU co-financing: EUR 800 000

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Description

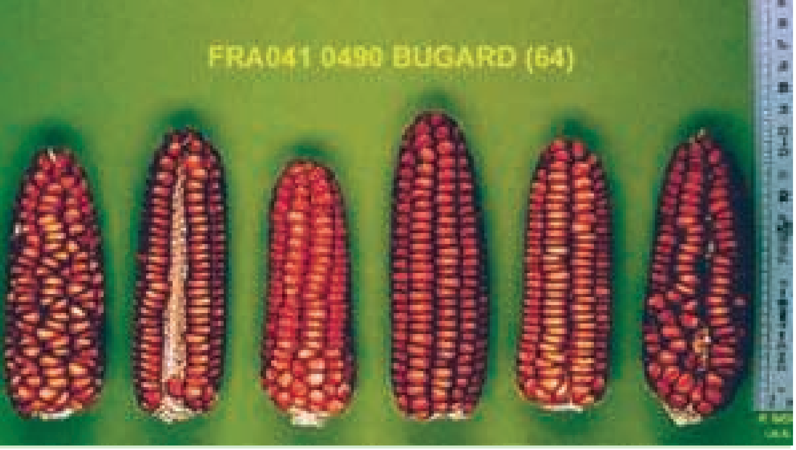
General information

Since the introduction of maize into Europe five centuries ago, great differentiation has occurred in landraces according to environments and the needs of farmers. Today, native landraces are no longer cultivated except in the highlands of north-west Spain and Portugal, where there is a large variability. Some time after the introduction of the first commercial hybrids, the necessity to preserve genetic resources appeared and led to the constitution of many national maize collections. Most of them have a flint kernel and are insensitive to photoperiod. Since the beginning of the 1950s, this diversity has been exploited in order to derive inbred lines. These inbred lines have proven highly complementary to inbred lines of US origin to produce hybrids for cultivation in Europe. For northern and central Europe, the most commonly groups are European flint × American dent. The first European inbred lines bring specifically early vigour and cold tolerance to hybrid combinations with dent material. Lacaune landrace has been at the origin of the inbred lines F2 and F7 very largely used in the hybrids adapted to the climatic conditions of northern Europe. Thus, European landraces could be a source of variability for the objectives of diversification and preservation of the environment: source of pest tolerance (European corn borer, virus), drought tolerance, cold tolerance, grain quality (human use, poultry breeding) and forage quality.

Many landraces were collected by national research organisations of different countries of the European Union and of eastern Europe over recent years. Although a meeting took place in order to explore the possibility of these countries to cooperate in a common database of maize germplasm (Rome, 1996), no coordination has existed for the conservation of the maize genetic variability so far. In this project, seven countries, Germany, Greece, Spain, France, Italy, Portugal and the Netherlands decided to elaborate a common programme to conserve, evaluate and use their maize landrace genetic resources.

Objective

The objectives were: (1) the constitution of a European network and general survey of maize landraces genetic resources for rational management; (2) the elaboration



of a maize database for European accessions with passport data and primary descriptors used by IPGRI (International Plant Genetic Resources Institute) and FAO (Food and Agricultural Organisation), in consultation with the ECP/GR network (European cooperative programme for crop genetic resources networks); identification of duplicates; (3) the secondary characterisation of the chosen accessions by the use of agro-morphological and molecular descriptors; (4) the sorting and creation of national representative collections by the use of agro-morphological and molecular descriptors and then of a European core collection by the use of molecular descriptors; (5) the final evaluation of the European core collection according to the Common agricultural policy criteria; constitution of the network for the conservation of the landraces; and (6) the diffusion of the main results in the form of national and international publications and journals, accessibility and diffusion of the genetic material after regeneration.

As a consequence, global costs of managing maize landraces in gene banks were expected to be reduced. Furthermore, the genetic variability of maize germplasm should be maintained, and the use of genetic resources by breeders improved in order to diversify agriculture (industrial uses, low pesticides, and nitrogen and water consumption). The core collection is a means to manage a large database by evaluating a part of the collection representing the total. This is then an 'access code' to utilise the whole collection.

Achievements

A review of the situation relating to conservation of maize genetic resources in Europe was the first result of the project. Then the participants agreed a number of self-regulations regarding the work during and after the project. They include regeneration methods, experimentation protocols for characterisation and evaluation of germplasm, conservation process, definition of descriptors to be used in the database and definition of common arrangements concerning the diffusion of information. As a next step, the European Union maize landraces database (EUMLDB) was created and set up on the website of the project (http://meleze.ensam.inra.fr/gap/resgen88). This database gathered about 2 900 landraces originating in the EU and it contains 23 passport data and 11 primary descriptors. Interchange of data in a global and multi-crop network will be possible in the future.

Next, each partner established secondary descriptors on a national level, analysed them and built up his national maize landrace representative collection (NMLRC). For this, passport data and agro-morphological descriptors were used, and landraces that are representative of the whole collection of each country were gathered. All the NMLRCs were then merged into a European Union maize landrace representative collection (EUMLRC) gathering 394 landraces. The collection's neutral diversity was analysed through isoenzymatic and molecular markers.

Subsequently, the European Union maize landrace core collection (EUMLCC) containing 96 landraces was constituted on the basis of the calculation programme MSTRAT. It is designed to build up core collections by maximising allelic or phenotypic richness. Firstly, reference maize landraces such as those used for breeding, analysed in former studies and/or of key historical importance were chosen. This first sample is called 'kernel core' (22 landraces). Secondly, the genetic diversity (allelic or class richness) of the core collection sample was maximised by adding iteratively new accessions to the kernel core and by using MSTRAT. At the same time, the data such as passport data, primary and secondary characterisation, isoenzymatic and molecular data made it possible to structure the genetic diversity of the European germplasm, which constitutes an interesting scientific result. The molecular characterisation included two kinds of genetic characters: isoenzymes and the restriction fragment length polymorphism (RFLP) markers. Both were useful to generate complementary information about the diversity met in the populations in order to define the EUMLCC. All the populations of the NMLRC were analysed (9). Full analysis was carried out on all 25 RFLP loci populations, of which 20 by frequency and five by presence/absence. In all, 258 alleles were found, with an average of 10.3 alleles per locus and an average of 2.53 populations per locus. The inter- and intra-population diversity was high. Inter-population diversity represented 25 % of the total diversity. Finally, an evaluation was conducted. First, it resulted in data relating to 394 landraces (the EUMLRC) for digestibility and other useful agronomic data. Second, agronomic and grain quality traits data were obtained on the 96 landraces belonging to the EUMLCC.

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(9) On isozymes: Revilla, P. et al. On RFLP: Gauthier, P. et al.

This major result, which is mainly information on germplasm, is available on CD-ROM. Additionally, measures have been taken to make these 96 landraces easily available for European breeders. They are identified on the ad hoc databases such as EUMLDB or Eurisco or EMDB. The seeds can be obtained from each national institution partner of the project which is in charge of their regeneration (see the list below). All the contact details are mentioned in the EUMLDB.

This project contributed to a better knowledge of the variability of the European maize germplasm. Some tools were made available: a database, which can be used to implement other ones, especially the European maize database (EMDB) set up in Lemon Polie, Yugoslavia. Above all, the core collection is a remarkable tool to investigate the variability of European maize landraces.

With the kernel core, breeders have reference landraces to better understand EUMLCC evaluation. French maize breeders of the association PRO-MAIS, one of the partners of the project, were invited to a meeting on the results of the project (Montpellier, 12 and 13 June 2003). In addition, some results of the final evaluation, such as grain quality or silage digestibility are directly usable. Some sound indications, such as the good performance of some early French or late Portuguese landraces under limited input cropping conditions, are available too. Results have been published for two evaluated traits: forage quality (10) and insect tolerance (11). Other evaluation experiments such as low nitrogen level tolerance and drought tolerance were presented at the Montpellier meeting. Some further experiments are still needed, since field experiments on environmental constraints take at least two years.

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Publications

Gauthier, P., Gouesnard, B. and Dallard, J., 'RFLP diversity and relationships among traditional European maize populations', *Theoretical and Applied Genetics*, Vol. 105, 2002, pp. 91–99.

Malvar, R. A., Butron, A., Alvarez, A. et. al., 'Evaluation of the European Union maize landrace core collection for resistance to *Sesamia nonagrioides* (*Lepidoptera: Noctuidae*) and *Ostrinia nubilalis* (*Lepidoptera: Crambidae*)', *Journal of Economic Entomology*, Vol. 97, 2004, pp. 628–634.

