



# Preserving genetic resources in agriculture

Achievements of the 17 projects  
of the Community Programme 2006-2011

Agriculture and  
Rural Development

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Cataloguing data can be found at the end of this publication.

ISBN XXX  
doi:XXX

Cover image: ©?????????

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*Printed in Belgium*

PRINTED ON ELEMENTAL CHLORINE-FREE BLEACHED PAPER

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# Preserving genetic resources in agriculture

Achievements of the 17 projects  
of the Community Programme 2006-2011



# # Foreword

Maintaining and developing sustainable uses for agricultural genetic resources is essential for ensuring food security in a sustainable manner.

Preserving and fostering the sustainable use of agricultural genetic resources is vital for the development of agricultural production, also with respect to being able to adapt to environmental changes and climate change and to react to evolving diseases. Furthermore, preserving agricultural genetic resources will maintain our traditions and provide end users with multiple opportunities, including the enhancement of food quality and additional options to sustain economically on changing markets.

The sustainable management of genetic resources is a key contribution to reaching the objectives of the EU Biodiversity Strategy towards 2020, in line with the commitments under the United Nations Convention on Biological Diversity and of the Food and Agriculture Organization (FAO).

The Community Programme, established by Council Regulation (EC) No 870/2004 on the conservation, characterisation, collection and utilisation of genetic resources in agriculture has been successfully implemented. The 17 supported projects of this programme represent important contributions to the conservation of cereals, fruits, vegetables, grapevine, forest resources and farm animals such as cattle and sheep. The projects involved around 180 partners located in 25 Member States and 12 non EU countries, with a budget of EUR 8.9 million. This publication compiles the executive summaries of the 17 projects established under the 'Community programme', dedicated to the conservation and use of both plant and animal genetic resources.

The Community programme has promoted the preservation of genetic diversity and the exchange of information across Europe. Those projects were dedicated to consolidating and enhancing the work of a wide range of gene banks and collections (*ex situ*) as well as conservation at farm level (*in situ*).

These achievements will form the basis for further reflections on future actions which will have a particular emphasis on encouraging the participation of end-users, including breeders, farmers, non-governmental organisations, and consumers. This new emphasis reflects the need for widening the basis for adding value to the conservation and sustainable use of genetic resources and facilitating related innovations at the level of agricultural practice.



**Dacian Cioloș**

*European Commissioner for Agriculture  
and Rural Development*

All the projects can be find at:

**[http://ec.europa.eu/agriculture/genetic-resources/index\\_en.htm](http://ec.europa.eu/agriculture/genetic-resources/index_en.htm)**

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# # Content

<b>Introduction</b>	<b>6</b>
<b>Map</b>	<b>8</b>
<b>Animal genetic resources</b>	<b>10</b>
Cattle	12
Farm animals	18
Sheep	24
Livestock breeds	30
Livestock globalview	34
<b>Arable crop and cereal genetic resources</b>	<b>42</b>
Rice	44
Crop biodiversity <i>in situ</i>	50
Oats	58
<b>Forest genetic resources</b>	<b>66</b>
Forest	68
<b>Fruit, vegetable and spice genetic resources</b>	<b>76</b>
Leafy vegetables	78
Grapevine	82
Saffron	88
Straw- and raspberries	96
Garlic and others	102
Artichokes	108
Nuts and almonds	114
Currants and gooseberries	120

# # Introduction

The second European Community Programme on the Conservation, Characterisation, Collection and Utilisation of Genetic Resources in Agriculture (2006-2011, Council Regulation (EC) No. 870/2004) followed up on the success of the first Programme (1994-1999, Council Regulation (EC) No. 1467/1994). The overriding objective of the second Community Programme was to complement and promote, at Community level, relevant work undertaken in individual Member States on these important activities regarding plant, microbial and animal genetic resources which are of use in agriculture.

In this context, the second Community Programme co-funded 17 individual projects, which dealt with animal resources of various livestock species, arable crop and cereal resources, fruit vegetable and spice resources, and forest resources. Overall, 12 projects addressed plant and 5 animal genetic resources.

This brochure presents the 17 projects' executive summaries, which were prepared by the implementing organisations.

As stated in the evaluation of this Community Programme, the 17 projects contributed to the objectives of the Programme and achieved, collectively, the following:

1. Addressed both *in situ* and *ex situ* conservation issues
2. Led to the phenotypic and/or molecular characterisation of about 14 500 new and existing collections of agricultural and forestry species.
3. Contributed to the collection of about 5 000 new accessions (samples) of agricultural and forestry species.
4. Established searchable databases, national inventory networks, genebanks and DNA repositories.

5. Developed and published useful guidelines including standards and requirements for genetic resource conservation and use of conserved material.
6. Developed strategies for the promotion of under-utilised genetic resources and local breeds.
7. Promoted scientific knowledge in the area of genetic resources in agriculture.
8. Built useful links and collaborations among key European stakeholders.
9. Promoted awareness and information exchange on issues related to agricultural biodiversity, rural sustainability, and food quality and security.

Considerable benefits are expected to accrue from the above outcomes for the stakeholders, the rural environment, the scientific community, and the society as a whole. The very nature of these benefits ensures that their effect will last beyond the formal end of the Community Programme. At the same time, however, further funding will be required for a follow up to these outcomes (e.g. database and genebank maintenance) in order to bring continuity to improving the conservation and utilisation of the European genetic resources.

In addition to successfully supporting the Programme's objectives, the 17 co-funded projects collectively contributed to the Programme's complementarities with other EC instruments. For example, some of these projects were submitted as follow-ups on projects co-funded by the first Community Programme (1467/94). Other projects complemented projects co-funded by the Research Framework Programmes. These were useful cases of the logical progression in science from research leading to innovation, discoveries and, finally, implementation and



application. There were also cases of complementarities of this Community Programme with national activities supported by Rural Development Programmes. All these cases exemplify the considerable scope in forming an uninterrupted continuum across diverse activities aiming at a similar overriding objective, namely the sustainable conservation, management and utilisation of genetic resources in agriculture. The challenge is to do so without redundancies and overlaps.

Throughout the second Community Programme, the preservation and management of genetic resources was linked with vital needs of the agricultural sector in the way the former contributes to food security as well as the rural economy. The latter can be fuelled by the use of local animal breeds and plant varieties. It should be recognised, however, that, more often than not, local breeds and varieties that require conserving are not the highest producing ones. On the other hand, their products may be differentiated from mass quantity to top quality, potentially yielding remunerative economic margins and sustainable benefits. In addition, these breeds and varieties are often hardier, better adapted and more resistant than their commercial, highly productive counterparts, and are preferred in low input systems, such as organic agriculture, and also when adverse circumstances, such as water shortage, prevail.

In conclusion, the second Community Programme stimulated significant interest and collaboration across Europe and beyond, and promoted a better understanding of local practices. The key outcomes of the Programme largely met its original objectives. At the same time, science, industry and the society evolve, and many new aspects and needs emerge warranting a continuation of activities on genetic resources in

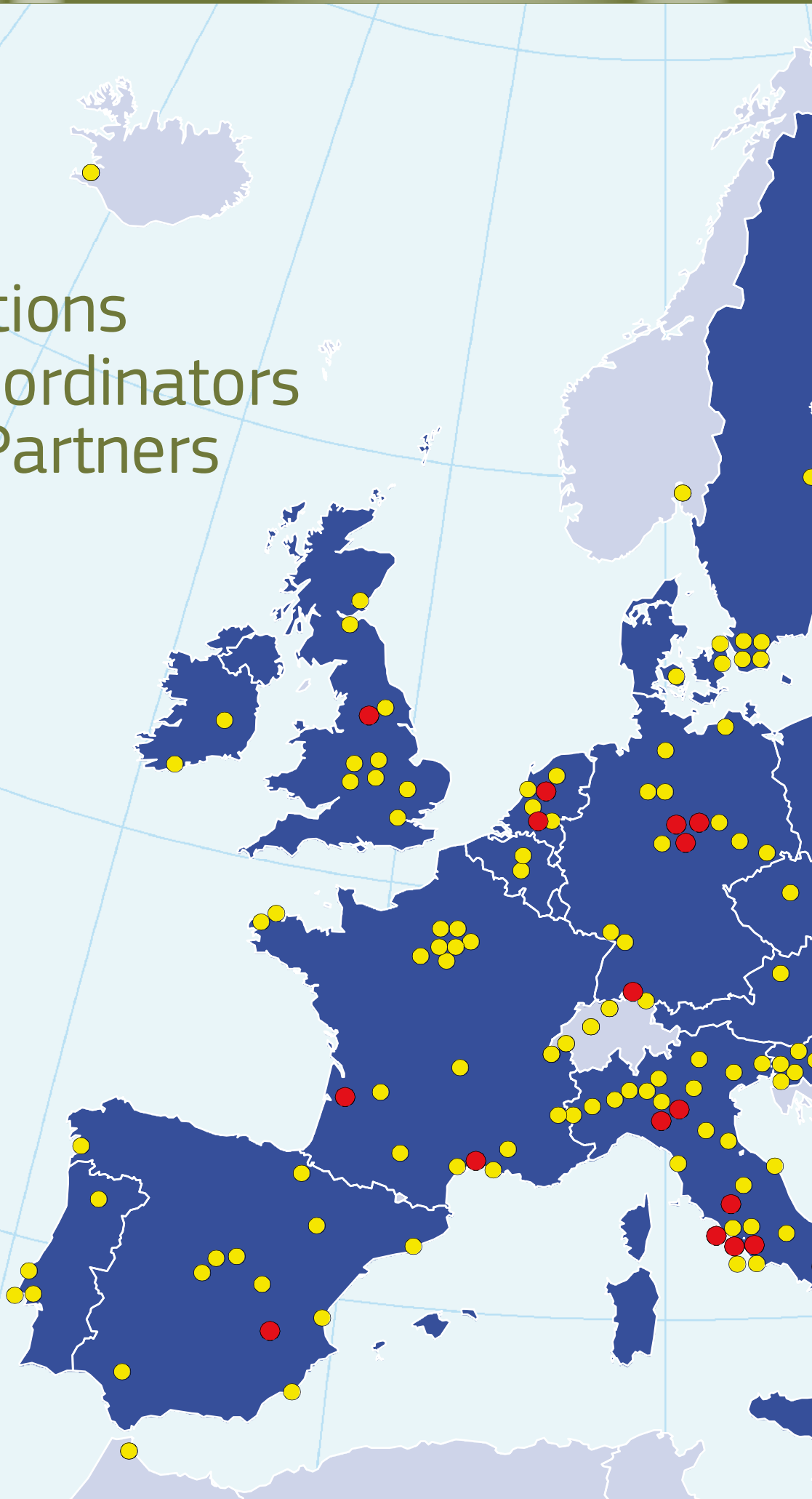
agriculture. Future activities should focus more on the optimal utilisation and management of these resources, directly involving end-users including Small and Medium Enterprises, and consumers organisations. These are considered essential to ensure that (i) the key stakeholder needs are fully understood and catered to and (ii) the uptake of scientific research results materialises effectively along with the necessary synergies for practical implementation. Indeed, the on-going scientific momentum and developments in the areas of genomics and post-genomics research promise a more effective use of genetic resources for the benefit of agriculture through a deepened understanding of the genetic mechanisms that control life. Harnessing this momentum will undoubtedly be a key in valorising the role of genetic resources in addressing the challenges of sustainable food production and security.

**Professor Georgios Banos**

*Chairman of the group of independent experts  
evaluating the Community Programme  
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# # Locations of Coordinators and Partners

- Coordinators
- Partners









# # Animals genetic resources

Cattle	12
Farm animals	18
Sheep	24
Livestock breeds	30
Livestock globalview	34





## Cattle

### Towards self-sustainable European Regional Cattle Breeds

The Regional Cattle action assessed 16 local cattle breeds across 9 Member States, studied national cryopreservation programmes and explored the use of decision making tools for the identification and selection of strategies and policies for the development and conservation of local cattle breeds. The EURECA experts' consortium provided recommendations to breed managers and stakeholders on how to improve strategies at breed level.

### Project details

<b>Duration</b>	36 months
<b>Start Date</b>	01/03/2007
<b>End Date</b>	31/10/2010
<b>Budget Total Cost</b>	979 056 €
<b>Budget EU Co-funding</b>	460 098 €
<b>Actual EU Co-funding</b>	459 948.34 €
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### Background

Cattle started living in close proximity to humans in Central Europe approximately 7 500 years ago and in the Northern parts of Europe a thousand years later. Since then cattle have played an important role in food production as well as in social, cultural and political development of the European societies and individual farmers. Currently, the FAO database DAD-IS lists 534 cattle breeds in European countries, of which 464 are classified as local or regional ([www.fao.org/dad-is](http://www.fao.org/dad-is), January 1st, 2011). Cattle have been used for many purposes from food production to transportation, and from draught power to social insurance. They also serve as pets and ritual animals, like bulls in Spain. Many cattle breeds have been developed for either milk or beef production. At the same time, according to DAD-IS, 130 European cattle breeds have already disappeared and a large proportion of local cattle breeds are now under threat of extinction.

The importance of conservation between and within breed genetic diversity is widely recognised. Irreversible loss of breeds, or genetic variation within breeds, is undesirable. Conservation of farm animal genetic diversity is important for economic, social and cultural reasons. The FAO Global Plan of Action on AnGR (FAO, 2007), as well as the Convention on Biological Diversity (CBD, 1992) and EU policies, address the importance of conservation and sustainable use of genetic resources. These international agreements form the basis for national policies related to the management of AnGR and several European countries have developed *in situ* or *ex situ* conservation strategies for Animal Genetic Resources, including local cattle breeds. Key questions remain: what have been the main drivers for the trend in cattle diversity and animal production in Europe, and what does the future hold for the local breeds? Given the current and future socio-economic, cultural, ecological and genetic values of local cattle breeds, the question is how to improve strategies and policies to support conservation and sustainable use of local cattle breeds in Europe. For this purpose it is important to understand the factors affecting sustainability of breeds, and to share information and experiences between countries and relevant stakeholders.

There are many different factors that support or limit the future sustainability of a breed or that may influence the risk status of a breed. Some factors clearly contribute to the success of particular breeds. Other factors may lead to a critical situation for the breeds. We can distinguish between genetic and non-genetic factors that can affect the state of endangerment of a breed. Genetic factors include the impact of breeding and/or conservation activities. Market changes and changing farmer preferences are examples of non-genetic factors.

### State of local cattle breeds in Europe in the EURECA project

We recognise that local cattle breeds will continue to face problems – even the possibility of extinction in the near future.

From this perspective, the EURECA project was proposed for co-funding by the European Commission, in order to study the factors that affect breed sustainability and to identify new ways to keep local cattle breeds more self-sustaining and to identify opportunities for the development of policies and strategies. EURECA partners in the Netherlands, Belgium, France, Spain, Italy, Poland, Estonia, Finland, Norway and Ireland identified 16 local cattle breeds and carried out detailed breed case studies among other activities in the project.

In order to get a better understanding of the factors affecting the demographic dynamics of local cattle breeds, we collected and analysed different sources of data. 16 breed cases across 9 European countries were selected to study the history, the status, and the development of the breeds. Farmer interviews and perceptions of stakeholders and experts were used to collect new data and to analyse the breed situation within European countries.

For each breed we also analysed the main strengths, weaknesses, opportunities and threats (SWOT) and in this way completed the individual breed assessments. Breed specific strategic opportunities were identified in close interaction with relevant stakeholders in order to strengthen the future prospects for the breeds.

In addition to the detailed assessment of 16 local cattle breed cases, we studied similarities and differences between national cryopreservation programmes, given the relevance of cryopreservation for the long and short term conservation of genetic diversity in local cattle breeds. Moreover, we reviewed available methodologies and software, which can be used for better genetic management of genetic variation within populations by persons or stakeholders responsible for the breed.

The farmer interviews across Europe showed that the sustainability of local breeds may in particular increase when (1) the social awareness about the positive roles of farmers of local

breeds for the society is raised, (2) collaboration among farmers of local breeds is promoted, and (3) the transfer of farms to the next generation is stimulated. It is a general trend that the number of farmers will further decrease and that farmers are ceasing to farm – in part due to the ageing population of farmers, the reluctance of their children to carry on the farm or to continue to keep the local breed.

Five breeds were analyzed in a 'willingness to pay' study among approximately 850 European citizens from four countries. 'Willingness to pay levels' can be used to support the design of cost-effective conservation initiatives, including payment for environmental services schemes. The EURECA study resulted in information on:

- which are the most important market and non-market values provided by local breed cattle?
- to what degree are people willing to trade-off these values?
- does willingness to pay for local breed cattle conservation differ by household type and do attitudes to conservation differ by country?
- which households could be targeted as part of the implementation of a least-cost conservation programme?

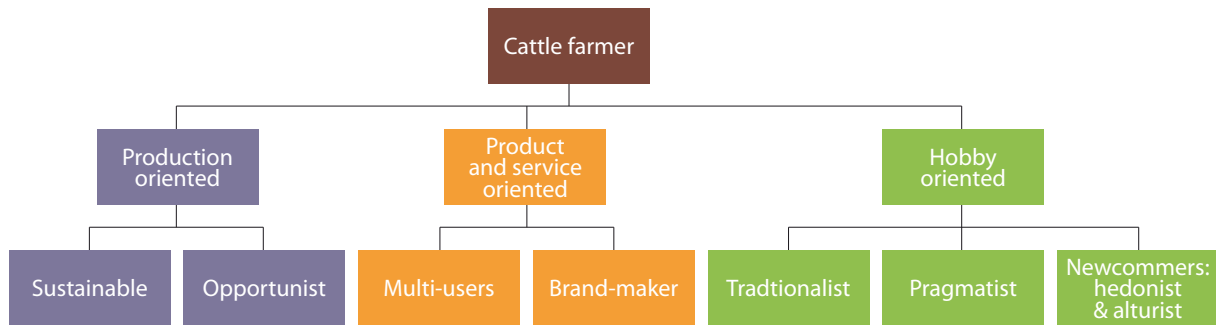
Results from four countries indicate substantial differences how citizens value different attributes associated with local breeds. Moreover, the willingness to contribute financially to certain values associated with local breeds appears also to be quite different between countries/breeds.

### Local breeds are being conserved by farmers

The conservation of local cattle breeds is a complex challenge. It integrates economic, social, environmental and technical issues, and involves many different stakeholders. Those stakeholders range from direct users, such as farmers and consumers, to indirect users that benefit from local breeds, such as the inhabitants of the farming areas. Some stakeholders may be

Groningen White Headed cow – one of the breeds analyzed





Types and subtypes of European cattle farmers keeping local breed animals

involved in several economic activities, some of which may compete with local cattle breeding.

We have explored the use of decision making tools for the identification and selection of strategies and policies for the development and conservation of local cattle. But in the end, it is still the farmer who decides whether or not to keep a local cattle breed, and which breed.

In the EURECA project, we identified common farmer types regarding the attitudes towards local cattle farming, across Europe. Based on a qualitative analysis, three main *types of farmers* could be identified according to the farming goals: 'Production-oriented', 'Product-oriented', and 'Hobby-oriented'. These three types could be further divided into seven subtypes (Figure above). In order to develop (breed) policies for the future it is important to realise that there is diversity of farmer types and farmer characteristics may change dramatically.

*Production-oriented* farmers mainly base cattle farming and its economic profitability on milk and/or meat production. This economic profitability can be either on the long term (*Sustainable*) or in the short term (*Opportunist*). This is also reflected in their

contribution to conservation of local cattle on farms. Sustainable farmers consider that conservation strategies are needed for preserving the good traits of cattle for future breeding, but also to continue the old tradition of their farm. Opportunists, on the other hand, consider farming with local cattle as a necessity to earn income. Their main focus is on profitability, and they do not have any special interest in conservation issues.

*Product- and service-oriented* farmers acknowledge the unique and multiple values of the local cattle, as a basis for various economic activities, and as a response to new challenges in agriculture. We distinguish two subtypes of these farmers: *Brand-makers* and *Multi-users*. The Brand-makers are primarily interested in the gastronomic quality of cattle products, and the Multi-users look at local cattle farming more broadly. For both groups, reasons for the conservation of breed diversity cattle range from genetic to culture and ethics.

For the *Hobby-oriented* farmers the economic profitability of cattle farming is not as important as other factors. For all three subtypes (*Traditionalists*, *Pragmatists* and *Newcomers*) production or breeding is not so important, but the animals themselves are. They all feel the need to contribute to conserving the local breed.

#### Storage of gene bank material in liquid nitrogen tanks





Development of measures to support conservation of local cattle breeds should always take into account the (future) farmers' profiles and attitudes, since each (type of) farmer has a different reason to conserve local cattle on their farm and will be appealed and stimulated by different kinds of supports and policies.

### Gene banks as insurance for long term conservation of local breed diversity

*In situ* conservation of local breeds – often regarded as the preferred method for maintaining the variation in local cattle breeds – greatly benefits from being complemented by cryopreservation of genetic material (*ex situ* – *in vitro*). When *in situ* conservation programmes are not properly planned, breeds may be threatened by inbreeding, by high selection pressure or unbalanced use of some family lineages, by genetic drift or even by extinction. As a backup to overcome such possible shortcomings, cryopreservation of germplasm is not only a very useful tool to maintain genetic diversity within breeds and to support the genetic management of breeds, but also, in the worst case, the cryopreserved germplasm could be used to re-establish the breed.

Some EU Member States are well organised in collecting germplasm from local cattle breeds at threat of extinction and store it in a gene bank, deep frozen in liquid nitrogen. The stores can be seen as an archive and are available to restore a breed in the event of a disaster or to (re-)introduce a particular genetic characteristic.

The inventory performed during the EURECA project in the four countries in Europe (e.g. Finland, France, Italy and the Netherlands) gives an indication about substantial semen gene bank collections, developed from before 1980 until today. Freezing semen is a cost-efficient method to preserve genetic variation. Countries have different ways to organise cryopreservation programmes at a national level, depending on the role and responsibilities of the stakeholders. However, in all four countries studied, the close involvement of breed associations and AI centres in linking the cryopreservation schemes with routine breeding and AI operations, was considered as the most important factor for the development of efficient cryopreservation programmes.

### Strategy development at breed level in a multi-stakeholder process

Improved strategies at breed level require a proper assessment of the main strengths, weaknesses, opportunities and threats (SWOT) by relevant stakeholders. In the EURECA project, breed specific strategic opportunities were identified, to strengthen their future prospects. To solve complex problems we first identified and analysed the key driving factors of the system to understand how they act and how they can be controlled.

SWOT analysis, identification of strategic opportunities and implementation of the strategy is preferably done in

a multi-stakeholder process. Conservation of local cattle breeds is a complex issue and the environment of local cattle production is dynamic. Agro-ecosystems, functions of cattle, products demanded by society, technologies, etc., are all changing in time. Strategic decisions can be made based on the analysis of the current and expected future situations by using the SWOT matrix. Strategies can be developed, by using a SWOT matrix, in four ways; (1) to maximise both opportunities and strengths, (2) to minimise weaknesses while maximising opportunities, (3) to maximise strength while minimising threats, and (4) to minimise both weaknesses and threats. We have concluded that such decision making tools provide a proper framework for approaching the further development and implementation of sustainable, breed specific strategies.

Breed strategies can be developed by using a SWOT matrix, in four ways; (1) to maximise both opportunities and strengths, (2) to minimize weaknesses while maximising opportunities, (3) to maximise strength while minimising threats, and (4) to minimise both weaknesses and threats. SWOT analysis has been implemented in the context of the EURECA project and used for the purpose of identification and selection of strategies for the development and conservation of European local cattle breeds.

### EURECA recommendations

The EURECA Consortium presents the following recommendations and finding to breed managers, policy makers or other stakeholders in this field:

1. Continued development of policies and strategies on how to make breeds more self-sustaining should be included in the National Action Plans for Animal Genetic Resources.
2. Indicators to assess the risk status of local cattle breeds should contain both demographic and non-demographic information. More research in this area is needed and as a result, some (non-demographic) factors should be included in international breed databases.
3. Development of measures to support conservation of local cattle breeds should always take into account the (future) farmers' profiles and attitudes.
4. Strategic planning at breed level should make use of decision making tools, in particular the SWOT methodology, and cover all relevant stakeholders in such analysis.
5. Common policies should avoid unbalanced effects across Europe and should be accompanied by local policies tailored to specific country/breed situations.
6. Breed managers should give proper attention to the management of genetic variation in order to avoid high rates of inbreeding and to keep the population vital. Researchers and technicians should further develop user-friendly software and strategies.
7. Breed managers should strengthen breeding programmes and optimise breeding policies in order to minimise the productivity or profitability gap compared to mainstream breeds.

8. Countries should (further) develop cryopreservation within the framework of a national programme for AnGR.
9. The process for independence from economic support should be initiated for all breeds, making an appropriate use of all breed strengths and opportunities.

### Communication value

The GENRES project has enabled the EURECA Consortium to study local cattle breeds across partner Member States, and discover how best to develop policies and strategies to protect and conserve the numbers and value of the local cattle breeds.

All of this information is also described in our book entitled 'Local cattle breeds in Europe: Development of policies and strategies for self-sustaining breeds' and can be downloaded from our website <http://www.regionalcattlebreeds.eu/publications/publications.html>

The main chapters of the EURECA book were presented at a joint meeting with the GENRES project GLOBALDIV on Livestock Biodiversity in Rome (May, 2010).

Local cattle breeds are a resource to their farmers and communities, and their importance will become increasingly recognised as the need for sustainable farming becomes urgent. To be able to put more attention to these breeds, we have compiled brochures for several of the breeds both in English and in the native language. These brochures include information

about the history of the breed, analyses of population data and outcomes of SWOT analyses based on the farmer interviews. These brochures can also be downloaded from the EURECA website ([www.regionalcattlebreeds.eu](http://www.regionalcattlebreeds.eu)). Specific technical aspects will also be published in scientific journals.

### More information

If you would like to know more about local cattle breeds in Europe, we would be glad to hear from you and provide contacts. Visit our website <http://www.regionalcattlebreeds.eu> or email us on: [SipkeJoost.Hiemstra@wur.nl](mailto:SipkeJoost.Hiemstra@wur.nl)

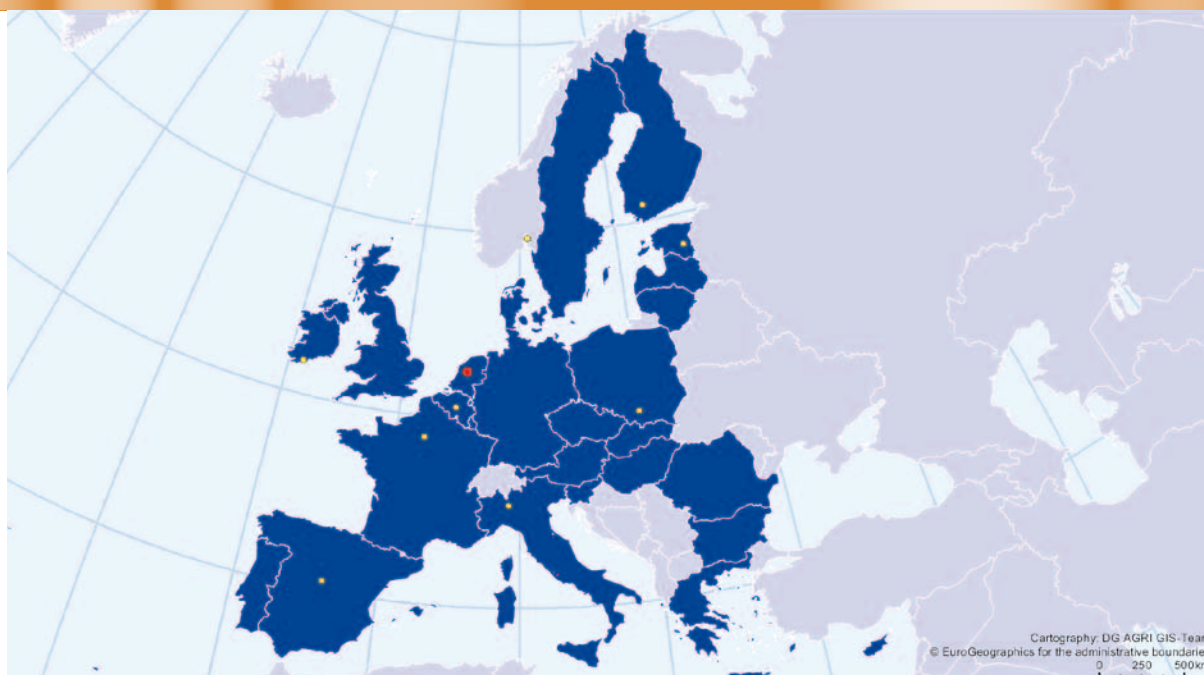
### Publications

The EURECA book entitled 'Local cattle breeds in Europe: Development of policies and strategies for self-sustaining breeds' and other publications can be downloaded from the EURECA website <http://www.regionalcattlebreeds.eu/publications/publications.html>



Consortium Meeting, Lodi, Italy (2008)





## Coordinator and Partners details

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## Farm animals

An integrated network of decentralized country biodiversity and genebank databases

The European Farm Animal Biodiversity Information System network (EFABISnet) action set up decentralised national inventories of animal genetic resources in 16 additional countries, installed 14 CryoWEB databases, linked them into the existing EFABIS and FAO DAD-IS databases and developed a unique network of animal genetic resources biodiversity information systems in Europe comprising 32 databases in 17 countries.

### Project details

<b>Duration</b>	46 months
<b>Start Date</b>	01/01/2007
<b>End Date</b>	31/12/2010
<b>Budget Total Cost</b>	907 296 €
<b>Budget EU Co-funding</b>	349 965 €
<b>Actual EU Co-funding</b>	347 890.32€
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<b>Coordinator's Website</b>	<a href="http://www.eaap.org/content/efabis_net.htm">http://www.eaap.org/content/efabis_net.htm</a>

## Background

One cannot protect what one does not know. This simple truth might have lead in the 80s of the last century to start a survey in Europe on the breeds used in animal production. Personal contacts served as a basis and ensured that questionnaires sent out returned with useful information such as breed description, performance, use and population numbers. The idea to make this information available to the public was the birth of the first European Database on Animal Genetic Resources (AnGR) then located at the Veterinary School at Hannover/Germany which soon got under the umbrella of the then European Association of Animal Production (EAAP) and to be known as the EAAP Animal Genetic Databank (EAAP AGDB) in 1987.

## What is EFABIS?

In the wake of the Rio Conference, Earth Summit in Brazil 1992, the Food and Agriculture Organization of the United Nations (FAO) started developing a WEB based system to record and present information from the breeds of the world, using the EAAP database as a model. DAD-IS, the domestic animal diversity information system, served as a basis for the state of the world report which was the first comprehensive report on the breeds of the world.

However, EAAP AGDB and DAD-IS were operating in parallel, which required the European countries to enter largely identical data in two systems. At the same time it became clear, that the demand had outgrown the capabilities of the meanwhile rather dated information systems. So the logical conclusion was to develop a new platform with modern technology and the objective to replace both the EAAP database and DAD-IS by a new system with extended networking and automatic data exchange capabilities. The idea lead to the development of a proposal which got funded in the EU Research Framework Programme 5 from 2002-2006 to become the European Farm Animal Biodiversity Information System (EFABIS) project.

EFABIS is:

- a register of domesticated animal breeds;
- a repository for documents related to the management of AnGR;
- a contacts folder for the National and Regional AnGR Coordinators;
- an advanced information and communication tool.

Immediately, the EFABIS project offered the option of installing many decentralized country biodiversity databases, each in their own language to serve as a national focus on their own national biodiversity, yet exchanging automatically information amongst them. At the end of the EFABIS project the software had been developed and three functional databases were established: one in Poland as an example of a national database or node with national specificities, one EAAP database aggregating European data and its own set of specificities and one FAO DAD-IS database



collecting all the worlds' data. This new network of communicating databases was called the Farm Animal Biodiversity Information System network (FABISnet).

### What are FABISnet, FABISnet databases and software?

FABISnet is an integrated network of decentralised country biodiversity and genebank databases for AnGR by making regional and national databases websites run under the national and regional European (EAAP) responsibility integral parts of the FAO structure. So called National Focal Points have been mandated by their national governments to report their national biodiversity data regularly to FAO's global DAD-IS database. With the emergence of FABISnet this data entry could be done at national and regional level followed by automatic data transfer to all other systems including FAO's DAD-IS.

FABISnet databases are websites accessible publicly on the internet. They are:

- registers of domesticated animal breeds with descriptions and population numbers;
- repositories for documents related to the management of animal genetic resources;
- contacts folder for the National and Regional Animal Genetic Resources Coordinators;
- advanced information and communication systems;
- used as reporting and early warning tools.

As all FABISnet software was developed using free software components (Open Source) it was possible to make any number of new installations free of license costs. Therefore, it was natural to expand the national database to as many European countries as wanted to join, to provide them with an own focus on their own genetic resources easily accessible and usable in their own national language and even character set.

### The *ex situ* conservation in genebanks

Apart from *in situ* conservation of breeds, it has long been accepted that *ex situ* conservation in genebanks has to play an integral part of any conservation strategy. In animals, this implies storage of deep frozen material like semen, embryos, and somatic cells.

Obviously, an efficient long term register of all material stored in a national gene bank is of paramount importance for its possible future use. Developing such a system for each genebank individually is often beyond the technical software development means. Furthermore, one system with a unified data set will make a European view on all genebanks so much easier. Such a system had been developed at the Friedrich-Loeffler-Institut (FLI) Mariensee/Germany and therefore served as a starting point for the setup of national genebanks by providing the informational bracket and procedure on what data had to be collected and what agreements among partners had to be reached to establish a genebank.

The EFABIS database collects – as a European specificity – aggregate count on stored genebank material on a per breed basis, information that is not available on the global level. As genebanks require long term documentation of individual animal material like semen and embryos stored, the per breed total would then in fact constitute the actual figure recorded in the EFABIS databases. All of this lead to the second project 'EFABISnet' which got funded as EFABISnet AGRI GENRES O20 action.

### Three major objectives of the EFABISnet project

Conservation of animal genetic resources requires public support. This is why visibility of a country's wealth of breeds in animal agriculture is of great importance.

The first objective of the project was to set up decentralized national inventories of animal genetic resources on the basis of the EFABIS database system in 12 additional countries, in addition to Poland. This gives countries the opportunity to present all their knowledge on their breeds in their own language and writing (for instance Greek and Georgian). Furthermore, documents related to these breeds can be stored on their own national FABISnet website. This helps to create ownership and instills responsibility, both being important components in gaining support for the countries' management and conservation of these resources. While serving as a national focus with information and data being only available in the country's database, it additionally serves as a collection and reporting point for each country's obligation to deliver a well defined set of data to FAO, via the EAAP EFABIS database and from there to FAO's DAD-IS.

Twelve countries (AT, CY, EE, IRL, IT, NL, SI, SK, UK, and outside EU, CH, IS and GE) will become partners to have national FABISnet database installed which are publicly accessible on the Web. The twelve national coordinators of animal genetic



resources (NC) will furthermore bring their inventories up to date to create a much more complete European register of countries' animal genetic resources than was available before.

The second objective of the project was the establishment of decentralized national inventories of national gene bank collections on the basis of the CryoWEB database software.

A CryoWEB database runs as a website to manage a national genebank recording data from individual animals as opposed to the breeds data in FABISnet database:

- it is a documentation system for national genebank inventories for any material and species;
- it collects minimal data set for ensuring usability of the material after many years;
- it has the options to enter also specific data like images and documents;
- it has restricted access to sensitive data, thus generally not open to the publication;
- its software is freely available without licensing costs;
- it uploads per breed totals of genebank material to FABISnet databases.

Genebanks are considered very important. However, their establishment requires much work in both the organizational framework as well as in the technical aspects of documentation.