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(10) Mieg, I. B. et al.

(11) Malvar, R. A. et. al.

MINOR FRUIT TREE SPECIES: CONSERVATION, EVALUATION, EXPLOITATION AND COLLECTION OF MINOR FRUIT SPECIES

URL: http://www.unifi.it/project/ueresgen29/Welcome.html

Project details

Start date: 1 April 1996
End date: 31 March 1999
Duration: 36 months
Project reference: Genres CT95 No 29
Project total cost: EUR 240 000
Project EU co-financing: EUR 240 000

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Description

General information

Minor or underutilised fruit tree species are part of a group of potentially relevant woody species with low importance on the market of crop production and consumption. Their production is limited by the reduced attention paid to them by research institutions, nurseries, fruit-growers and industry. Nevertheless, they could represent a relevant resource for diversifying production and human diet and for obtaining healthy fruits and fruit products, since most of them are hardy species requiring low input. Furthermore, these forgotten or underutilised accessions are threatened by genetic erosion.

During the third meeting of the Réseau Agricole Méditerranéen, held in Florence in September 1994, a working group was created to collect, evaluate, manage, conserve and use collections of minor fruit tree species belonging to and cultivated in the Mediterranean basin. The chosen species were*:* *Ficus carica* (fig), *Punica granatum* (pomegranate), *Diospyros kaki* (Japanese persimmon), *Eryobotria japonica* (loquat), *Opuntia ficus-indica* and *O. amyclaea* (prickly pear), *Cydonia oblonga* (quince for fruit production), *Castanea sativa* (European chestnut), *Pistacia vera* (pistachio), all of them already collected, and *Morus alba*, *M. nigra*, *Morus spp.* and other *Moraceae* (mulberry), *Ceratonia siliqua* (carob tree), *Crataegus azarolus* (azerole), *Mespilus germanica* (medlar), *Arbutus unedo* (strawberry tree — madrona), *Cornus mas* (Cornelian cherry), *Zizyphus vulgaris* (jujube) and *Sorbus domestica* (sorb), which are still uncollected species. From 1996, the project was supported by the EU and it was finalised in 1999.

Objective

The main objectives of the project were: (1) to establish a basis for the conservation and utilisation of 16 minor fruit tree species of the Mediterranean basin; (2) to create a European inventory; and (3) to develop a database on germplasm collections which would include both first and advanced characterisation descriptors, linked to the agronomic evaluation of collected material.

Achievements

The work carried out can be divided into three sections: coordination tasks, technical tasks and diffusion tasks.

Coordination tasks

First of all, common descriptor lists were created for each genus, the passport was defined with accession data and collection data, and first and secondary characterisation rules were established. This was followed by the creation of a database documentation system for all species, the European minor fruit tree species database (EMFTS database), used for data manipulation, as well as the 'First inventory of collected accessions of minor fruit tree species' which takes into account the accessions held by each partner. Data input in the EMFTS database can be consulted through different queries structured on the basis of species (selection by crop) and of data sets (typology of data, i.e. passport, first characterisation and further characterisation and evaluation). Moreover, data can be examined on institutions holding collections, on environmental aspects of sites of collection and on statistics. The EMFTS database and the inventory were diffused and regularly updated on the Internet (http://www.unifi.it/project/ueresgen29/).

Technical tasks

A total of 1 381 collected accessions have been studied by the partners within this project, of which the majority (91.3 %) are *ex situ* accessions and 66.3 % belong to the eight already inventoried species (12) Among those species that had not been inventoried (13), the majority are *in situ* collected accessions (121), and all of them represent newly entered material.

The technical tasks of the project regarded mainly the collection of data passport (14), first characterisation (15) and further characterisation (16) for the eight already inventoried species and passport and characterisation (17) for the eight non-inventoried species.

About 66.7 % of all collectable data have been computed. More precisely, 66.3 % of data have been collected on accessions of the eight inventoried species, 60.3 % on *ex situ* non-inventoried species and 76.3 % on *in situ* non-inventoried species. Data for each species are reported in the table.

Collected and computed passport data for the eight already inventoried species represent 92.8 % of all

Table: Percentage of collected and computed data

Ex situ **inventoried species**	**Percentage of collected data**	***Ex situ*** **non-inventoried species**	**Percentage of collected data**	***In situ*** **non-inventoried species**	**Percentage of collected data**
Fig	52.8	Strawberry tree	no accession	Strawberry tree	83.8
Pomegranate	86.7	Cornelian cherry	79.3	Cornelian cherry	70.2
J. Persimmon	78.3	Medlar	64.0	Medlar	70.0
Loquat	91.7	Jujube	no accession	Jujube	63.1
Cactus Pear	67.3	Azerole	69.0	Azerole	68.2
Quince	85.6	Sorb	61.5	Sorb	72.1
E. chestnut	71.1	Mulberry tree	83.3	Mulberry tree	66.6
Pistachio	54.3	Carob tree	83.3	Carob tree	87.9
Total	66.3	Total	60.3	Total	76.3

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(12) *Ficus carica* (fig), *Punica granatum* (pomegranate), *Diospyros kaki* (Japanese persimmon), *Eryobotria japonica* (loquat), *Opuntia ficus-indica* and *O. amyclaea* (prickly pear), *Cydonia oblonga* (quince for fruit production), *Castanea sativa* (European chestnut*), Pistacia vera* (Pistachio).

(13) *Morus alba*, *M. nigra*, *Morus spp* and other *Moraceae* (mulberry), *Ceratonia siliqua* (carob tree), *Crataegus azarolus* (azerole), *Mespilus germanica* (medlar), *Arbutus unedo* (madrona), *Cornus mas* (Cornelian sherry), *Zizyphus vulgaris* (jujube) and *Sorbus domestica* (sorb).

(14) The passport (accession and collection data) is formed by descriptors common to the species (around 13 for the already inventoried species and for the *ex situ* non-inventoried species, 16 for *in situ* non-inventoried species).

(15) The first characterisation of the collected accessions was carried out on the basis of a descriptor list for each species, the typologies of conservation (*ex situ* and *in situ*) and the importance of the species (eight main inventory species, eight secondary non-inventoried species).

(16) For further characterisation and evaluation data, both biometric and qualitative traits (frequently linked to commercial aspects) have been gathered from experimental fields using a homogenous methodology for each species.

(17) Characterisation descriptors are common for *ex situ* and *in situ* collected accessions and take into account the most important biological and productive traits of each species.

observable passport data for the 1 206 accessions of these species; 77.4 % of observable data were collected and computed for first characterisation and 53.4 % for further characterisation and evaluation.

Passport and characterisation data collected and input for *ex situ* collected accessions of non-inventoried species were respectively 89.5 % and 42.2 % of all observable passport and characterisation data on the 54 collected accessions of this group of species. Passport and characterisation data collected and computed for the 121 *in situ* accessions of non-inventoried species were respectively 85.4 % and 67.6 % of observable data for this group.

Documents on the 'state of conservation in Europe' have been released for fig, pomegranate, Japanese persimmon, loquat, cactus pear, quince, strawberry tree, medals and sorb. In addition, new accessions among the already inventoried *ex situ* collected species were acquired by partners during the project and some accessions have also been duplicated by partners.

Diffusion tasks

The webpages of the project have been improved year by year with new information and illustrative material, with the 'First European inventory of collected accessions of minor fruit tree species', with the proceedings and pictures of the international workshop and the pomological exhibition and, finally, with the link to the online EMFTS database.

The 'International workshop on the conservation of minor fruit tree species in Europe', was held in Florence on 27 November 1998. A pomological exhibition (including fruits and derivatives), a book exhibition and a philatelic exhibition were organised for this event. A book was published on the conservation and use of minor fruits in Europe.

About 2 500 persons visited the collection fields of different species. Propagation material has been released to about 80 farmers, nurseries and scientific institutions.

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National Agricultural Research Foundation, associated to SPOTI	Naoussis	Greece	C. Tsipouridis

Publications

Bellini, E. and Giordani E., ‘Conservation of under-utilised fruit tree species in Europe’, *Acta Horticulturae*, Vol. 522, 2000, pp. 165–173.

Bellini, E., *I fruttiferi minori in Europa*, Edizioni L’Informatora Agrario, 2002, Verona.

POTATO: GENETIC RESOURCES OF POTATO, INCLUDING CONSERVATION, CHARACTERISATION AND UTILISATION OF SECONDARY POTATO VARIETIES FOR ECOLOGICAL PRODUCTION SYSTEMS IN EUROPE

URL: http://www.genebank.nl/eupotato/

Project details

Start date: 1 March 1996
End date: 31 March 2000
Duration: 49 month
Project reference: Genres CT95 Nos 34–45
Project total cost: EUR 642 666
Project EU co-financing: EUR 400 000

Coordinator

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Description

General information

The potato is the second most important crop in Europe (wheat is the most important). It is susceptible to a large number of diseases and pests, making it one of the heaviest users of chemical inputs of any crop. European companies engaged in the breeding of potatoes are active throughout the world. There is a continuous need for new traits to improve potato varieties. It is the only important crop in Europe that is vegetatively propagated, which raises particular problems for the conservation of old varieties and previously developed breeding lines.

This project is a fusion of Genres 45 'Genetic resources of potato' and Genres 34 'Conservation, characterisation and utilisation of secondary potato varieties for ecological production systems in Europe'. The contractors consist mainly of research institutes, but also private breeders and non-governmental organisations.

Objective

The general objective of the project was to make better use of European potato collections, in order to produce material for low-input agriculture (e.g. reduction of pesticides and/or fertilisers) and of higher quality for the consumer.

The specific objectives were: (1) to coordinate potato genetic resources in Europe, harmonise the databases already existing within the EU and establish a central EU potato database; (2) to improve the health status of a chosen set of European potato genetic resources for European farmers, breeders and scientists and improve its accessibility; (3) to characterise potato genetic resources for economically important traits such as resistance against pests and diseases (e.g. late blight and cyst nematodes), quality traits for eating and processing, and other traits such as low nitrogen requirements; (4) to rationalise the potato collections included in the network; and (5) to diffuse material and results to farmers, advisers, breeders and scientists.

Achievements

This EU project made great progress in improving the accessibility (via Internet: http://www.genebank.nl/eupotato/) of the material and its data as well as identifying useful characteristics of the germplasm. The database holds over 11 600 records of old potato varieties and previously developed breeding lines (maintained in a clonal form) and over 11 700 records of wild and primitive species of potato (maintained as population). More than 38 000 evaluation results are available on important potato diseases and quality traits. The database maintenance will continue in the framework of the ECP/GR working group on potato, and additional data will be included. Data on European potato variety collections are stored in the European cultivated potato database and have been made available by SASA (http://www.europotato.org/).

Although several cultivars or accessions still remain to be virus cleaned and evaluated, virus-free material for this vegetatively propagated crop was produced. In total, 771 clones were virus eradicated and 1 220 accessions were successfully regenerated after the plants had been screened for quarantine diseases. The field evaluations have led to the characterisation, for about 40 traits, of more than 80 varieties. Resistance against pests and viruses as well as quality traits, both for consumption and processing, were characterised. European potato breeders will now be able to identify new germplasm for the development of more sustainable varieties and in the long run the consumer may benefit from potatoes produced in a more sustainable way.

Even though the rationalisation of the collections (identification of redundancies) needs further action, wild material of potatoes has been stored, mainly as seed, and cryopreservation of clonal material was also undertaken, which considerably reduces the storage costs.

A real breakthrough of this project was the cooperation between traditional institutions (gene banks) with private breeders and particularly with NGOs who are in close contact with organic farmers. The latter were mainly interested in promising varieties for biological production and, although the perfect fit for organic farming was not found because each variety has its drawbacks, interesting clones for organic growers have been identified.

Other participants

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Organisation name	Town	Country	Contact person
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Publications

Carnegie, S. F., Hoekstra, R., Schüler, K. et al., 'EU project on potato genetic resources: goals and achievements', 14th triennial conference of the European Association for Potato Research, *Abstracts of conference papers, posters and demonstrations*, 1999, p. 571.

Hoekstra, R., 'Availability, evaluation and use of potato genetic resources', in: Peter, K. (ed.), *Beiträge zur Züchtungsforschung — BAZ — Proceedings of the International Symposium Breeding Research on Potatoes*, 23–26 June 1998, Groß-Lüsewitz (Rostock), Germany, 1998, Vol. 4(2), pp. 70–72.

Hoekstra, R. and Carnegie, S. F., 'The establishment of the European potato genetic resources database', in: Van den Berg, R. G., Barendse, G. W. M., et. al. (eds.), Solanaceae V. — *Advances in taxonomy and utilization — Proceedings of the fifth International* Solanaceae *Conference*, 23–29 July 2000, Nijmegen, Nijmegen University Press, Netherlands, 2001, pp. 363–368.

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Lennartsson, M., Manchett, R., Schauer, C. et. al., 'Characterisation and utilisation of secondary potato varieties for organic farming', in: Alfoldi, T., Lockeretz, W., Niggli, U. (eds), *The world grows organic — Proceedings of the 13th International IFOAM Scientific Conference*, Basel, Switzerland, 28–31 August 2000, p. 223.

PRUNUS: INTERNATIONAL NETWORK ON *PRUNUS* GENETIC RESOURCES

URL: http://europa.eu.int/comm/agriculture/res/gen/61a.htm; for database see: http://www.bordeaux.inra.fr/urefv/base/

Project details

Start date: 1 March 1996
End date: 28 February 1999
Duration: 36 months
Project reference: Genres CT95 No 61
Project total cost: EUR 486 650
Project EU co-financing: EUR 325 000

Coordinator

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Description

General information

The genus *Prunus* includes both forestry species (cherry is a noble hardwood) and fruit species (almond, apricot, cherry, peach, plum, prune, Japanese plum and other related species used for the creation of rootstocks). Most of the *Prunus* species originate outside Europe with the exception of two sections (*Euprunus* and *Eucerasus*). However, many varieties have been bred in Europe since the Renaissance.

Collections of these species exist in many Member States and since 1982 an ECP/GR (European cooperative programme for crop genetic resources network) *Prunus* group of the International Plant Genetic Resources Institute (IPGRI) has met regularly.

The Genres CT95 No 61 project comprises eight countries and 12 institutes. Those belonging to EU Member States were financially supported through Council Regulation (EC) No 1467/94. Those who are situated in non EU-Member States were financially supported by IPGRI.

The group has established or revised the list of descriptors and the database using these descriptors. Initiated in 1983, the database used to be held at the Nordic Gene Bank in Sweden. In 1993, the database was transferred to Bordeaux, France. It now contains data on 8 500 accessions. In 2005, the ECP/GR *Prunus* group comprises 29 countries in Europe.

Objective

The objective of the project 'International network on *Prunus* genetic resources', Genres CT95 No 61, was essentially to increase the utility of the collections in the EU Member States and in a more general way of the European countries. The essential points to be improved were the structure of the existing database, its updating and completion, in particular by adding agronomic information, after having defined the descriptors. The project also had to prepare the harmonisation of the collections at a European level and to create the European *Prunus* collection.

Achievements

During the three years of the contract, work started on all the main components of the project. The data were transferred to an Access database by the INRA so as to transform a data file into a genuine basic data structure. The descriptors were completely revised and were harmonised by all the partners, by incorporating the international criteria recommended by the IPGRI (International Plant Genetic Resources Institute) and FAO (Food and Agriculture Organisation) into the data passport.

The common and specific primary descriptors' revision was carried out in the same spirit while relying on UPOV (International Union for the Protection of New Varieties of Plants) standards. The majority of the passport and primary descriptors data were transferred to this database. These data are available on the Internet (http://www.bordeaux.inra.fr/urefv/base/). The transfer of the European database *Prunus* onto the Internet makes it possible to widely diffuse the state of characterisation of the European collection.

After the consultation with the international experts on each *Prunus* species, agronomic evaluation descriptors were generated. Classes and reference witnesses were established for each type of descriptor. The agronomic characterisation of the selected accessions was carried out during the last year of the project for the descriptors that had been established.

Ultimately, even though the management of the collections at European level is yet to be developed, a solid base for a European organisation on the *Prunus* genetic resources was established. The material's diffusion and utilisation could be considered in the future insofar as material free from quarantine organism and could be propagated in a favourable health environment.

Other participants

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Institute of Plant Genetics and Crop Plant Research, Fruit Gene Bank	Dresden	Germany	M. Fischer
HRI Wellesbourne	East Malling	United Kingdom	K. R. Tobutt
Istituto sperimentale per la frutticoltura	Rome	Italy	F. Grassi
Swiss Federal Research Station for Fruit Growing, Viticulture and Horticulture	Wadenswill	Switzerland	M. Kellerhals
Servicio de Investigación Agraria	Saragossa	Spain	R. Socias i Company
Estación Experimental Aula Dei	Saragossa	Spain	A. Arbeloa Matute

Publications

Dosba, F., Tobutt, K., Zanetto, A., Grassi, F. and Maggioni, L., 'Extraordinary meeting of the ECP/GR *Prunus* working group and third coordination meeting of the EU project GENRES61', 3–5 December 1998, Rheinfelden, Switzerland, 1999, 42 pp.