Most countries would like to have genebanks as part of their conservation strategy. They often have semen or embryos stored somewhere that could be considered genebank material. However, setting up a national genebank requires resolving many practical and legal issues. Instead of first defining the legal status of a national genebank, the EFABISnet projects tries to jump start the development of national genebanks (where they had not yet been defined) by focusing on the practical issues of documenting what is already available through

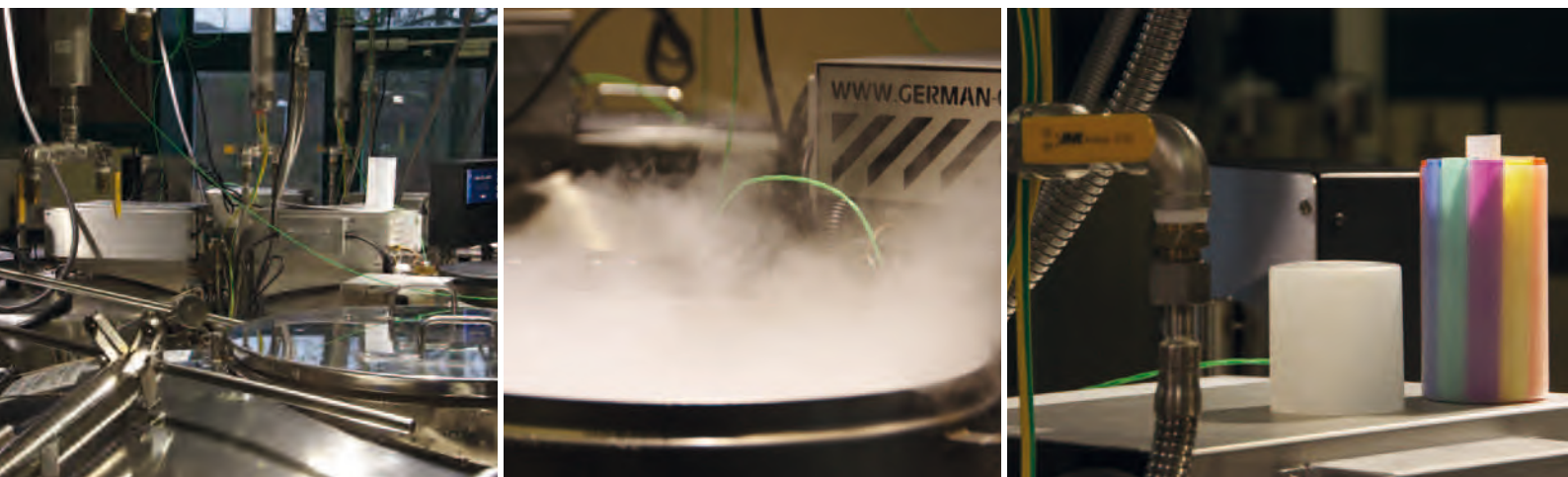
the WEB based CryoWEB information system. Being a fully developed database system, countries do not have to put efforts into defining the structure of data to be recorded and software development. Instead, CryoWEB can be used right away, and can even be translated into the national languages. In parallel, countries can focus on resolving the other issues around the creation of a national genebank, and at the same time can, as a resource for sharing experience, use the group of CryoWEB users of the project.

Ten countries (AT, EE, FIN, NL, SI, SK, UK, and outside EU, CH, IS and GE) will become members of the CryoWEB part of the EFABISnet project, linking their new genebank registers into the existing European EFABIS and FAO DAD-IS databases.

The third objective of the project focused on the development of a permanent management structure of the European network of animal genetic resources inventories on the national, European and international FAO level comprising 25 databases (the 3 first ones already existing before the project, + the 12 for EFABISnet + the 10 for cryoWEB) in 14 (AT, CY, EE, FIN, IRL, IT, NL, PL, SI, SK, UK, and outside EU, CH, IS and GE) countries for the sustainable management.

The long term maintenance of the network created under the EU projects beyond the actual project time to ensure the long term operation and development of this unique web of biodiversity databases. Such a network needs much more coordination than an equal number of stand alone databases because they exchange information through the web largely automatically. This means, that the individual systems need to be known uniquely in the network, modification in one of the databases must be such, that the data exchange with the other systems is not impeded, there has to be a policy in place that allows for coordinated bug fixes or further improvement and even expansion of the network.

#### Genebank equipment and liquid nitrogen cryo tanks



## Overview of EFABISnet project's implementations

The net result of implementing these objectives was that more countries than originally foreseen did join and therefore more databases were implemented. Currently, the EFABIS network consists of 14 CryoWEB installations and 18 FABISnet nodes (16 national country nodes are feeding data into the European node (E) hosted by EAAP in Rome, which in turn synchronizes data with the worldwide node (D) hosted by FAO also in Rome).

In total, 32 databases have installed in 17 countries (AT, CY, DE, EE, FIN, GR, HU, IRL, IT, NL, PL, SI, SK, UK, and outside EU, CH, IS and GE).

The FABISnet nodes and CryoWEB installations are available in 9 languages (Dutch, English, Estonian, Georgian, German, Greek, Icelandic, Italian and Slovenian) and the public has access in 12 countries to their data in their national languages; [in case of the CH in 2 of the national languages].

## Project details

EFABISnet offers a new development component in production environmental descriptors. EFABISnet's main thrust was the large scale introduction and dissemination of national biodiversity databases all over Europe and its updating to reflect the countries' current state of biodiversity. Similarly, CryoWEB had been developed at FLI earlier with the intent to provide countries with the means to document their national genebanks without having to embark on own software development.

The EAAP coordinated the action and the technical coordination and software development, including CryoWEB, was performed at FLI and the Production Environment Descriptors (PED) development done at FAO. Members of the management committee were EAAP, FAO, FLI and UNIMI; the European Regional Focal Point (ERFP) was a regular participant.

The objective of introducing large scale databases and websites all over Europe resulted in the structure of the action: one central resource person, who was available to all partners, helped to install and to setup new national databases and to integrate them into the transnational network, additional to develop the software further. This central resource person was located at FLI in Mariensee/Germany; FLI also provided the technical coordination of EFABISnet project.

## Communication value

EFABIS is all about communication: communicating the breeds of the country, the region, the world to the general public, to schools, to universities. This is why the EFABIS websites are designed to be multi lingual and with an infrastructure to be translated into any language. As publicly accessible websites, they present the breeds of the world with images and textual information about them. Being websites, the data is accessible

from anywhere around the globe. Enhanced accessibility of nationalized FABISnet websites is also a boon to many users. Not everybody easily reads English, so being able to browse and read information on breeds in one's mother tongue opens this segment of agriculture and national heritage to a whole new segment of society.

FABISnet databases have been set up to contain the relevant public data of the world presented under the control of the respective countries. As a result, within a country users can not only inform themselves about their own genetic resources but also about the breeds of neighbouring countries of Europe and indeed the world. This makes each FABISnet node a one-stop-website to access national and indeed the international breeds of the world.

The initial assumption during the development of the EFABISnet project was, that decentralized national biodiversity websites would create ownership and help to make the national breeds known to a much wider audience, thereby enhancing support for conservation measures. This view was not only taken by the initial project partners but also by three more countries (FI, GR, HU) who, at their own cost, had a national FABISnet node set up during the project. For similar reasons, while the UK installation was not done as planned, five (DE, GR, IR, IT, PL) additional CryoWEB installations were done outside the project.

Therefore, communication has been at the center of the EFABISnet project and been very successful with a high visibility of 18 publicly accessible FABISnet websites and 14 CryoWEB installations documenting in a harmonized manner national genebanks in Europe.

## Links

The EFABISnet project website can be reached at:  
<http://efabisnet.tzv.fal.de>

All 18 FABISnet nodes can be reached at:  
[http://efabis.tzv.fal.de/fabisnet\\_graph\\_links.htm](http://efabis.tzv.fal.de/fabisnet_graph_links.htm)

## The databases

EFABISnet is possibly the project that has created the largest number of communicating databases all over Europe and has certainly changed the management of data on animal genetic resources. Scientists and the general public are invited to browse the EFABIS databases (see list below) with its more than 5 000 breeds from 30 species used in animal production in Europe, with its images, general descriptions and population sizes as they developed over time together with extensive reports which users can customize and execute. To ensure future long term operation of these facilities an agreement between EAAP and the ERFP including a financial commitment has been reached.

### *FABISnet databases*

During the EFABISnet project the number of FABISnet databases increased from 3 to 18 all accessible through the web. Out of these, the databases can be used in different languages as far as user interface and in part also as far as content goes. Thus, countries have developed an ownership that goes well beyond the use of one centralized system that would have had to be used in case EFABISnet had not been established.

In total, 16 additional countries have FABISnet national nodes installed with 11 of them using the node in at least one of their national languages.

Interestingly, FABISnet databases were set up in 3 additional countries (FI, GR and HU) initially not foreseen in the EFABISnet project, resulting in a total of 18 FABISnet databases all publicly accessible through the web. This just goes to show, that the strategy and software developed during the EFABIS and EFABISnet projects has lived up to the initial expectation as providing a software framework, which is generally applicable and useful to the international community at large.

### *CryoWEB databases*

In total, 14 countries decided to use CryoWEB as register of their own genebank, in many cases thereby starting for the first time the formal process of setting up such a facility. Being a database of individual animal records, access is usually not public. However, CryoWEB and EFABISnet are integrated in such a way, that cumulative breed statistics can get electronically transferred to EFABIS and thereby providing exact data of cryo conservation.

The net result is that dissemination went well beyond the initial scope of the EFABISnet project with 5 additional installations (IR, IT, GR, PL, DE). In total, 14 countries chose to have CryoWEB installed as registers of their national gene banks with 10 of them using it in at least one of their national languages.

### *List of publications*

Duchev ZI, Groeneveld E (2006) – Synchronization of APIIS based farm animal biodiversity systems. *Bioinformation* 1(5):146-152.

Duchev ZI, Groeneveld E (2006) – Improving the monitoring of animal genetic resources on National and International level. *Arch. Tierz., Dummerstorf* 49(6):532-544.

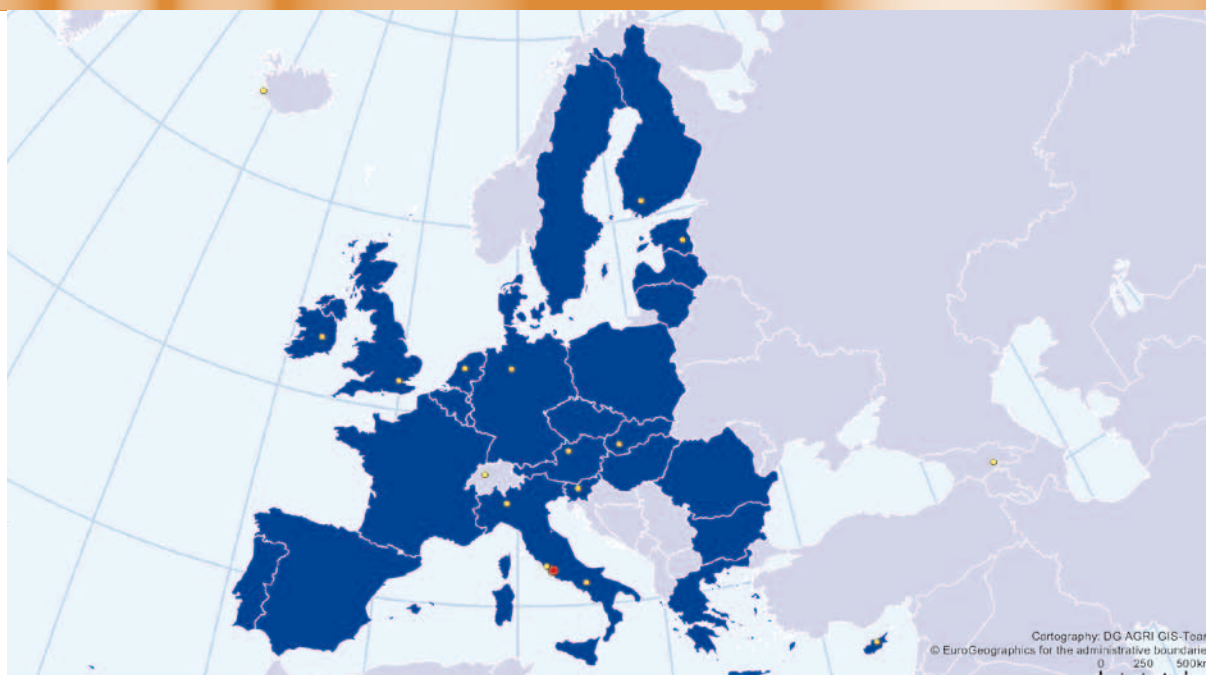
Duchev ZI, Distl O, Groeneveld E (2006) – Early warning system for loss of diversity in European livestock breeds. *Arch. Tierz., Dummerstorf* 49(6):521-531.

For the full list of publications, see the project website:  
[http://efabisnet.tzv.fal.de/?page\\_id=23](http://efabisnet.tzv.fal.de/?page_id=23)



Final EFABISnet conference in Palermo 2010





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## Sheep

### Heritage Sheep

The Heritage Sheep action studied Heritage Sheep Breeds across 5 Member States, contributed to a European genebank and how best to develop markets as a means of protecting and conserving the numbers and value of regional sheep breeds.

#### Project details

<b>Duration</b>	24 months
<b>Start Date</b>	01/04/2007
<b>End Date</b>	30/09/2009
<b>Budget Total Cost</b>	720 757 €
<b>Budget EU Co-funding</b>	356 000 €
<b>Actual EU Co-funding</b>	307 608.38€
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#### Background

There are many different breeds of sheep currently existing in the world. Out of a total number of some 1 200 breeds, more than a third of them – 417 are native to the European Union. Selected by generations of farmers, each sheep breed has evolved over the centuries. Today, some are known for the special quality of their meat, their milk and cheese, or their wool; other breeds are specifically adapted to a harsh life grazing the heather on mountains, living off seaweed on beaches, or surviving life on fenland marshes. These local Heritage Sheep Breeds are distinct to their regions, adapted to their environments and provide low-input farming systems that protect landscapes and encourage tourism. Importantly, these regional native sheep breeds contribute to social communities and provide a commercial opportunity to sustain local economies.

Unfortunately this situation is increasingly threatened – and the native sheep breeds of Europe are now losing numbers at such a rate that the breeds are at risk of becoming lost forever. Farmers are preferring intensive agriculture, using foreign breeds that grow rapidly but need much higher levels of management and food than the local breeds. Disease outbreaks and epidemics are also ever-present threats, with risks made much worse when each Heritage breed is concentrated within a single region.

These sheep breeds are a resource for future generations – people will need to turn to more sustainable farming systems protect the environment and encourage rural development to support a secure food supply for expanding cities and the rising global population.

We need to learn urgently how best to protect these valuable farm animals from extinction – before it's too late.

#### Breeds in the project and the threats they face

When the foot and mouth disease epidemic hit certain regions of the United Kingdom in 2001, the local breeds of those regions were nearly killed out [1] (Bowles et al, 2003). Policy makers realised for the first time that concentration in a particular region could pose a real threat from disease – and 'Heritage Breed' became a recognised definition. When the whole of Europe was surveyed [2] (Jones & Bowles, 2006), it was realised that all the Member States had their own unique regional Heritage Sheep Breeds – each supporting their local communities and helping to sustain economies and environments.

As animal scientists and farmers we recognised that these breeds were facing increasing problems – even the possibility of extinction in the near future. For this reason, we gained funding from GENRES project to study the breeds in more detail and work out new ways of protecting the sheep and their commercial potential. As partners in the United Kingdom, France, Netherlands, Greece and Slovenia we each identified our national Heritage Sheep Breeds for the project.

France			
Basco Bearnaise	Bizet	Causses du Lot	Corse
Grivette	Limousine	Manech Tête Noire	Manech Tête Rousse
Mourerous	Mérinos d'Arles	Rava	Tarasconnais
Velay Black			
Greece			
Boutsiko (Orino)	Frizarta	Katsika	Kefallinias
Sfakia			
Slovenia			
Bela Krajina Pramenka	Bovec Sheep	Istrian Pramenka	Jezersko Solcava
The Netherlands			
Black Blazed	Blue Texel	Drenth Heath	Flevolander
Kempen Heath	Mergelland	North Holland	Schoonebeek
Swifter	Texel	Veluwe Heath	Zeeland milksheep
United Kingdom			
Brecknock Hill Cheviot	Cheviot	Clun Forest	Dalesbred
Derbyshire Gritstone	Devon Closewool	Exmoor Horn	Herdwick
Lonk	Romney	Rough Fell	Shetland
South Welsh Mountain	Southdown	Welsh Hill Speckled	

We prepared questionnaires and contacted local breed societies to collect as much information as possible. This included recording the special values of each breed, the range and number of threats facing the breeds, the numbers of breeding animals that currently exist and whether in the future, those numbers were likely to go up or down. All of the answers to the questionnaires were built into a database <http://www.heritagesheep.eu/Default.aspx> that can be rapidly accessed for information on each of the breeds in each partner Member State.

The most serious general threat highlighted by all breed societies, across the EU, was farms ceasing to farm – in part due to

the ageing population of sheep farmers, the reluctance of their children to carry on the farm and the decision of many farmers, young as well as old, to go out of sheep farming completely because of decreasing returns for the work needed. This is a very real risk – just when food security is becoming recognised as an urgent issue.

Changes in government policies and reform of the Common Agricultural Policy were also political issues perceived to threaten the livelihoods of sheep farmers. And new diseases now appearing in Europe for the first time can rapidly reduce sheep numbers.

Veluwe Heath sheep of The Netherlands



Heritage Sheep of Greece





Our survey showed that the Heritage Sheep Breeds were far more regionally concentrated than previously thought. In the UK, we worked with breeders to get information on individual flocks – and for the first time accurately geo-referenced these Heritage Breeds – putting each and every flock ‘on the map’ [3] (Carson et al, 2009). This showed for example that more than 95 % of the Herdwick breeds, a famous sight in the Lake District national park, are all found within an upland area just 40km across. Clearly this presents an immense risk if the worst were to happen and there was a disease outbreak in the area. Already in the Netherlands and France there have been significant numbers of sheep lost due to the disease called Bluetongue Virus, which until 2006 had never been found in Northern Europe.

### The best way to protect a breed – conservation on the farm

It is said that the only long-term solution to protect a breed is to ensure there are markets for its produce – whether meat or milk or cheese or wool – or breeding animals to maintain and share the best of the breed’s qualities. If there are these markets, there will be sufficient reason to continue to farm the breeds commercially and their numbers can be sustained economically at a high level.

Our French partner studied reasons for the success of three Heritage Sheep Breeds that continue to be commercially farmed in the French Pyrenees and are used for milk production. Through regional economic support for the sheep dairy industry, there has been a doubling of outputs over the last 20 years and very importantly, new special-label products have been developed, particularly the Label Rouge Agneau de Lait des Pyrénées. Flocks of each breed are managed locally with the farmers working closely with the breed society to maintain top quality animals – through flock records, selective breeding and progeny testing – all aimed to help ensure the milk products from the Heritage Sheep will attract growing markets.

We also looked at all the different ways that sheep breeders in the different partner Member States promoted their products and analysed any difficulties they had encountered to see if there was a common theme for success – such as help from regional governments and more closely monitored breeding programmes for the sheep.

### Protecting genetics as a long term safeguard – genebanks

Some Member States are well organised in collecting germplasm from sheep breeds at threat of extinction and keeping it stored frozen in genebanks. The germplasm can be semen from rams or very young embryos flushed from ewes after artificial insemination. The stores can be an archive and are available to restore a breed or a particular genetic characteristic that could be lost in the event of a disaster.

We wanted to find out the best methods in use across the Member States such as those for collecting semen from rams – whether living animals or taken from dead rams at slaughterhouses – and the range of procedures used for freezing of germplasm. Our partner in the Netherlands took the lead in this work and collated the information into a computerised ‘Conservation Planner’, available as a downloadable zip file at the website

<http://www.cgn.wur.nl/UK/CGN+Animal+Genetic+Resources/Tools/>

This is based on standard population genetics and data collected through this project. We hope that breeders and breed societies planning an *ex situ* conservation scheme for a Heritage Sheep Breed will find the planner a useful resource.

The Bovec heritage sheep of Slovenia



A partner from the Heritage Sheep consortium working with a local farmer in the Netherlands



Based on data collected throughout the project, each of our five partners chose two Heritage Breeds in their countries from which to collect germplasm. Semen from these rams is now safely stored and represents the beginnings of a European-wide genebank of Heritage Sheep Breeds.

### Communicating value

The GENRES project has enabled us to study Heritage Sheep Breeds across our partner Member States, contribute to a European genebank and discover how best to develop markets as a means of protecting and conserving the numbers and value of the sheep breeds.

All of this information is now available for everyone to see on our website: <http://www.heritagesheep.eu>. Our Greek partners have developed the site to communicate the values of the Heritage Sheep Breeds to the public and to policymakers. They have designed and set up a unique database that you can easily search and use.

These sheep breeds are a resource to their communities and their importance will become increasingly recognised as the need for sustainable farming becomes urgent. We want our information resource to grow – and include studies of the unique sheep breeds of other Member States beyond those of the six partners in the GENRES project.

We are also writing up the technical aspects of our work. A paper describing the geographical concentration of British breeds of sheep is recently published [3] and also was presented to the United Kingdom National Committee that protects farm animal genetic resources. More articles are in preparation and will be additional outputs from the project's work, together with a short report specifically aimed at policy-makers across Europe.

### More information

An extension of three months was provided given the difficulties encountered in germplasm collection during the Blue Tongue virus epidemic of 2008. We, The University of York, coordinated the action. Our partners were specialists from organisations located in five EU Member States – France, Greece, Slovenia, the Netherlands and the United Kingdom.

### Links

This section lets you know how to find out more about the 'outputs' of the Heritage Sheep project – how to access the sheep breed societies and genetic resources that have been collected in genebanks, how to access the information that we have found about the sheep breeds, and how to obtain copies of the scientific, technical and other publications that we have produced.

### The genetic resources

If you would like to know more about Heritage Sheep Breeds, and perhaps start to keep and breed these sheep, we would be glad to hear from you and provide contacts. Please email us at The Sheep Trust on: [info@thesheeptrust.org](mailto:info@thesheeptrust.org)

### The database

Our database aims to serve as a tool to promote the sustainable use of the Heritage Sheep Breeds, integrating information on the characteristics of the breeds, their uses, the threats they are exposed to and the values attached to the breeds and their products. You can find it on our website at:

<http://www.heritagesheep.eu/Default.aspx>



The Basco Bearnais Heritage Sheep Breed of France

## List of publications

We are writing technical, scientific and policy reports and publications. Publications that were already available at the time of writing are listed in the below.

Our study of British breeds and their geographical concentration is listed as Reference [3] (Carson et al, 2009). The report on that study made to the UK Standing Committee on Farm Animal Genetic Resources [4] can also be accessed at: <http://www.defra.gov.uk/fangr/pdf/sheeptrustrpt-090205.pdf>

## Other publications and links

For other publications and links, see the project website <http://www.heritagesheep.eu/Dissemination.htm>

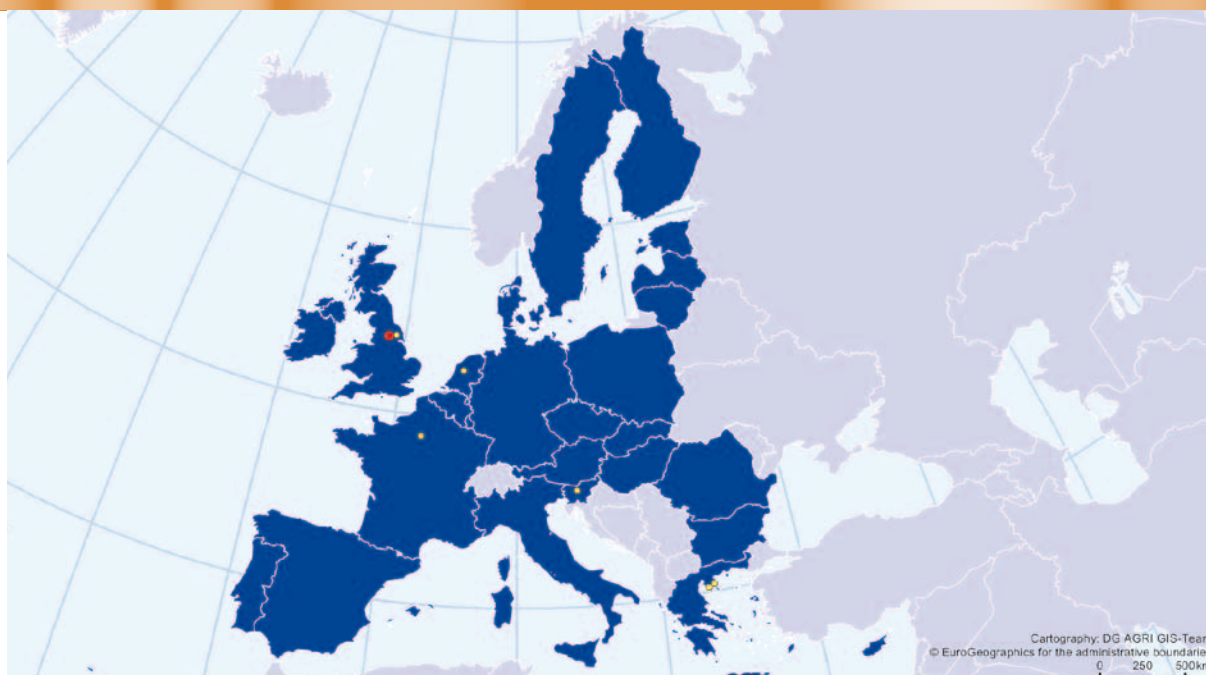
Other actions co-funded by the European Commission's Community Programme on the conservation, characterisation, collection and utilisation of genetic resources in agriculture can be found at: [http://ec.europa.eu/agriculture/envir/biodiv/gen-res/index\\_en.htm](http://ec.europa.eu/agriculture/envir/biodiv/gen-res/index_en.htm)

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First meeting  
of the partners



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## Livestock breeds

### European Livestock Breeds Ark and Rescue Net

The Livestock Breeds action developed a European-wide concept and network for the in-situ conservation of livestock breeds. The concept provided a policy framework within which conservation can take place and covers the themes of Rescue and Quarantine, Breeding, Characterisation and Marketing. A database networking over 400 "Ark Farms" working for the survival of endangered European farm animal breeds in 43 European countries was published online. Breed descriptions of representative breeds for each country were published on the ELBARN website. Action plans were published for the whole of Europe to highlight the action required to conserve breeds. The concept and

## Background

### Introduction to ELBARN 2007-2010

ELBARN is the European Livestock Breeds Ark and Rescue Net (ELBARN). The origin of ELBARN lies in rescue actions undertaken in Switzerland in the 1980s. From these early rescue actions a vision emerged of a pan-European network to ensure that valuable livestock can be protected from slaughter in times of crisis. Additionally, a pilot project began, in the German-speaking area of Europe, to create an online 'guide-book' of all centres with rare livestock breeds that are open to the public. This took the form of the Arca-Net website, promoting a network of 'Ark Centres'. In 2006, these two ideas were combined to create the concept of the European Livestock Breeds Ark and Rescue Net.

ELBARN began in 2007 with a three year project funded by the European Commission under the work programme of **Council Regulation (EC) No 870/2004**. This project (AGRI GENRES action 066 or ELBARN 2007-2010) was completed in 2010. The three year concerted action has resulted – among other things – in a well-networked and motivated group of people; this resource is an asset to the future work on conservation of indigenous animal breeds in Europe. ELBARN 2007-2010 was the start of the European network for livestock breeds. It will be continued under the leadership of the SAVE Foundation and by using the now well-established label ELBARN.

The following executive summary outlines ELBARN 2007-2010.

### Project objectives

The project objectives were presented at the Central Workshop held in Kutna Hora, Czech Republic in February 2008. Within the framework of the workshop, four work groups discussed these themes, with the aim of producing a set of guidelines to be used for shaping the rest of the project.

### Project details

<b>Duration</b>	36 months
<b>Start Date</b>	01/06/2007
<b>End Date</b>	31/05/2010
<b>Budget Total Cost</b>	497 550 €
<b>Budget EU Co-funding</b>	398 040 €
<b>Actual EU Co-funding</b>	396 958.93€
<b>Coordinator</b>	EuroNatur Foundation (The European Nature Heritage Fund)
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<b>Coordinator's Website</b>	<a href="http://www.euronatur.org/elbarn">http://www.euronatur.org/elbarn</a>





## Rescue

The ability to act rapidly to protect endangered livestock breeds in emergencies or unforeseen circumstances is the central theme of ELBARN. For this to be possible, much prior planning is required. A review of existing laws and regulations is required to make sure that they are compatible with this idea. It is also necessary to raise awareness of the importance of animal genetic diversity amongst veterinarians and official bodies. The ELBARN Ark and Rescue Centres (A&RCs) can provide a framework for successful rescue actions – but this has to be supported by adequate national law and knowledgeable practitioners.

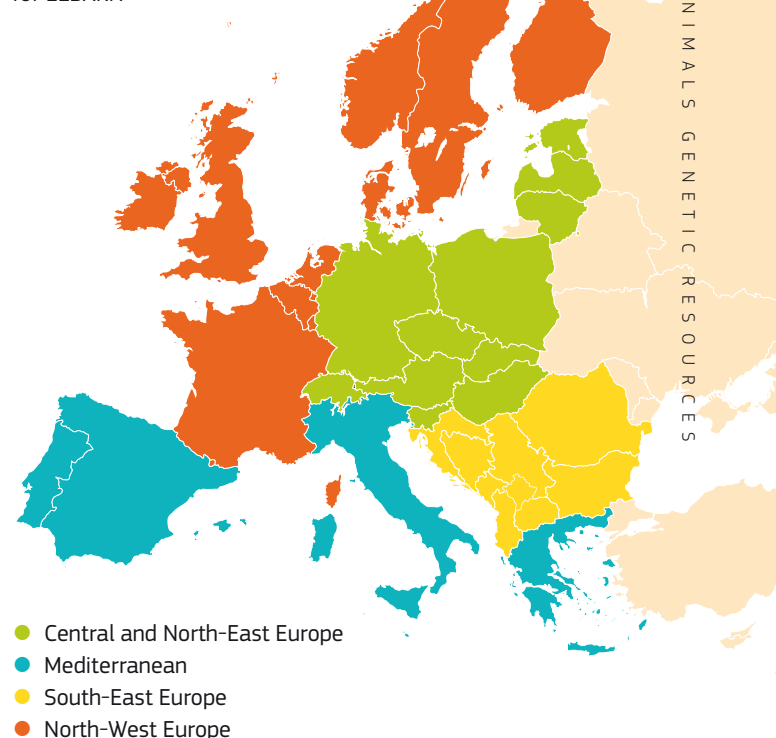
## Ark and rescue centres

The primary goal of ELBARN is to network existing 'Ark Centres' and to provide a policy framework within which they can provide a professional service for conservation of the breeds through breed management. This service also includes the promotion of the products and services of rare breeds along with raising awareness within the public sphere of the importance of animal genetic diversity. Awareness raising and the inclusion of endangered traditional livestock breeds into agricultural production are important tools for safeguarding their future. Discussions showed that a 'Rescue Centre' needs to be capable of saving herds of endangered farm animals from slaughter or, in the case of political unrest, military conflicts, flooding, etc. Suitable facilities are acquainted with caring for animals and have room, time and personnel available to welcome additional animals. Furthermore, they should have a suitable sanitary status and contingency plans for accepting animals at short notice and also be able to provide isolation of incoming animals.

## Breeding

Managing the breeding of endangered traditional livestock breeds is the most important tool for safeguarding genetic variety, especially if the population is a small one. The ELBARN

## Area Workgroups for ELBARN



A&RCs can provide a framework for this management where there is none already in place. By keeping nucleus herds and coordinating breeding with other farms and A&RCs, an essential part of the work for *in situ* conservation will be achieved.

## Marketing

Marketing is an important part of the process to find ways to finance A&RCs. They should be as self-sufficient as possible, as dependence on state subsidies can be dangerous in times of cut-back. Besides marketing the actual products from rare breeds



like milk, meat and wool, it is possible to market services such as landscape management, promoting tourism and education. The marketing strategies strongly depend on the type of A&RC, its location and market potential, end customers and outlets. The various European countries have vast differences in marketing, culture, income, purchasing parity and consumer behaviour, which results in a complex and diverse starting point for setting out generally accepted guidelines.

In spite of this it is possible to isolate general consumer requirements and general marketing tools for the producer.

### Elbarn areas

In early 2009, four 'Area Workshops' were held in Ghent (Belgium), in Roznov (Czech Republic), in Legnano (Italy) and in Blagoevgrad (Bulgaria). Each workshop was a meeting of a wide range of stakeholders from the area, all of whom has special interest and expertise in the field of *in situ* conservation of agrobiodiversity. For each area an 'Area Action Plan' has been developed, tailored to perceived local needs. The Action Plans have been developed together with local partners and, therefore, can be seen as a representation of the views of the current participants in the ELBARN project.

### Outcomes

The main outcomes of ELBARN 2007-2010 are publications, the database and the website.

**ELBARN Guidelines:** a set of guidelines that can be used by Ark and Rescue Centres. The guidelines cover the subjects of Rescue and Disease, Ark and Rescue Centres, Conservation Breeding and Marketing of Products and Services.

**Workshop Results:** all the presentations plus photos and other documents from all workshops held. These are all to be found on the website [www.elbarn.net](http://www.elbarn.net)

**Questionnaire Report:** a short report that sets out the main results of the ELBARN fact-finding questionnaire.

**Area Action Plans:** for four areas of Europe, setting out the needs and requirements to continue the ELBARN project into the future.

**ELBARN Book:** The final publication – a highly illustrated short book outlining the project and the importance of agrobiodiversity. It is comprehensive and explains what agrobiodiversity is and why it is endangered. It is complete with many examples, case studies, pictures, maps and contact points.

**Database with breed descriptions:** Descriptions of currently 505 different animal breeds typical for Europe related to 13 farm animal species: ass (4), buffalo (6), cattle (113), chicken

(26), dog (5), duck (3), goat (60), goose (7), horse (61), pig (39), rabbit (2), sheep (176) and turkey (3).

[www.elbarn.net/elbarn/Breeds/tabid/123/Default.aspx](http://www.elbarn.net/elbarn/Breeds/tabid/123/Default.aspx)

**www.elbarn.net:** a website presenting all the above mentioned outcomes, plus a fully searchable database of over 500 arc farms and rescue centres in more than 40 European countries, which makes this a unique collection of farms, open air museums, nature reserves, etc., all conserving the traditional breeds of their region.

### Communication value

ELBARN 2007-2010 has resulted in a well-networked and motivated group of people; this resource is an asset to the future work on conservation of indigenous animal breeds in Europe.

ELBARN was an NGO-run project. NGOs have played an important part in both international discussions and local action for over two centuries. European NGOs, adapted to local needs and structures, have been working successfully to achieve on-farm conservation of agrobiodiversity.

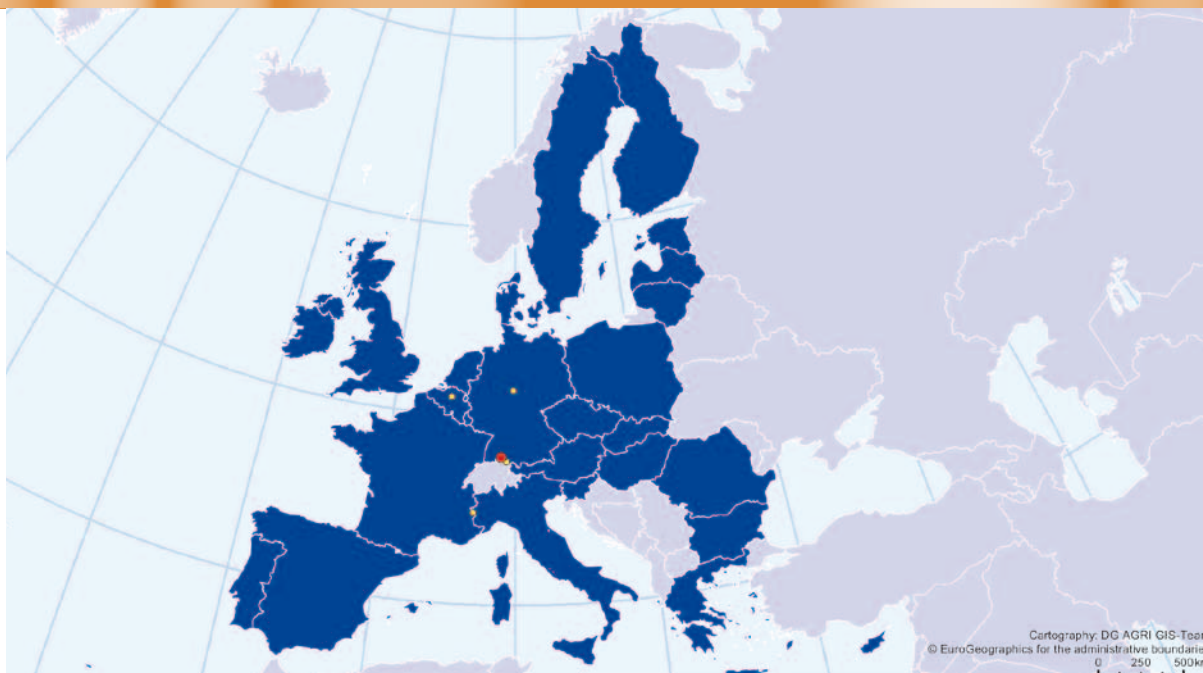
Through ELBARN over 400 Ark Centres from 43 European countries are now presented in a searchable, online database. Each listing includes a short description of the Centre, its opening times, directions of how to find it, which animals can be seen there and if there are farm products available. This function is available on the website [www.elbarn.net](http://www.elbarn.net) and the list of Ark Centres is continually growing.

NGOs have played an important part in both international discussions and local action for over two centuries. European NGOs, adapted to local needs and structures, have been working successfully to achieve on-farm conservation of agrobiodiversity.

Tours through Eastern Europe have identified a number of potential Rescue Centres and, where the owner is in agreement, an inventory sheet has been completed. This information will be made available to the relevant National Contact points.