Dosba, F. and Zanetto, A., 'The *Prunus* European cooperative programme for genetic resources: a networking activity for the European *Prunus* database and the challenge for European collections', in the *Journal of Fruit and Ornamental Plant Research*, Vol. 12, special edition, 2005.

Zanetto, A., Dosba, F., Tobutt, K. R. and Maggioni, L., 'Report of an extraordinary meeting of the ECP/GR *Prunus* working group and the second coordination meeting of the EU project GENRES61', 13–15 November 1997, Saragossa, Spain, 1998, 50 pp.

Zanetto, A., Maggioni, L., Tobutt, K. R. and Dosba, F., '*Prunus* genetic resources in Europe: achievement and perspectives of a networking activity', *Genetic Resources and Crop Evolution*, Vol. 49, 2002, pp. 331–337.

RICE (*ORYZA SATIVA*): CONSTITUTION, DESCRIPTION AND DYNAMIC MANAGEMENT OF RICE GENETIC RESOURCES

URL: http://www.cirad.fr/presentation/programmes/cult-alim/projets/rgriz.html

Project details

Start date: 1 February 1996
End date: 30 April 2000
Duration: 51 months
Project reference: Genres CT95 No 37
Project total cost: EUR 435 150
Project EU co-financing: EUR 275 000

Coordinator

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Description

General information

Considerable research efforts are devoted to rice throughout the world, illustrated in particular by the International Rice Research Institute (IRRI) based in the Philippines, but these efforts primarily target tropical areas which account for around 98 % of the rice grown in the world. Temperate rice (cultivated at latitudes of 40° or above) represents only 2 % of the total, and in Europe, rice is at the northern limit of its cropping area. Most of the European rice cropping area has traditionally been located in economically and ecologically fragile zones with hydromorphic and/or saline soils, such as large alluvial plains or river deltas. In these regions, rice growing today represents an important share of total economic activity and has even become emblematic, contributing strongly to the image of these regions and their overall development. However, this particular agro-ecological context requires adapted varieties with a short plant life cycle and specific tolerance of the biotic and abiotic constraints of southern Europe.

In addition, EU rice production faces two issues. One is quantitative, with a rough deficit of 450 000 tonnes of paddy (i.e. 300 000 tonnes of processed grain or white grain). The other is qualitative, given the increasing preference among European consumers for *indica*-type rice (long and thin hard cooking grain), while local production (approximately 390 000 ha in the five southern countries of the Union) is mainly of *japonica* type (round or short tender cooking grain).

In order to develop new varieties that will address these multiple issues (productivity, earliness, cold tolerance, insect resistance, etc.), European breeders need to have access to all the rice genetic resources of potential interest for this very specific context. Until now, each country of the Union has individually collected and developed its own genetic resources, but they are of obvious interest for all the partners.

Objective

The aim of the project was to characterise and analyse the variability of the rice genetic resources available within the European Union, in order to optimise their conservation, management and utilisation in breeding programmes geared towards European requirements. It was organised in five stages: (1) an exhaustive inventory of the rice genetic resources in Europe on the basis of passport data; (2) characterisation of this genetic material with the aid of appropriate descriptors; (3) creation of a computerised database allowing easy access to and use of this information; (4) analysis and structuring of the genetic variability of European resources and establishment of a 'core collection'; (5) release of project results and assets for European selection purposes.

Achievements

All in all, the work carried out led to the collection and identification of 2 700 accessions, from which 433 genotypes were selected, on the basis of passport data, to be subjected to in-depth characterisation with more than 50 phenotypic traits (agronomic, morphological, technological, pest and disease resistance, etc.) and 16 genetic markers (SSR). Cooking quality tests were also performed for the 433 genotypes. Genotypes with characters of interest were identified among them, to be used in future breeding programmes.

A combined analysis of these 433 accessions, using original methods based on phenotypic and genetic markers, led to the design of a 'diversity tree', giving a good picture of the overall genetic diversity of the European rice breeders' collections. Two different strategies were tested in order to define a core collection, leading to the establishment of a final core collection with just 120 individuals, representative of European rice variability.

All the elementary results were compiled in an Excel® file, and are available on paper, as an Excel® file and on CD-ROM. A specific database including the adjusted descriptors and the pathological and microsatellite profiles of all the varieties was compiled by CIRAD using Sister (Système d'information pour le stockage, le traitement et l'évaluation des résultats), and is also available on CD-ROM.

Over and above the selection-aid tool developed for European breeders, the project offers a large number of additional prospects in the short, medium and long term.

Among the major achievements of this project were the management and joint enrichment of European genetic resources, the standardisation of grading scales and evaluation methods used among Europeans, and the improvement of information flow between breeders and partners in the rice sector. Furthermore, the project contributed to developing the methodology for identifying all the varieties cultivated in or imported into Europe, without ambiguity, even from a single processed grain. This involves very efficient methods as regards traceability, quality control, fraud limitation, trade transparency, etc.

In the medium term, one of the project's major achievements is the development of rapid methods for the appraisal of important parameters for rice quality. Another is the marketing of varieties which suit even better the specific agro-ecological conditions in Europe, the industrial processing requirements, and the new tastes among European consumers, etc., based on traditional genetic solutions.

In the long term, the economic competitiveness of European Union rice production and the socio-economic and ecological stability of the major European rice areas should also benefit from the project.

Other participants

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Publications

Chantereau, J., Giner, M. and Feyt, H., 'Rice genetic resources at CIRAD and the European rice collection', in: *Rice genetic resources and breeding for Europe and other temperate areas*, Proceedings of Eurorice 2001 symposium, CIRAD–IRD–KSAU–VNIIRISA, 3–9 September 2001, Krasnodar, Federation of Russia, Editions CIRAD, Montpellier, 2002.

Clement, G., Delbosc, G., Aguilar Portero, M. et al., 'Diversités génétiques et ancrage socio-culturel: les riz européens veulent valoriser leurs atouts', in: *Perspectives Agricoles*, No 264, 2001, pp. 72–81.

Feyt, H., Dubois, C., Clément, G. et. al., 'Analysis of the diversity of rice genetic resources for use in Europe — Determination of a core collection', in: *Rice genetic resources and breeding for Europe and other temperate areas*, Proceedings of Eurorice 2001 symposium, CIRAD–IRD–KSAU–VNIIRISA, 3–9 September 2001, Krasnodar, Federation of Russia, Editions CIRAD, Montpellier, 2002 (CD-ROM).

ROSA: EUROPEAN NETWORK FOR CHARACTERISATION AND EVALUATION OF GENUS *ROSA* GERMPLASM

URL project: http://ec.europa.eu/comm/agriculture/res/gen/52a.htm

Project details

Start date: 1 April 1996
End date: 31 Mars 1998
Duration: 24 months
Project reference: Genres CT95 No 52
Project total cost: EUR 70 000
Project EU co-financing: EUR 70 000

Coordinator

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Description

General information

The rose is a European symbol and part of the continent's heritage, as attested by the many important public and private collections existing throughout Europe. The rose also has an important economic impact: it is the most widespread crop plant and the most important decorative species with more than 3 000 ha of production in Europe. Despite significant genetic resources it is recognised that the current commercial varieties rest on a very narrow genetic basis and that they exhibit inherent consanguinity symptoms.

The principal cause of the under-exploitation of rose genetic resources is the absence of centralised knowledge of their existence and their characteristics. This is in particular connected to the lack of cooperation and of harmonisation between the various collections, the objectives of which are only defined locally. In particular, there is a fear that lack of cooperation could lead to a dilution of the native gene pool in the short run, if this has not already occurred. It would mean the loss of resources of special interest.

Objective

This joint action was intended to set up a European rose collection network with an aim of managing, conserving, evaluating and developing rose tree genetic resources. In order to fulfil this objective, an essential phase was the census of accessions according to concerted and harmonised methods. The following stages had then to be set: (1) definition of basic descriptors that characterise accessions in a simplified and reliable way, and evaluation of the descriptors in the partners' collections; and (2) definition of accessions' detailed description modalities. In parallel, contacts were established at the European level to present the work in progress and to invite potential partners to participate in a broader action by using the established characterisation standards.

Achievements

In accordance with the objectives of the project and in order to conduct the partners' collection variety census, a consensus on the characteristics to be observed was reached. This led to the construction of a list of passport data and first characteristics (i.e. pest and disease resistance) containing about 28 descriptors. Unfortunately, due to the late availability of these elements and notation problems, the achievements were

limited in relation to the programme initially envisaged. Nevertheless, the linking of the data resulting from the notations carried out allowed the construction of a file including 6 000 entries which is available on CD-ROM. This file made it possible to define the varieties to be safeguarded within the framework of the destruction of the collection of the Wageningen CPRO-DLO (Centre for Plant Breeding and Reproduction Research — DLO).

In addition, the contacts established within the framework of the joint action have allowed the preparation of a research programme 'Breeding healthy Europe for roses' between the Ahrensburg Institute, London University, Wageningen CPRO-DLO and INRA. The aim of the programme is to develop genotypes that are resistant to pests and diseases. In France, an identification programme of rose varieties with molecular markers, associating GEVES Sophia-Antipolis, INRA and the European Horticultural Obtainers' Association was also set up.

With regard to the genetic resource aspects as such, a network of collections of rose trees within Europe will have to be established. This will happen through the census of accessions and characterisation on the basis of the elements defined within the framework of this joint action. At the end of this phase, management of genetic resources concerning rose trees could start. This would lead to a limitation of the inter-collection redundancies, a duplication of present accessions in only one collection to ensure that they are safeguarded and a provision of accessions in particular for the selection programmes. This second phase could be envisaged only after the adoption of the national networks has occurred and the census of the collections' varieties of each State has been completed in a reliable way.

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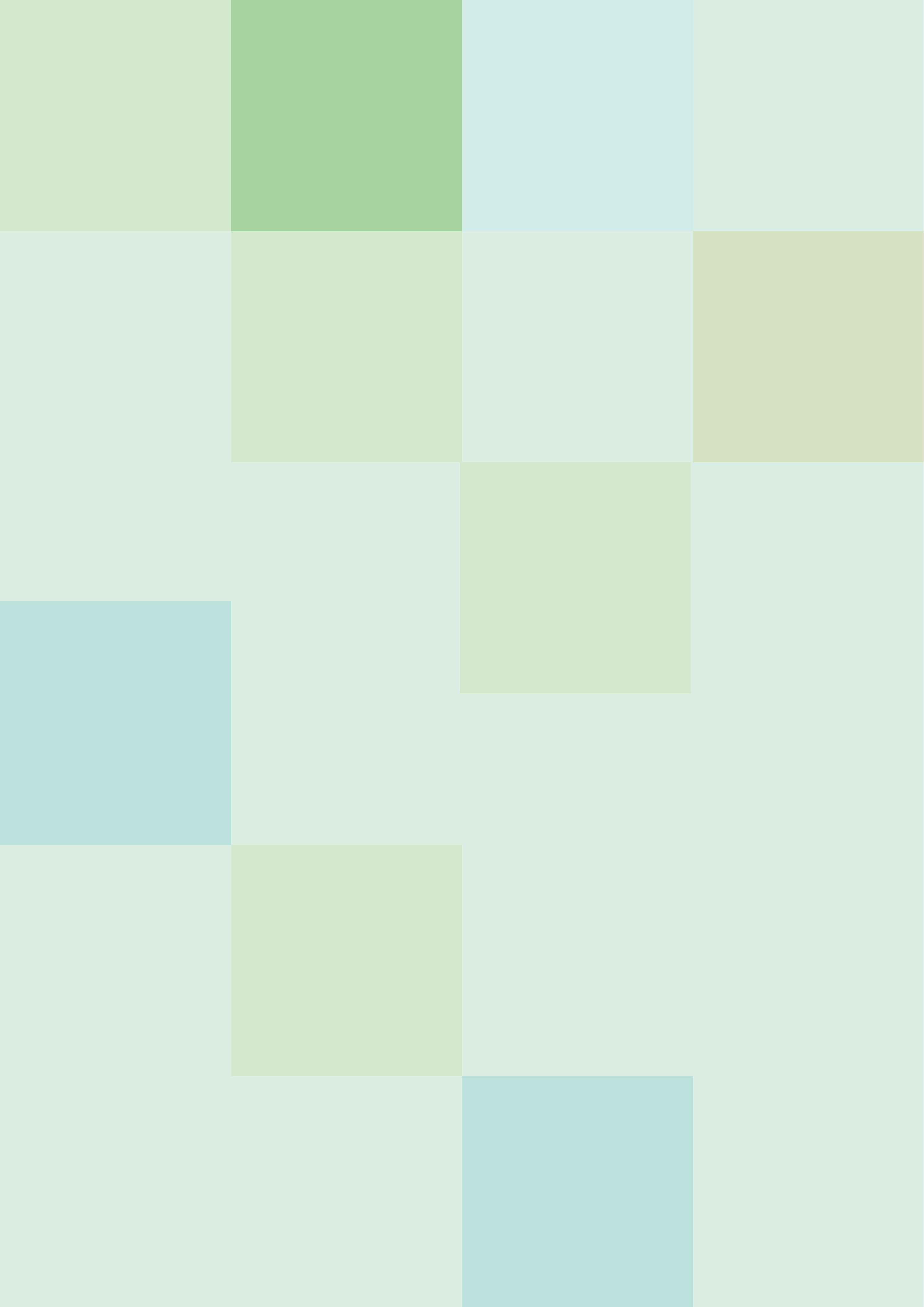

CONCLUSION

The projects mentioned in this brochure have enabled scientific institutes, gene banks, users and private companies to mobilise and bring together national know-how and knowledge in decentralised databases, while preventing duplication of efforts. The projects have contributed to the preservation and exploitation of genetic resources which are native to the European region but which are endangered since they are not competitive in the market. Furthermore, the project has supported the European Community in fulfilling international obligations arising from the Convention on Biological Diversity and obligations arising from the European biodiversity strategy of 1998 (http://ec.europa.eu/comm/environment/docum/9842sm.htm).

Because of the close cooperation with partners outside of Europe, Council Regulation (EC) No 1467/94 has become widely known as an important Community instrument for improving the management of genetic resources for food and agriculture.

PERSPECTIVE

Even though the projects have contributed to the conservation and exploitation of genetic resources in Europe, there are still areas in which further improvements could be made. Moreover, following the meetings and measures that were mentioned throughout the brochure, new priorities in the conservation of genetic resources in agriculture have been identified. In parallel, conferences took place and agreements were made at international level. The next major step after the Convention on Biological Diversity was the FAO 4th International Technical Conference on Plant Genetic Resources in 1996 with the publication of a 'Report on the state of the world's plant genetic resources for food and agriculture' and the approval of a 'Global plan of action on plant genetic resources for food and agriculture' (http://www.fao.org/waicent/faoinfo/agricult/agp/icppgr/itc/itc.htm). Furthermore, the EU adopted the International Treaty on Plant Genetic Resources for Food and Agriculture in 2001 (http://www.fao.org/ag/cgrfa/itpgr.htm). This plan, which has to be implemented by individual Member States, comprises a series of recommendations for priority activities such as *in situ* conservation and development, *ex situ* conservation, utilisation of plant genetic resources, as well as institution and capacity building.

Because of the essential need to maintain biological and genetic diversity in agriculture and the positive impact of the conservation work on plant and animal genetic resources, the Commission adopted in 2004 a second Community programme on the conservation, characterisation, collection and utilisation of genetic resources in agriculture (Council Regulation (EC) No 870/2004 (http://ec.europa.eu/comm/agriculture/envir/index_en.htm#genres) ([18]). Both, *in situ* and *ex situ* methods are fully taken into account in the new Community programme, since genetic diversity can only be secured when different conservation strategies are employed. Through these efforts, the European Community and the Member States contribute to the goal of halting biodiversity loss in agriculture, to safeguard the genetic heritage and to foster the use of almost forgotten varieties and species that have qualities which may become important for sustainable agriculture in the future.

([18]) A list of the selected projects is available on the Commission's "Agriculture and Rural Development" website: http://ec.europa.eu/agriculture/funding/index2_en.htm

TERMS AND DEFINITIONS

Main sources:

http://www.fao.org/biotech/index_glossary.asp

http://www.ipgri.cgiar.org/publications/pubseries.asp?id_serie=13

http://filebox.vt.edu/cals/cses/chagedor/glossary.html

http://cahe.nmsu.edu/news/aggloss.html#A

http://bch-cbd.naturalsciences.be/glossary.htm

http://www.bookrags.com/sciences/genetics/amplified-fragment-length-polymorph-wog.html

Abiotic stress: Outside (non-living) factors which can cause harmful effects to plants, such as soil conditions, drought, extreme temperatures.