The Area Workshops emphasised the need for a pan-European group who would communicate the national and area interests of stakeholders up to a governmental level. This is required to gain recognition for problems and needs on a national level and also act as a lobbying instrument to improve legislation in Europe, on all levels, affecting native breeds. The ELBARN project partners decided to already create a small but effective Task Force to tackle some of the most pressing needs. This Task Force made up of ELBARN partner organisations and other people who have shown interest and commitment to the project.

It is the opinion of the ELBARN Task Force that this type of coordination work – collaborative, cross-border, inclusive of all



## Coordinator and Partners details

### Coordinator

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### Partners

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### SLE (Living Heritage Centre)

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 Rotselaarsebaan 45  
 3220 Holsbeek, Belgium

### RARE (Razze Autoctone a Rischio di Estinzione)

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stakeholder levels – is essential for the long-term success of conservation in general and ELBARN in particular.

Therefore, we will be striving towards a sustainable future based on the good work started under the current Community programme on genetic resources in agriculture so that it can continue at a European level.

## Links

[www.elbarn.net](http://www.elbarn.net)  
[www.euronatur.org](http://www.euronatur.org)  
[www.save-foundation.net](http://www.save-foundation.net)  
[www.g-e-h.de](http://www.g-e-h.de)  
[www.SLE.be](http://www.SLE.be)  
[www.associazionerare.it](http://www.associazionerare.it)



The ELBARN 2007-2010 Team l-r: Martin Schneider-Jacoby (EuroNatur), Antje Feldmann (GEH), Markus Dressnandt (EuroNatur), Laura Milone (RARE), Hans-Peter Grünenfelder (SAVE), Elli Broxham (SAVE), Riccardo Fortina (RARE), Gabriel Schwaderer (EuroNatur), Staf Van den Bergh (SLE), Jef Aerts (SLE). Missing from picture are Ulrich Donath (SAVE) and Anja Zimmermann (GEH).





## Livestock globalview

### A global view of livestock biodiversity and conservation

The Livestock global view action reviewed different aspects vital to the characterisation, exploitation and conservation of Farm Animal Genetic Resources (FAnGR), offered interdisciplinary training for 109 young researchers during three summer schools, and promoted the networking among 35 scientists working in Europe and for five international organisations.

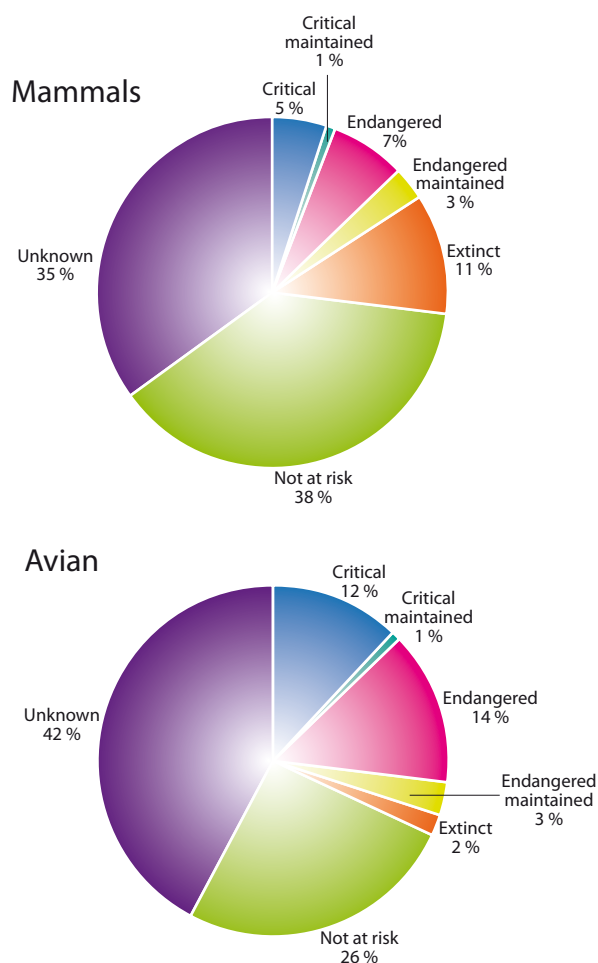
#### Project details

Duration	36 months
Start Date	01/03/2007
End Date	28/02/2011
Budget Total Cost	664 709 €
Budget EU Co-funding	382 375 €
Actual EU Co-funding	380 063.12€
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Coordinator's Website	www.globaldiv.eu

## Background

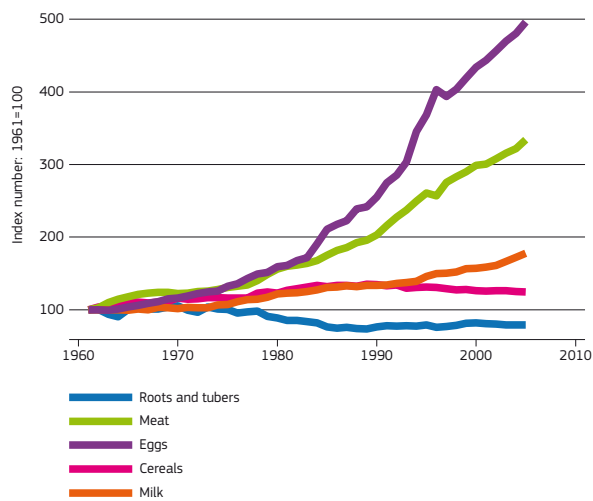
The future of Farm Animal Genetic Resources (FAnGR) is extremely uncertain. The FAnGR contain the genetic makeup of the thousands of local breeds worldwide which are well-adapted for producing in harsh environments, and which for millennia have been fundamental in sustaining human communities. Nowadays, animal production is increasingly based on a limited number of cosmopolitan breeds (e.g. Holstein-Friesian cattle and the Large White pig), which are favoured because they are more suitable for industrial production. While this is not negative per se, the secondary effect of this trend is the undesirable loss of FAnGR. This loss is occurring at an increasing pace; to date, one in fifteen livestock breed is extinct, one in four is known at risk and one in three has unknown risk status (FAO, 2007), notwithstanding the fact that genetic diversity is very important for the survival, the evolution and the adaptation of both wild and domestic species to changing conditions. Rapid loss of FAnGR equals an equally rapid loss of genetic diversity which, if taken too far, will make it more difficult or even impossible to breed for production in new environmental conditions, for resistance to new diseases or for novel consumer needs.

Figure 1 | Proportion of the world's breeds by risk status category. Adapted from FAO (2007).



This loss is particularly worrying in the present uncertain scenario as regards market demand, climate change, pollution, energy policy and the global economy. The demand for animal products is expected to increase worldwide, particularly in emerging and developing countries, at a rate higher than that of human population growth. Farm animal breeding is therefore expected to grow in numbers and in market share in order to meet this demand.

**Figure 2 | Growth in market demand for animal products (percent increase compared to demand in 1961 in the period 1961-2006. Re-elaborated from 'Livestock in the balance', FAO 2010.**



However, farm animals in general and ruminants in particular contribute a significant share of greenhouse gases, which play a part in climate change. The precise extent and consequences of climate change are difficult to predict, but undoubtedly higher temperatures, droughts, desertification, extreme climatic events

and the shortening of the growing season will affect food security primarily in the southern and already poorer parts of the world, where consequences will be more dramatic. This uncertain scenario calls for flexible solutions (e.g. rapid selection for adaptation, change in species/breeds raised in specific geographic areas) in terms of animal breeding. Genetic diversity grants this flexibility, and FAnGR grants this diversity; once lost, it is gone forever.

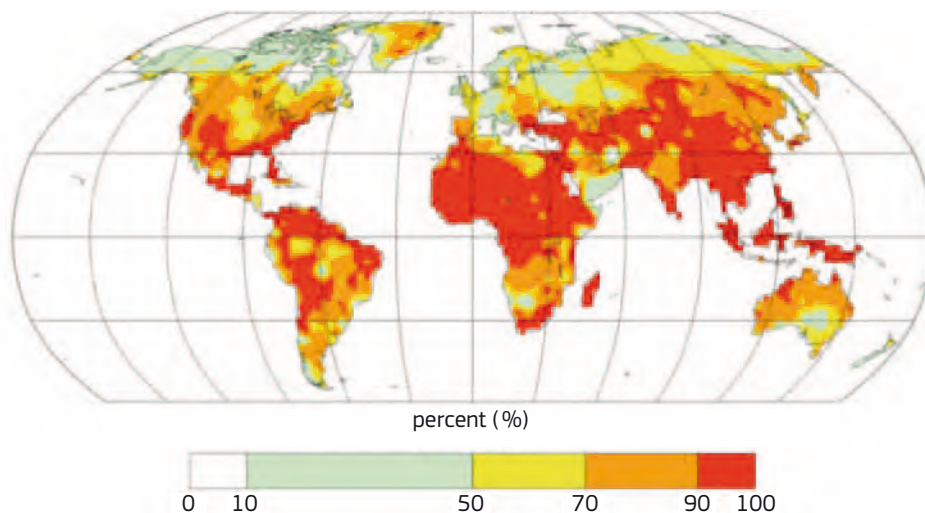
### Project objectives

Globaldiv's main objective was to gather international experts from different fields related to the characterization of FAnGR to review the main drivers of biodiversity loss and the main strategies for FAnGR conservation. Specific objectives were:

- to disseminate current advanced and integrated methodologies for the characterization, exploitation and conservation of livestock genetic resources. The recent development of novel DNA analysis technologies and statistical methods offers new opportunities for better understanding genetic diversity and biology. This increased knowledge can be exploited in genetic improvement and conservation programs;
- to offer interdisciplinary training to a new generation of young scientists, fostering the creation of new knowledge across the boundaries of different research fields related to livestock diversity;
- to promote the networking of researchers across different areas of the world. Biodiversity characterization, valuation and conservation are issues of global concern that need a coordination of local efforts.

Globaldiv has achieved all planned objectives. As results, the project constructed a world-wide network 35 experienced scientists, from Europe, and 5 International Organizations ILRI (International Livestock Research Institute), FAO (Food and

**Summers in 2080-2100 Warmer than Warmest on Record**



**Figure 3 | Likelihood (in percentage points) that average future summer temperatures will exceed the highest summer temperature on record (1900-2006) for 2090. From Science, 2009, 323: 240.**

Agriculture Organization), EAAP (European Association of Animal Science), International Atomic Energy Agency (IAEA) and WAAP (World Association of Animal Production) have collaborated in the analysis of the present critical situation of FAnGR and the study of current technologies and socio-economic measures available, with the aim of indicating new and better ways to achieve sustainable diversity conservation with the limited resources available. Experts have met in nine working groups (WGs) focusing on a) the characterization of diversity; b) the meta analysis of existing molecular datasets; c) the socio-economic aspects of conservation and d) the integration of genetic, environmental and socio-economic information and the setting of conservation priorities. Finally, WG participants defined recommendations for future research needs.

### Characterization of FAnGR diversity

In the framework of the Globaldiv project, recommendations and guidelines were defined for the sampling and collection of information on FAnGR phenotype, genotype and local environmental variables. In addition, Globaldiv has evaluated the new options offered by novel powerful genomic tools for the characterization of FAnGR, giving concrete support to the FAO in the definition of new guidelines for the molecular characterization of livestock. Molecular tools permit the furthering of our understanding of the origin and past history of FAnGR and of demographic events and evolutionary forces that have shaped genetic diversity in farm animals. In addition, the molecular tools have the potential to identify the portion of the total diversity that is functional and therefore invaluable for conservation purposes. Nevertheless, genomics should be used with an awareness of the fact that some molecular tools have not yet been optimised for the investigation of biodiversity.

### Meta analysis of diversity

Globaldiv efforts have focussed to unify large independent datasets produced by a number of previous national and international projects involving cattle, sheep, goats and chicken. A combination of statistical tools and newly-produced data, that could 'bridge' existing datasets, has produced the largest existing overview of livestock diversity.

The best results have been obtained for chicken and cattle. Worldwide diversity studies of chicken are well-coordinated and the combined microsatellite genetic marker datasets (mark DNA characteristics that can be revealed by laboratory analysis. Microsatellite are a very informative class of genetic marker) produced in different studies cover 163 chicken breeds worldwide.

Almost all published cattle microsatellite data sets have been made available to the Globaldiv participants and share at least some of the FAO-recommended microsatellite markers. This has permitted the compilation of a microsatellite meta-dataset of 231 cattle breeds, 171 of which are of European origin.

Fig. 5 shows a successful meta-analysis (statistical methods to join in a single analysis different set of data) of goat microsatellite datasets analysed with the same markers. Combination with data from other African and Asian breeds and meta-analysis of sheep datasets is less straightforward, because the datasets share only a few markers. This work is continuing beyond Globaldiv project lifetime.

In the long term, high-density SNP (Single Nucleotide Polymorphism) genotyping and genomic sequencing will facilitate meta-analyses and render them straightforward. Globaldiv has



Figure 4 | In the picture: Bergamasca sheep, Italy. Characterization of livestock includes the measurement of their phenotype (animal morphology, physiology and production), the environment in which animals are raised (left side) and genotype (animal DNA sequence) (right side).



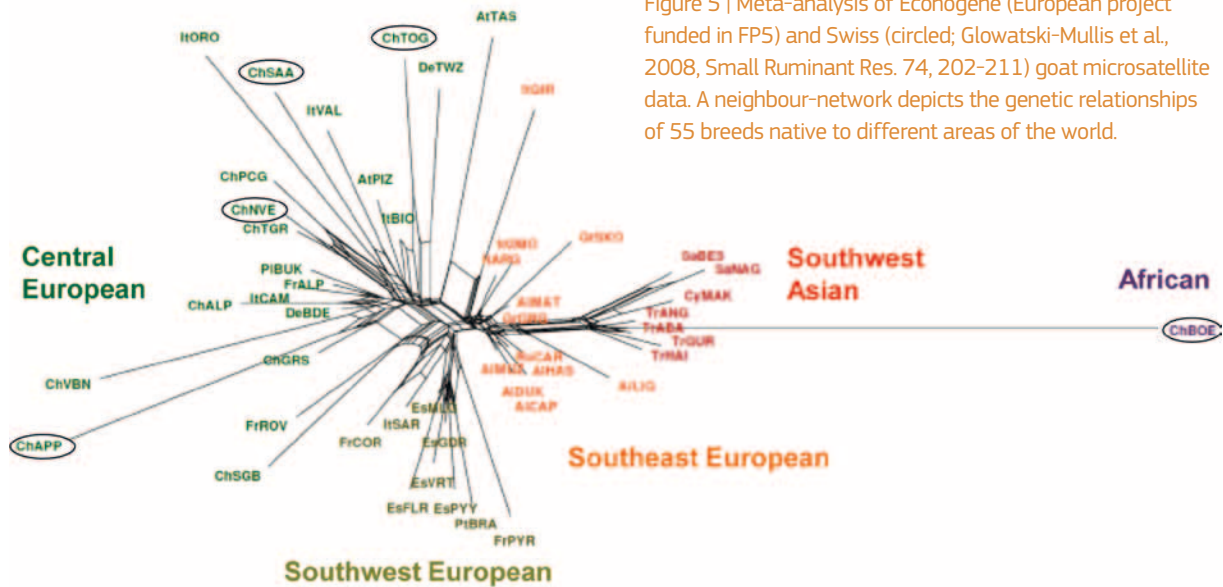


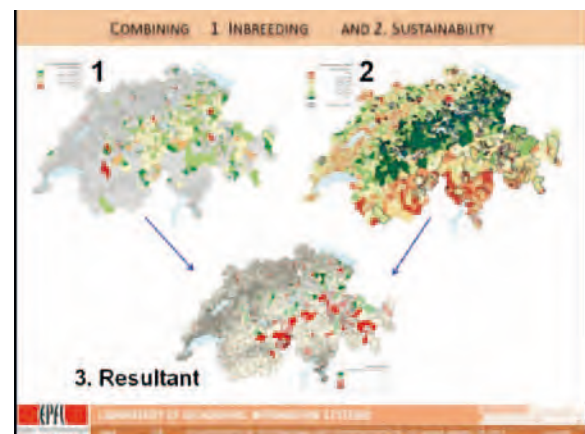
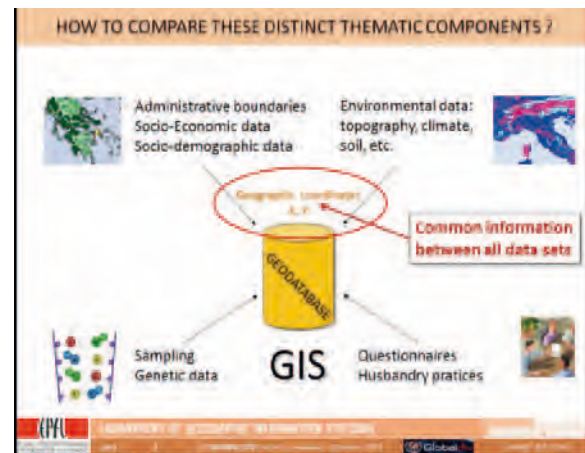
Figure 5 | Meta-analysis of Econogene (European project funded in FP5) and Swiss (circled; Glowatski-Mullis et al., 2008, Small Ruminant Res. 74, 202-211) goat microsatellite data. A neighbour-network depicts the genetic relationships of 55 breeds native to different areas of the world.

demonstrated this with sheep SNP data sets. The information obtained so far and expected to become available in the near future will be most useful for the classification of breeds, the reconstruction of genetic histories of livestock, and decision-making as regards conservation.

### Socio-economic aspects of conservation

The economic evaluation of FAnGR plays a potentially key role in developing effective breeding and/or conservation programs and in developing policy and management decisions. Under intensive animal breeding, the economic value of the genetic improvement of most species lies in (increased) productivity, with a limited value also being attributed to survival and reproduction characteristics, and occasionally to a small degree, also to disease resistance and product quality. Conversely, in low-input farming production systems, the highest value lies in adaptation, disease resistance and in other functions such as traction and nutrient recycling. This means that low-input farming production systems typically require a greater range of genetic attributes; hence, the value of livestock breeds is not captured completely by the market price. For this reason, methods evaluating livestock biodiversity have to go beyond the marketplace and consider changing agricultural practices, environmental impact, the sustainable intensification of production systems, and national and international policy context. Case studies indicate that possible successful solutions in the policy area might be based on the enforcement of labelling, the development of demand for specific quality-differentiated products such as local meats and cheese, support for mixed farming systems and for the multifunctional role of FAnGR in environment management. Globaldiv has also reviewed the costs and benefits of conservation activities in Europe.

Figure 7 | Integration of distinct thematic components (up) and combination of two different indices, inbreeding and sustainability, (below) through a Geographic Information System (GIS) approach.



## Integrating data and setting priorities for conservation

In livestock genetic resources conservation, decision-making regarding breed prioritization should be based on the simultaneous analysis of several different criteria (genetic and demographic characteristics, environmental conditions, role of the breed in the local or regional economy, etc.) that may contribute to long-term sustainable breeding conditions.

Geographic Information System's (GIS) monitoring tools provide decisive advantages when the aim is to evaluate these criteria simultaneously. They permit the setting up of an early warning system, able to evaluate demographic and genetic information according to geographical criteria. They also provide functions supporting livestock research and management at many stages: case study identification, characterization of the environment, characterization of livestock systems, etc. Moreover, outputs from GIS (maps, graphs, plots, tables) provide efficient decision-making support, rapidly usable by experts involved in the management and conservation of FAnGR.

Many methods are available for livestock breed prioritization, each having advantages and drawbacks. No golden standard yet exists and debate continues as to the relative weights to be attributed to different breed demographics and genetic characteristics (e.g. extinction probabilities, within- and between-breed diversity, breed distinctiveness). Models that also consider special traits and socio-economic parameters are presently under development. These do not produce unconditional solutions but will greatly help decision-makers in setting priorities in specific complex conditions, providing breed ranking under different scenarios.

## Future needs and perspectives

As is clear from the analysis presented in the previous sections, the research agenda is far from being exhausted. Many issues should remain at the top of the priority list, ranging from the use of genomic information in conservation and breeding for new traits (e.g. decreased carbon footprint), to socio-economic issues and to the definition of conservation priorities. In addition, farming systems need to be developed further that imply coexistence between a very efficient, productive and industrialized animal husbandry model for feeding the world's growing population, and more traditional farming models that maintain biodiversity for future use. Making both models sustainable from an economic and environmental point of view is an aim which urgently needs to be achieved.

## Communicating value

The Globaldiv project has enabled partners and experts to review different aspects vital to the characterization and conservation of FAnGR with a global perspective. Globaldiv has made an effort

to communicate this knowledge to different stakeholders at different technical levels.

- *Three summer schools* have trained at a high scientific level **109** young researchers and Ph.D. students from **45** different countries of all **5** continents (Europe, Asia, Africa, America and Australia), focusing on new genomic technologies, their use, and methods for the integrated analysis of genetic, geographic, environmental and socio-economic data in conservation decision-making.
- Dissemination among scientists by means of scientific journals. A *special issue of Animal Genetics*, the official journal of the International Society of Animal Genetics (ISAG), has presented the outcomes of the Globaldiv project. Other papers have been published by or are presently undergoing the submission process of high-ranking ISI journals (see List of publications 4).
- *Two workshops* and a *final conference* informed a less specialist scientific community, who have also been informed through **14** review papers published in journals dedicated to sciences other than genetics, e.g. anthropology, and through scientific conferences.
- A total of **104** (lectures and talks given in summer schools and workshops can be downloaded from the Globaldiv project Web <http://www.globaldiv.eu/SummerSchool/Home.html>
- *Nineteen Newsletter* issues intended for an even wider stakeholder community have been disseminated through FAO's and EAAP's mailing lists and published on the Globaldiv Web at: <http://www.globaldiv.eu/Newsletter.htm>
- They have been downloaded more than **67000 times** since 2007, reaching a vast community worldwide.
- In addition, Globaldiv participants produced **9 seminars**, *several papers* and this executive summary addressed to the *general public* (mainly high school students and teachers).
- The table below summarizes the project communication activities.

Figure 7 | Vorwerk cock (Germany).





Table 1 | Globaldiv products

DELIVERABLE	DESCRIPTION	NOTES
<b>Involvement of the scientific community</b>	35 scientists from 11 European countries and 5 International Organizations	Close collaboration with ISAG (International Society of Animal Genetics) and FAO working group on Animal Genetic Diversity
<b>Summer schools</b>	3 Globaldiv summer schools held in Piacenza, Italy in September 2008, 2009 and 2010. A total of 109 researchers and students from 45 countries and all 5 continents	Excellent evaluations from students, who were most content with the lectures and with the opportunity for networking and initiating collaborations
<b>Training material</b>	104 summer schools and workshop presentations	Freely available at <a href="http://www.globaldiv.eu/SummerSchool/Home.html#">http://www.globaldiv.eu/SummerSchool/Home.html#</a>
<b>Meta-analyses of existing continental scale datasets</b>	In cattle, sheep, chicken and goats	Selected breeds were genotyped with selected markers to create datasets bridging existing ones
<b>Scientific papers</b>	One open access Special issue of Animal Genetics and other publications in peer reviewed scientific papers	Papers in the special issue were the 1st, 2nd, 3rd, 5th and 13th most downloaded Animal Genetics papers in 2010
<b>Communication towards the scientific community</b>	Posters/communications/seminars	
<b>Communications towards the general public</b>	9 Seminars for breeders, decision-makers and other stakeholders	
<b>Website</b>	Presenting the Globaldiv project and its outputs	<a href="http://www.globaldiv.eu">www.globaldiv.eu</a>
<b>Newsletters</b>	19 issues, more than 67 000 downloads	<a href="http://www.globaldiv.eu/Newsletter.htm">http://www.globaldiv.eu/Newsletter.htm</a>
<b>Documents</b>	Four technical guidelines and one document with recommendations	<a href="http://www.globaldiv.eu/Final_Report_and%20Deliverables/Final%20Report%20&amp;%20Deliverables.html">http://www.globaldiv.eu/Final_Report_and%20_Deliverables/Final%20Report%20&amp;%20Deliverables.html</a>
<b>Collaboration with International Agencies</b>	FAO, IAEA (International Atomic Energy Agency) ILRI, EAAP, WAAP	Active contribution to FAO guidelines for the molecular characterization of Animal Genetic Resources
<b>Collaboration with other AGRIGENRES and FP7 projects</b>	AGRIGENRES projects: Eureca, Heritage Sheep, Elbarn, Efabis-Net FP7 project: NextGen	One joint Globaldiv-Eureca Workshop Rome (Italy), 2010
<b>Spin-off of other projects</b>	European Science Foundation (ESF) 'Genomic Resources' project, an interdisciplinary research and training programme, covering different branches of animal genetics, breeding, physiology, husbandry, socio-economics and geographic analysis <a href="http://genomic-resources.epfl.ch/">http://genomic-resources.epfl.ch/</a>	Objective: education of a new generation of scientists in cutting edge approaches to the characterization, evaluation, management and conservation of FAnGR
<b>Workshops</b>	2 Workshops on modern methods for the characterization, valuation and conservation of FAnGR	Bydgoszcz (Poland), 2009 FAO, Rome (Italy), 2010
<b>Conference</b>	Final Conference joint with the ESF project 'Genomic Resources'	EPFL, Lausanne (Switzerland), 2011

## More information

The project was led by a multi-disciplinary consortium with strong experience in FAnGR characterization and conservation and included the coordinator (Università Cattolica del S. Cuore of Piacenza) and 6 partners from Europe, Southern America, and Africa, all having international project coordination experience. In addition to partner organisations, 35 scientists have generously contributed to the success of the Globaldiv project, discussing ideas, co-authoring papers, presenting their research, and last but not least disseminating the project's results and significantly increasing the project's impact around the world. The list of their name and affiliation is posted at <http://www.globaldiv.eu/experts.html>

## Links

### Project web-site

All the GLOBALDIV information is available at: [www.globaldiv.eu](http://www.globaldiv.eu)

### List of publications

- Special Open Access Issue of 'Animal Genetics' 'A Global View of Livestock Biodiversity and Conservation' – Special issue Coordinators: Paolo Ajmone-Marsan and Licia Colli. ANIMAL GENETICS Volume 41, Supplement 1, May 2010. Wiley-Blackwell Publisher, ISSN 0268-9146 <http://onlinelibrary.wiley.com/doi/10.1111/age.2010.41.issue-s1/issuetoc>
- Geographic indication of animal products and farm animal biodiversity case of twelve Northern and five Mediterranean member states of the European Union. M. Zjalic, A. Rosati, A. Dimitriadou and E. Murelli. Proceedings of the 11th biennial Mediterranean

Symposium of the European Association for Animal Production (Zadar, Croatia 27-29th October 2010).

- **Molecular tools for the characterization of farm animals genetic diversity.** J.A. Lenstra, L.F. Groeneveld, H. Eding, J. Kantanen, J.L. Williams, P. Taberlet, E.L. Nicolazzi, J. Sölkner, H. Simianer, E. Ciani, J.F. Garcia, M.W. Bruford, P. Ajmone-Marsan and S. Weigend, Animal Genetics 2012, in press.
- **Domestication and worldwide migrations of cattle.** P. Ajmone-Marsan, J.F. Garcia and J.A. Lenstra, Evol. Anthropol. 2010, 19:148-157.

For the full list of publication, see the Globaldiv web-site: [http://www.globaldiv.eu/Final\\_Report\\_and%20Deliverables/Final%20Report%20&%20Deliverables.html](http://www.globaldiv.eu/Final_Report_and%20Deliverables/Final%20Report%20&%20Deliverables.html)

### Globaldiv Summer Schools

They were held in Piacenza, Italy, in 2008, in 2009 and 2010. All the lecturers' presentations and the materials made available to the students can be consulted on the Globaldiv web-site at: <http://www.globaldiv.eu/SummerSchool/Material%20available.html>

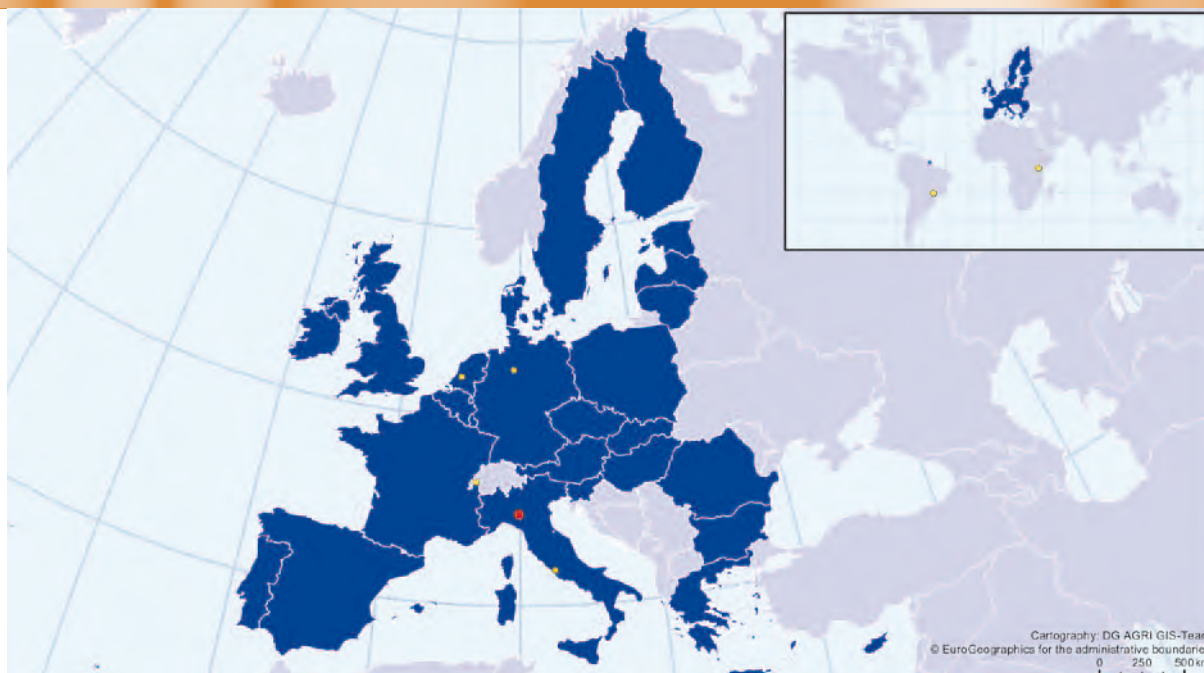
### Globaldiv International Workshops and Conference

During the course of Globaldiv project, two international Workshops and a final conference were organized:

- 1st Globaldiv Workshop 'A global view of livestock biodiversity and conservation', held at the University of Technology and Life Sciences, Bydgoszcz, Poland, 18-19 March 2009. The workshop material is available at: <http://www.globaldiv.eu/Poland/documents%20available.html>



Figure 8 | Partners and Experts attending the 2nd of 9th Globaldiv Joint Working Group Meetings, 18-19 March 2008, Mariensee, Germany.



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- 2nd Globaldiv Workshop 'Livestock Biodiversity Workshop', hosted by FAO Food and Agriculture Organization Rome, Italy, 5-6 May 2010. The workshop material is available at:  
[http://www.globaldiv.eu/Livestock\\_Biodiversity\\_Workshop/Presentations.html](http://www.globaldiv.eu/Livestock_Biodiversity_Workshop/Presentations.html)
- Final Conference 'International EU Globaldiv & ESF Genomic-Resources Workshop', held at the Ecole Polytechnique Federale de Lausanne EPFL, Lausanne, Switzerland, 8-9 February 2011. The workshop material is available at:  
<http://www.globaldiv.eu/Lausanne%20presentations.html>

## Globaldiv Newsletters

All 19 issues of the newsletters are available on the project Web at the following link:  
<http://www.globaldiv.eu/Newsletter.htm>

No further issues are planned.





# # Arable crop and cereal genetic resources

Rice	44
Crop biodiversity <i>in situ</i>	50
Oats	58



## Rice

### Genotyping for the conservation and assessment of the European rice germplasm

The Rice Germplasm action acquired, evaluated and conserved existing European rice accessions and identified valuable sources of new genes and alleles for relevant agronomic and quality traits to be employed in rice breeding programmes at EU level. The results of the action will support sustainable development of rice culture in the Mediterranean area.

### Project details

Duration	36 months
Start Date	01/03/2007
End Date	30/06/2010
Budget Total Cost	1 639 698 €
Budget EU Co-funding	768 660 €
Actual EU Co-funding	765 951.75€
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### Background

Cereals are by far the World's most important source of food, both for direct human consumption and indirectly, as inputs to livestock production: genetic resources in the cereal sector are therefore crucial to world food supplies. Since the mid-1960s the world has managed to raise cereal production by almost a billion tonnes. Over the next 30 years, another billion tonnes of cereal production is needed to feed the increased world population. Among the long list of cereal crops, wheat and rice are the most important ones. Rice serves as major staple food for almost one third of the world population and this is due to the extreme adaptability of this species to various environments.

Europe cultivates rice since the XIVth century, mostly in the southern area of the Mediterranean basin. The varieties that are grown derive from national breeding programmes using germplasm of the *Oryza sativa* ssp. *japonica* of the temperate regions of the world.

The total area devoted to rice cultivation in Europe covers approximately 440 000 ha with a production of 2.9 Mt of paddy rice in 2009, representing about 0.5 % of the total rice world paddy production (<http://faostat.fao.org>). The main producing countries are Italy and Spain, followed by Greece, Portugal and France, with an average yield of 6.5 t/ha.

Although rice is not the major crop in Europe with respect to the growing area, it represents a historical and traditional crop for European countries. Rice growing areas are mostly located in the deltas of big rivers into the Mediterranean Sea: Rhone for France, Ebro and Guadalquivir for Spain, Tejo and Mondejo for Portugal, Po for Italy and Axios for Greece. Inner areas are also present, the North-West part of the Po Valley in Italy and Oristano plane in Sardinia being the most important ones.

Increased productivity and quality stability, resistance to actual and emerging diseases, resistance to old and new environmental constraints such as water shortage, increased soil salinity and cold





are major requirements to provide European rice production chain to sustain competitiveness at the international level.

In the last half century, Europe has enhanced its production in terms of yield and quality of the product with increasingly high inputs agricultural practices. This has elevated the European rice production mostly in terms of quality and safety of the product, making Italian rice highly appreciated in the international market.

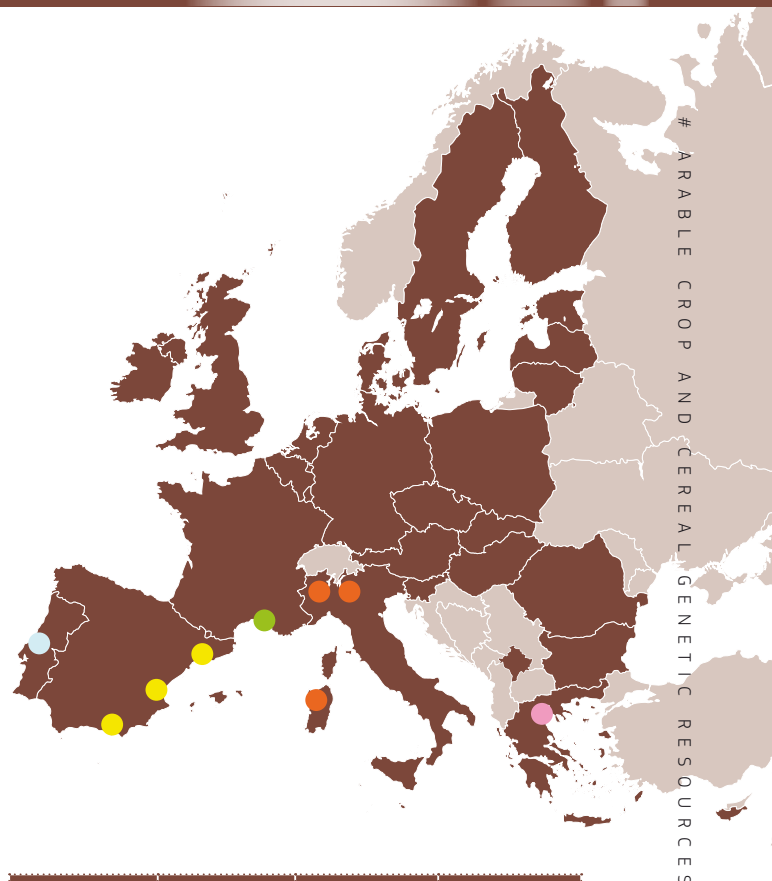
However, the competitiveness of the European rice production does not only rely on the above reasons. There is an increasing concern about the adoption of more sustainable agricultural systems, aiming at the valorisation of the national products together with the use of practices more respectful of the environments and of the natural habitats.

These aspects are today considered a driving force for the European policies in agriculture. The adoption of the Community agro-environmental measures according to the current and future CAP policies specifically addresses the exploitation of genetic resources in terms of the identification of varieties better suited for cultivation in accordance to the above mentioned priorities.

### Rice in Europe: environmental and biotic constraints

Biotic and abiotic constraints significantly affect rice productivity in the agrosystems of the Mediterranean basin. In these areas, the major source of biotic stress is primarily represented by the pathogenic fungus *Magnaporthe oryzae*, causative agent of rice blast and, at a minor extent by *Bipolaris oryzae*, causative agent of brown spot disease. Moreover, some areas, like in Greece, the insect *Sesamia nonagrioides* represents a major pest.

Because most of the rice growing areas are located in the deltas of rivers to the Mediterranean sea, sensitivity to salinity is a major abiotic constraint, while inner areas, such as in Italy and in Spain, may suffer for water deficit and implies strict water management policies.



Country	Area (ha)	Total Paddy Rice production (tons)	Yield (tons/ha)
Italy	238 500	1 500 000	6.3
Spain	119 300	899 400	7.5
Greece	29 000	205 000	7.1
Portugal	27 900	159 000	5.7
France	24 200	138 100	5.7

### Rice leaf and neck blast

The pathogenic fungus *Magnaporthe oryzae* is the causative agent of the rice blast. This is a well-known disease studied in detail at the cellular, genetic and molecular levels. It affects all plant tissues resulting in serious damage in sensitive varieties, up to a complete loss of harvest. The disease is detected at different stages of the plant growth cycle, as leaf blast during the vegetative phase, and as neck blast during grain filling and maturation stages. Breeding for resistance to the rice blast disease has been carried out for a long time, but the frequent occurrence of new virulent isolates (able to overcome resistance) shortly after the release of new cultivars is a strong limiting factor for the use of this strategy as a control method of the pathogenic fungus. The use of resistant rice cultivars is a major, cost effective method to control the disease and can be incorporated as component of an integrated pest management (IPM) plan. The evolution of the pathogen population cannot be stopped and the populations will always tend to adapt to the host, i.e. to overcome the resistance genes deployed. Breeding for high level of partial resistance, which is known to be broad-spectrum, has

also been proposed to obtain a durable control of the blast disease. The identification of genetic resources characterized either by the presence of broad resistance genes (Pi genes) and/or QTLs (Quantitative Trait Loci) for partial resistance is a major requirement in breeding strategies of new rice varieties at EU level.

### *Water shortage constraint*

With global shortages of water and increasing competition with non-agricultural water usages, reducing water consumption has now been generally recognized as an important strategy for rice production, even in areas where water supplies are currently not a limiting factor. In addition, reduced levels of irrigation will decrease levels of water contamination and energy consumption, thus producing a significant positive impact on the environment. Cultivation in aerobic soil has also positive effects on the reduction of greenhouse gas emissions, such as methane, CO<sub>2</sub> and others. Several research programs are currently underway to improve the tolerance of irrigated rice to water-limiting conditions such as IRRI Aerobic Rice Program (<http://www.irri.org>). The identification of rice genetic resources to be used as donors for these relevant traits, and the combined approach of conventional breeding and marker-assisted selection, with the aim to improve growth in water-limited conditions of European varieties, is considered an important step towards breeding for rice cultivation in aerobic soil.

### *Salinity Tolerance*

In many European rice growing areas, rice cultivation is not a choice but a necessity for the sustainable agricultural use of these areas. The main reason is the need for these soils to be cultivated, periodically, under flooded conditions to 'wash' the soil and avoid salt accumulation due to natural evaporation. Presently, rice is the only crop which can be grown in flooded conditions. Given the prevalence of salinity stress, salt tolerance is one of the important breeding objectives of European breeding program.

At the 2001 EURORICE Conference, held in Krasnodar, Russia, on the theme of '*Rice genetic resources and breeding for Europe and other temperate areas*', the above-mentioned topic was included into the main priority actions for rice varietal improvement, to keep and increase the competitiveness of rice in Europe and other temperate areas.

### *Project objectives*

The general aim of the EURIGEN project was the characterization and exploitation of European rice genetic resources of the temperate rice growing area, to enhance competitiveness of Europe in rice production, and alleviate the impact of biotic and abiotic constraints typical of the Mediterranean area.

The project has achieved two major objectives: i) the acquisition, evaluation and conservation of existing rice accessions; ii) the identification, taking advantage of the most updated genomic tools, of valuable sources of new genes and alleles for relevant agronomic and quality traits to be employed in rice breeding programs at EU level.

The results of this project will support sustainable development of rice culture in the Mediterranean area by means of the exploitation of novel sources of agronomically valuable traits.

### *The EURIGEN European Rice Germplasm Collection*

In the framework of the EU-funded RESGEN (1999-2002) and EURIGEN projects, the main public breeding institutions in Europe decided to share their rice genetic material and characterize the resulting EUROPEAN RICE GERMPLASM COLLECTION at phenotypic and molecular levels. This collection now consists of 455 rice accessions, mainly originating from European breeding programs that used genetic combinations potentially useful for the Mediterranean temperate areas.



A standard germplasm and information management system was developed, that resulted in the establishment of a European Rice Germplasm Bank facilitating rice germplasm exchange ([http://golo.cirad.fr/CRB\\_T\\_WEB/UK/CRB\\_T\\_Collections.awp](http://golo.cirad.fr/CRB_T_WEB/UK/CRB_T_Collections.awp)) at EU and international levels.

The genetic diversity of the whole collection was assessed using a set of 30 SSR neutral markers. Based on the phylogenetic data, a sub-sample of 200 accessions representing the genetic diversity of the European rice germplasm was selected as a CORE collection for in-depth phenotyping for elite traits, including resistance to biotic and abiotic constraints.

### Phenotyping in three different EU locations for agronomic and quality traits

The EURIGEN CORE COLLECTION was phenotypically characterized in different agro-climatic conditions. Three locations were chosen as representative of the European rice growing areas: the North-West of the Po river valley (Italy), Makedhonia (Greece) and the Tejo and Mondego river sites (Portugal). A total of 40 morphological, phenotypic and quality traits were evaluated in parallel in the three different locations.

The 200 EURIGEN accessions were also evaluated for their response to the main fungal (blast: *Magnaporthe oryzae*; brown spot: *Bipolaris oryzae*) and insect (pink stem borer: *Sesamia non-agrioides*) pathogens, increased soil salinity and reduced water availability (aerobic soil) in field and in controlled conditions.

All phenotypic data were collected, elaborated and uploaded in the EURIGEN Database and made available through the EURIGEN website, providing a valuable source of information to assist the European rice breeding community.

### Biodiversity of the EURIGEN RICE CORE COLLECTION

A high-throughput genotyping analysis of the EURIGEN CORE COLLECTION of 200 rice accessions was carried out using one of the most advanced genomic technologies, the ILLUMINA BeadArray. This study allowed assessing the existing genetic diversity for further genotype/phenotype association studies. A panel of 384 SNPs (Single Nucleotide Polymorphisms) was selected in a set of candidate genes controlling the main traits targeted in this project: resistance to blast disease, salt stress tolerance and adaptation to water-limited conditions. In the genotyping analysis a reference set of 62 accessions representative of the four main rice varietal groups (indica, japonica, aus and basmati), known as mini-GB collection [1] (Glaszmann et al. 1995) was also genotyped. The obtained results revealed the existence of seven main groups according to their origin and grain phenotype.

### Genotype/phenotype association studies for blast resistance and salt tolerance

The phenotyping and genotyping data collected in the course of the EURIGEN project enabled to run targeted association analyses to identify molecular markers in the most relevant candidate genes correlating to increased levels of blast resistance, and to tolerance to salinity. The results of this activity provide a set of molecular tools available to the European rice breeders to develop marker-assisted strategies for the improvement of these agronomically relevant traits.

### Molecular characterisation of domestication-related genes

The genetic diversity of two domestication-related genes (Rc and qSH1) was assessed in a sub-set of 96 EURIGEN accessions representing the genetic diversity of the European Rice







Germplasm collection. The main goal was to explore some aspects of the mechanisms and processes involved in crop domestication and uncover new sources of functional, haplotype variation. Specific genetic variants leading to the pigmented pericarp phenotype were revealed providing novel insights in the molecular mechanisms subtending rice domestication-related events in European rice germplasm.

### Dissemination

A range of promotion activities were carried out by the EURIGEN partners to ensure wide dissemination of the EURIGEN project to the scientific community and to relevant stakeholders in the main rice-producing EU countries. A number of explanatory documents were published by the EURIGEN partners and results obtained during the three years of the project presented at National and International Scientific Meetings (see <http://www.eurigen.net/documents.html>).

### Communication value

#### The EURIGEN Seed Repository

A centralised European Rice Germplasm Bank was established at CIRAD-Montpellier (France), which guarantees the conservation of genetic resources through the collection, classification, maintenance and routine regeneration of the temperate rice germplasm.

The Seed Repository contains seed stocks for each of the 455 EURIGEN accessions examined at phenotypic and genotypic levels in the course of the EURIGEN project. For each accession, the amount of seeds available and the corresponding germination rate are registered, alongside with its passport data (e.g. country of origin).

All the information are accessible via web at the EURIGEN Seed Repository Database ([http://golo.cirad.fr/CRB\\_T\\_WEB/UK/CRB\\_T\\_Collections.awp](http://golo.cirad.fr/CRB_T_WEB/UK/CRB_T_Collections.awp)) or through the link in the EURIGEN Portal. Seeds of the desired accession are available upon request through the web site.

### The EURIGEN DNA Biorepository

Large quantities of high quality genomic DNA of the 200 rice accessions of the EURIGEN CORE COLLECTION were generated at the PTP Genomics Platform using an automated 96-well plate system, quantified and stored in bar-coded 96-well plates. The genomic DNA stocks are available to the scientific community on a cost-recovery basis for future genomic analyses. DNA requests can be addressed to [pgp@tecnoparco.org](mailto:pgp@tecnoparco.org)

### More information

The six partners involved in the EURIGEN projects belong to the main Institutions involved in rice and crop genetic research in Europe.

### Links

#### The EURIGEN portal

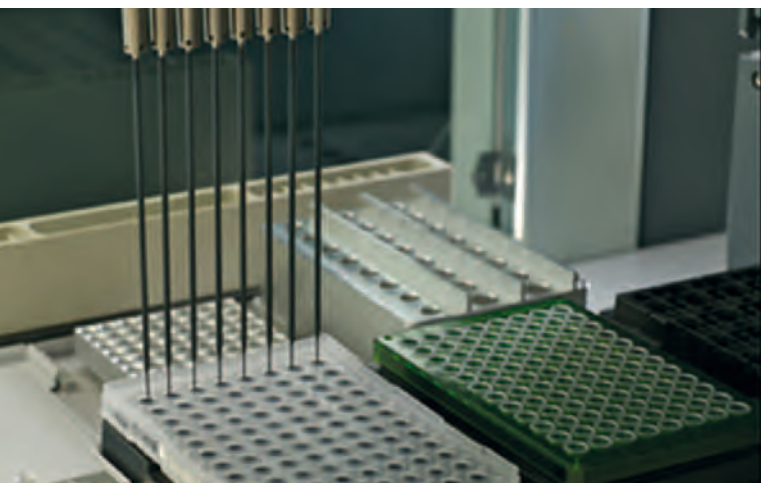
A dedicated EURIGEN portal was created to disseminate the objectives and results obtained in the course of the project and made available to the scientific community, to rice breeders and to stakeholders. The URL is <http://www.eurigen.net>. From the EURIGEN portal it is possible to access all the other resources developed within the EURIGEN project.

#### The EURIGEN database

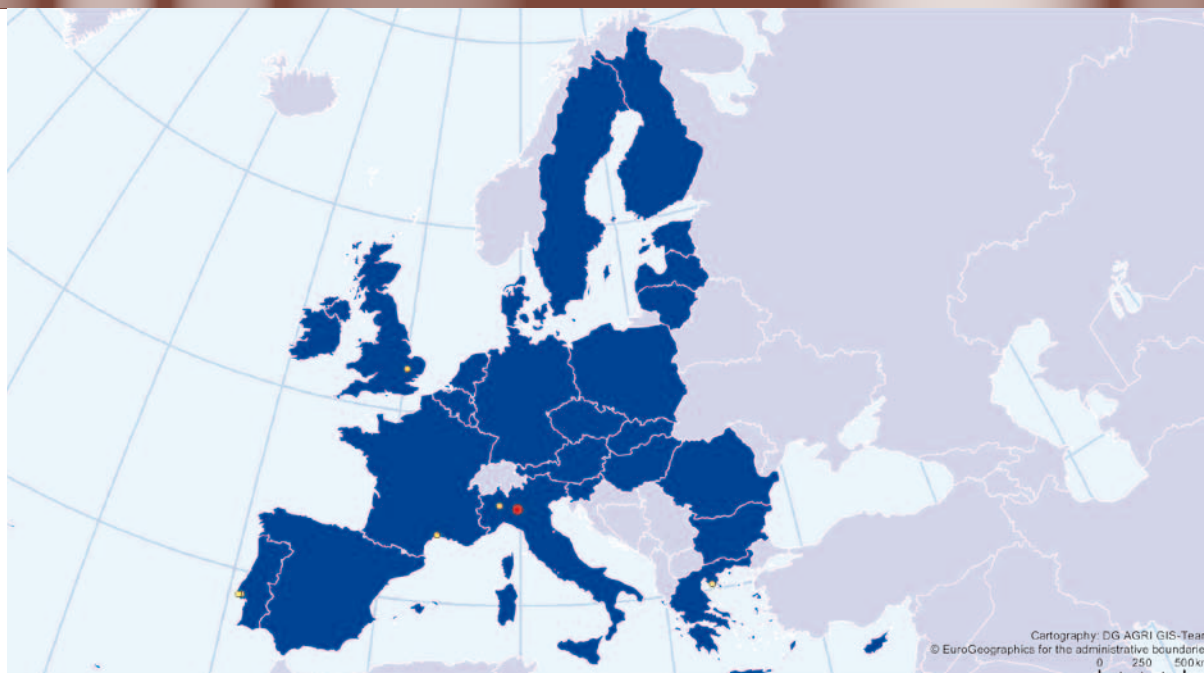
The EURIGEN Database manages all the phenotyping and genotyping data generated in the course of the three years of the EURIGEN project for the accessions of the European Rice Germplasm Collection. It also includes phenotypic data generated in the previous EU-funded RESGEN project and additional genomic information. The Database is maintained by CIRAD-Montpellier (France) and can be consulted on the web at <http://eurigendb.cirad.fr> or via the EURIGEN Portal <http://www.eurigen.net>

The EURIGEN Database is open to the rice scientific community since June 1st 2011.

The DATA Menu on the Home page of the database (see image below) enables to access the QUERY module. Queries can be







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made on all the different data (phenotypes, genotypes, germ-plasm, markers, QTLs) recorded in the database. The results of a query can be exported in MS Excel or text format.

## List of publications

Courtois B., Greco R., Bruschi G., Frouin J., Ahmadi N., Droc G., Hamelin C., Ruiz M., Evrard J.C., Katsantonis D., Oliveira M., Negrão S., Cavigiolo S., Lupotto E. and P. Piffanelli. Molecular characterization of the European rice collection in view of association mapping. *Plant Genetic Resources*, 2010.

Negrão S., Courtois, B., Ahmadi N., Abreu L., Saibo N. and M. Oliveira. Recent updates on salinity stress in rice: from physiological to molecular responses. *Critical Reviews in Plant Science*, 2010.

For the full list of publications, see the project website <http://www.eurigen.net/documents.html>

## Other links

Other actions co-funded by the European Commission's Community Programme on the conservation, characterisation, collection and utilisation of genetic resources in agriculture can be found at: [http://ec.europa.eu/agriculture/envir/biodiv/genres/index\\_en.htm](http://ec.europa.eu/agriculture/envir/biodiv/genres/index_en.htm)

## References

[1] Glaszmann J.C., Mew T., Hibino H., Kim C.K., Mew T.I., Vera Cruz C.H., Notteghem J.L., Bonman J.M. Molecular variation as a diverse source of disease resistance in cultivated rice. In G.S. Khush, editor, *Rice Genetics III*:460-466. International Rice Research Institute, Los Baños, Philippines, 1995. doi: 10.1142/9789812814289\_0048.



## Crop biodiversity *in situ*

An integrated European *in situ* management workplan: Implementing genetic reserves and on-farm concepts

The Crop biodiversity project enhanced methodologies and techniques to improve crop specific management of Crop Wild Relatives (CWR) and landraces diversity *in situ* and on-farm based on the genetic reserves concept. Four crops were selected for crop-specific case studies. The project revealed the constraints of creating genetic reserves; a list of 52 sites in 11 Member States was suggested for establishing genetic reserves within protected areas.

### Project details

Duration	36 months
Start Date	01/10/2007
End Date	31/03/2011
Budget Total Cost	829 625 €
Budget EU Co-funding	413 077 €
Actual EU Co-funding	403 055.91€
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## Introduction

Crop wild relatives (CWR) are wild plants closely related to species of socio-economic importance. A landrace can be defined as a variable population of cultivated plants, which lacks formal crop improvement and is associated with the traditions of the people who grow it. Genetic resources can be conserved *ex situ* in genebanks and *in situ* in their natural environment.

According to Article 2 of the Convention on Biological Diversity '*ex situ conservation means the conservation of components of biological diversity outside their natural habitat*' and '*in situ conservation means the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surrounding and, in the case of domesticated or cultivated species, in the surroundings where they have developed their distinctive properties*'. The natural surroundings of CWR are natural and semi-natural habitats, while the natural surrounding of landraces is any cultivated land where the crops are reproduced and grown. The term 'on-farm conservation' is also used when referring to the conservation of landraces and CWR in an agricultural context. Both methods are complementary elements of a holistic conservation strategy.

Appropriate *in situ* conservation methodologies for CWR were developed by the European Crop Wild Relative Diversity Assessment and Conservation Forum (PGR Forum) research project. A part of the PGR Forum project team, together with experts of the working groups on *Avena*, *Beta*, *Brassica* and *Prunus* of the European Cooperative Programme for Plant Genetic Resources (ECPGR) in 2006, joined and continued to collaborate within AEGRO from 2007 to 2011.

Wild beet on La Gomera, Spain



### Why do we need to protect the crop wild relatives and landraces in their natural surroundings?

The survival of CWR *in situ* is increasingly threatened by an unsustainable environmental management. In addition, despite their socio-economic importance, the European CWR represent only 9% of PGR accessions in European gene bank holdings and only 6% of European CWR have been sampled until now. Thus, CWR are neither sufficiently protected *in situ* nor sufficiently conserved *ex situ*.

In the past, all agricultural activities were based on a large number of crop landraces. The risk of losing potentially valuable donors of novel genetic variation through the displacement of landraces by modern varieties was already addressed by the International Plant Breeders Association in the early 1930s. As long as there is no clear comprehension of the magnitude of genetic erosion within crop species, we should try to maintain prudently as many landraces as possible.

While crop landraces are reasonably adapted to the *ex situ* conservation method, many CWR are more difficult to maintain *ex situ*. Wild species are often not at all adapted to the environmental conditions of genebank locations far off the species' natural distribution area and will often lose genetic variation during the first *ex situ* seed reproduction cycle. Non-adapted plants may not survive until the reproductive stage and as a result only a fraction of the original genetic variation is passed on to the next generation. Once a sample conserved in a genebank has suffered a loss of genetic variation, this variation cannot be replaced if the source population does no longer exist in its natural surroundings.

Garden beet landrace with orange skin and yellow flesh



### How to ensure that CWR and landraces are better protected?

#### *The genetic reserve conservation technique*

Without sufficient genetic variation the ability of a species to adapt to the climate change is impaired and as a consequence a species can become extinct. Therefore, approaches are needed to target the management of genetic diversity of wild species including CWR and landraces.

#### *CWR conservation approaches*

Methodologies and conservation techniques such as the genetic reserve conservation technique are required to realise the *in situ* conservation strategy. Genetic reserves are areas designated for the active, long-term *in situ* conservation of CWR populations where the primary consideration is to preserve their genetic diversity. In most cases, the strategies for *in situ* conservation of CWR involve the establishment of genetic reserves within protected sites by authorities responsible for the management of these protected sites. These strategies tend to lead to greater sustainability and efficacy of conservation actions. However, while this is relatively safe, this is not a necessary prerequisite and *in situ* conservation of CWR may also be necessary outside protected areas.

#### *Landrace conservation approaches*

Contrary to CWR growing in their natural habitat, landraces would not continue to exist without active maintenance by the people interested in their use. Conservation actions have to consider not only the conservation *per se* but also the

Several sugar beet varieties carry a root cyst nematode resistance gene of the species shown left





promotion of the economic use of landraces, preferable at the local or regional level. People reproducing and cultivating landraces would like to receive similar revenue when compared to cultivating mainstream crops and commercial seeds or other planting materials. This can be achieved by reinforcing the interest of people in the typical traditional products belonging to their own regional culture.

In addition to the fact that landraces are evidently an important genetic resource used in crop enhancement programmes since decades, there are two more strong arguments for their conservation. Firstly, landraces that are still managed by people today are a vivid cultural heritage and also contribute to the identity of people in the EU regions they are living in. The cultural heritage is a value in itself. Secondly, the promotion of landrace management on-farm would help to maintain a seed supply system in Europe similar to the specialized seed producing farmers in the late 1800s and early 1900s. Such seed supply system will increase the resilience of agricultural production by increasing the number of independently managed breeding populations in Europe. The conservation of landraces on-farm thus contributes to the flexibility and security of agricultural production.

The EU member states are already adapting their agricultural policies with the objective of encouraging (strengthening) the development of regional products. *Firstly*, the European Commission released a number of directives ('the conservation variety directives') providing for certain derogations for marketing of seed of landraces and varieties, in order to facilitate the trade of seeds and other propagating materials of landraces and varieties that have been traditionally grown in particular localities and regions. *Secondly*, direct payments to farmers growing landraces are foreseen in the European Agricultural Fund for Rural Development (EAFRD), in order to facilitate the development of products based on these landraces and to promote the expansion of market niches. Both these measures,

The market hall at Funchal, Madeira, Portugal.  
A great diversity of local landrace products is offered.



the conservation variety directives and the EAFRD, facilitate the development of specific landrace products and thus support the maintenance of landrace in regional agricultural production.

## Objectives of the project

The main objectives of the AEGRO project were (i) to improve the conservation of CWR and landrace diversity *in situ* and on-farm, (ii) to enhance methodologies and techniques, and (iii) to reveal the constraints impairing the application of the genetic reserve conservation technique in practice, as well as to find solutions to deal with such constraints.

The AEGRO landrace workpackage focused on a specific European area, i.e. Central Italy, which is composed of Lazio, Marche, Tuscany and Umbria regions. It was known beforehand that local institutions and regional authorities had gathered landrace distribution data, which could be used for the case study on landraces. For the further development of *in situ* conservation management concepts for CWR, four crops (oat, sugar beet, brassica crop, and sweet cherry) were selected for crop-specific case studies.

## Results of the project

### The CWR In Situ Strategy Helpdesk

The CWR *In Situ* Strategy Helpdesk (<http://aegro.jki.bund.de/aegro/index.php?id=188>) is a guide and information facility for national programmes, research institutes, non governmental organisations (NGOs), protected area managers or individuals involved or interested in the development of a CWR *in situ* conservation strategy.

A detailed survey on the sources of CWR data was undertaken, categorized into taxonomic, distribution, conservation and environmental data and the results made available via the Helpdesk. The CWR *In Situ* Strategy Helpdesk was completed and published as a major component of the project website. The Helpdesk provides a step-wise methodology for identifying CWR genetic reserve sites for a target crop gene pool, a national CWR flora methodology, the above-mentioned data source and a list of references. The methodology was successfully applied to the crop gene pools of oat, beet, brassica crop, and sweet cherry. The methodology can now be used to develop conservation strategies for other important crop gene pools.

### Case study on landraces

A detailed analysis of existing definitions of the terms 'landraces', 'geographic origin' and 'genetic erosion' was carried out. The key objective was to find criteria for landrace conservation allowing for the development of a more systematic approach for conservation of vivid landraces which are still embedded in social and cultural context. Such definitions were found and





Distribution of wild oat species

a strategy for establishing on-farm conservation areas was developed and assessed by using landrace distribution data available for Central Italy. It turned out that CWR are occurring in areas of high landrace diversity. Therefore, these areas can be considered as the Most Appropriate Areas (MAA) for protecting plant genetic resources for food and agriculture *in situ*.

### Case study on oat (*Avena*)

Oat was chosen to develop *in situ* conservation actions within the EU-27 which are complemented by the global strategy for the *ex situ* conservation of oats (*Avena* spp.) compiled for the Global Crop Diversity Trust. In addition, CWR of oat are examples of gramineous species having biological and ecological characteristics very different from cherry, beet and brassicas.

A list of *Avena* species and population distribution data has been produced. A species priority list was produced following the step-wise methodology for identifying CWR genetic reserve sites for a target crop gene pool. Plant material sampled during field surveys in Cyprus, Spain and Italy (with a focus on Sicily) was genetically analysed to establish a preliminary demographic and genetic baseline for *A. ventricosa*, *A. insularis* and *A. murphyi*. Seven sites located in these three countries within protected areas have finally been suggested for the establishment of genetic reserves for *A. longiglumis*, *A. hirtula* and *A. murphyi*.

### Case study on Beta

This group of species was chosen because of (i) the very limited number of wild species related with cultivated beets, and (ii) the likelihood of being able to establish during the duration of the AEGRO project a genetic reserve for the threatened wild relative, *Beta patula*. The cultivated species, *Beta vulgaris* ssp. *vulgaris*, includes the cultivar groups sugar beets, fodder beets, garden beets and leaf beets.

The step-wise methodology for identifying CWR genetic reserve sites for a target crop gene pool was applied resulting in the Crop case study *Beta* L. (including *Patellifolia* A. J. Scott *et al.*). It was inferred from the study that 26 genetic reserves for seven species should be established. For these species a genetic reserve guideline was developed. We established a demographic and genetic baseline for *B. patula* using 25 genetic markers. Finally, we established a genetic reserve action plan in cooperation with the regional nature conservation agency in Madeira, responsible for the Natura 2000 site where *Beta patula* occurs.

### Case study on Brassica crops

This species group was chosen to represent a very complex gene pool. The crop gene pool includes 240 species, a number of them are widely used as important sources of vegetables

(such as cabbage, broccoli, etc.) as well as spice and edible oils (such as Indian mustard) as well as industrial oils (such as canola). A literature study on CWR of the *Brassica* crops to delineate the primary gene pool of the crop *Brassica* was carried out.

For the EU-27 region the need to establish genetic reserves for species belonging to the *Brassica oleracea* species complex was assessed and species ranked. The list of populations found in Sicily during a series of field surveys was then added to the Population Level Information System (see below) to complete the population distribution data. Plant material sampled during field surveys in Sicily was morphologically and genetically analysed to establish a preliminary demographic and genetic baseline for four *Brassica* species and a total of 8 sites. In collaboration with the Sicilian nature conservation agency the national legal framework was analysed to prepare the next steps towards the establishment of genetic reserves for *Brassica* CWR.

#### *Case study on cherry (*Prunus avium*)*

Cherry represents a crop and a valuable timber species as well. The interest in the conservation of genetic resources of the species is shared by the European Cooperative Programme for Plant Genetic Resources (ECPGR) and the European Forest Genetic Resources Programme (EUFORGEN). Cherry was chosen as a model for information and knowledge exchange between the agricultural genetic resources and forest genetic resources sectors.

Raw data on *Prunus avium* and its occurrences have been acquired from various data sources, compiled, and processed and improved by geo-referencing. Botanic Gardens were visited in the United Kingdom (UK), Austria, France, Georgia, and Russia and records on *P. avium* occurrences not yet digitized by these botanic gardens were added to the list. The final data set of European occurrences comprised approximately 15 000 records.

Criteria for selecting cherry genetic reserves were established and applied as well as a list of recommended genetic reserve sites published. Genetic marker data that are compatible with the existing UK data were compiled for the complete geographic range of *P. avium* in Europe. The project proposed five genetic reserves sites, three sites in Belgium, Denmark and, Germany, and two sites in the U.K. These sites are shown by the Genetic Reserve Information System (GenResIS) <http://www.agrobiodiversidad.org/aegro/>. Owners of genetic reserves have been contacted to promote appropriate management. The results were taken into consideration by the EUFORGEN programme.

#### *Establishment of the Population Level Information System and the AEGRO web portal*

Four independent database modules, collectively called Population Level Information System, (PLIS) were developed for *Avena*, *Beta*, *Brassica* and *Prunus*. PLIS, hosted by the Julius Kühn-Institute, exemplarily extends the Crop Wild Relative Information System (CWRIS) hosted by the University of Birmingham at <http://www.pgrforum.org/cwriscwris.asp> (PGR Forum, 2005). PLIS is an essential data source which can be used by crop experts to take informed decisions on the selection of genetic reserves. PLIS allows searching for occurrences by (i) location, (ii) protected area, (iii) a specific combination of a species name and a location. The search results can be displayed on a web based map or downloaded as a list.

#### *Development of the Genetic Reserve Information System and quality standards*

In the context of the AEGRO project, the Genetic Reserve Information System (GenResIS), hosted by Rey Juan Carlos University, Madrid provides information on recommended locations across Europe, mainly in protected areas, suitable for the establishment of genetic reserves for CWR of *Avena*, *Beta*, *Brassica*, and *Prunus*.

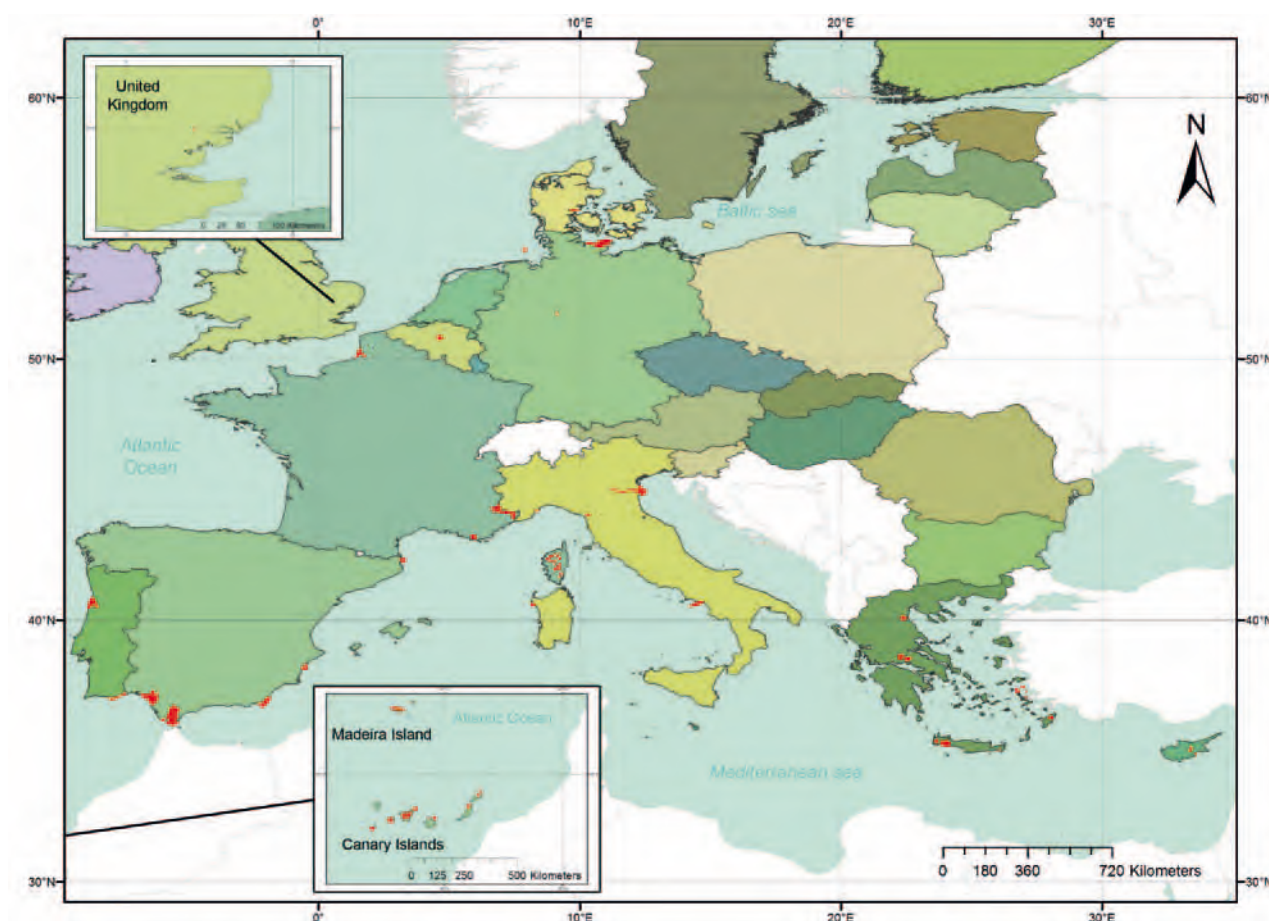
Wild *Brassica* species, Italy



Wild cherry, United Kingdom







The map shows the areas of the suggested 52 genetic reserve sites in the EU-27

The selection of sites for the establishment of genetic reserves at the European level by the case study work packages teams was a central element of the AEGRO project. A Geographic Information System, hosted by the University Rey Juan Carlos (Madrid), was developed to provide the case study work packages with data and tools required to take informed decision. On one side, information has been extracted for the case study work packages from the PLIS database on the species occurrences within Natura 2000 sites. On the other side, a systematic methodology has been developed on how to select and rank genetic reserve sites for the creation of a European genetic reserve network. An important step of this methodology is the development of a European ecogeographical land characterization map exclusively based on environmental variables that are deemed important for each group of related species. The results of the work are presented in the GenResIS (<http://www.agrobiodiversidad.org/aegro/>).

For oat, beet, brassica crops and cherry species, the GenResIS identifies the single species genetic reserve sites recommended by the case studies and combines this with information on geographic location, habitat, conservation status of the selected sites and status of the populations.

Furthermore, other CWR species were identified that can be conserved under the umbrella of the recommended single species genetic reserves. Such single species sites could be further developed towards habitat specific multi-crop genetic reserves. For the establishment and operation of an integrated network of genetic reserves in Europe a set of minimum quality genetic reserves management standards is required. The project developed this management standard.

### Communicating value

From the beginning, the AEGRO project involved members of the European Cooperative Programme for Plant Genetic Resources (ECPGR) working groups in project meetings and project partners have reported on the progress of the AEGRO project during ECPGR meetings. The information on AEGRO and our tools, such as the CWR *In Situ* Strategy Helpdesk, the Population Level Information System for *Avena*, *Beta*, *Brassica* and *Prunus* and the Genetic Reserve Information System can be accessed via the AEGRO website at <http://aegro.jki.bund.de/aegro/> which has been developed to communicate the objectives and achievements of the project to the ECPGR community, other interest groups such as the European Forest Genetic Resources Programme (EUFORGEN) and the nature protection sector, as well as to policymakers and the wider public.

The AEGRO project's results were presented during the symposium 'Towards the establishment of genetic reserves for crop wild relatives and landraces in Europe. Joint meeting of the ECPGR *In situ* and On-farm Conservation Network and final meeting of the EU project AEGRO' held in Funchal (Madeira, Portugal), from 13 to 16 September 2010. This symposium and a previous meeting in Almeria (Spain) with the association of Spanish conservation biologists enabled us to debate our visions and results with a wide range of experts at the policy making level, the crop expert level and the regional/local protected area manager level as well.

The presentations given during the symposium can be downloaded via the AEGRO homepage. Most of the presentations were published by Maxted *et al.* (eds.) (2012) in the book 'Agrobiodiversity Conservation: Securing the diversity of Crop Wild Relatives and Landraces', CAB International.

The collaboration on aspects of *in situ* conservation management with partners in Europe created synergies. The most visible joint product is a list of 52 sites in 11 EU countries suggested for establishment of genetic reserves within protected areas.

### More information

The project was composed of four cross-cutting tasks and five crop specific work packages.

### Links

The results and tools, such as the guide and database of the AEGRO project are available on our project webpage at: <http://aegro.jki.bund.de/aegro/>. Links point to presentations given during the Symposium held at the University of Madeira and to other projects co-funded under Council Regulation (EC) No 870/2004.

Furthermore, a collection of useful links points to related projects, information systems and stakeholder groups.

### List of publications

The results of the AEGRO project were published in:

Maxted, N., Dulloo, M.E., Ford-Lloyd, B.V. Frese, L., Iriondo, J.M. and Pinheiro de Carvalho, M.Â.A. (eds.), Agrobiodiversity Conservation: Securing the diversity of Crop Wild Relatives and Landraces, CABI, Wallingford, UK. Chapters 1-10, 16 and 31.