Accession: A plant or seed sample, strain or population held in a gene bank or breeding programme for conservation and use.

Agro-morphological descriptors: Characters observed in the field, such as plant height, colour of grain, size of grain, etc.

Agronomic: Application of the various soil and plant sciences to soil management and crop production; scientific agriculture.

Allele: Alternate forms of a gene or DNA sequence, which occur on either or both homologous chromosomes in a diploid organism (see DNA polymorphism).

Ampelographic descriptors: Primary descriptors and secondary descriptors, mainly based on the recording of morphological and agronomical characteristics and on the measurement of parameters relevant to the description of vine leaves, vegetative buds and grapes morphology. Leaf biometry proved in fact to have a significant impact on ampelography, decreasing description subjectivity and providing parametric data suitable to specific statistical tests.

Ampelography: 1. The science of describing and identifying grape varieties by their appearance.

2. A reference book used by growers to identify grape varieties in their fields. The book is based on the science of grape varietals identification.

Amplified fragment length polymorphism (AFLP): A technique for DNA profiling that is based on the selective polymerase chain reaction (PCR) amplification of genomic restriction fragments, and displaying genetic variation, corresponding to restriction enzyme fragment polymorphisms (RFLPs).

Aphid (superfamily Aphidoidea): Small plant-feeding insects with piercing-sucking mouthparts (stylets).

Artificial inoculation: Introduction of certain substances, or pathogens, into or on plant tissues, or to the placement of microrganisms into culture media (for experimental or diagnostic purposes).

Biallelic markers: Genetic marker with gene or DNA sequence presenting two alleles.

Biological diversity: Richness and abundance of species, and variety of natural communities. Both the number of species, and the number of individuals within each species, is important in considering the extent of biological diversity in an area. Also referred to as biodiversity.

Biotic stress: Stress caused by living organisms such as viruses, fungi, bacteria, and harmful insects, which can harm plants.

Cash crop: Agricultural produce marketed for cash rather than retained for household use.

Characterisation: Description of qualities or particularities of an individual, based on descriptors. Description of the essential properties of an organism or system. It refers to the assessment of characters that enable an easy and quick discrimination between phenotypes. They are generally highly inheritable, can easily be seen by the eye, and find equal expression in all environments. These are typically morphological (including taxonomic) characters and they may include biochemical and molecular marker data recorded subsequently.

Chloroplast: Specialised plastid that contains chlorophyll. Lens-shaped and bounded by a double membrane, chloroplasts contain membranous structures (thylakoids) piled up into stacks, surrounded by a gel-like matrix (stroma). They are the site of solar energy transfer and some important reactions involved in starch or sugar synthesis. Chloroplasts have their own DNA; these genes are inherited only through the female parent, and are independent of nuclear genes.

Chloroplast DNA: The DNA present in the chloroplast. Although the chloroplast has a small genome, the large number of chloroplasts per cell ensures that chloroplast DNA is a significant proportion of the total DNA in a plant cell.

Clonal selection: The production of a population of plasma cells, all producing the same antibody, in response to the interaction between a B lymphocyte, producing that specific antibody, and the antigen bound by that antibody.

Clone: An exact genetic replica of a specific gene, cell or an entire organism.

Collecting data: Data that are recorded at the collecting site. Any information included in plant or animal collections. The information can be accessible in computerised databases. Users can query the database to identify accessions within a collection with attributes of interest. The amount of evaluation data varies considerably, depending upon the trait evaluated and on the specific species examined.

Common descriptor list: For plants, this includes morphological descriptors such as flower colour, leaf size, growth habit, and height and width, providing standardisation for users and gene banks, thus permitting comparability. Generally, morphological descriptors are called primary descriptors.

Consanguinity symptoms: Genetic relationship, due to common ancestry, which increases the chance of causing a recessive genetic disease.

Core collection: Consists of a limited set of accessions, derived from an existing germplasm collection, to represent the genetic spectrum in the whole collection.

Crop rotation: Growing of different crops, in recurring succession, on the same land.

Cross breeding: The mating of animals of different breeds.

Cryopreservation: Freezing of embryos, specific plant parts (e.g. gametes, buds, seeds, pollen) or any biological material.

Cultivar: A race or variety of a plant that has been created, or selected intentionally, and maintained through cultivation.

Dendrogram: A visualisation method to illustrate the outcome of clustering in statistics. It is represented as a tree format with a specified branching order. It is used for the genetic analysis of population data, in epidemiological and environmental studies, in bacteria, plants and higher organisms.

Dent: The grain texture of maize is dependent of the type of starch it contains. Dent corn grain has a high level of soft starch in its central part. During maturation, this starch loses water and, consequently, the top of the mature grain shows a depression. Dent types grains are generally long and flat. These traits give grains the shape of a horse dent. Most American material is 'dent' type.

Descriptors: Standardised quotation of a trait of an individual. Traits may belong to different classes: passport data, morphological, physiological or agronomical characteristics, chemical content, molecular markers, etc.

Diploid cell or plant: A cell or a plant which contains two copies of each chromosome.

DNA: Abbreviation for deoxyribonucleic (former spelling: desoxyribonucleic) acid. A long chain polymer of deoxyribonucleotides, housed inside the cell of the organism. DNA constitutes the genetic material of most known organisms and organelles, and usually is in the form of a double helix, although some viral genomes consist of a single strand of DNA, and others of a single- or a double-stranded RNA.

DNA polymorphism: Any variation in DNA sequence, like point mutations, insertions, deletions or variation in the number of repeated nucleotide units.

Duplicates: More or less identical sub-samples of accessions. 1. Gene banks store security duplicates at a second location to prevent accidental loss of accessions. 2. Duplication is also caused by sharing samples, after a collecting mission, exchange of germplasm between countries, and uncoordinated, repeated inclusion of germplasm, such as obsolete varieties in national holdings. These kinds of duplicates are generally not considered as a contribution to the *ex situ* maintenance of germplasm but as redundant, superfluous material.

Duplication: 1. A double occurrence of a DNA sequence within a defined length of DNA.
2. A double occurrence of a specific segment in the same chromosome or genome.

Ecogeographic survey: An ecogeographic survey is an essential first step in the development of a comprehensive strategy for the conservation and use of plant genetic resources.

ELISA: Enzyme-linked immunosorbent assay (ELISA) is a detection method based on the fixation of either antigens or antibody to the plastic well of a microtiter plate and on the detection of the antibody–antigen binding via enzymatic staining.

***Ex situ* conservation:** The two basic approaches to conservation are *in situ* and *ex situ* methods. *Ex situ* conservation refers to maintaining organisms outside their original habitats in facilities such as gene banks, conservation herds (animals), field gene banks or zoological or botanical gardens.

F2, F7: These are two maize inbred lines registered by INRA in 1958. They were used very intensively by many breeders for about 30 years and they are a component of a huge number of early European hybrid maize.

Fingerprinting: Modern technology, allowing DNA molecules to be cut into specific segments through specific enzymes, which enables a kind of bar code to be established. This bar code, specific to each individual, constitutes the genetic fingerprint. This technology is used to distinguish closely related strains, to deduce phylogenetic relationships between strains, and to study their diversity in a variety of ecosystems.

Flint: The grain texture of maize is dependent on the type of starch it contains. Flint corn grain has a high level of hard vitreous starch. Consequently, its shape is ovoid and its surface is smooth. Most European maize landraces are 'flint' type.

Gamete: For diploid species: a haploid sex cell, egg or sperm that contains a single copy of each chromosome. For polyploid species: a sex cell, egg or sperm that contains half of the number of each chromosome. For example, from a hexaploid species ($2n = 6x$) the gametes are $n = 3x$.

Genetic marker: Variable DNA sequence used to identify (or tag) chromosomes, sub-chromosomal fragments, genetic map positions, individuals or populations.

Genotype: The structure of DNA, usually at a given locus, that determines the expression of a trait.

Genus: A taxonomic category including closely related species. Interbreeding between organisms within the same category can occur.

Germplasm: A breed, a line, or any defined group of individuals (e.g. a collection of genotypes), understood as a genetic resource. The original meaning, now no longer in use, is the genetic material that forms the physical basis of inheritance and which is transmitted from one generation to the next by means of the germ cells.

Glucosinolates: A class of molecules produced in the seeds and green tissue of a range of plants, in particular *Brassica* species. Their natural role is thought to be involved in plant–insect interactions. Their importance in plant breeding is largely due to their negative influence on taste and their positive effect on the prevention of cancers of the alimentary tract.

Habitat: The place or type of site where an organism, population or species naturally occurs.

Herbarium specimens: A collection of preserved plants or plant parts, mainly in a dried form. These specimens are often used as the reference material to define a plant taxon.

Hexaploid oats: The genus *Avena* L. (Poaceae) has a basic chromosome number $x = 7$ and contains diploid, tetraploid and hexaploid species. *Avena sativa*, the cultivated and most important commercial oat, is a hexaploid species ($2n = 6x = 42$).

Homonym: A taxonomic name identical to one previously applied to a different species or genus, and therefore unacceptable in its new use.

Hybrid: Individual organism resulting from a cross between parents of differing species or subspecies (strains, breeds, lines). Hybrids may be fertile or sterile, depending on qualitative and/or quantitative differences in the genomes of the two parents. Hybrids are most commonly formed by sexual cross-fertilisation between compatible organisms, but techniques for the production of hybrids, from widely differing organisms, are being developed by cell fusion and tissue culture.

Hydromorphic soils: Soils formed under conditions of poor drainage in marshes, swamps, seepage areas, or flats.

***In situ* conservation:** The two basic approaches to conservation are *in situ* and *ex situ* methods. *In situ* refers to maintaining plants and animals in their original habitat, most notably in farmers' fields (also known as on-farm conservation), or wild plants in their natural habitat.

***In vitro*:** Biological processes that take place in an artificial environment outside a living organism.

***In vivo*:** Biological processes that take place within a living organism or cell.

Inbred lines (F2, F7): Lines or cultivars obtained by self-fertilisation (crossing together male and female flowers of the same plant) so, after a few generations, seeds of the inbred line produce plants similar to the seed parent. Inbred lines are used to be crossed to make hybrid cultivars, or directly used as cultivars, mainly in autogamous plant. In animals, inbred lines are produced by mating sibs.

Indicine (zebu) component: Specific allele of zebu species (*Bos indicus*) allowing for the study of the crossbreeding occurring between zebu and taurine cattle populations.

Introgression: Pairwise crossing and backcrossing technique to introduce specific genes into elite breeding material. This breeding technique is often used to rapidly introduce genes from wild crop relatives into the cultivated form, or from a highly productive breed into a less productive local breed for upgrading.

Isoenzyme or isozyme: A genetic variant of an enzyme. Isozymes for a given enzyme share the same function, but may differ in level of activity as a result of minor differences in their amino acid sequence. Electrophoretic separation of isozymes has been used to distinguish between individuals and varieties.

Landrace: 1. A dynamic population of a cultivated plant that has historical origin, distinct identity and lacks formal crop improvement. It is often genetically diverse, locally adapted and associated with traditional farming systems (Maxted et al., personal communication).
2. The name of a breed of pigs.

Locus: A specific location or site on a chromosome.

Meristem culture: A tissue culture containing meristematic dome tissue, without adjacent leaf primordial, or stem tissue. The term may also imply the culture of meristemoidal regions of plants, or meristematic growth in culture.

Micropropagation: *In vitro* multiplication and/or regeneration of plant material, under aseptic and controlled environmental conditions.

Microsatellite: A segment of DNA characterised by a variable number of copies (typically 5–50) of a sequence of around four (see 'Simple sequence repeat') or fewer bases (called a repeat unit). At any one locus (genomic site), there are usually several different alleles in a population, each allele identifiable according to the number of repeat units. This existence of multiple alleles (high level of polymorphism) has enabled microsatellites to be developed as powerful markers in many different species. They are detected by the polymerase chain reaction.

Microsatellite profile: Fingerprint based on data obtained from microsatellite data analysis.

Molecular characterisation: Characterisation done at molecular level.

Molecular descriptors: Characters related to the physical constitution of the chromosomic matter. They are free of any influence of the environment, so they are good markers of the membership of a genetic group.

Molecular marker: A genetic marker which is assayed at the DNA level.

Morphological description: See 'Primary characterisation'.

MSTRAT: A program for building germplasm core collections by maximising allelic or phenotypic richness.

Myostatin gene: Myostatin is a protein. It is a major regulator of muscle growth, acting through a complex signalling pathway, involving a large number of molecules. The gene encoding this protein is responsible for the phenomenon of increased muscle mass (muscular hypertrophy). Mutations in the myostatin gene result in hypermuscular so-called double-muscled cattle.

Neighbour-Net graphs: A network representation of a matrix of genetic distances.

Nematodes: Roundworms, often internal parasites of animals and plants. The latter are significant economic pests on food crops as few crops are immune to attacks of these creatures which inhabit the soil about the roots of plants. The development of nematode-resistant varieties of crop plants is important to food-growth economics.

Nuclear DNA characterisation: Characterisation of DNA, carried out at the level of the nucleus of the cell and made by amplified fragment length polymorphism (AFLP) or microsatellites molecular biology techniques.

Oilseed crop: Primarily *brassica*, soybeans, palm trees, peanuts, cottonseed and flaxseed used for the production of oils for cooking, protein meals and non-food uses. Less common oil crops include sunflower, safflower, castor beans and sesame.

Oleosity: The state or quality of being oily or fat; fatness.

Organoleptic: Having an effect on one of the organs of sense, such as taste or smell.

Parthenocarpic aptitude: Aptitude to the development of fruit without fertilisation.

Partial resistance: Characterised by slow development and reproduction of the pathogen. Partial resistance leads to a delayed onset of infection (longer latent period), a reduced final extent of attacked leaf area (lower infection frequency) and reduced spore production. Synonyms: horizontal, quantitative or minor gene resistance.

Passport data: Data that record the identity and provenance of a gene bank accession. They are composed of accession descriptors (e.g. accession number, scientific name, cultivar name) and collecting descriptors (e.g. collecting number, location of collection site).

Pathogen: A disease-causing organism (generally microbial: bacteria, fungi, viruses; but can extend to other organisms (e.g. nematodes). Synonym: infectious agent.

Pathological profile: Evaluation of resistance, or susceptibility of an individual to various pests or diseases.

Pedigree: A diagram showing the parents of an individual over several generations. Pedigrees may cover whole animal populations or crop plant cultivars.

Phenotype: The observable characteristics of an organism, the expression of gene alleles (genotype), as an observable physical or biochemical trait. Sum of genotypic value and environmental effects.

Photoperiod: The length of the day. Tropical maize, like other tropical plants, flowers on short days. When cropped in temperate areas, tropical maize will flower very late, around September, and will mature in winter. This is a genetic trait which does not exist in the varieties suitable for temperate areas. Such varieties are said to be insensitive to photoperiod.

Polymorphism: Presence in a given population of several forms, more precisely named alleles, of the same gene or haplotype. Polymorphism in nucleotide sequences has provided powerful diagnostic tools.

Pomology: The scientific study and cultivation of fruit.

Primary characterisation: Characterisation of plant or animal species, based on simple morphological characters (e.g. size, shape, colour). These characters must be useful in terms of immediate and easy identification by any breeder, and easy to record by simple observation of the species at different developmental stages.

Refractometric index: In the food industry, a unit for measuring the approximate amount of sugars in fruit juices, wine, soft drinks and the sugar production industry. It can be measured by a refractometer.

Resistance: The genetically based ability of a host plant to reduce, or to prevent the development of a pathogen.

Saline soils: Soils containing a considerable amount of salt (sodium chloride), which hinders crop growth. For efficient crop production, salt must be leached from the root zone by regular application of irrigation water, and eliminated with drainage water.

Sample: The part of a population, which is actually observed. In normal scientific practice, we demand that it is selected in such a way as to avoid presenting a biased view of the population. If statistical inference is to be used, there must be a way of assigning known probabilities of selection to each sample. If the probabilities of different samples are all equal, for example, the method is called simple random sampling.

Saponins: Natural surfactants, or detergents, found in many plants, but they are most abundant in the desert plants Yucca and Quillaja. Extracts from these plants are commonly used as foaming agents for beverages such as root beer. These biochemicals also have commercial applications, such as ore separation in industrial and mining operations, and are useful in products such as photographic emulsions, cosmetics and shampoos.