Further publications are available at: <http://aegro.jki.bund.de/aegro/>

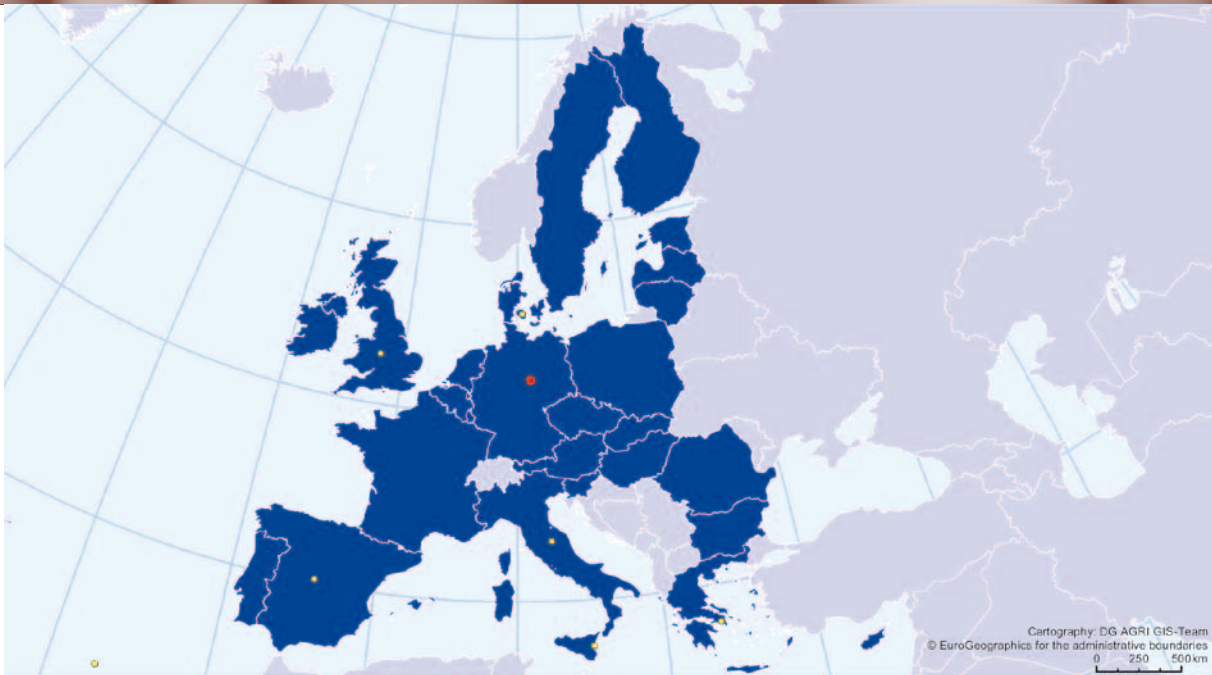
### References

The complete list of literature cited in the executive summary is also provided on the AEGRO web site at <http://aegro.jki.bund.de/aegro/>

Participants of the symposium held at the University of Madeira







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# Oats

## Avena genetic resources for quality in human consumption

The Oats action evaluated and characterised Avena genetic resources for traits relevant for the quality of oats in human nutrition, analysed resistance to *Fusarium* infection and mycotoxins contamination and tested three cultivars to cold tolerance. All the traits evaluated are of high importance for breeding cultivars and for the crop production of oats in European agriculture. All results are available in the European Avena database.

### Project details

Duration	48 months
Start Date	01/03/2007
End Date	28/02/2011
Budget Total Cost	1 037 882 €
Budget EU Co-funding	490 375 €
Actual EU Co-funding	473 054.81€
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### Background

#### Oats quality in human consumption

Oat is a crop with an important European history and tradition. Nutritive substances determine the physiological quality of oats in human nutrition. From a nutritionists point of view oat is our most valuable cereal, based on the following traits:

- high protein content of oat grain and high biological value of the protein;
- high fat content in oat grain. Oat fat has a high proportion of polyunsaturated fatty acids and has a positive impact on the aroma of oat products. However, the oat fat also re-duces storage stability of extruded products;
- high contents of dietary fiber. Of special value is the oatmeal gruel, which is chemically the soluble and highly viscous mixed linked (1->3)(1->4)-β-D-glucans. It reduces serum cholesterol levels mainly by increasing the viscosity in the gut. Thus molecular weight distribution of β-glucans is important as well. Oat products can be added to carbohydrate containing food for reducing insulin requirements.

Recent research focused on antioxidants as additional health promoting ingredients of oat products. These are tocols, also known as vitamin E, and avenanthramides, a recently detected family of compounds, which play a role for the plant as substances protecting from diseases (phytoalexins), and are chemically very similar to Tranilast, an anti-allergenic pharmaceutical.

The unique nutritional value of oats is widely recognized and resulted in health claims for oat products, initially only in the USA, but since end of 2011 also in the European Union (The European Commission 2011). Thus, oat has potential for the production and marketing of premium quality priced products. Beginning in

Figure 2 | A diversity of oat products is available primarily in health oriented and organic food markets.



the Nordic countries new products and markets emerged. A market dedicated to health products will also direct to sustainable agricultural production.

### Oats in sustainable agriculture

Oats rank seventh among cereals in world production, following maize, rice, wheat, barley, sorghum and the millets. Oats are intrinsically a low input cereal crop: their nutrient requirements are less when compared to wheat or corn; they are amongst the least demanding in regard to suitable soil; they have low susceptibility for cereal diseases and high competitiveness to weeds. This makes oat a crop highly adapted to sustainable management and, together with its unique nutritional quality in whole grain cereal products, an ideal crop in organic farming systems. Comparable yields and technical quality can be easily achieved with oats in organic farming. Oat is considered valuable for disease reduction in cereal crop rotations, which are dominating throughout European agriculture. Growing oat can lead in the succeeding cereal crops to a reduced need for chemical plant protection.

### The preservation of oats in genebanks

Most oat species can be easily stored as seeds in genebanks. The European oat collection, available through web based information systems, contains approximately 35 000 entries (accessions), stored and made available as seed samples. They comprise four cultivated and about 20 wild species in the genus *Avena*. Figure 2 shows the impact of domestication on the appearance of seeds. Seeds of the wild species (upper row) have hairs and awns, which facilitate their distribution by wind and animals. But they are not suitable for mechanical operations, like sowing and harvesting, or for animal feeding. Cultivated forms in the middle and lower row have mostly lost hairs and awns, although most cultivated oats are still a husked cereal.

Nevertheless, free threshing forms (so called naked oats) have already been bred of the sand oat (diploid) as well as of the common (hexaploid) cultivated types (right hand side of the middle and lower row).

### Objectives of the project

The main objectives of the AVEQ project were the evaluation of oat genetic resources for traits relevant to the physiological quality of oats in human nutrition: contents of protein, fat, minerals, dietary fibre – especially  $\beta$ -glucan, antioxidants and phenolic compounds. Furthermore, resistance to *Fusarium* infection and the resulting risk for humans of contamination with mycotoxins was evaluated in field experiments by means of artificial inoculation with strains of the most important *Fusarium* species known to occur on oats. Another aspect dealt with cold tolerance in field and growth chamber tests. Cold tolerance is important for oat in several European regions, because oat is sown early or even as a winter crop in order to maximize the yield potential.

All the traits evaluated are of high importance for breeding cultivars needed for the production of premium quality oat raw products to meet an increasing demand for healthy food in Europe, and for the competitiveness of oats as a crop in European agriculture. A further objective was to make all results available with an internet accessible database.

### Results of the project

#### The working collection

*Avena* species with 14 (diploid), 28 (tetraploid) and 42 chromosomes (hexaploid) have originated from crosses between primitive species with 14 chromosomes. Wild and cultivated species are available at all ploidy levels. More than 600 accessions and cultivars from 25 germplasm collections and 31 breeders in



Figure 2 | The evolution of seeds during the domestication process from wild *Avena* species to cultivated oats. Seeds of wild species are in the upper row of seeds, cultivated species in the middle and lower rows, with naked oats at the very right.



14 European countries were compiled to a work-ing collection, which was multiplied and managed to serve the project purposes. Biological classification (taxonomy), together with data on geographic origin and the assumed time of use in agriculture have been used to a great extent for selecting a working collec-tion with a maximum of biological diversity. It included current commercial and obsolete cultivars, land-races and wild species, representing 12 different *Avena* species, more than 100 years of breeding history and more than 50 countries of origin.

A. Cultivated hexaploid oats – *A.sativa* and *A.byzzantina*

Currently, commercially available oat cultivars belong to the hexa-ploid species *A.sativa* and *A.byzzantina*. *A.byzzantina*, also known as red oat, is close to *A.sativa* and not generally accepted as another species. 554 accessions of *A.sativa* and 24 accessions determined by holders as *A.byzzantina* have been grown at seven field sites widely distributed over Europe, and were analyzed for protein and fat. All harvests from three of seven participating countries were also analyzed for total  $\beta$ -glucan and 123 of these accessions, grown on the three sites, were additionally analyzed for other car-bohydrates and antioxidants.

B. Marginally cultivated oats – *A.strigosa* and *A.abysynica*

Forty six accessions of the diploid *A.strigosa* and five accessions of the Ethiopian oat have been grown in the field experiments and analyzed for protein, fat and total  $\beta$ -glucan, 20 respectively two were additionally analyzed for other carbohydrates and antioxidants.

The diploid *A.strigosa* has been grown for feed and fodder already in the old Celtic cultures in west Scotland and the Hebrides, where its tolerance to acid soils, manganese and cop-per deficiency was crucial. As a result, *A.strigosa* remained the most grown oats in Great Britain and Ireland until the 17th cen-tury. It was also cultivated in Romania (Karpaty), Portugal, Poland, and Denmark. It is considered an important genetic resource for oat breeding for earliness and stress tolerance. The tetraploid *A.abysynica* (Ethiopian oat) has long been grown in Ethiopia in mixture with barley and has been used for the flat national bread, local beer and other products like roasted snacks. It is well adapted to the high elevations, the climatic and soil conditions in Ethiopia.

C. Wild relatives of *Avena*

Wild relatives in the genus *Avena* are ordered into a gene pool con-cept according to their ability of crossing with the cultivated hexa-ploid oat. The hexaploid wild species (*A.fatua*, *A.sterilis*, *A.hybrida*) are easily crossed with *A.sativa*. The project used 16 accessions of *A.fatua*, five accessions of *A.sterilis* and one accession of *A.hybrida*. Twelve, four and one of these accessions, respectively, were analyzed for protein, fat and total  $\beta$ -glucan; eight and four and one additionally were analysed for other carbohydrates and antioxidants. The use of tetraploid and diploid species in breeding of hexaploid oats is more difficult. Thirteen accessions of *A.barbata* (tetraploid), *A.canariensis*, *A.damascena*, *A.hirtula*, and *A.wiestii* (diploid) have been included in the evaluation field exper-iments and most of them were analysed for protein, fat, total  $\beta$ -glucan, carbohydrates and antioxidants.

Figure 3 | A small set showing the variability in the hexaploid cultivated oats

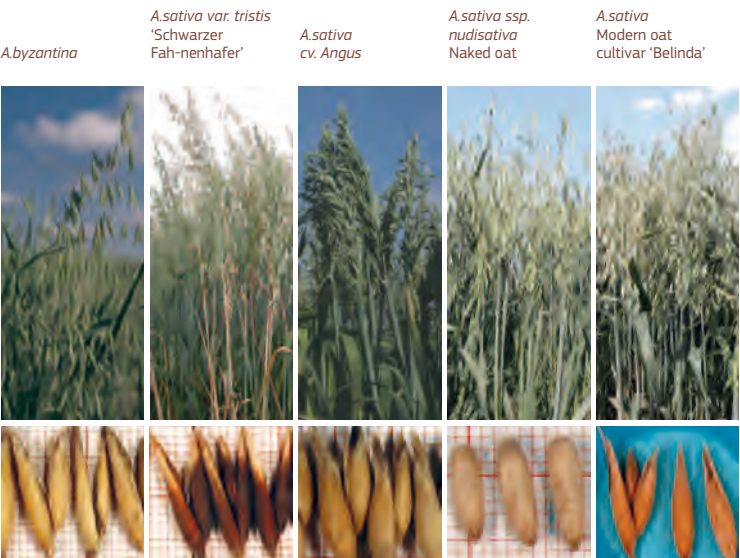
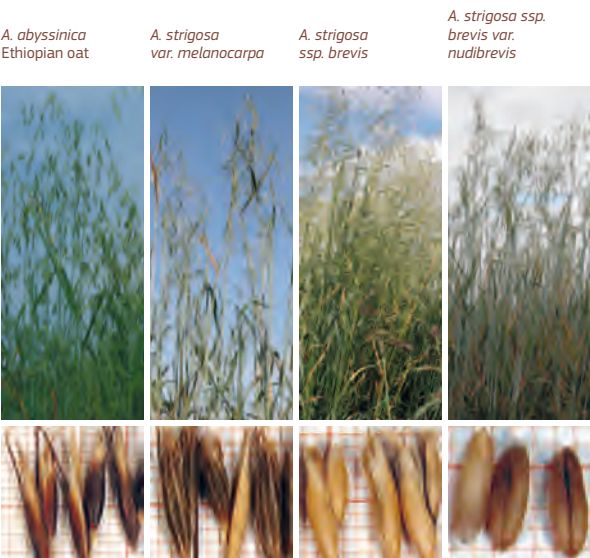


Figure 4 | Marginally cultivated tetraploid and diploid oats





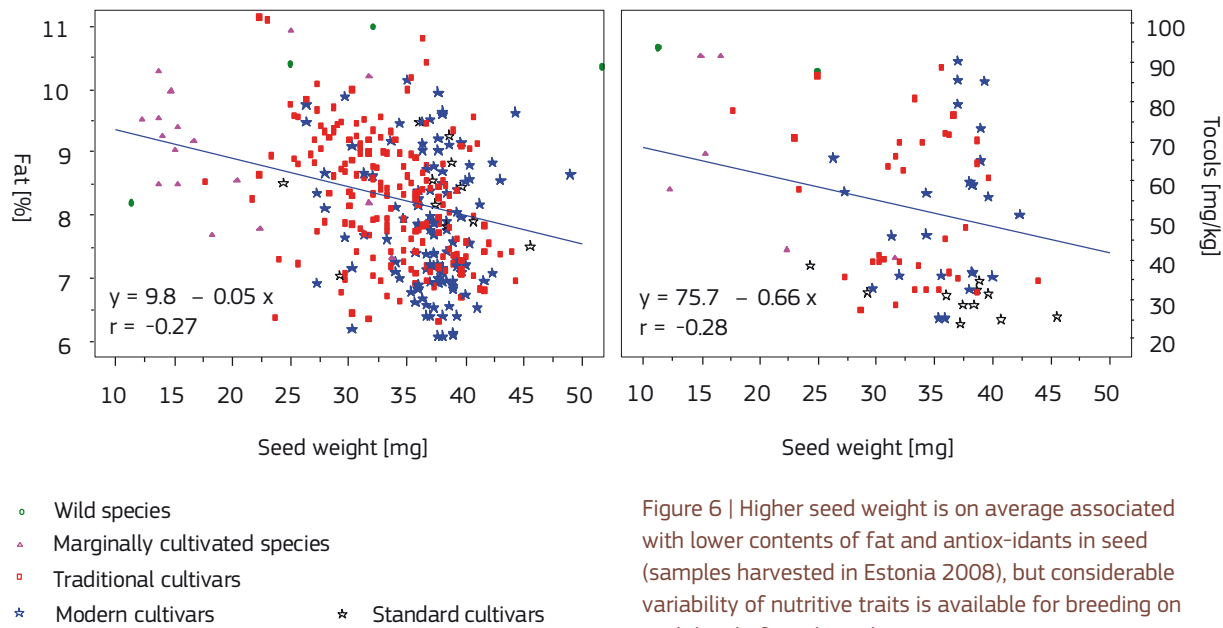


Figure 6 | Higher seed weight is on average associated with lower contents of fat and antioxi-dants in seed (samples harvested in Estonia 2008), but considerable variability of nutritive traits is available for breeding on each level of seed weight

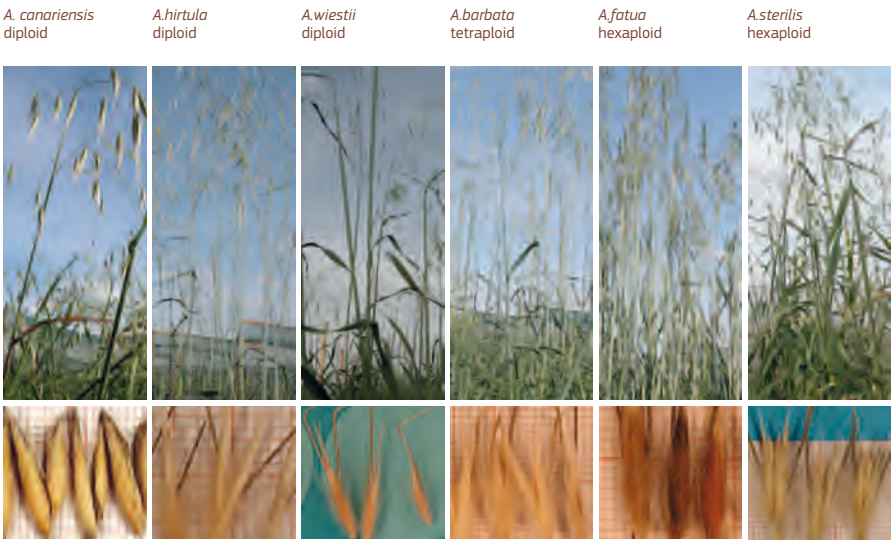
Quality for human nutrition in oat breeding – the potential of genetic resources

Nutritive substances define the physiological quality of oats in human nutrition. However, easily determinable traits of relevance for processing such as grain size, grain weight and husk content dominate the commercial perception of the quality of oat as a raw material. High kernel size is considered of special

importance for industrial quality, because it makes mechanical processing easier and more efficient. But high kernel size is likely associated with lower contents of valuable compounds as e.g. fat and vitamin E (tocols).

Figure 7 indicates that selection for high yield and seed weight in oat breeding may not en-sure valuable characters regarding health effects and taste. Eleven very popular more or less

Figure 5 | Wild relatives of oats from the genus *Avena*



modern cultivars from different countries were selected as standard cultivars for the project and grown for comparison reasons in both years and in replications.

In all genetic resources groups, including the modern cultivars, a high range of variation for protein, fat, total  $\beta$ -glucan, carbohydrates and antioxidants can be exploited. High contents of each compound were also found in different wild relative species. Remarkable is the high content of antioxidants in the diploid bristle or sand oat (*A. strigosa*). This suggests that valuable traits for nutritional quality can be made available also from less developed species.

### *Mycotoxins, a danger in oats?*

Mycotoxins contamination of food products is of serious concern to health authorities. Commission Regulation (EC) No 1881/2006 sets up limits for contaminants in cereal foodstuff. Different species of *Fusarium* produce the major target toxins. Thus a mixture of *Fusarium* species had to be inoculated in field experiments with artificial *Fusarium* inoculation to cover all relevant mycotoxins contamination risks. Among the targeted toxins the Trichothecenes (T-2 and HT-2 toxin) are of special importance, because they occur primarily on oats and have high toxicity, however, an analysis methodology is not yet readily available.

*Fusarium* infection of oats unlike wheat causes hardly visible symptoms in the field or on the grain. Typical symptoms were found only in Romania in 2008, after extremely wet weather conditions (Figures 7 a, b). A freezing blotter test, where seeds

killed by freezing are incubated on moist filter paper (Figure 7c), has been found an appropriate method to detect *Fusarium*. Also in germination tests contaminating fungi identifiable as *Fusarium* were frequently found (Fig. 7d). Mycotoxins contents differed significantly already in the standard cultivars. A wheat cultivar included for comparison showed much higher contamination with the mycotoxin deoxinivalenol (DON), while T-2 contamination was generally higher in oats. Naked oats were less contaminated, indicating that most mycotoxins are located in the hulls. Genotypes were identified with consistently low mycotoxins contamination. An old landrace found in Schenkenfelden, Austria was very low for both mycotoxins DON and HT-2.

### *Frost tolerance would allow earlier sowing for higher yields*

Field screening for frost tolerance was done for all working collection in Bulgaria and Romania. The field results were in line with frost injury measured under controlled conditions (growth chamber) with chlorophyll fluorescence in the first leaf stage as an indicator. Even though only spring oats were evaluated in the AVEQ project considerably frost resistant genotypes were found (see figure 8).

### **Communicating value**

AVEQ was an initiative out of the *Avena* Working Group of the European Cooperative Programme for Plant Genetic Resources (ECPGR). Leading working group members, if not participating as

Figure 7 | *Fusarium* symptoms in the field (a) and on seeds (b), as observable only after extreme weather conditions, in the freezing blotter (c) and germination tests (d)



partners, were invited to project meetings. The final meeting held at Bucharest (Romania) in October 2010 was a joint meeting of the AVEQ project group with the ECPGR *Avena* working group. One overlapping day of the meetings was used by the AVEQ partners to present their results and discuss them with experts and stakeholders from the ECPGR *Avena* working group. A report of these meetings is available at the ECPGR web site.

A publicly accessible website has been set up to communicate the objectives and achievements of the project. The project used expertise available in only one or few EU countries, e.g. for the analysis of avenanthramides, tocopherols or mycotoxins. The possibility to collaborate with partners in Europe on aspects in genetic resources and quality analysis created synergies, which would not have been possible without funding from the GENRES Programme.

### More information

This project has been realised with the financial support from: Peter Koelln KGaA, Germany, Emco spol. s r.o., Czech Republic, and Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung e.V. (GFP), Germany.

The donations are: 20 000 €, from Peter Kölln KGaA Germany, 7 000 €, from Emco spol s.r.o., Czech Republic, 2 000 €, from Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung e.V., Germany, as well as 518 507 € as own contribution from the project partners. The project had 10 work packages and was implemented by 15 partners.

## Links

### The AVEQ project portal

The project results and products can be found on the web portal at <http://aveq.jki.bund.de>

The web site presents the objectives and gives a short introduction into the project. It lists the partners and main sponsors with links to their web representations.

Technical reports, presentations given during meetings and conferences and publications can be downloaded from the documents section. Links are provided to further information systems relevant for the project: the production and test version of the project management and information system and the European *Avena* database, hosted by the Julius Kühn Institute.

### The AVEQ project database

A project database has been created to support the management of the action and to provide facilities to upload and download project results. It is accessible as a production version (<http://aveqprod.jki.bund.de>), and a testing version (<http://aveqtest.jki.bund.de>). The latter will be used to demonstrate and popularize the software modules and concepts developed.

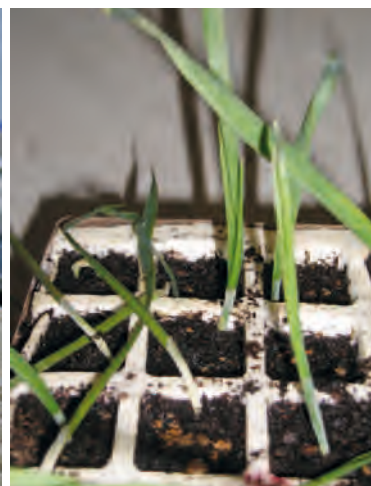
The working collection and observation methodology used, observation results and pictures can be researched, viewed and downloaded by everyone without a login being needed.

Figure 8 | The method based on chlorophyll fluorescence is non invasive (left) and useful to monitor leaf injury in a less subjective way compared to visual observations.

The leaf clip of the PAM2000 Walz fluo-rometer



The use plants at first leaf stage in polystyrene containers allows high throughput of analyses



In addition, field plans, sowing and observation lists, direct data input or downloading Excel templates to input observations, or uploading data and pictures are available to project partners via login and password.

### The European Avena Database

The European *Avena* database (EADB) was created by the former Braunschweig Genetic Resources Collection and is now maintained by the Julius Kühn Institute on behalf of the European Cooperative Programme for Crop Genetic Resources (ECPGR) <http://www.ecpgr.cgiar.org/> as one of the European Central Crop Databases. It provides an information tool on oat genetic resources for the ECPGR *Avena* Working Group and for other end users interested in the use of oat genetic resources in agriculture, breeding and re-search. The developmental focus during the last years was on evaluation and characterization data, which have been generated in AVEQ and a preceding project (GENRES 99-106)

The EADB web application allows for a combined search of passport (origin), characterization and evaluation (trait observation) data. Various result sets can be displayed and partly also downloaded as lists of passport data, trait observation data, descriptions of observation methodology, field experiment details, photos and some genetic and allelic information. Further information is available at: <http://eadb.jki.bund.de>

### List of publications

Scientific publications are under preparation. The full list of publications will be published on the project web site at <http://aveq.jki.bund.de>

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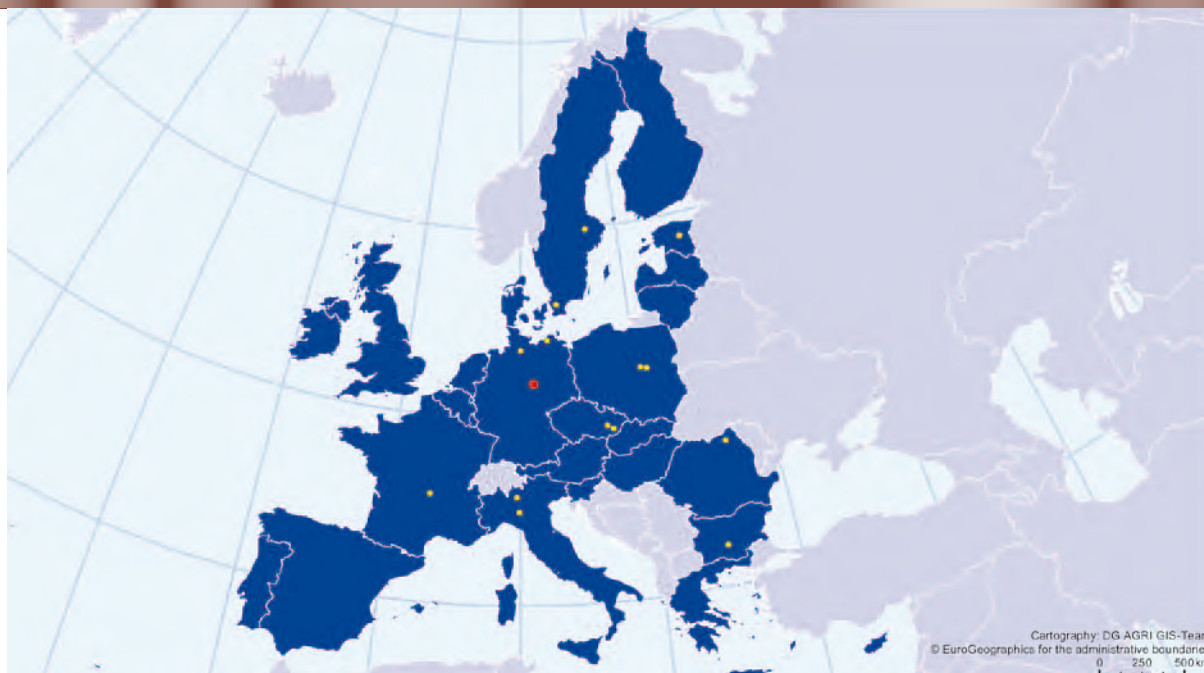
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Figure 9 | Second project meeting of the partners in the coordinator's institute







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# # Forest genetic resources

Forest

68



## Forest

### Establishment of a European Information System on Forest Genetic Resources

The Forest action strengthened national inventories of forest genetic resources (FGR) and supported the practical implementation of FGR conservation as part of sustainable forest management in Europe. The data collected during the project provides a comprehensive picture of the dynamic FGR conservation efforts in Europe. The conservation network consisted of 2 360 samples, which are managed for the genetic conservation of nearly 100 tree species.

#### Project details

<b>Duration</b>	42 months
<b>Start Date</b>	01/04/2007
<b>End Date</b>	31/03/2011
<b>Budget Total Cost</b>	1 107 721 €
<b>Budget EU Co-funding</b>	553 860 €
<b>Actual EU Co-funding</b>	511 823.17 €
<b>Coordinator</b>	Bioversity International
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## Background

### Forest genetic resources and the threats they face

Forests provide a vast array of products, socioeconomic benefits and environmental services. Sustainable forest management aims at managing forests in such a way that the capacity of forests to provide these products, benefits and services for human well-being does not diminish over time. Within the European Union (EU), there are 157 million hectares of forests and 35 million hectares of other wooded land, together covering 42 percent of the land area (1). Some 56 percent of the population in the EU Member States live in rural areas (2), i.e. within or nearby forest and other wooded land, and the EU forest sector employs a total of 2.5 million persons (1).

The genetic diversity of forest trees is crucial for adaptation of forests to climate change (3) and for sustaining other species and entire forest ecosystems (4). Genetic diversity is also needed to maintain the vitality of forests and to cope with pests and diseases. However, forest genetic diversity is facing several threats, such as habitat destruction, fragmentation, poor silvicultural practices and inappropriate use of forest reproductive material. Therefore, special attention should be given to conservation of forest genetic diversity while implementing sustainable forest management.

Forest trees differ from other plant species in their capacity to maintain high levels of genetic diversity within populations rather than among populations (5). This is partly due to extensive gene flow as pollen typically travels distances of up to several kilometers in both wind and animal pollinated tree species (6). Furthermore, trees have outcrossed mating systems, a long generation time, large population sizes and overlapping generations. Subsequently, trees can resist to some extent the negative consequences of forest degradation and fragmentation (7). Despite the extensive gene flow, forest tree populations also demonstrate adaptation to local environmental conditions (8).

During the past 2.6 million years (Quaternary Period), the distribution ranges of tree species in Europe have not been stable but dynamically contracting, expanding or shifting as a result of climatic changes. Recent genetic and paleoecological studies have provided insights into the past dynamics of the distribution ranges by locating refugia areas and postglacial migration routes (9, 10). Climate conditions will continue influencing the migration and distribution of forest trees in the future (11) but it is unclear how well tree populations, especially those ones on the trailing edge of the distribution range (12), can cope with the speed of the current climate change.

### Conservation of forest genetic resources in Europe

In Europe, the need to improve conservation of forest genetic resources, i.e. genetic variation in trees valuable for present or future human use, was recognized by policymakers in 1990



when the first Ministerial Conference on the Protection of Forests in Europe (now FOREST EUROPE) adopted a resolution on these resources. In 1994, the countries established the European Forest Genetic Resources Programme (EUFORGEN) to facilitate and coordinate pan-European collaboration in this area. The Ministerial Conference in 1990 and the adoption of the Convention on Biological Diversity (CBD) in 1992 prompted many countries to develop specific national programmes or strategies for managing their forest genetic resources.

*In situ* conservation is commonly the preferred approach for maintaining the genetic diversity of forest trees. Some forest trees are also conserved *ex situ* in seed banks, seed orchards, clone collections, provenance trials and planted conservation stands to complement *in situ* conservation efforts (particularly when population size is critically low in the wild). However, *in situ* conservation has several advantages as compared to *ex situ* conservation. Firstly, *in situ* conservation is dynamic allowing temporal and spatial changes in genetic diversity while *ex situ* conservation is mostly static maintaining the once-sampled genetic diversity. Secondly, trees within an *in situ* conservation unit remain exposed to evolutionary processes as they continue interacting with their environment and competing with other species. Thirdly, it is usually easier and cheaper to conserve tree populations in their natural habitat than in *ex situ* conditions. Finally, larger population sizes can be managed *in situ* than *ex situ*.

Europe is an example of a region where the distribution ranges of tree species extend across large geographical areas and include many countries. Conservation of forest genetic resources in Europe has been hampered by a lack of common understanding on the management requirements for genetic conservation units, and complexities of national legal and administrative structures. These have made it difficult to identify gaps in the conservation efforts and to develop genetic conservation

strategies at the pan-European level. Furthermore, the diverse practices applied by the countries have complicated international reporting efforts, such as the monitoring of implementation of sustainable forest management in Europe. However, nearly all countries use the same conservation approach; networks of forest stands or areas harbouring tree populations which have adapted to specific environmental conditions or have distinct characteristics. Such stands, i.e. genetic conservation units, are typically located in forests managed for multiple uses, protected areas or seed stands.

As part of EUFORGEN, European experts have so far developed technical guidelines for genetic conservation and use of 33 tree species in Europe (available at [www.euforgen.org](http://www.euforgen.org)). These guidelines provide basic conservation recommendations but they do not specify where new genetic conservation units should be established or how genetic conservation units should be managed. Several years ago, EUFORGEN also initiated the development of pan-European action plans for selected tree species to facilitate national conservation efforts and to identify gaps in the existing conservation efforts.

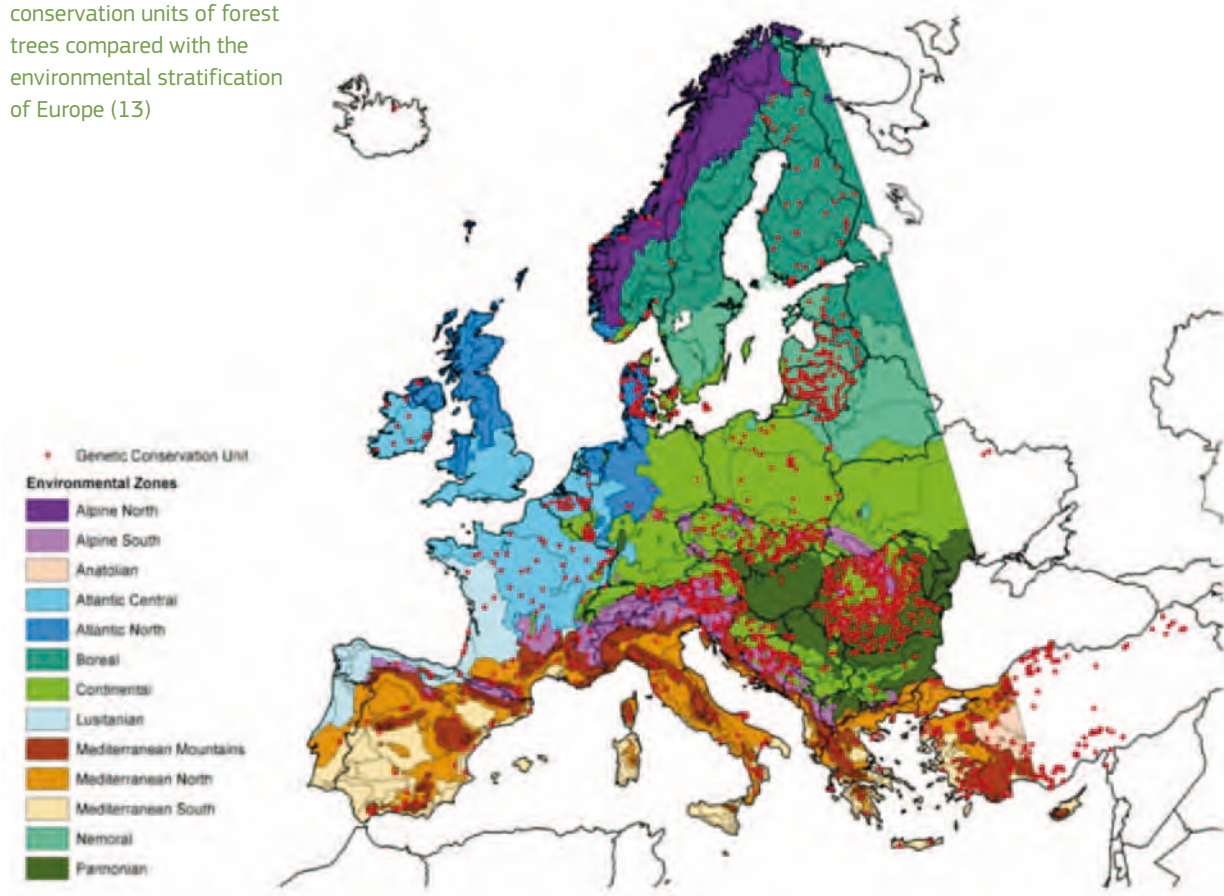
Unfortunately, the development of these action plans made slow progress as no harmonized and geo-referenced data on tree populations conserved in Europe was available. Subsequently, the EUFGIS project was designed by the EUFORGEN community to address these problems and to develop an online database on the genetic conservation units as well as pan-European minimum requirements and data standards for these units.

### Project objectives

The overall goal of the project was to strengthen national inventories of forest genetic resources (FGR) and support practical implementation of FGR conservation as part of sustainable for-



The location of the genetic conservation units of forest trees compared with the environmental stratification of Europe (13)



est management in Europe. The specific objectives of the project were to:

- establish a network of FGR inventories in 40 countries to provide data for the information system;
- develop minimum requirements for genetic conservation units of forest trees and common data standards for these units at pan-European level;
- provide training on FGR documentation to national focal points in these countries;
- create a web-based information system to serve as the European documentation platform for national FGR inventories; and
- make available, as a first step, harmonized data on the conservation units of 20 tree species from at least 80% of the countries within each species' distribution range in Europe.

### Network of national FGR inventories

The project created a network of national focal points in 36 countries across Europe (Austria, Belarus, Belgium, Bosnia and Herzegovina, Bulgaria, Croatia, Czech Republic, Denmark, Estonia,

Finland, France, Georgia, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Former Yugoslav Republic of Macedonia, Moldova, Netherlands, Norway, Poland, Portugal, Romania, Serbia, Slovakia, Slovenia, Spain, Sweden, Turkey, Ukraine and United Kingdom). The national focal points are experts who are involved in collecting and maintaining information on forest genetic resources as part of national inventories or any similar documentation arrangement a country may have in place. They were nominated by the EUFORGEN National Coordinators (or relevant authority in case of non-member countries) to compile information on the genetic conservation units of forest trees in their country and to provide the data to the EUFGIS database. The national focal points also received training for this purpose during the project.

### Pan-European minimum requirements for genetic conservation units of forest trees

The pan-European minimum requirements for genetic conservation units of forest trees integrate scientific knowledge on population genetics into practical conservation of forest genetic resources. They are scientifically sound and practically

feasible to implement for this purpose. The minimum requirements are based on the concept of dynamic conservation of genetic diversity which emphasizes the maintenance of evolutionary processes within tree populations to safeguard their potential for continuous adaptation. This means either managing tree populations at their natural sites within the environment to which they are adapted (*in situ*), or artificial, but dynamically evolving populations, elsewhere (*ex situ*). In the face of climate change, this approach is crucial for the long-term sustainability of forests and forestry in Europe.

The units entered into the EUFGIS database have a designated status as genetic conservation areas of forest trees at national level. The minimum requirements also specify a minimum population size depending on tree species and conservation objectives. One or more tree species have been recognized as target tree species for each unit. Active management measures and silvicultural techniques are applied, as needed, to favour genetic processes within target tree populations. The monitoring of the units is carried out by field inventories every 5-10 years and between the inventories, the units are visited regularly to observe that they still serve their purpose and that they have not been damaged or destroyed.

### Data standards

The data standards define the format, accuracy, quality and range of the information on the dynamic conservation units entered into the EUFGIS database. The units are characterized using 26 data standards at the unit level (designated forest area) and 18 data standards at the population level (target tree species within a unit).

### Genetic conservation units in Europe

The data collected during the project provides a comprehensive picture of the dynamic FGR conservation efforts in Europe.

In September 2011, the conservation network consisted of 2 360 units, which are managed for genetic conservation of nearly 100 tree species in Europe. The units harbour a total of 3 145 tree populations.

### The EUFGIS information system

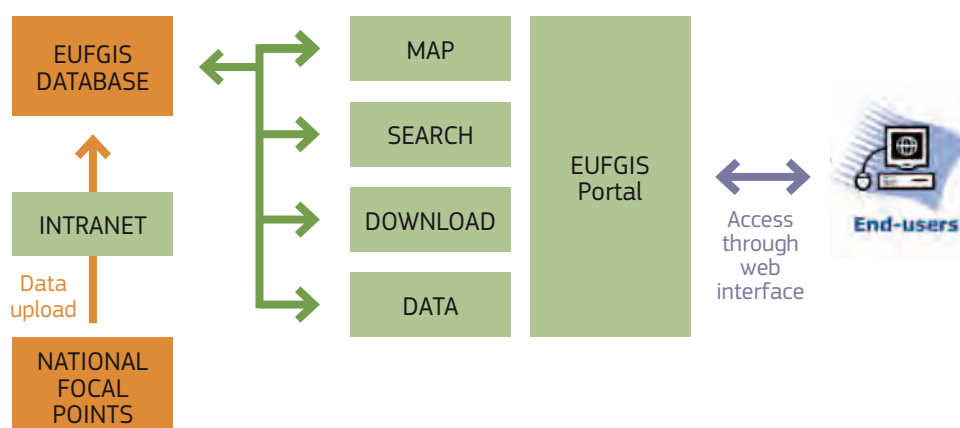
The EUFGIS information system consists of three components, 1) the intranet, 2) the database, and 3) the portal. The intranet is designed for uploading the national datasets into the database. Access to the intranet is limited to the national focal points and each of them has been given a username and a password. The data on each unit are stored in the database at two different levels (unit and target tree species) and it can be uploaded in a file format (e.g. Excel) or typed into online tables. The portal allows the end-users to view and search the data. The location of the units is displayed using a solution based on Google Maps.

### Communicating value

#### Main outcomes of the project

The EUFGIS project constitutes a major step for improving the management of forest genetic resources in Europe. The pan-European minimum requirements for the genetic conservation units of forest trees have prompted several countries to enhance active management of their genetic resources. The minimum requirements have been particularly useful for small countries with limited budgets and human resources available for genetic conservation by helping them to focus their efforts to key issues. Forest owners and managers, forest geneticists and the broader biodiversity conservation community have increased collaboration to explore whether existing protected areas or production forests meet the minimum requirements, and whether new units could be established within these areas. There are still few countries with no units that meet the

#### The structure and components of the EUFGIS information system





minimum requirements. Subsequently, the project has also been useful for making managers and policy makers in these countries aware of the shortcomings in dynamic conservation of forest genetic resources.

The project has strengthened regular monitoring of the genetic conservation units. In addition, the countries have already used the EUFGIS Portal for international reporting efforts, such as the State of Europe's Forests 2011 report and the forthcoming State of World's Forest Genetic Resources report.

Further efforts are underway as part of EUFORGEN to use the EUFGIS Portal for identifying gaps in genetic conservation efforts across Europe and developing pan-European genetic conservation strategies for forest trees. The project has also facilitated discussions on the development of a genetic monitoring system for the units in Europe. The EUFGIS Portal provides a platform for implementing such a new monitoring system in the future.

### Dissemination

Numerous dissemination efforts were carried out during the project. They were targeted to policy-makers, forest managers, conservation specialists and the scientific community, as well as to general public and students.

The dissemination efforts included oral and poster presentations at the sessions of international policy processes and bodies (e.g. FOREST EUROPE, FAO Committee on Genetic Resources for Food and Agriculture, and FAO Committee on Forestry), technical meetings (e.g. EUFORGEN, national FGR committees or programmes, SBSTTA <sup>(1)</sup> of the Convention on Biological Diversity, and UNECE <sup>(2)</sup> /FAO Team of Specialists on monitoring of sustainable forest management), and scientific conferences (e.g. 'Forest Ecosystem Genomics and Adaptation', San Lorenzo de El Escorial, Spain, 9-11 June 2010). Furthermore, articles for

newsletters and professional magazines, leaflets and audio interviews were prepared.

In addition, two case studies were carried out to demonstrate the use of the information system for assessing FGR conservation efforts and for improving the FGR conservation strategies at the pan-European level. The first case study assessed the status of dynamic FGR conservation in Europe and identified gaps in the geographical coverage of the pan-European network of the genetic conservation units. The second case study focused on quantifying the impact of climate change on the genetic conservation units and identifying those units which are at the climatic limit of the species' distribution range and thus most susceptible to climate change. Furthermore, a review paper was written based on the pan-European minimum requirements for the genetic conservation units of forest trees.

Detailed list of the dissemination efforts can be found in the final technical report. Most of the articles and presentations on EUFGIS are also available on the project website: <http://www.eufgis.org/dissemination.html>

### More information

#### Project details

The EUFGIS project was launched on 1 April 2007 for a period of 42 months and it was later extended by additional six months as data screening and revision took more time than originally planned. The extension was also needed for finalizing two case studies based on the database and to carry out more dissemination efforts to non-scientific audience, users of the information system and other stakeholders

The EUFGIS project was coordinated by Bioversity International and participated by six other partners from Austria, Denmark,



France, Slovakia, Slovenia and the United Kingdom. A large group of European experts and scientists from the EUFORGEN member countries also contributed to the implementation of the project activities.

## Links

### The EUFGIS project website

The project website ([www.eufgis.org](http://www.eufgis.org)) was released soon after the project was launched in April 2007, and it was then used as a dissemination platform and a repository of project outputs.

### The EUFGIS Portal

The EUFGIS Portal (<http://portal.eufgis.org>) was launched at the final project meeting that took place in Vienna, Austria from 13-15 September 2010.

### List of publications

Koskela, J., Lefèvre, F., Schüler, S., Kraigher, H., Olrik, D.C. Hubert, J., Longauer, R., Bozzano, M., Yrjänä, L., Alizoti, P., Rotach, P., Vietto, L., Bordács, S., Myking, T., Eysteinnsson, T., Souvannavong, O., Fady, F., De Cuyper, B., Heinze, H., von Wühlisch, G., Ducousso, A. and Ditlevsen, B. Translating conservation genetics into management: Pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity Biological Conservation (in print).

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Schüler, S., Lefèvre, F., Koskela, J., Hubert, J., Kraigher, H., Longauer, R., Olrik, D.C., and Bozzano, M. Forest genetic resources under threat: quantifying the impact of climate change on dynamic conservation units of forest trees in Europe (manuscript).

### Other links

Further information on EUFGIS and other projects co-funded by the European Commission's Community Programme on the conservation, characterisation, collection and utilisation of genetic resources in agriculture can be found at the following website [http://ec.europa.eu/agriculture/envir/biodiv/genres/index\\_en.htm](http://ec.europa.eu/agriculture/envir/biodiv/genres/index_en.htm)

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- (4) Whitham, T. G., et al. 2006. A framework for community and ecosystem genetics: from genes to ecosystems. Nature Reviews Genetics 7: 510-523.



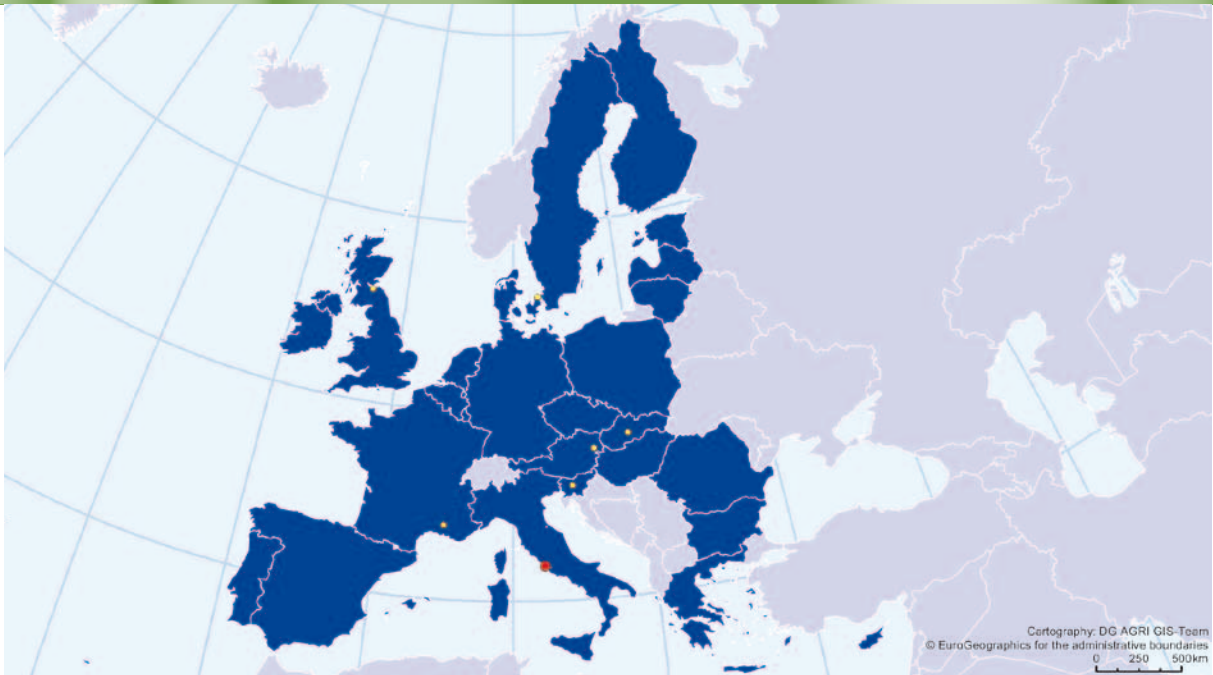
Pictures from the final project meeting in Vienna, September 2010

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Examples of dissemination materials produced in different languages (Newsletter for Europe in English, an article in the Danish journal 'Skoven' and a poster in Slovenian).





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# # Fruit, vegetable and spice genetic resources

Leafy vegetables	78
Grapevine	82
Saffron	88
Straw- and raspberries	96
Garlic and others	102
Artichokes	108
Nuts and almonds	114
Currants and gooseberries	120





## Leafy vegetables

### Leafy Vegetables Germplasm, Stimulating Use

The Leafy Vegetable project conserved, characterised, and collected leafy vegetables across 9 Member States and one non EU country, developed leafy vegetables databases and increased the level of safety duplication. 1 950 accessions were characterized for morphological traits and 770 accessions were evaluated for disease and pest resistance and organic compounds involved in taste.

## Background

Currently around 7.5 million seed samples are stored in genebanks worldwide and large collections exist of staple crops like cereals and legumes. However only around 50 000 accessions of vegetables are present in crop collections worldwide. Given the fact that so many vegetable species exist, it means that large gaps in collections must be present. However a good overview on the current state of the art on vegetable collections worldwide is currently not present, which hampers the adequate conservation of these crop species.

In the context of the GENRES programme the present project dealt with this important issue. Leafy Vegetables were chosen as a target group as this group consists of economically important crops. The group of leafy vegetables encompasses around twenty crops of which lettuce, spinach and chicory are most known. However there are also a large number of minor leafy vegetables such as Valerianella, Eruca, Rheim and Diplotaxis. Currently around 4 000 leafy vegetables cultivars are commercially marketed in the European Union of which fifty percent consists of various types of lettuce cultivars. Next to an inventory and analysis of leafy vegetables held in genebanks worldwide, key challenges of the project are the regeneration and evaluation of these crops in Europe in order to facilitate the use of these valuable genetic resources in the breeding of new cultivars but also in the cultivation of old leafy vegetable landraces (Figure 1).

## Project objectives

The Leafy Veg project was necessary due to a number of reasons. First of all there were no adequate crop databases for spinach, chicory and minor leafy vegetables at the start of this project. Furthermore the international lettuce database needed serious updating. This implied that the European genebank

## Project details

Duration	48 months
Start Date	01/01/2007
End Date	31/12/2010
Budget Total Cost	1 118 600 €
Budget EU Co-funding	358 846 €
Actual EU Co-funding	335 657 €
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Figure 1 | An Italian rucola (*Eruca sativa*) variety

community did not have a good overview of their stored leafy vegetables germplasm at the start of the project. A consequence of the lack of overview was that strategies to acquire new germplasm were insufficiently determined. As a third point safety duplication was lacking for part of the collections maintained by the partners, which is very risky. Fourthly there were serious backlogs in regeneration, characterization, and evaluation of the leafy vegetables collections of the partners meaning that collections managed by them were not conserved in an optimal way. Last but not least there was limited access to trait data in leafy vegetables databases which made it difficult for the user to select the right accessions.

### The Leafy Vegetables crop portal

In order to tackle the first objective of the project, namely the development of adequate crops databases, we developed a unique leafy vegetables crop portal on the web (<http://documents.plant.wur.nl/cgn/pgr/leafyveg/introduction.htm>). In this portal most if not all leafy vegetables crops present in genebanks worldwide can be found. Furthermore all the information can be retrieved using the same format for all the crops that are included.

The building of the leafy vegetables crop databases also allowed for a detailed analysis of gaps in the collections. We showed that in the case of lettuce large gaps are present concerning their close wild relatives. These crop wild relatives are of significant importance for breeding and research. Therefore recommendations were given which species to collect and where to collect.

The limited access to trait information in leafy vegetables crop databases has been addressed by the implementation of a download utility in the crop portal developed. The download facility constructed by the project allows the easy downloading of passport data, characterization & evaluation data and

utilization data of the crop concerned. It will be clear that the Leafy Veg download facility will help users to more efficiently select for accessions and traits in which they are interested.

### Regeneration, evaluation and safety duplication

Regeneration, characterization and evaluation are crucial aspects of proper genebank management. In this project most of the time was devoted to these activities. The targets set for these three activities were overdelivered by the partners: seed was produced on 1 386 accessions, 1 950 accessions were characterized for morphological traits and 770 accessions were evaluated for disease and pest resistance and organical compounds involved in taste. In summary, the current leafy vegetables genebank collections in Europe have been drastically improved through the GENRES Leafy Vegetables projects.

The lack of safety duplication of several leafy vegetables collections maintained by the partners is a threat for the long term sustainability of these collections. After an project to increase the level of safety duplication, all Leafy Veg base collections maintained by the partners are safety duplicated now (Figure 3).

### Communicating value

The information generated by this project can be found on the internet at: <http://documents.plant.wur.nl/cgn/pgr/leafyveg/introduction.htm>. The site gives an overview of the current state of the art on leafy vegetables genetic resources and consists of a leafy vegetables portal having currently the best database on leafy vegetables genetic resources worldwide.

The users of the Leafy Veg website are various ranging from breeding companies looking for new germplasm which may contain genes which can be used for the development of new cultivars, research institutes who need germplasm for fundamental



Figure 2 | Regeneration of two types of lettuce at IPK (Germany)



Figure 3 | Long term storage facility at CGN (the Netherlands) which is also used for safety duplication of other genebank collections



research, non-governmental organizations who are interested in obtaining forgotten landraces and farmers' varieties with a specific taste, colour or growth habit and genebanks who are for example interested in filling gaps in their collections.

In this context the work of the non-governmental organizations, like Arche Noah (Austria), Garden Organic (UK) and ProSpecieRara (Switzerland) in the project was important as they had a very direct link with the general public than any organization within the Leafy Veg consortium. This resulted for example in the testing for consumer acceptance for various accessions amongst which landraces (Figure 4).

### More information

To obtain more information about leafy vegetables this section provides the links to the leafy vegetables portal developed in this project on the web and a list of interesting publications and other links.

### The genetic resources and database

If one wants to have a good overview of what is currently present worldwide in genebanks concerning leafy vegetables, the home page of the GENRES Leafy Vegetables project should be consulted. It can be reached via:

<http://documents.plant.wur.nl/cgn/pgr/leafyveg/introduction.htm>

### List of project publications

The entire list of publications originating from this project can be found at the website of the Leafy Veg project:

<http://documents.plant.wur.nl/cgn/pgr/leafyveg/introduction.htm>

### Key publications

Kik (C.) (2007). European leafy vegetables project is not just rocket science. Bioversity Newsletter for Europe 34, 17.

Kik (C.), van Treuren (R.), Pink (D.), Astley (D.), Coquin (P.), Cadot (V.), Boerner (A.), Lohwasser (U.), Thumm (S.), Lebeda (A.), Kristkova (E.), Solberg (S.), Antonius (K.), Maisonneuve (B.), Lerch (F.), Sumption (P.), D'Antuono (F.), Meglic (V.) and Bartha (B.) (2011). Leafy vegetables GENRES project successfully completed! Newsletter for Europe 42, 12.

### Other publications

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Figure 4 | Consumer acceptance testing at Garden Organic (UK)

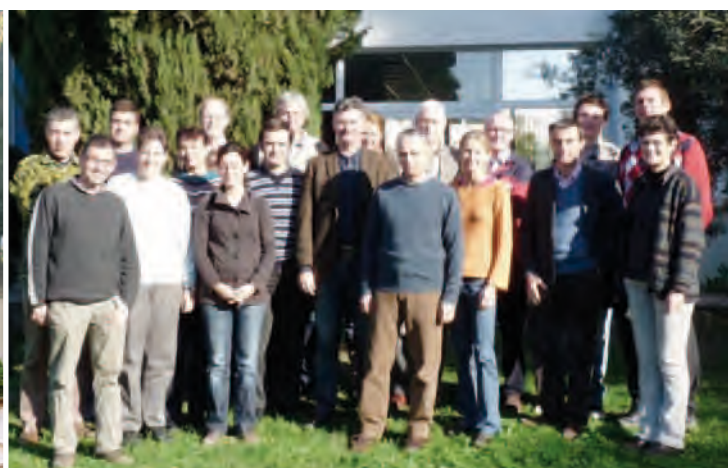
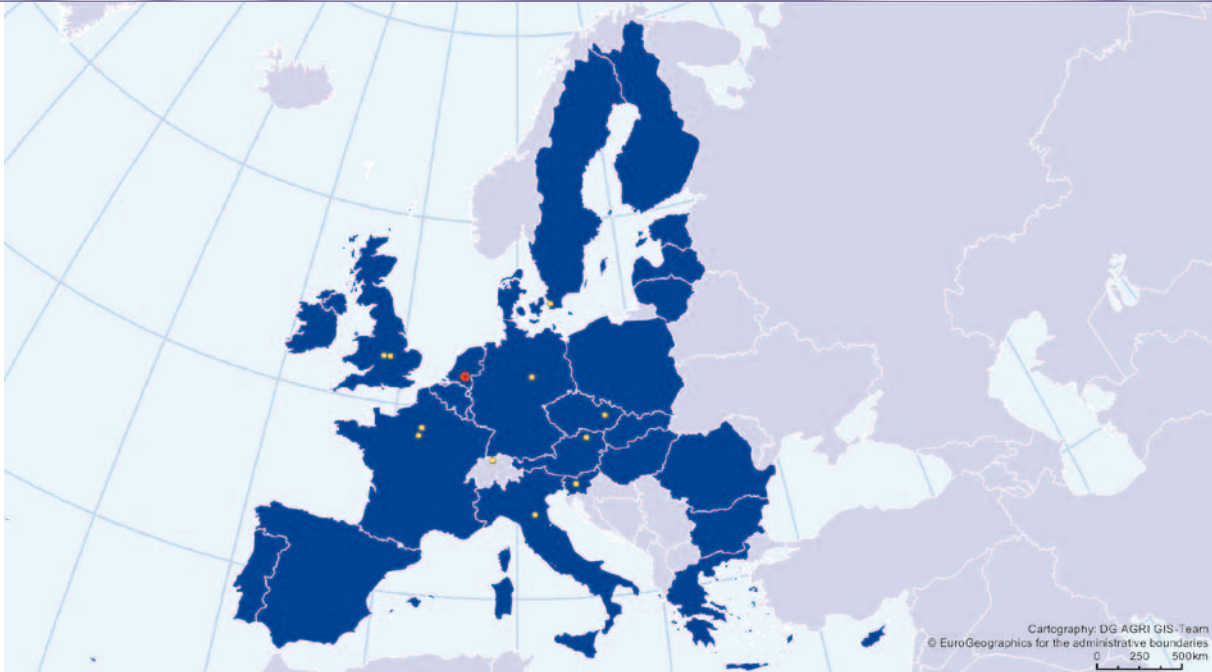


Figure 5 | Partners and observers at the final meeting of the GENRES Leafy Veg in Montfavet (France) in November 2010





Coordinator and Partners details

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## Grapevine

### Management and conservation of Grapevine Genetic Resources

The Grapevine action collected, monitored, characterised, and conserved wild and cultivated *Vitis vinifera* germplasm across 11 Member States and 6 countries outside the European Union. Around 4 000 accessions have been analysed by using molecular markers. The data were included into the European *Vitis* database. These activities contributed to ensure the long term protection of grapevine genetic resources in Europe.

### Project details

Duration	48 months
Start Date	01/01/2007
End Date	31/12/2010
Budget Total Cost	1 527 216 €
Budget EU Co-funding	585 178 €
Actual EU Co-funding	532 120.55 €
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### Background

From ancient times till today, grapes have played an outstanding role in human life, being used directly as fruit and raisins, or transformed into grape juice, wine and spirit. Findings in the Zagros mountains of Northern Iran have dated the oldest samples of wine back to the 5th millenium before Christ (Mc Govern 2000). At that time the wild grape (*Vitis vinifera* L. *ssp. sylvestris* Gmel.) was abundant in the Caucasus region and it was in this region that grape domestication first took place. Along trade-routes, through migration and colonisation efforts, domesticated grapes were then brought to areas with suitable climatic conditions, where they did not exist before. Through great civilizations such as the Phoenicians, Greeks and Romans, grape varieties of Eastern origin reached the Mediterranean and Western Europe. From the Middle Ages onwards, the Roman Church extension became the main cause favouring grape expansion to the entire world.

The encounter of grape varieties from Eastern and Western Europe with local *Vitis vinifera* L. *ssp. sylvestris* Gmel. populations gave rise to a multitude of new grape varieties which were further selected by man to adapt to specific local conditions

From the approx. 8 000 varieties which are believed to exist in the world, only 200-300 are cultivated on a large scale (Galet, 2000). Today, owing to an ongoing preference for a small number of 'global-player' varieties like Chardonnay or Cabernet-Sauvignon, autochthonous varieties with an interesting potential for market or genetic improvement are endangered and knowledge about their use and characteristics is quickly disappearing. Fortunately, most of these potentially interesting grapevine genetic resources are presently held in collections around the world (Dettweiler and Eibach, 2003). The *Vitis* International Variety Catalogue (<http://www.vivc.de/>) lists 137 collections in the world with a total of 48,826 accessions, more than half of

Wild *Vitis sylvestris* accession:  
Lambrusque Grésigne 9,  
Accession number  
FRA139-8500Mtp128  
(Photography INRA)



them held in EU. Because multiple local names and errors in identification accumulated over the centuries, many synonyms and homonyms exist in collections rendering quite complex any precise comparison of content among collections. It is thus difficult to estimate the real extent of grape germplasm diversity in European collections.

Furthermore, the wild European grapevine *Vitis vinifera* L. ssp. *sylvestris* Gmel. (*Vitis sylvestris*) also declined during the 20th century, due to *Phylloxera* infestation, various diseases and human activities. This wild species is at present reduced to very small and rare populations, sometime with a single tree for a given location, not all of them identified, which has led to its registration on the red list of the International Union for Conservation of Nature and Natural Resources. Any action to prevent the extinction of this species in Europe and avoid loss of diversity and of genes of potential interest, first needs a general survey of this resource all over EU and then specific actions can be taken for *ex situ* conservation in grape collections or *in situ* conservation in protected areas such as National Parks.

The GrapeGen06 project was launched in 2007 for 4 years (Bacilieri, 2007). The long term objective of the project was to increase our knowledge of European grapevine genetic germplasm and to enhance its preservation, management and promotion for future utilisations.

This objective included preservation and study of *in situ* populations of *Vitis sylvestris* as well as of old and neglected varieties, especially from Eastern Europe and, in some extent, from Eastern non-European regions where interesting resources are present but still scantily known. A special interest was given to the characterization of agronomical and technological characteristics of old autochthonous varieties in more conventional conditions (on-farm), to the management of the partners' collections by the identification of synonyms, homonyms and misnamers

within and between collections, and to the development of alternative conservation means.

It is expected that the envisaged enlargement of the existing European *Vitis* Database, based on a comprehensive regional network covering all interesting primary resources, will be of inestimable use for grapevine genetic resources management and monitoring and its long term safeguard, to the benefit of European growers and competitiveness as well as regional cooperation.

### The exact extent of genetic resources in Europe

The grapevine collections of the 25 GrapeGen06 partners presently hold approx. 25 583 accessions, but we do not know the actual number of different cultivars they represent. In the project, several actions were taken in order to determine the accurate content of these collections: approx. 4 000 accessions have been analyzed using molecular markers in order to define their DNA fingerprints. With this molecular data, coupled to morphological data recorded on 2 382 cultivars, we were able to identify 234 cases of 100 % identical profiles within and among collections (involving a total of 1 124 accessions), 50 of them revealed either synonyms or errors. (Even if more work is necessary to sort out the whole germplasm, the project clearly demonstrated the feasibility of the use of these data for the accurate comparison of collections.

In the project, a list of all the national catalogues of the participant countries was established. It is a first step towards a European Grapevine Catalogue (Lacombe et al, 2011).

Similarly, several prospecting trips to many regions of Europe enabled the discovery of 218 populations of *V. sylvestris* totaling 1 854 individuals. DNA fingerprinting of part of this material (269 accessions) as well as morphological descriptions (631 accessions) were obtained.





### The need for increased characterization of the European germplasm in order to encourage its use

During GrapeGen06, a portion of the accessions held in the EU and in neighbouring non-EU countries (Azerbaijan, Croatia, Georgia, Moldova, Morocco, Switzerland) was analyzed. This analysis was performed both in the collections (by molecular markers and morphology analyses) but also at a larger scale in on-farm sites. This work enabled the estimation of technical characteristics of the cultivars, since vinification was performed and tasting sessions organized during open days. This provided a better description and an easier presentation of autochthonous cultivars to both growers and consumers.

The germplasm held in the partners collections represents an inestimable treasure which can allow Europe to increase its competitiveness, to create new products and open up new markets for the horticultural and wine industries

### Protecting genetic resources as a long term safeguard

The long term aim of the project was also to ensure a safe conservation for the genetic resources in Europe. Several actions of the project enabled us to make steps in this direction.

First, the management of the collections, by the reduction of redundancy (elimination of synonyms & homonyms) or in contrary duplication of endangered accessions (wild and cultivated), together with the availability of the 'variety identity card' in a web based database, was a first milestone towards a well managed germplasm in Europe. The development of alternative conservation means was also achieved, such as cryoconservation of pollen and seeds. Intensive research work during the project succeeded to achieve cryoconservation of dormant buds for a limited number

of accessions, showing the feasibility of this process and producing a protocol for the conservation community. More work is nevertheless needed for the development of safety duplicates in liquid nitrogen as performed for animal semen.

### Communication value

The GrapeGen06 project enabled us to monitor the wild and cultivated *V. vinifera* germplasm across Europe (EU and non EU countries), to contribute to its description by DNA fingerprinting analysis and by morphology descriptions, and to enter all these data into the European Vitis database held by Julius Kühn Institute at <http://www.eu-vitis.de/index.php>. The project enabled the improvement of collection management by more accurate identification of accessions and promoted an overall optimized conservation scheme for the safe conservation of the *Vitis* germplasm including *Vitis sylvestris*, currently threatened of extinction, and involving several conservation means (*ex situ* collections, cryopreservation and on-farm conservation by farmers and professionals). Finally, the project ensured the overall accessibility of the information by diverse media (scientific papers, technical papers, general public publications, websites, online database,...) and the availability of well characterized autochthonous cultivars for European growers.

All of this information is now available to the public on our website (<http://www1.montpellier.inra.fr/grapegen06/>) and in the European Vitis database. The data are thus easily available for all to see. Indeed, during the project's duration, several external teams have asked to access the database, showing the interest it rises in the conservation and for the scientific communities.

We are also writing the technical aspects of our work. Several papers have been published (see list of publications). More articles are in preparation and will be additional outputs from the project's work.

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## More information

Twenty-four partners were involved in the project as specialists from organisations located in 11 EU Member States (Austria, Czech Republic, Cyprus, France, Germany, Greece, Hungary, Italy, Portugal, Slovakia, Spain) and 6 non EU countries (Azerbaijan, Croatia, Georgia, Moldova, Morocco, Switzerland). Four additional external contributors joined on the way and contributed to the analysis of additional material.

## Links

This section lets you know how to find out more about the 'outputs' of the GrapeGen06 project – how to access the genetic resources that have been collected in collections, how to access the information that have been found about the grape germplasm, and how to obtain copies of the scientific, technical and other publications that we have produced.

### The GrapeGen06 website

The documents prepared during the 4 years of the GrapeGen06 project are available on our website (<http://www1.montpellier.inra.fr/grapegen06/accueil.php>). You will find the annual interim technical reports and the final report as well as most of the working documents prepared during the project.

### The European Vitis database

The establishment of the European Vitis Database with free access via Internet has been carried out in the scope of a previous GENRES CT96 European Project (Genres081, 1997-2002, Dettweiler and This, 2002). The follow up and enlargement was accomplished within GrapeGen06 project.

This database aims to serve as a tool to promote the sustainable use of the autochthonous cultivars (Maul et al., submitted). You can find it at <http://www.eu-vitis.de/index.php>

### How to retrieve data on cultivars from the database

Thanks to the work performed within GrapeGen06, it is now quite easy to retrieve data from the database on any cultivars, both autochthonous and international cultivars.

Go to the database, select Public access/catalogue of varieties and enter several criteria for the search. You can get 'pdf documents' for specific cultivars with data collected within the project and generate your own cultivar catalogue as presented in the following figure for Mouyssagues noir, an old French cultivar.

### List of publications

We are writing technical, scientific and policy reports and publications.

For the publication list, see the final technical report and the executive summary on the web site of the project: <http://www1.montpellier.inra.fr/grapegen06/accueil.php>

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Third Meeting  
at Geilweilerhof

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## Saffron

### Genetic Resources of Saffron and allies (Crocus spp.)

The Saffron action created the World Saffron and Crocus Collection (WSCC), a unique collection for conservation which contains a representation of genetic variability present in saffron crop and wild relatives at global scale. The action also characterised and evaluated the WSCC, including morphological, phenological, cytological, phytochemical, molecular and physiological traits and created a DNA bank. All the accessions and descriptors are available in a database.

### Project details

Duration	48 months
Start Date	01/06/2007
End Date	31/05/2011
Budget Total Cost	1 859 041 €
Budget EU Co-funding	929 507 €
Actual EU Co-funding	922 454 €
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### Background

The genus *Crocus* (*Iridaceae*) contains ca. 100 small, corm-bearing, perennial species distributed in Central and Southern Europe, North Africa, and from Southwest Asia to Western China. These species are highly valued as ornamental plants for their colorful flowers, horticultural varieties and for industrial applications. Among the long list of *Crocus* species, cultivars and/or varieties, *C. sativus* L. is the most fascinating and intriguing species commercially cultivated for the production of the well known spice saffron.

### Why saffron? Saffron is a high value agricultural product

Saffron, which consists of the dried long-dark-red stigma of the plant, has three exceptional quality attributes, *i.e.* aroma, taste and color, a set of characteristics bringing about its uniqueness for pharmaceutical, food and textile industries. Saffron is mostly used as a spice and food colorant due to the presence of pigments (apocarotenoids) in the flower stigmas, and less extensively, as a textile dye or perfume. However, due to its analgesic and sedative properties, traditional Eurasian herbal medicines have used saffron for the treatment of numerous diseases. Saffron has been indeed one of the oldest plants used as medicine (as shown in the frescoes of Thera, Greece). The renewed importance of saffron as nutraceutical and functional food is being sustained by increasing number of scientific publications. In addition, saffron is considered to be the most expensive spice in the World, and in fact, saffron is one of the most valuable food products (e.g. the cost of 1 kg saffron equals, based on the prices of end 2011, approximately to 2 kg of silver). Several areas in different European countries are considered to produce high quality saffron, which is guaranteed by specific 'Protected Denominations of Origin' (PDO).

Saffron flowers showing the long-dark-red stigmas



## Saffron in Europe: the European saffron industry is in crisis

Commercial production of saffron is currently based mainly in Iran (80–90% of world production, about 200 tonnes). India, Morocco, Greece, Spain, Italy, China, and Afghanistan also produce significant amounts, whereas micro-scale production is found in France, Switzerland, Turkey, Azerbaijan, Japan, Tasmania, New Zealand, Argentina, USA and others.

The European production of saffron is associated to a prestigious added value in gastronomy and a cultural importance in history and arts. However, the saffron crop has disappeared in some European countries such as Germany, Austria and the United Kingdom (there it was grown in great quantities in Essex, especially near the town Saffron Walden). Saffron was cultivated in France during five centuries. Saffron produced in Gâtinais, France, was one of the most reputed in quality. Its production stopped after the 1st World War. After having been the leaders of saffron production and commercialization at World scale for centuries, European countries only produce a scarce 3% nowadays. Nevertheless, the reputation for quality in the market is still held by European Protected Denominations of Origin, which are established in different countries, such as Greece (*Krokos Kozanis*), Italy (*Zafferano dell' Aquila*, *Zafferano delle Colline Fiorentine*, *Zafferano di San Gimignano* and *Zafferano di Sardegna*), Spain (*Azafrán de La Mancha*), and Switzerland (*Munder Safran*). Others PDO's are currently being requested: *Azafranes de Jiloca* and *Campo Bello* in Teruel (Spain), *Safrans du Gâtinais* in Quercy, *Font Saint Blaise* in Limousin and *du Tarn et du Lauragais* (France), and *Zafferano di Cascia* (Italy). The purpose of these quality labels is to preserve cultivation, manufacturing and merchandising of saffron in their specific areas. In this connection, excellence and gourmet quality of saffron has always been associated to European productions. During the last

40 years, the intensive manual labour required for flower harvesting and processing, among other reasons, has caused a significant reduction of the saffron cultivated area in many European countries. This has resulted in corresponding significant genetic erosion of the cultivated species, which means the irreversible loss of local varieties or landraces of the crop.

## Preserving genetic resources of saffron and allies

*C. sativus* is a hybrid sterile species which cannot produce seeds. The propagation of the crop is exclusively vegetative, and for this reason the genetic variability is suspected to be very low. This characteristic, joined to the reduction or disappearance of the crop in many producing areas, as explained above, makes necessary the urgent implementation of actions to protect what still remains of the European saffron biodiversity for its potential interest in future breeding programs and applications. Until now, germplasm collections rarely include species with nutraceutical, therapeutic or medical applications, aromatic plants, and ornamental and spice producing plants. In the case of saffron, collecting and preserving materials from currently producing and commercial areas, or from places where the crop is relictic, or even collecting single plants remaining in fields where the crop was abandoned several years or decades ago, is the most appropriate approach to create a germplasm collection.