Secondary characterisation: Characterisation based on more complicated morphological characteristics with agronomic value. For example, for plants it concerns resistance to specific diseases and pests, good fruit-set at low temperature, reduced vegetation under winter cultivation or chemical value. Other characteristics like DNA polymorphism are also concerned to distinguish between close morphological types. Any descriptor of secondary characterisation needs for its measurement the use of specific techniques (e.g. artificial inoculation, growing at low temperature, etc.).

Simple sequence repeat (SSR): Synonym of microsatellite, defined as a DNA sequence, made of the repetition of a short sequence of two, three or four base pairs, e.g. (CA)*n* = adenin/cytosin motive repeated *n* times.

Somatic cells: Any non-germ cell that composes the body of an organism, and which possesses a set of multiploid chromosomes (diploid in most organisms).

Species: A taxonomic classification of related organisms that can freely interbreed.

Steroidal alkaloids: Organic compounds normally with basic chemical properties, and usually containing at least one nitrogen atom in a heterocyclic ring, occurring chiefly in many vascular plants and some fungi. Many alkaloids, such as nicotine, quinine, cocaine, and morphine, are known for their poisonous or medicinal attributes.

Sustainable field clonal banks: A clonal bank is a living collection of selected clones (asexually propagated plants), which are maintained for conservation and breeding work.

TAGs (triacylglycerols): TAGs are storage lipids stored mostly in adipose (fat) cells and tissues, which are highly concentrated stores of metabolic energy.

Taxon (pl. taxa)**:** The named classification unit (e.g. *Panthera tigris*, *Panthera*, Felidae, Carnivora or Mammalia) to which individuals or sets of plant or animal species are assigned. Lower taxa are those at subspecies and species level (e.g. *Panthera tigris sumatrae*). Higher taxa are those above the species level, e.g. genus, family, order, class, (*Panthera*, Felidae, Carnivora, Mammalia).

Terpenes components: Terpenes are a class of hydrocarbons produced by many plants, particularly conifers. They are major components of resin, and of turpentine produced from resin. The name 'terpene' comes from 'turpentine'.

Tolerance: The genetically based ability of a host plant to recover from the attack of a pest and/or from infection by a disease, without any or with low reduction of fitness and yield.

Traits: One of the many characteristics that define an organism. The phenotype is a description of one or more traits. Synonym: character.

Upgrading: Import or use of exotic genetic material can be used to 'upgrade' breeds.

Variation: Differences in the frequency of genes or traits, among individual organisms, within a population.

Vector: 1. An animal (e.g. an insect) that carries and transmits pathogens.

2. A small DNA molecule (plasmid, virus, bacteriophage, artificial or cut DNA molecule) that can be used to deliver DNA into a cell. Vectors must be capable of being replicated and contain cloning sites for the introduction of foreign DNA.

Vertical resistance: A resistance mechanism, which is specific to an isolated pathogen, based on a single or very few genes. Synonyms: qualitative resistance, major gene resistance.

Ward's minimum variance method: Statistical method used to analyse genetic diversity in germplasm accessions, breeding lines and populations.

Zootechnical: Related to zootechny. Sciences aimed at the domestication, breeding and improvement of animals; the technology of animal husbandry.

ANNEX 1

PROJECT IMPLEMENTATION: ORGANISATION OF THE WORK

(Each project followed the same step-by-step progression)

Step 1	**Establishment of the workplan:** Draw up a minimum list of primary descriptors. The descriptors should be highly heritable, expressed in all environments and they should be inexpensive to evaluate. Then, design and test a common database and a common format for data exchange for the particular project. It is required that the databases used in all actions supported by the programme be compatible and able to intercommunicate. The essential requirement is that the database should be able to export and to import information as a flat format comma delimited ASCII file, and that the field definitions should correspond to those published by a recognised international organisation. Common fields for plant collections should be those designated by either the Hunt common exchange format or the IBPGR format. Common fields for farm animal collections should be those designated by the FAO/EAAP database. Some references to the appropriate documents are given in the appendix.
Step 2	**Characterisation of the collections:** Once step 1 has been concluded, create the database by assembling passport data (passport data are defined as data that are recorded at the collection site), characterising the primary descriptors, and recording this information in the database. Material that was stored without completing its primary characterisation may be regenerated and characterised. The information acquired at this stage will be published and material stored will, so far as possible, be made available to interested parties.
Step 3	**Evaluation/utilisation** (secondary characterisation): Once step 1 has been concluded and step 2 started, where relevant, add data from other screening tests to the database. Examples of such screening tests are: • the routine screening of conserved agricultural material for sources of useful and relevant genes conferring for example product quality, resistance/tolerance to diseases, to pests and to environmental stress, general combining ability, male sterility, grazing behaviour, mothering behaviour and other unique traits; • the recording of other non-economic characters that are useful operationally, e.g. for faster or more precise identification of genotypes or, especially in the domain of genetic resources of farm animals, for the estimation of 'genetic distance'; it may also be appropriate, particularly in the case of collections of genetic resources of farm animals, to record information on minimum population size; • the routine evaluation of the agronomic performance of conserved material in practical conditions; the multiplication of candidate material and its trialing in field conditions; • the acquisition of relevant information from users who have received germplasm from the gene bank in the past, and the collection of relevant information from the literature. Material stored and information gathered, so far as possible, will be made available to interested parties.
Step 4	**Sorting of the collections:** Once step 2 has been concluded, identify duplicates and gaps in collections, with the objective of improving the coordination of collections in the Member States and minimising duplication of effort. To this end, it may be appropriate, especially in the context of collections of plant genetic resources, to designate a fraction of the total collection as a 'core' or 'minimal population'. The information acquired at this stage will be published and material stored will, so far as possible, be made available to interested parties.
Step 5	**Rationalisation of the collections:** Once step 3 has been concluded and where there is duplication between collections, rationalise and harmonise the holdings, aiming to pool the resources for the common good. Some overlap of holdings is necessary to guard against accidental loss. The collection as a whole may be spread over several designated sites. The minimal criterion is that duplicates of core material should be held in dormant condition at at least two designated sites. The information acquired at this stage will be published and material stored will, so far as possible, be made available to interested parties.
Step 6	**Acquisition (collection) of further genetic resources:** Once step 4 has been concluded and step 5 has been started, collection of germplasm is an eligible activity in two situations: where there are gaps in the collection which demonstrably limit their utility; or where there is uncollected material which is reasonably suspected as being unique and which if not collected would be lost. Good collecting practice will be followed and the collected material will be documented and entered in the database (steps 1 to 5). In particular, when collections are recorded and new collections are undertaken, steps will be taken within the programme to ensure that the traditional regional experience and knowledge of the users (farmers, horticulturists) on methods of cultivation, specific uses, processing, taste, etc., are also included. The information acquired at this stage will be published, and material stored will, so far as possible, be made available to interested parties

ANNEX 2

MAJOR FIELDS OF ACTIVITIES COVERED BY EACH PROJECT

Project	*Conservation*	*Characterisation*	*Collection*	*Utilisation*	*Rationalisation*	*Coordination*
Animal projects						
Cattle	🟩	🟩	🟩			🟩
Farm animals		🟩	🟩			🟩
Pig	🟩	🟩	🟩	🟩		🟩
Rabbit	🟩	🟩	🟩	🟩		🟩
Plant projects						
Allium	🟩	🟩	🟩		🟩	🟩
Avena		🟩		🟩	🟩	🟩
Barley		🟩		🟩	🟩	🟩
Beta	🟩	🟩		🟩	🟩	🟩
Brassica	🟩	🟩		🟩	🟩	🟩
Carrot	🟩	🟩		🟩		🟩
Eggplants	🟩	🟩		🟩		🟩
Elms	🟩	🟩		🟩	🟩	🟩
Fruit trees	🟩	🟩	🟩	🟩		🟩
Grapevine		🟩		🟩	🟩	🟩
Maize	🟩	🟩		🟩	🟩	🟩
Melon		🟩	🟩	🟩		🟩
Potatoes		🟩		🟩		🟩
Prunus		🟩			🟩	🟩
Rice		🟩		🟩	🟩	🟩
Roses		🟩			🟩	🟩

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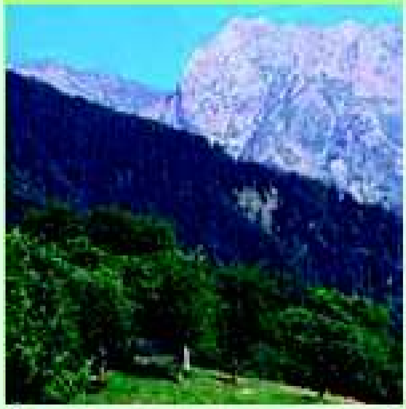

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