In addition, around 100 *Crocus* species are currently known, most of them living in different areas of the Mediterranean region, but probably new species are still being recognized. The inclusion of wild related species has been proved to be useful for any crop improvement as sources of a variety of valuable traits taking into account that the wild portion of a crop gene-pool generally contains a much greater genetic variation than that contained in the own crop. In addition, some *Crocus* species are highly

Harvesting saffron flowers in Spain

© María Ángeles Serrano, in Minaya, near Albacete



*Crocus biflorus* Mill

*Crocus sieberi* J. Gay





Some of the wild and gardening *Crocus* species preserved in the WSCC:

- A** *C. sativus* L.
- B** *C. sativus* L. var. *Cashmeriensis*
- C** *C. cartwrightianus* Herb. cv. *Albus*
- D** *C. cartwrightianus* Herb.
- E** *C. hadriaticus* Herb.
- F** *C. mathewii* Kernd. et Pasche
- G** *C. asumaniae* B. Mathew et T. Baytop
- H** *C. pallasii* Goldb.
- I** *C. thomasi* Ten.
- J** *C. kotschyianus* K. Koch
- K** *C. ochroleucus* Boiss. et Gaill.
- L** *C. imperati* Ten.
- M** *C. minimus* DC.
- N** *C. corsicus* Vanucc.
- O** *C. serotinus* Salisb.
- P** *C. nevadensis* Amo
- Q** *C. carpetanus* Boiss. et Reut.
- R** *C. fleischeri* J. Gay.

appreciated for their colorful flowers and extensively used in many gardens. Other possible applications (therapeutic, industrial, etc.) of such interesting group of plants remain to be discovered.

### The CROCUSBANK Project and the World Saffron and Crocus Collection

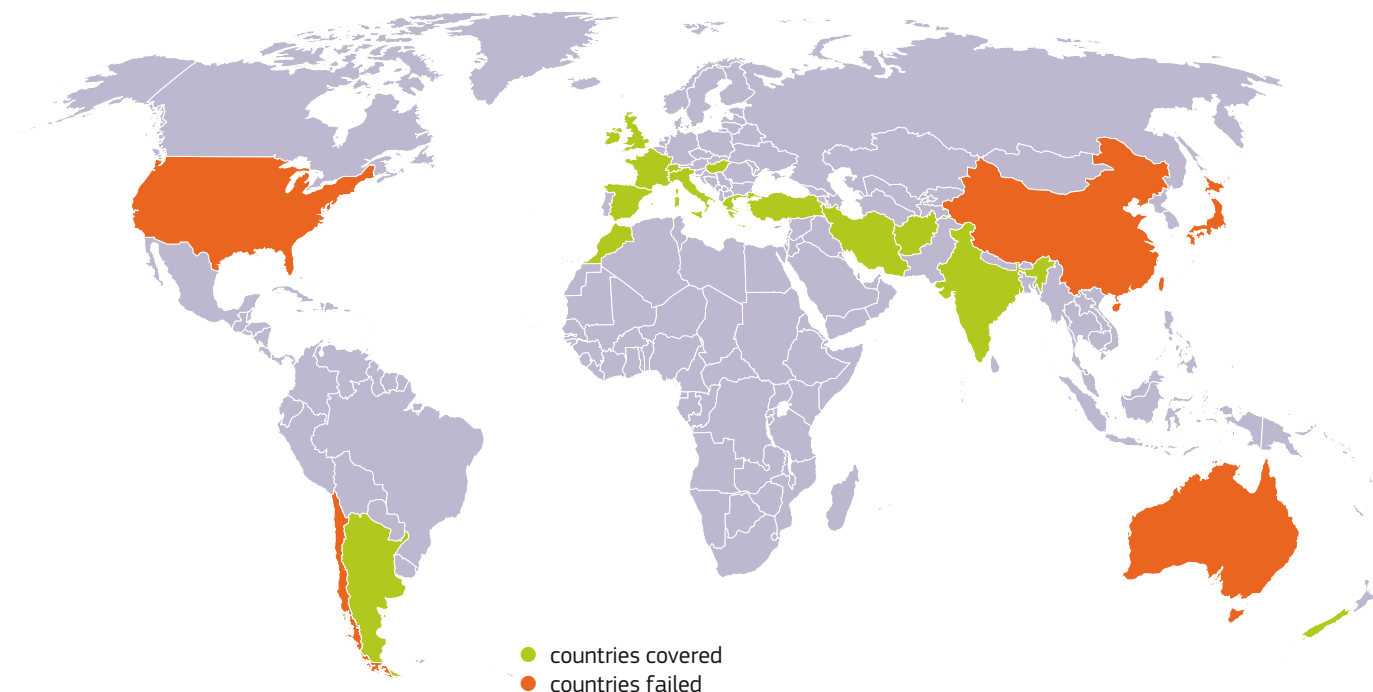
The main objectives of the CROCUSBANK project were the creation and management of a germplasm collection (bank) of *Crocus* species, including saffron *Crocus* (*C. sativus* L.), and the multidisciplinary characterization of the preserved materials for further exploitation. In this context, the CROCUSBANK project has allowed the creation of the *World Saffron and Crocus Collection* (WSCC), a unique germplasm collection which contains a representation of the genetic variability present in saffron crop and wild relatives at global scale. The different tasks implemented in the project to achieve the objective were developed by the members of the CROCUSBANK consortium. These tasks can be summarized in the following points: Acquisition of materials; Conservation and management; Documentation of the collection; Elaboration of a list of descriptors; Characterisation of the collection.

#### Acquisition of materials

Saffron corms were collected from different localities all around the World to be integrated in the WSCC. Most of these materials were collected in commercial areas of a total of 15 countries, including 6 European Union countries (Italy, France, Greece, Hungary, Spain and United Kingdom) and 9 non-EU countries (Afghanistan, Argentina, Azerbaijan, India, Iran, Morocco, New Zealand, Switzerland and Turkey). These materials involve the most important saffron commercial areas, including the 5 PDO's currently established in the UE, although other interesting sources of acquisition are well represented in the collection such as crop relictic areas, abandoned fields and specialised nurseries. In general, the results are satisfactory in terms of geographical origin of the materials, although saffron materials from some other minor producing countries (p. ej.: Australia, Chile, China, Japan and USA) remain to be collected in the future.

The most interesting source for the acquisition of other *Crocus* species is the exploration and collection of plants from the natural habitats, although it is very expensive method and not always rendered the expected results. Anyway, near 400 *Crocus* accessions have been collected from the wild in 13 different countries. Other sources of *Crocus* acquisition, such as botanical gardens, commercial nurseries, etc. have been quite useful too. Near 70 % of the currently described *Crocus* species have been acquired in the frame of the CROCUSBANK project (a representation of the *Crocus* diversity integrated in the WSCC can be observed in the figure page 94). However, more than 20 species remain to be acquired in the future, because their natural habitats fall in countries where collecting has been not possible due to legal restrictions.

World map indicating countries of origin of saffron materials included in the WSCC (green color) and other countries where saffron is currently grown but no samples has been achieved until now (red color)



### *Conservation and management of the WSCC*

The WSCC is currently integrated by 761 effectively preserved accessions, 225 correspond to saffron materials and 536 to other *Crocus*, including 62 different species. The materials are preserved and managed in the facilities of the Bank of Plant Germplasm of Cuenca, dependent on the regional government

of Castilla – La Mancha (Spain). Taking into account the biological characteristics of the materials and in order to minimize the risk of losing materials, a specific design has been established in the bank, including a Reserve Vegetative Collection in flower-pots (greenhouse), an Exchange Vegetative Collection in the field, and a Seed Collection in hermetic jars in refrigerated chamber (exclusively for seeds of non-saffron crocuses).

Aspect of the bank design developed for conservation and management of the WSCC, including a Reserve Vegetative Collection (left), a Interchange Vegetative Collection (middle) and a Seed Collection (right)





In addition, alternative procedures for *Crocus* germplasm conservation have been implemented in the frame of the CROCUSBANK project. For the conservation of sensible materials or for quick multiplication, the development of *in vitro* techniques are specially useful. This way, the basic protocol for saffron micropropagation has been improved, and promising results have been obtained for other *Crocus* species. In addition, the extraction techniques for *Crocus* DNA have been optimised, which can be considered the first step for the creation of DNA bank for this genus, which can be used in molecular studies.

### Documentation of the collection

A relational database was developed to store effectively the large volume of data generated during the conservation and characterisation of *Crocus*. The database includes descriptors grouped according to the categories proposed by *Bioversity International* (passport, management, site and environment and characterisation). For rapid dissemination of the information, a Central Information System (CIS) was developed. This CIS is accessible via the CROCUSBANK website at: <http://www.crocusbank.org>. The CIS is a comprehensive electronic platform that provides users an interactive documentation system of the WSCC. In addition, in order to provide access to the information stored in the WSCC an online database is available at: <http://www.crocusbank.org/Database/buscador.asp>. In this connection, a powerful search function was designed, providing easily access to the information included in the germplasm collection.

### Development of a list of descriptors for the genus *Crocus*

Lists of descriptors have been elaborated and published to describe the variability observed in the most important crops and wild related species at World scale. However, there was not any list of descriptors for saffron and other *Crocus*, so it was an essential task in this project to make possible the characterisation of the materials integrated in the collection. In this way a total of 177 descriptors have been defined, including traits related to the morphology, aspect and size of the different organs, agronomic traits (production of flowers and corms, etc.), resistance to pest and pathogens, chemical composition (p. ej.: pigment content, etc.), molecular markers to detect differences at DNA level, cytogenetic markers (p. ej.: chromosome number, etc.). Some of the descriptors are highly interesting for plant breeders, because they are useful in crop improvement and domestication of new materials.

### Characterisation of the collection

The characterisation of *Crocus* genetic resources is useful for different purposes: breeding programs, commercial gardening, bank rationalisation, taxonomic studies, etc. As mentioned above, the characterisation of the materials must be based on previously defined descriptors, and including all the traits of the crop and/or related species that could be useful to highlight

the differences among materials for further selection and utilisation. Due to restrictions in material availability for the experiments, only a part of the collection has been characterised, but interesting results have been obtained in most of the disciplinary approaches.

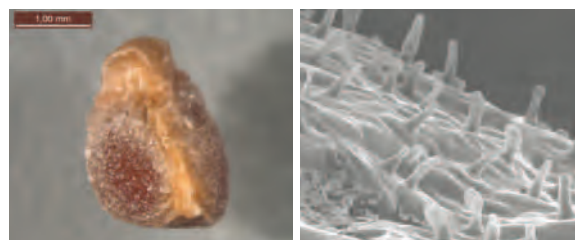
In relation to morpho-agronomical traits 66 saffron accessions from different countries have been characterized taking into account quantitative and qualitative traits. Different levels of intraspecific variability were detected suggesting the existence of genetic differences among accessions related to geographic origin of the materials, which is surprising taking into account the low variability generally assumed for this crop. For other *Crocus* species, a total of 183 accessions from 50 different species have been characterized for morphological traits (aspect of the tepals, stamens and style, morphology of leaves, seeds and corms, etc.). High levels of inter-specific and intra-specific variability were observed in most of tested traits, as expected, but even intra-accession variability in some cases.

Some *Crocus* materials, including saffron, have been also evaluated for resistance to abiotic (salinity) and biotic stresses (fungal infestation). The differences in saffron are not significative, but interesting results have been found in other species. In this sense, a certain degree of tolerance to salinity was detected in *C. laevigatus* Bory et Chaub., and some resistance to the fungus *Fusarium oxysporum* f. sp. *gladioli* was detected in *C. serotinus* Salisb. individual plants.

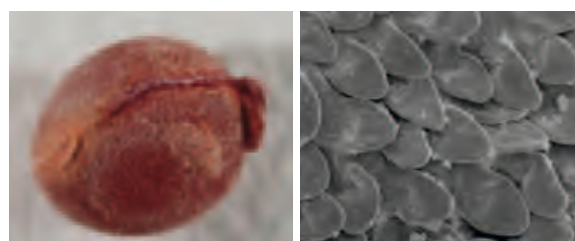
The chemical characterisation of a subset of accessions from the WSCC was based on different analytical methods. Some quantitative differences in the compounds responsible for the

### Examples of the variability detected in the shape and in the surface ultrastructure of seeds of some wild *Crocus* species

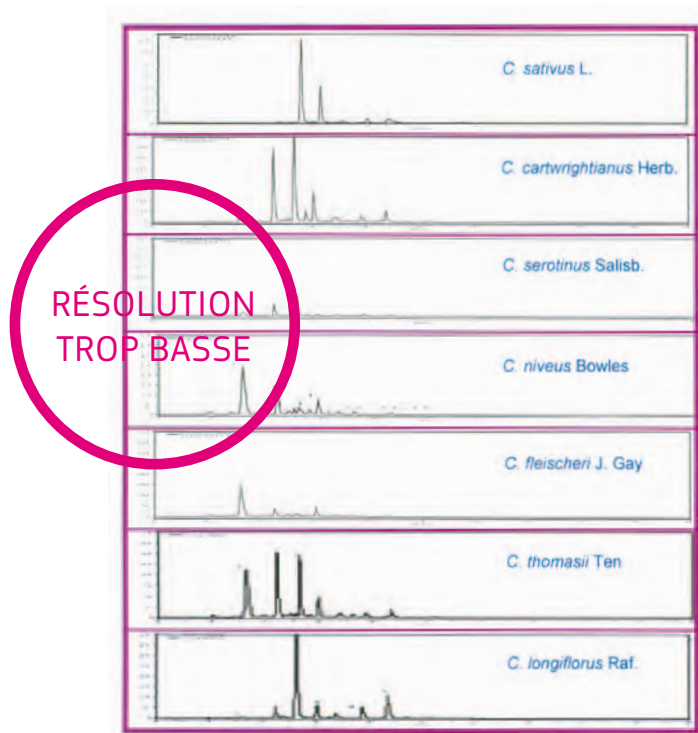
#### *C. cambessedessi* J. Gay



#### *C. vernus* (L.) Hill







Significative differences can be observed in the profiles of apocarotenoids (pigments) obtained from samples of styles in different *Crocus* species using the same analytical method (RP-HPLC-DAD at 440 nm)

color (crocin), bitterness (picrocrocin) and aroma (safranal) have been detected in samples of styles from different saffron accessions, but the exact origin of that variability in saffron must be established in further experiments. As expected, in other *Crocus* species, the differences in the chemical composition are much more evident than in saffron, from both the quantitative and the qualitative points of view, and as a result, some of these methods are appropriate to differentiate style samples of *C. sativus* from other *Crocus* species, and can be utilized in the development of valid chemical descriptors for the genus *Crocus* in the future.

For the molecular characterisation several types of molecular markers were used to detect differences (polymorphisms) at DNA level between saffron accessions and between different *Crocus* species. Some of them, mainly AFLP (Amplified Fragment Length Polymorphism), which detect differences in the length of the DNA fragments obtained after the digestion of genomic DNA with a specific type of enzymes (restriction enzymes), has revealed interesting and previously unreported genetic variability in saffron. In addition, those molecular markers seem to be an appropriate tool for taxonomic studies in the genus *Crocus*.

Other interesting approach for further research and application of the WSCC initiated in the frame of the CROCUSBANK project, is the detection and isolation of bioactive molecules

against pests, pathogens and weeds. For this purpose, crude extracts of different parts of the plant (leaves, corms, etc.) of saffron and other *Crocus* have been evaluated for detection of antifeedant properties against insect pests, nematicidal, fungicidal and phytotoxic activities. Preliminary results indicate that different types of bioactivity can be found depending on the *Crocus* species utilized, the part of the plant considered and the target species for a specific activity.

## Dissemination

Many activities have been focused to ensure wide dissemination of the CROCUSBANK project by the usual ways of communication to the scientific community and the public. A wide range of communication channels has been exploited including Internet, project meetings (<http://www.crocusbank.org/CBankMandW/CbankMandW.html>), international workshops (<http://www.crocusbank.org/CBankMandW/SaffronMeetings.html>), press releases (<http://www.crocusbank.org/Index52En.htm>), brochures (<http://www.crocusbank.org>), papers ([http://www.crocusbank.org/PDFFiles/Administrative/CrocusBank-Outputs\\_Dissemination.pdf](http://www.crocusbank.org/PDFFiles/Administrative/CrocusBank-Outputs_Dissemination.pdf)), etc.

## Communication value

### Germplasm collection

The WSCC is preserved in the facilities of the Bank of Plant Germplasm of Cuenca (Albaladejito Research Center, Government of Castilla – La Mancha, Cuenca, Spain). This bank is integrated in the Spanish and International Networks of germplasm banks (institutional FAO code ESP124), and took on the responsibilities of the acquisition, conservation and management of this unique germplasm collection. The collection contains already a wide representation of the *Crocus* germplasm from around the World, preserving 761 accessions, of both saffron of different geographical origin (225 accessions) and other crocuses (536 accessions, 62 species). The WSCC will be increased by the acquisition of new materials, even after the conclusion of the CROCUSBANK project. New expeditions, donations, interchanges, etc. are being currently developed in the frame of other national or international actions, and in this sense, it is highly probable that an important part of the saffron research developed in the next years will be based on this important collection, at least at European level. Anyway, the administrative and technical management of the materials integrated in the WSCC is performed following the rules and recommendations of the International and Spanish Institutions related to Conservation and Utilisation of Plant Genetic Resources, taking always into account the agreements established with the donors and other legal aspects for the transference of the materials.

A complete set of passport data on the accessions integrated in the WSCC, is accessible via the CROCUSBANK portal at <http://www.crocusbank.org>, including information about date of acquisition, donors, origin countries, collecting localities, taxonomy, etc.

## More information

A delay for submission of the final technical report by December 2011 was needed to include an additional flowering and harvest period of saffron need to obtain new interesting data and complete the on-going experiments.

## Partners details

The 14 partners included in the CROCUSBANK consortium are experienced in different areas of saffron research (Agronomy, Breeding, Botany, Genetics, Chemistry, Food Technology and Commercialisation). Saffron being such a minority crop, we can assert that this consortium includes the majority of the best saffron researchers at World scale.

## Links

### The website of the project

The website is continuously being updated to provide administrative and technical information associated to the CROCUSBANK project. Until now the website addresses the needs of CROCUSBANK partners, and other users (local farmers, private companies and nurseries, scientific and specialized breeders, networks on genetic resources, politicians and stakeholders) as well as general public. Detailed information about WSCC can be found in the website. A powerful search function was designed, providing easily access to the information. In addition, direct links have been created to provide quickly access to the main statistics of the collection as:

- Accession passport data: <http://www.crocusbank.org/Database/ConsultPassportDataAccession.asp>
- Collecting passport data: <http://www.crocusbank.org/Database/ConsultPassportDataCollecting.asp>
- Species: <http://www.crocusbank.org/Database/ConsultSpeciesGen.asp>
- Donors: <http://www.crocusbank.org/Database/ConsultDonorInstituGen.asp>
- Source countries: <http://www.crocusbank.org/Database/ConsultCountriesGen.asp>
- Germplasm gallery: <http://www.crocusbank.org/GGALLERY.html>
- Library: <http://www.crocusbank.org/Login.asp>

## List of publications

Fernández, J.A., Santana, O., Guardiola, J.L., Molina, R.V., Heslop-Harrison, P., Borbely, G., Branca, F., Argento, S., Maloupa, E., Talou, T., Thiercelin, J.M., Gasimov, K., Vurdu, H., Roldán, M., Santaella, M., Sanchís, E., García-Luis, A., Suranyi, G., Molnár, A., Sramko, G., Gulyas, G., Balazs, L., Horvat, O., Rodríguez, M.F., Sánchez-Vioque, R., Escolano, M.A., Reina, J.V., Krigas, N., Pastor, T., Renau-Morata, B., Raynaud, C., Ibadli, O., Polissiou, M., Tsimidou, M.Z., Tsaftaris, A., Sharaf-Eldin, M., Medina, J., Constantinidis, T., Karamplianis, T. & De-Los-Mozos-Pascual, M. (2011) The World Saffron and Crocus Collection. Strategies for establishment, management, characterisation and utilisation. *Genetic Resources and Crop Evolution*, 58: 125-137.

A complete list of scientific publications and other scientific or technical contributions can be consulted in the project website:

<http://www.crocusbank.org/PDFFiles/Administrative/CrocusBank-papers.pdf>

## Other related links

- Collection of EST sequences from saffron (*Crocus sativus*) stigmas <http://www.saffrongenes.org/>
- Denominations of Origin (DOP) and traditional areas of saffron cultivation <http://www.crocusbank.org/Index51En.htm>
- The 17 actions on genetic resources in agriculture [http://ec.europa.eu/agriculture/genetic-resources/actions/index\\_en.htm](http://ec.europa.eu/agriculture/genetic-resources/actions/index_en.htm)
- COST action FA10101: 'Omics technologies for crop improvement, traceability, determination of authenticity, adulteration and origin in saffron' [http://www.cost.eu/domains\\_actions/fa/Actions/FA1101](http://www.cost.eu/domains_actions/fa/Actions/FA1101)



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## Straw- and raspberries

### European small berries genetic resources

The Strawberries and Raspberries action improved the conservation of the small berries genetic resources and developed their characterisation, focused on the diversity available in collections, identified genotypes for some traits, such as health compounds and diseases resistances, initiated cryopreservation method and established a core collection and a database for strawberry. All these activities contributed to the conservation and sustainable use of small berries.

### Project details

<b>Duration</b>	37 months
<b>Start Date</b>	01/09/2007
<b>End Date</b>	31/03/2011
<b>Budget Total Cost</b>	710 099 €
<b>Budget EU Co-funding</b>	329 507 €
<b>Actual EU Co-funding</b>	317 700.11€
<b>Coordinator</b>	Institut National de la Recherche Agronomique (INRA) – Bordeaux BP81
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<b>Coordinator's Website</b>	<a href="http://www.bordeaux.inra.fr/genberry/pages/sum.htm">www.bordeaux.inra.fr/genberry/pages/sum.htm</a>

### Background

Horticultural crops have always played a vital role as fresh foods in the human diet. Some of them such as strawberries and raspberries are particularly interesting for consumers due to the special taste value and high content of health benefits, including dietary fibre, macro and microelements (K, P, Ca, Mg, Fe, Zn), and vitamins (A, B<sub>1</sub>, B<sub>2</sub>, B<sub>6</sub>, PP, C, E) in the fruits. Annual world production of these berries amounts approximately 4.0–4.8 Mt with a total harvested area of over 300 000 ha.

In Europe, the total area devoted to berry cultivation covers approximately 190 000 ha (100 000 ha for strawberry, 30 000 ha for raspberry and 60 000 ha for other berries such as blueberry, gooseberry, currant, cranberry).

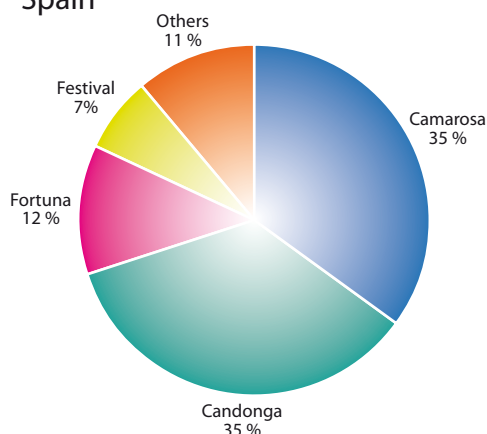
Europe produces annually 1.1 Mt of strawberry and 0.14 Mt of raspberry.

Table 1 | Countries with highest production of strawberry and raspberry in 2010 (based on FAO statistics). EU countries are marked with \*

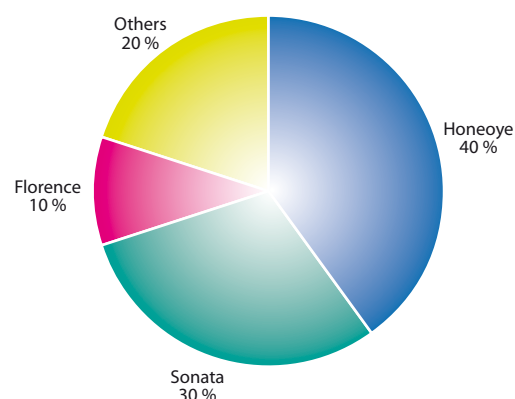
Country	Annual strawberry production in tones
USA	1 292 780
Turkey	299 940
Spain *	275 300
Republic of Korea	231 803
Mexico	226 657
Japan	177 500
Poland *	176 748
Russian Federation	165 000
Germany *	156 911
Italy *	153 875

Country	Annual raspberry production in tones
Russian Federation	125 000
Poland *	87 556
Serbia	83 870
USA	31 207
Ukraine	25 700
Mexico	14 343
Canada	11 864
Azerbaijan	10 100
Spain *	10 000
Bosnia and Herzegovina	7 937

### Spain



### Sweden



In general, cultivation of strawberry and raspberry is largely extended in Europe, thanks to the plants high adaptability to environmental conditions and improved growing techniques. However, despite the high adaptability of strawberry to environmental conditions, varieties are very specific to countries. For example, the varieties cultivated in Spain are very different to the ones cultivated in Sweden (see figures above).

### The preservation of diversity of the cultivated strawberry and raspberry

Genetic resources are important for breeding programmes mainly because of 1) food security, 2) possible adaptation to changing environment (climate change) and 3) plant diseases resistance. It is therefore crucial to continue the effort of evaluation of varieties well adapted to the different European climates, Eastern, Western, Northern and Southern Europe. This effort should include also the new demand of consumers such as fruits with more flavour and with less or no fungicides and pesticides.

The project of GenBerry aimed to evaluate genetic resources that are representative of all available variability, including old strawberry cultivars for identifying the best varieties and genotypes. These varieties and genotypes represent potential parents for original traits (e.g. disease resistances, flavour, climate adaptability) and are consequently of great importance for breeding programmes.

### History of the common wild and cultivated strawberry, *Fragaria x ananassa*

Strawberry belongs to the genus *Fragaria* which displayed a polyploid series of wild species ranging from diploids ( $2n = 2x = 14$ ) (two haploid genome) to decaploids ( $2n = 10x = 70$ ) (10 haploid genomes). In addition to these wild species, the common cultivated octoploid species, *F. x ananassa* ( $2n = 8x = 56$ ), was created only recently (about 250 years ago), which explain its narrow diversity compared to its widespread genitors. This species results

from a hybridization by chance between two related octoploid species, North American origin scarlet strawberry (*F. virginiana* Mill.) and South American domesticated *F. chiloensis* (L.) Mill (please delete all scientific references). This hybridization occurred in a French botanical garden in the early 1700s, resulting in a new cultivated fruit species, *F. x ananassa*.

While diploid strawberry species such as the woody *F. vesca*, contains 14 chromosomes, the octoploid species are genetically complex since they contain four times the chromosome's number of the diploid species.

Strawberry breeding began in England in the late 1700s, followed by France and Germany. The first selected European cultivars were used as genitors in early American breeding programmes, together with American native cultivars. Therefore, the origin of strawberry and these early breeding practices reduced initial genetic variability. During the around 200 years of strawberry breeding, initial diversity increased thanks to the use of wild strawberry germplasm or unrelated progenitors in breeding programmes which allowed to integrate new traits in varieties (introgression). However, the use of exotic germplasm was limited and therefore, the genetic diversity of the cultivated strawberry in modern strawberry cultivars is limited compare to its two relative wild American species.

In this context, it is of extreme importance to keep and breed all sources of wild and cultivated strawberries. The project was concerned with the conservation of the cultivated strawberry, and particularly varieties from Europe where breeding of strawberry has started.

### History of the cultivated raspberry, *Rubus idaeus*

*Rubus* is a member of the family *Rosaceae* and is one of the most diverse genera in the plant kingdom, comprising over 400 species subdivided into 12 subgenera. Ploidy levels range from diploid to 14-ploid.

The domesticated subgenera contain the raspberries, blackberries, arctic fruits and flowering raspberries, all of which have been utilised in breeding programmes. The most important raspberries are the European red raspberry, *R. idaeus* L. subsp. *idaeus*, the North American red raspberry *R. idaeus* subsp. *strigosus* Michx and the black raspberry (*R. occidentalis* L.). *Rubus* subgenus *Idaeobatus* is distributed principally in Asia but also East and South Africa, Europe and North America. There is another subgenus, *Eubatus*, which is mainly distributed in South America, Europe and North America.

Raspberries have always been attractive as fresh dessert fruits or for processing from frozen berries into preserves, purees and juices. In most European countries, USA bred cultivars have led the industry, such as 'Meeker', 'Willamette' and 'Tulameen'. Primocane-fruiting cultivar 'Heritage' has led the industry in many countries. In Scandinavia, the hardy Norwegian variety 'Veten' has been the mainstay for many years, now 'Glen Ample' has taken the lead.

### *Collections of the cultivated strawberry and raspberry in Europe*

Both strawberry and raspberry can be maintained in collections during several years. However, the turnover is much shorter for strawberry (2 years or even 1 year for some partners) than for raspberry (8 years).

Maintaining collections for several years can lead to sanitary problems such as *Phytophthora* (*Phytophthora rubi* for raspberry or *Verticillium dahliae* for strawberry).

Due to a large worldwide interest in strawberries and raspberries, numerous breeding programmes mainly in the Northern Hemisphere occurred in the past for strawberries and raspberries. In addition, strawberry fruits are produced in annual cultures,

which leads to a relative quick turnover of the varieties. Therefore, a large number of varieties or genotypes of strawberries and raspberries exist.

### *Project objectives and activities*

The first objective of the GENBERRY project was to **continue maintaining the European genetic resources of cultivated strawberry and raspberry** and to build the European small berries collections for strawberry and raspberry.

The second objective was to **characterize the strawberry and raspberry collections using passport data and primary and secondary descriptors**. The major descriptors were linked to health nutritional values such as vitamin C and plant disease resistances, e.g. *Phytophthora cactorum* and *Verticillium dahliae* resistances for strawberry and *Phytophthora fragaria* var *rubi*, *Botrytis cinerea* and *Didymella applanata* for raspberry. For strawberry, these descriptions were **integrated in a European database**. Characterization was also conducted using **microsatellite markers** for studying the genetic diversity of strawberry and raspberry.

All descriptions of the strawberry including analyse of the genetic diversity was used for identifying the best possible core collection.

Preservation of agricultural biodiversity and characterization of this diversity will be of benefit to European breeding programmes as well as gardeners.

### *Maintaining collections*

As the plants of the collections must be maintained vegetatively, some specific growing system must be used to keep them authentic and free of diseases such as insect proof tunnels or

Different types of strawberry conservation: at the top left, in pots; top right in boxes and below in field with straw





cryoconservation (conservation in -80° C). These growing systems are different for each partner according to their locations and the strawberry or raspberry species.

### Strawberry

For strawberry, collections can be maintained in open field in box systems or directly in field rows or under insect proof tunnel. The new plants are collected in winter as bare root plants and stored as frigo plants in cold rooms at -2° C.

Soilless systems, substrate type – peat, can be used to avoid some diseases such as *Verticillium dahliae* or *Phytophthora cactorum*. The runners (new plantlets that are on the stolon) are collected during the summer, planted in small pots and stored in winter.

Almost all partners used explants cleaning methods such as in vitro culture to have viruses free plants. The in vitro technique allows obtaining healthy plants which can be further planted in greenhouses or in fields. In vitro culture (culture in glass tubes) conditions are quite similar between partners.

For adaptation in greenhouse conditions, all partners used standard procedure – transferred plants to a peat substrate and covered them for 1-4 week in the greenhouse.

Cryopreservation:

The use of cryopreservation has been initiated. Pieces of plants are placed in -80° C which will allow a more efficient long term preservation of plant materials.

### Raspberry

Raspberry collections can be maintained in open field organised in rows. Clean straw, rotted sawdust, screened bark or similar organic mulch can be used in field rows for weed control and moisture preservation. The raspberry must be kept free of weeds, watered when necessary, fertilized, pruned regularly, kept free of insect and disease pests, and in some cases, supported with trellis.

### Characterisation of the collections

Descriptors for characterising collections of strawberry and raspberry were separated into primary and secondary descriptors. Primary descriptors are stable whatever the condition of cultivation, in greenhouse or in field, while secondary descriptors can be more. Primary descriptors were mandatory and recorded by all partners. Secondary descriptors were established when available according to each location.

A table for descriptors was set up.

For strawberry, there are 8 primary descriptors for the plant and 10 for the fruit, and 33 secondary descriptors for other plant and fruit characteristics diseases, pathogens and abiotics stresses behaviour. The characterisation of each strawberry cultivar also includes the passport data for the identification of the cultivar.

For raspberry, there are 9 primary descriptors for the plant and 8 for the fruit, and 33 secondary descriptors.

For strawberry:

all the primary and secondary descriptors are available at: <https://www.bordeaux.inra.fr/genberry/doc/dissemination/genres036/GENRES036-Strawberry-sheet-for-notations.pdf>

For raspberry:

all the primary and secondary descriptors are available at: <https://www.bordeaux.inra.fr/genberry/doc/dissemination/genres036/GENRES036-Raspberry-sheet-for-notations.pdf>

The passport data for strawberry cultivars are available on the Genberry portal at: <https://www.bordeaux.inra.fr/genberry/>

### Towards a core collection for strawberry

For strawberry, a core collection was established for old European varieties selected before 1940. These varieties have shown specific diversity compare to varieties from more recent origins. In addition, the collection includes varieties and genotypes (plants that were selected but not used commercially) that have original traits such as high health compound contents (e.g. total antioxidant compounds) or high level of disease resistances (e.g. *Phytophthora cactorum* and/or *Verticillium dahliae*). Finally, important varieties for European countries (including local varieties well adapted to a particular country) were also included in the collection.

For raspberry, this project allowed to initiate the collection of data on genetic resources available in Europe, to draw a list of passport data and descriptors and to characterise collections using these criteria. In contrast to strawberries no data base was established for raspberries because the objective of this project was to initiate the study of diversity of available collections.

### Communication value

A Genetic Resources Network has been set up by 10 partners of the project to maintain their collections.

For strawberry, this network lists a total of 790 genotypes of the cultivated strawberry which are located in one or several conservation sites of the project. This network is accessible via <https://www.bordeaux.inra.fr/genberry/>. Part of these varieties was maintained as *in vitro* culture.

Table 2 | Overview of varieties and genotypes (plants without names) of the cultivated strawberry (excluded wild species of *Fragaria*) maintained by the partners in collections

Partner's N° & name	Number of varieties
1 CRA-FRF, IT	232
2 UNIVPM, IT	27
3 INSAD, PL	196
4 LIH, LH	94
5 CIREF, FR	157
6 JKI, GE	279
8 IFAPA, SP	289
9 FRIP, RO	113

This represents a total of 1 387 individuals from which 1 228 were included in the database.

For raspberry, 90 varieties were maintained by the partners.

## More information

### Project details

The project was implemented by ten partners in the following eight EU Member States: Italy, Spain, France, United Kingdom, Germany, Poland, Lithuania and Romania.

## Links

### The Genberry portal

More information on the achievements, as well as the contact persons of the different partners, can be found at: <https://www.bordeaux.inra.fr/genberry/pages/sum.htm>

### The Genberry database for strawberry

For cultivated strawberry, a database was created and is accessible to the public at: <http://www.bordeaux.inra.fr/eustrawberrydb/> and contains 1 017 accessions (one accession represents a variety observed in one location). These accessions are physically represented by 1 228 individuals, where each one is represented by 2 to 10 plants, located in pots or in container, and is physically located in one of the conservation sites. For the cultivated strawberry, 8 conservation sites located in seven countries were included in the study (see Table 2).

Primary descriptors, fruit descriptors and passport data were mandatory, secondary descriptors were recorded (see section Characterisation of the collections). Molecular markers were recorded in three locations, France, Italy and Spain.

The core element of the GenBerry database is the ACCESSION (variety and genotype observed in one location). The accession can be represented by one or several INDIVIDUALS (entity which was observed) physically located in a conservation site.

There were three different categories of descriptors: the standardized FAO/IPGRI Multicrop Passport Descriptors, the phenotypic traits descriptors and molecular descriptors. These descriptors were configured by the administrator of the database. The administrator can make also future changes, (ie. add new descriptors).

This database could be used as model for a raspberry database.

Portal of the GENBERRY strawberry database:  
<http://www.bordeaux.inra.fr/eustrawberrydb/>

## Publications from partners

Castillo, N.R.F., Reed, B.M., Graham, J., Fernández-Fernández, F. & Bassil, N.V. 2010. Microsatellite markers for raspberry and blackberry. *Journal of the American Society for Horticultural Science* 135, 271-278.

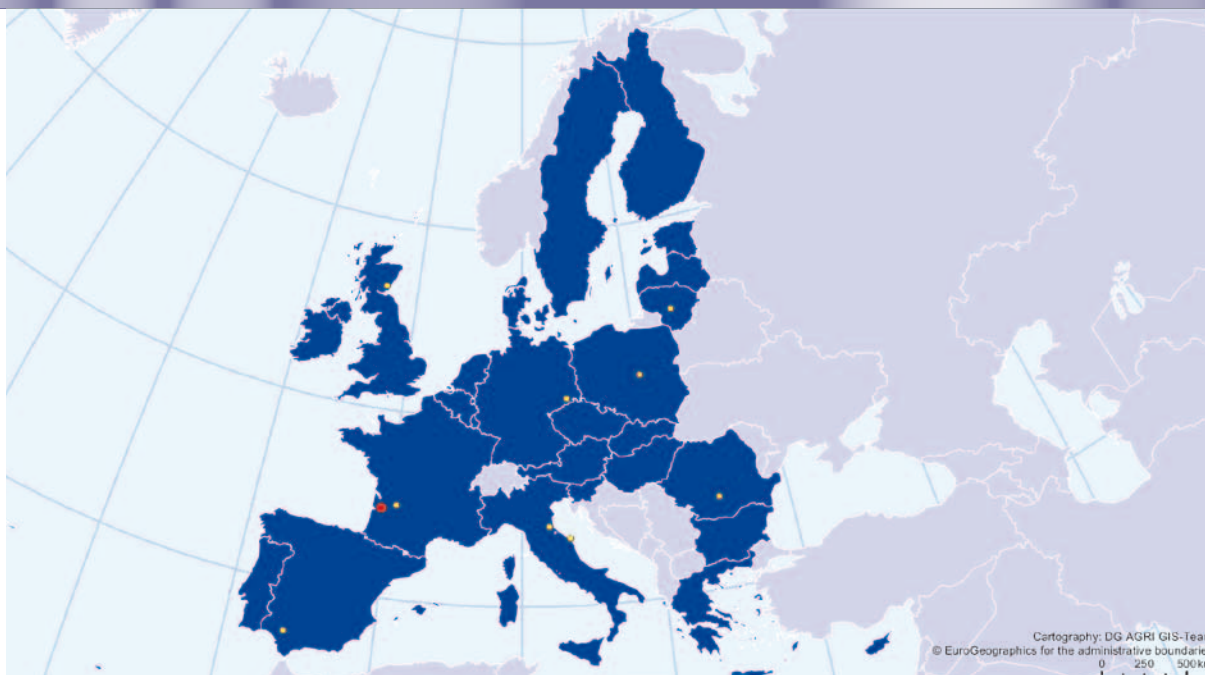
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Horvath A, Sánchez Sevilla JF, Punelli F, Sesmero Carrasco R, Leone A, Höfer M, Chartier P, Balsemin E., Barreneche T, Denoyes B. 2011. Structured diversity in octoploid strawberry cultivars highlights the importance of the old European germplasm. *Annals of Applied Biology* doi:10.1111/j.1744-7348.2011.00503.x.

Jęcz T, Korbin M. 2010. Inoculation of micropropagated plants with wounded roots as a tool for precise distinguishing strawberry genotypes tolerant and susceptible to *Verticillium* wilt disease. *Phytopathologia* 58: 33-42

Masny A., Zurawicz E. 2009. Porazenie wybranych odmian truskawki (*Fragaria x ananassa*) przez *Verticillium dahliae* (in Polish) (Plant infection of strawberry cultivars (*Fragaria x ananassa*) by *Verticillium dahliae*). *Zeszyty Problemowe Postępów Nauk Rolniczych, Polska Akademia Nauk (Advances of Agricultural Sciences – Problem Issues, Polish Academy of Sciences)*, vol. 539 (2): 483-490 (scientific paper).



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Final meeting of  
the GenBerry project  
in INRA – Bordeaux





## Garlic and others

Vegetative Allium, Europe's Core Collection, safe and sound

The Garlic and Shallot action integrated substantial initial steps to build up a core collection, contributed to the cryopreservation and virus elimination of well-characterized material, cryopreserved genebank collection and improved collaboration and consolidated the knowledge about the diversity of garlic and shallot in Europe.

### Project details

Duration	48 months
Start Date	01/04/2007
End Date	31/03/2011
Budget Total Cost	1 089 000 €
Budget EU Co-funding	544 500 €
Actual EU Co-funding	531 347.48€
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## Background

The crops and the threats they face

### Garlic

Garlic is a multipurpose crop of high importance. It is used as vegetable, spice and in increasing extent, also as medicinal plant (Koch and Lawson, 1996). The production of garlic worldwide is 22.28 million t (2009 – FAOSTAT), only 773 209 t of it in Europe (3.47 %), although Europe maintains the highest diversity of this crop. Garlic production has a long tradition, reports on its culture date back to the antique period (Rabinowich and Currah, 2002). Spreading out from its centre of origin in Central Asia, the introduction into Europe in ancient times led to a very high diversity of this crop, which is caused by the high extent of geographic diversity on this continent and many different cultures and traditions in its populations. This is reflected by the existence of different subgroups in this species, which are termed by many specific folk names in the various countries.

As an example, how the infraspecific grouping of garlic corresponds to its phylogeny, the bolting behaviour of the plants is described here. It is thought that garlic, during the history of its cultivation, lost gradually its generative reproduction strategy by permanent positive selection of the vegetatively most productive plants which are clearly those with smaller or no inflorescence stalk.

The inflorescence itself changed from structures with flowers and many small bulbils to a lower number of larger bulbils accompanied by total loss of flowers. Then, the stalk shortened more and more, ending finally in an inclusion of the inflorescence into the bulb. The bulbils appeared more and more clove-like. The resulting structure is then an irregular compound bulb with no separable inflorescences at all. One of the intermediate types of this evolutionary line is forming even bulbils in several, more than one, levels of the stalk.



At present, this diversity is extremely endangered by invading low-price garlic produced by some dominating countries. The FAO statistics present these figures clearly. The highest production is in China and India which dominate the world production by 80.64% and 4.80%, respectively. Europe is faced by the danger to lose its diversity due to reduction in income from trading the own material (Anonymous, 1998). This is a serious justification to protect and safe Europe's high genetic diversity by most appropriate methods. The danger of a worldwide production of only some types within a crop species, the monoculture, has been experienced in the history already several times as, e.g., in potato and maize. A safe bank of most representative garlic germplasm is an essential tool to counteract this danger.

### Shallot

Shallot, botanically representing the vegetatively propagated part of the species onion, has also high impact as vegetable and spice worldwide. The world production is 3.74 million t, production in Europe 355 824 t corresponding to 9.51 %. Though not so extremely, the endangerment of shallot's germplasm is similar to that of garlic, the market is dominated by such countries like China (23.72%) and Japan (15.24% of the world production, respectively – Figures given for 2009 by FAOSTAT for onion [incl. shallots], green). Due to the smaller production scale in comparison to garlic, also the state of research is behind that for garlic. This is the reason for the limitation of this project to characterization only. The well-characterized European shallot Core collection is so far maintained in de-centralized way by the various partners as a field collection. But it will undergo the AEGIS designation process like it is envisaged for other crops in the AEGIS process as well. Holding a well-structured core collection in permanent maintenance, its introduction into the activities of cryopreservation and virus elimination is well-prepared and easy to implement, as soon as the techniques for shallot will be, in future, at a comparable stage to garlic today.

Intraspecific groups of garlic and their bolting characters

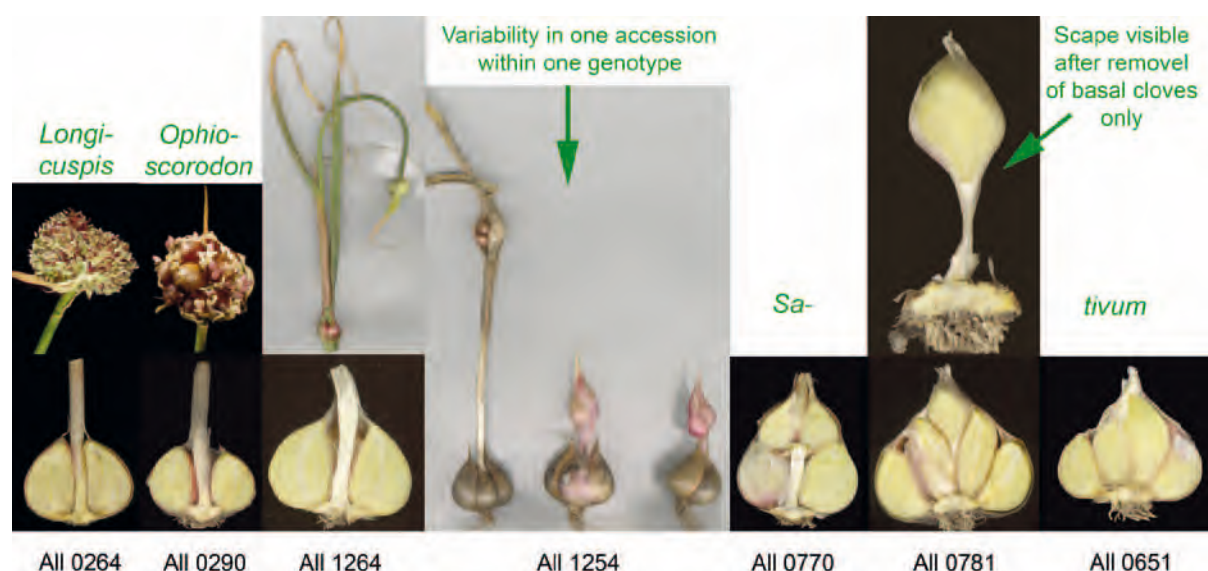
A part of the garlic core collection cultivated in the fields of the Gatersleben genebank

### Cryopreservation and virus elimination of well-characterized material – a prerequisite of future genebanking

Three aspects are important for maintaining germplasm for future: We must be sure about its identity, the material must be healthy and the material must be kept safely. The project integrated substantial initial steps to build up a core collection to which more and more material may be joined in future.

Characterization is done on various levels. It is not only to describe the material; it is also to exclude redundancy from the various individual collections. Morphological characters are recorded by using descriptors formulated in the IPGRI descriptor list (IPGRI et al., 2001). Comparing of passport data and considering past documents of material exchange between genebanks, a number of 81 duplicates were excluded from the collection. Finally AFLP markers were used to describe the diversity of the core collection. Passport and characterization data, infraspecific classification and images are provided to the public in a specific garlic and shallot database and the EURALLIVEG accession catalogue.

Vegetatively propagated plant collections are usually most endangered by accumulation of viruses. Five viruses and virus groups are present in garlic: onion yellow dwarf virus (OYDV), leek yellow stripe virus (LYSV), garlic common latent virus (GCLV), shallot latent virus (SLV), and the allexi virus group. They are differently harmful, and their elimination is also differently easy. Most important is to free the material from the first two viruses (OYDV and LYSV). Therefore, focus was laid on them. Among the accessions of garlic forming the core collection 24 accessions are free of all five viruses. The development of virus-free plantlets is slow in the first phases. Thus, the main aim was



introduction of the method. It was successfully introduced and may be used also in future for new material.

Finally, cryopreservation is the method to store the valuable material (Keller 2002, 2005). For this the shoot tips of garlic, derived from bulbils or *in vitro* plants, were trimmed to small explants of about 1 mm in diameter, dehydrated by osmotically effective and glass-forming substances (cryoprotectants) and placed in tubes containing the cryoprotectant solutions. These tubes were then quickly transferred into liquid nitrogen and stored in cryo-containers. A representative number of explants were rewarmed as control samples shortly after that in order to record the regeneration ability of the respective plant material.

### The cryopreserved genebank collection – the best way to maintain the genetic diversity of garlic and shallot

An integrated system of germplasm safety storage was urgently needed in order to protect the endangered material (Keller and Senula, 2003). Because of the very expensive field culture of vegetatively propagated crops, such a germplasm bank needs to be based on cost-efficient methods as well as high characterization and sanitary standards. At the same time, it connects a certain degree of centralization with a multi-local safety duplication system, which allows the access to the whole collection also after damage, destruction or closure of one storage site. This is provided by the Tripartite Cryopreservation Genebank, which is the main outcome of the present project. This collection is closely embedded into the European germplasm integration policy which is explained in the document of the European AEGIS system, for which *Allium* was one of the model crops in the first period.

The elimination of duplicates is thought for the Tripartite Cryobank only, which will be labelled as AEGIS collection. It will, however, not touch any interests of the partner countries to

keep their own germplasm in their own countries for their own interests. However, the well structured and characterized germplasm, which forms the core of Europe's garlic diversity, will also be the core subject for all further protection measures.

Whereas the time limit and the power of the project will allow characterizing the whole germplasm of the participants, it is not the case for cryopreservation and virus elimination, because the time frame for these treatments is longer than the possible duration of any projects. Therefore, for these methods the most valuable part of the germplasm is envisaged forming a virus-free core-in-core collection. This part will be then the nucleation point for further activities using the management experience derived from this first step and aggregating all the next charges of germplasm to this primary core.

The resulting cryopreserved garlic collection was safety-duplicated between the cryo-genebanks of Czech Republic, Germany and Poland.

### Exploitation of the genebank material

Due to the above explained different state of the art in garlic and shallot, the exploitation is also on a different level. It will be completely possible in garlic, but it will also be drastically improved in shallot.

In garlic, better exploitation will be possible by a permanent holding of the germplasm in cryopreservation. As resulted from former research, the availability of cryopreserved germplasm is in a similar timeframe like germplasm disseminated in form of bulbils. This ensures access to all germplasm in a feasible manner. The main advantage of cryopreserved material is, that once held in cryopreservation, it will be recovered through *in vitro* culture and can be sent as *in vitro* sample, which facilitates extremely all mailing and transfer procedures, because the

Details of a small technical meeting and a training course



Cryopreservation tanks of the genebank at IPK and first regeneration stage of an explant after rewarming from cryopreservation (insert)





material has been separated completely from soil, thus, reducing all endangerments by soil-borne pathogens.

The highest exploitation advantage is, finally, the use of virus-free material from the core collection, because this enables the user to rely on certified material, fully usable without additional cleaning needs. As the project is designed to build up the fundament for future activities in the same direction, it will lay the background for a drastic improvement of the germplasm health and, insofar, its implementation will have impact also in the further germplasm development strategy.

### Communicating value

The EURALLIVEG project improved collaboration and consolidated the knowledge about the diversity of garlic and shallot in Europe. Through the implementation and further maintenance of the Tripartite Garlic Collection stored in liquid nitrogen a fundament was created which can be enlarged in further time, also by joining of other European collections. The collection will be presented for common use in the EURALLIVEG catalogue and on the image database of the EURALLIVEG Garlic and Shallot Core Collection:

[http://www.ipk-gatersleben.de/databases/genetic\\_resources/gsc](http://www.ipk-gatersleben.de/databases/genetic_resources/gsc)

This website, which was implemented by the Bioinformatics and Information Technology Group together with the Genebank Documentation and In vitro Storage and Cryopreservation groups of IPK, containing the IPK priority accessions, will include all the material of the EURALLIVEG collection in near future. It will serve as the basic data source for all those that are interested to find out material with special characters for further utilization. A manuscript about this database has been submitted (Colmsee et al., submitted). Furthermore, the website of the EURALLIVEG project will be maintained for the next 10 years, in which all information on the material and its preservation will be available for all users.

Young inflorescence of bolting garlic and longitudinal cut of violet-flesh shallot



Further publications are in press or will be prepared about the results of the project.

The experience gained in the EURALLIVEG project has been and will be further discussed in the *Allium* Working Group of the Vegetable Network within the European Cooperative Programme of Plant Genetic resources ECPGR. The EURALLIVEG label will be attached to the accessions in the European *Allium* Database.

### Links

This section lets you know how to find out more about the 'outputs' of the EURALLIVEG project.

### The genetic resources

If you want to know more about preservation methods of garlic and shallot, we will be glad to hear from you and give you more information. For this, please, contact one of the email addresses given above in the partners' list or look at our websites.

### The database

The main advantage will be for both crops that, with a finally updated and complete database for both crops, the users worldwide, but especially in Europe will have immediately access to the information about the distribution of the desired germplasm within the partners' countries, its passport and characterization data, without getting confused by undesired redundancy. Another product facilitating exploitation is a much better knowledge about the genetic structure of both crops allowing identification of gaps for future germplasm collecting activities, for research on the crops and for further breeding activities.

<http://euralliveg.ipk-gatersleben.de/>

[http://www.ipk-gatersleben.de/databases/genetic\\_resources/gsc](http://www.ipk-gatersleben.de/databases/genetic_resources/gsc)

### List of publications

We are writing technical, scientific and policy reports and publications. Publications that were already available at the time of writing are listed below.

Altieri L., 2009. Aspetti diagnostici e risanamento di una collezione di aglio. Atti del Convegno Ricerca, Innovazione e Sviluppo nelle Biotecnologie Agro-alimentari. pp. 110-111.

Altieri L., I. Camele & V. Miccolis. 2010. Virosi e fitoplasmosi dell'aglio (*Allium* spp.) e possibilità di risanamento. Ricerca di base e innovazione nelle biotecnologie agro-alimentari: il corso di Dottorato di Ricerca in Biologia e Biotecnologie dell'Università degli Studi della Basilicata. pp. 88-94.

Altieri L., I. Camele & V. Miccolis. 2010. Aspetti diagnostici del risanamento da virus in accessioni di aglio locale. Atti del Convegno 'Orticoltura di qualità per un mercato in evoluzione', Foggia 30 April 39, 2009. Italus Hortus, 17:54-55.

Altieri L., I. Camele, V. Miccolis & G.L. Rana. 2010. Indagini virologiche su una collezione di aglio mediante ELISA e RT-PCR. Atti VIII Convegno Nazionale su 'La Biodiversità – Risorsa per Sistemi Multifunzionali', Lecce, 21-23 April, 21-23, 2008. Arti Grafiche Favia Modugno (BA). pp. 30-31.

Altieri, L. & V. Miccolis. 2011. Aspetti diagnostici e risanamento di una collezione di aglio. *Acta Italus Hortus* 1:90-91.

Keller, E. R. J. 2007. Cryopreservation for Maintenance of Plant Germplasm in Germany. *Advances in Horticultural Sciences* 21:228-231.

Keller E. R. J., A. Kaczmarczyk & K.J. Dehmer 2007. Proc. 18th EUCARPIA Genetic Resources Section Meeting, 23-26 May, 2007, Piešťany, Slovak Republic, p 39.

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Keller E.R.J., C. Zanke, H. Stavělková, J. Zámečník, T. Kotlińska, V. Miccolis, C. Kik, F. Esnault, A. Kolodinska, D. Fischer & D Astley. 2007. First Steps Of Integrating Europe's Genetic Resources In Garlic And Shallot In A New Genres Project. 5th International ISHS Symposium on Edible Alliaceae (ISEA), October 29-31, 2007. De Meerpaal, Dronten, The Netherlands. *Acta Horticulture* (in press).

Keller, E.R.J. & C. Zanke 2007. EURALLIVEG Project: 'Vegetative *Allium*, Europe's Core Collection, safe & sound'. *Bioversity Newsletter Europe* 34:17.

Kotlińska T. & M. Olas. 2009. *Allium* genetic resources in Poland. Report of a Vegetables Network. Second Meeting, 26-28 June 2007, Olomouc, Czech Republic. Bioversity International, Rome, Italy. pp. 59-64.

Final meeting of the partners in Prague



Kotlińska T. & M. Olas-Sochacka. 2010. Zróżnicowanie cech morfologicznych zasobów genetycznych czosnku pospolitego (*Allium sativum* L.) nie tworzącego pędów kwiatostanowych [Variability of morphological traits of non-bolting garlic (*Allium sativum* L.) germplasm]. *Nowości Warzywnicze* [Vegetable Crops News] 50:45-62.

Miccolis V., L. Altieri & V. Candido. 2010. EURALLIVEG: un progetto europeo per la valorizzazione dell'aglio e dello scalogno. Atti VIII Convegno Nazionale su 'La Biodiversità – Risorsa per Sistemi Multifunzionali', Lecce, April, 21-23, 2008. Arti Grafiche Favia Modugno (BA). pp. 275-277.

Olas M. & T. Kotlińska. 2010. Przechowywanie zasobów genowych czosnku pospolitego (*Allium sativum* L.) w ciekłym azocie [Long term storage of garlic (*Allium sativum* L.) germplasm in liquid nitrogen]. *Zeszyty Problemowe Postępów Nauk Rolniczych* [Advances of Agricultural Sciences Problem Issues] 555:133-13.

Olas-Sochacka M. & T. Kotlińska. 2010. Krioprezervacja zasobów genetycznych czosnku pospolitego (*Allium sativum* L.) tworzącego pędy kwiatostanowe [Cryopreservation of genetic resources of bolting garlic (*Allium sativum* L.). *Nowości Warzywnicze* [Vegetable Crops News] 50:69-74.

Zanke, C.D., E.R.J. Keller, J. Zámečník, T. Kotlińska & M. Olas. 2009. Cryopreservation of vegetative garlic for the establishment of a European Core Collection. *Acta Horticulturae* (in press).

## Other publications and links

For other publications and links, see the project website <http://euralliveg.ipk-gatersleben.de/>

Other actions co-funded by the European Commission's Community Programme on the conservation, characterisation, collection and utilisation of genetic resources in agriculture can be found at:

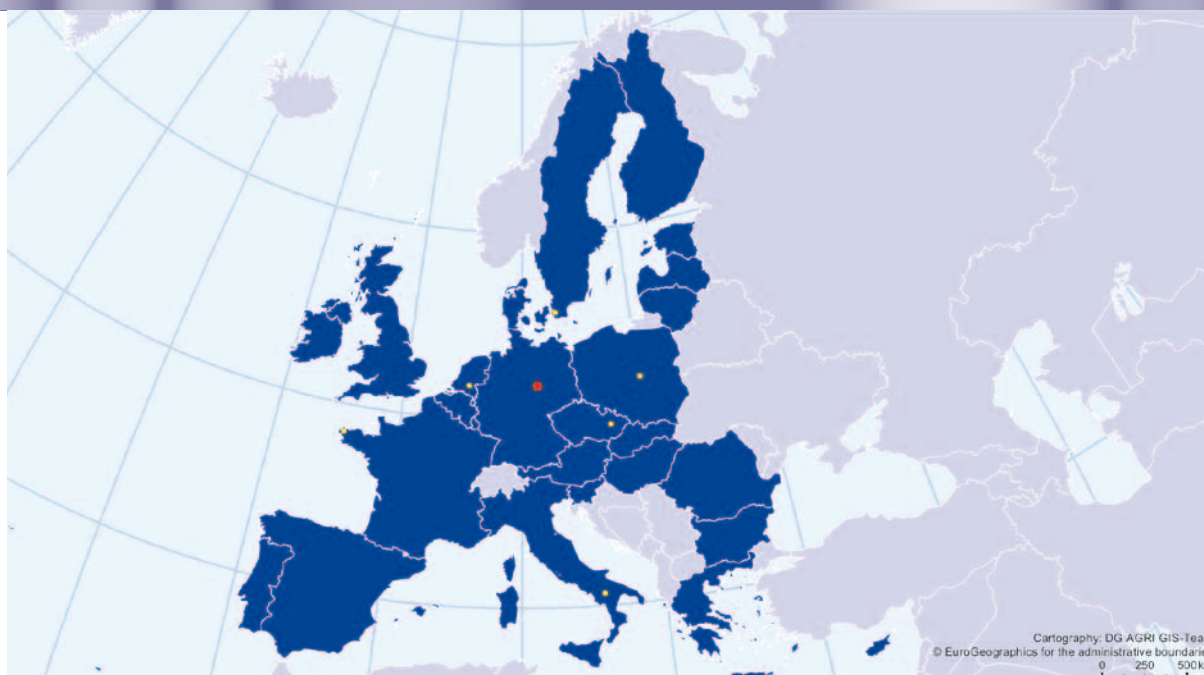
[http://ec.europa.eu/agriculture/envir/biodiv/genres/index\\_en.htm](http://ec.europa.eu/agriculture/envir/biodiv/genres/index_en.htm)

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FAOSTAT. Website <http://faostat.fao.org/default.aspx> Website contacted 24 June 2011



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## Artichokes

### European genetic resources of *Cynara* spp

The artichokes action collected, conserved, and characterised most of the European germplasm of globe artichoke, as well as wild and cultivated cardoon present in germplasm collections. In total, 229 globe artichokes, 85 wild cardoons and 82 cultivated cardoons accessions have been conserved. The action's data were collected in a shared database which contains more than 200 accessions with, in some cases, related maps and photos.

### Project details

Duration	48 months
Start Date	01/07/2007
End Date	30/06/2011
Budget Total Cost	1 971 760 €
Budget EU Co-funding	906 419 €
Actual EU Co-funding	869 113.86€
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### Background

The *Cynara* genera includes the wild cardoon (*Cynara cardunculus* var. *Sylvestris* (Lamk) Fiori), the globe artichoke (*Cynara cardunculus* var. *Scolymus* (L.) Fiori) and the cultivated cardoon (*Cynara cardunculus* var. *Altilis* DC) (Basnizki and Zohary 1994; Rottenberg and Zohary 1996; Rottenberg and Zohary 2005; Sonnante et al. 2007). The wild cardoon is the ancestor of the two cultivated subspecies, i.e. globe artichoke and cultivated cardoon. All three subspecies form fully fertile hybrids, although genetic studies of wild cardoon have shown them to be more closely related to the cultivated cardoon than to the globe artichoke (Sonnante et al. 2002, 2004, 2007).

### The wild cardoon

Wild cardoon belongs to the Asteraceae family, as do the Jerusalem artichoke and the sunflower. *C. cardunculus* is diploid ( $2n=34$ ) and has its origins in the Mediterranean basin, ranging from Cyprus [in the east] to Portugal and the Canary Islands [in the west]. The wild plant, a perennial, is found between 0-1100m above sea level, in arid, uncultivated areas, pastures and roadsides.

### The cultivated cardoon

The cultivated cardoon, a perennial composite, is native of Southern Europe. It grows up to 2 m in height, and has large pinnate leaves, greyish-green above, almost white beneath. In some varieties there is a yellow or brown spine, often over 1 cm long, in the angle of the leaf divisions. It is thought that Arabs probably played an important role in the diffusion of this crop, as in the case of other plants like eggplants and spinach; they had a particular interest in horticultural and garden crops (Idrisi 2005). The origin of the cultivated cardoon is therefore often associated with Arabs, who were prevalent in the Southern Mediterranean during medieval times. The cultivated cardoon is mainly used as a food for its edible leaf stems, but also as a source of biomass and milk-clotting.

### The globe artichoke

Globe artichoke is an allogamous and entomophilous plant, native from Southern Europe around the Mediterranean basin and North-Western Africa. Southern Italy and Sicily have been recently considered as the origin of its domestication (Pignone and Sonnante 2004).

The economic use of the globe artichoke includes mainly the consumption of the edible immature flower heads, eaten as a fresh, frozen or canned delicacy. Furthermore, the use of the plant is not restricted to its edible part, but also to the leaves, stem and roots that are utilised as sources of: (i) forage for live-stock; (ii) extraction of inulin; (iii) feedstock for the extraction of secondary metabolites; (iv) lignocellulosic biomass for energy and paper pulp; (v) seed oil for biodiesel fuel production (Raccuia

and Melilli 2004); and (vi) alcoholic beverages. Since ancient times, the leaves have also been widely used as hepatoprotectors and choleric agents in herbal medicine.

Production is dominated by Italy (50 000 ha with an annual harvest of 470 000 t), followed by Spain (189 000 t), Morocco (54 000 t), France (50 000 t), and USA (38 000 t). Since 1992, China (59 000 t) has emerged as a growing producer (FAOSTAT 2010) and also countries such as Peru and Argentina set up major artichoke crop productions.

In Italy, globe artichoke occupies the third place in terms of cultivated area, after tomato and potato. Its production is important for the economy and social development in a number of districts (mainly Apulia, Sicily, and Sardinia). In Spain, the globe artichoke growing districts are located around Alicante, Murcia, Valencia, Andalusia, and Catalonia. In France, the globe artichoke is grown mainly in Brittany but some local production is also seen in Southern France (Pyrénées Orientales).

In spite of its economic importance artichoke has not been extensively studied. International market standardization leads to concentration on a small subset of varieties and is a major threat to the conservation of artichoke genetic diversity. The main threats to the *Cynara* genetic resources are the low number of cultivated varieties, compared to the large diversity present originally, which is an index of genetic erosion. In addition, there is a lack of clarity in the nomenclature of *Cynara* germplasm due to years of cultivation in various geographical sites resulting in each cultivar named according to the place where it was cultivated. It is therefore unclear whether the varieties are genetically distinct or simply displaying a high degree of phenotypic plasticity.

### Project objectives and activities

The project aims to collect, conserve, characterize, and utilize the potential *Cynara* diversity. Moreover, an aim was the creation of a web site and online database in order to make the

information widely accessible. The project was divided into 5 work packages (WP) which focused on different objectives: (i) rationalize and enlarge the present germplasm collection of *Cynara* (WP1), (ii) conserve germplasm, adopting the different procedures both *in situ* and *ex situ* (WP2), (iii) characterize the *Cynara*'s germplasm (morphologically, bio-chemically, molecularly and for disease resistance) and standardize characterization procedures (WP3), (iv) register new varieties (WP4), (v) establish an interactive web-based documentation catalogue (WP4), and (vi) promote and protect the *Cynara* utilization (WP5). Clones (identical plants vegetatively propagated) registration into the national varietal register(s) does increase knowledge of farmers producing well-recognized varieties with known nutritional value.

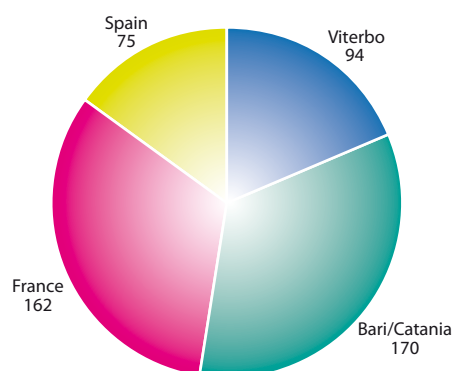
The conservation and use of *Cynara* spp. germplasm is based on international conventions and treaties, such as the Convention on Biodiversity (CBD), the Global Plan of Action of the Food and Agriculture Organization for Plant Genetic Resources for Food and Agriculture (FAO's GPA for PGRFA), and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA).

### Communicating value

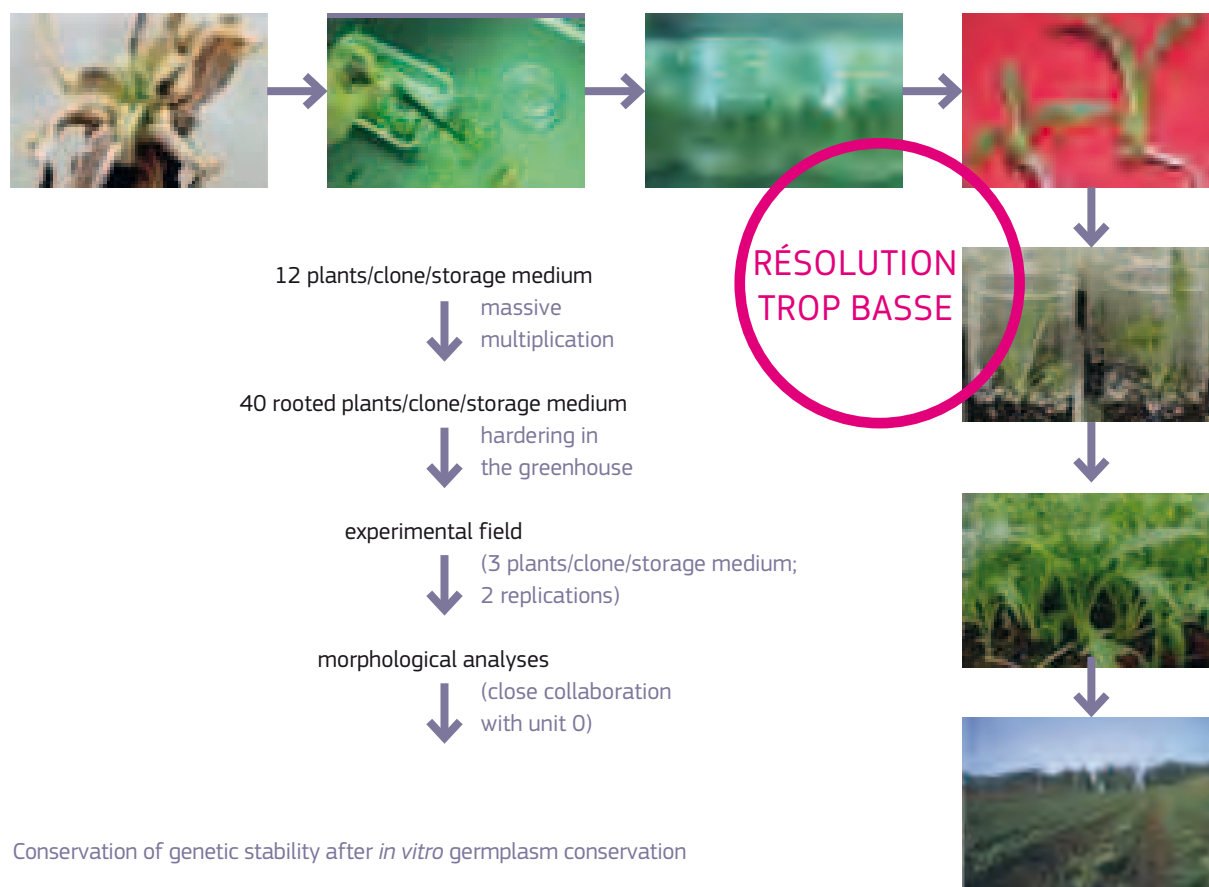
The CYNARES project collected conserved and characterized most of the European Germplasm of globe artichoke and wild and cultivated cardoon present in previous germplasm collections as well as material obtained during field collection missions. All the project information and results are available at the web site [www.cynares.com](http://www.cynares.com) created during the project.

In total, 229 globe artichoke lines, 19 globe artichoke Hybrids, 82 cultivated cardoon and 85 wild cardoon accessions have been conserved at the partners' institutions. Some of the collected accessions carrying the same name have been identified as different material, as well as some accessions with different names turned out to be similar.

Wild cardoon (*Cynara cardunculus* var. *Sylvestris* (Lamk) Fiori)



Germplasm Distribution among Partners

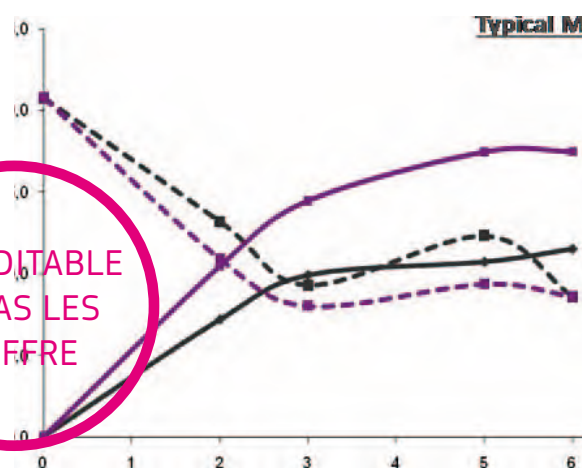




## Germplasm conservation

Germplasm conservation was achieved through different conservation strategies: (i) Living collections in the field (i.e. field gene bank) integrated with seed collections, where applicable; (ii) *In vitro* (in tube) conservation of selected genotypes; and (iii) Cynara DNA bank where DNA of each accession was conserved at the Partner 2 (CNR-IGV, Bari, Italy).

The *in vitro* conservation technique of selected genotypes was achieved either by short-term preservation (micro propagation) or medium-term conservation (slow growth storage). The *in vitro* conservation was also tested by molecular markers in order to quantify the somaclonal variation occurred during *in vitro* conservation, moreover several media were tested in order to improve *in vitro* efficiency and to reduce its costs.



Accessions	No.	Plants anal. (no.)	reaction to fungus	Trans-planted plants (no.)
<b>Cultivated cardoon</b>				
Pleinblanc	2	34	S	-
Nizza	3	27	S	-
Gig.inerme	4	89	S	-
Belgio	3	44	S	-
259fog. P.	3	70	S	-
Gigante	5	95	S	-
C. altilis	3	77	S	-
Madrid bis	4	89	S	-
Ignoto	3	36	S	-
Madrid	4	78	MR	12
V. Romagna	2	35	S	-
<b>Wild cardoon</b>				
Siéna	4	96	MR	20
C. silvestris	4	118	S	-
Cardone 1	5	35	R	35
Cardone 2	4	49	R	49

## Germplasm characterization

Most of the conserved germplasm was **characterized** by different methods:

- molecular method**, by analysing the DNA with different molecular markers. This gives information of the genetic diversity regardless of the environmental situation.
- morphological method**, utilizing different morphological traits in order to obtained a description for each accession with the most important characteristics. It is also possible to compare accessions and to relate them to each other.
- biochemical method** both as chemical compound and post-harvest evaluation.
- method to analyse **disease resistance** to *Verticillium dahlia* (fungus disease). Plants were infected to detect their resistance to verticillium.

## Cynares charter

Finally, the CYNARES Charter for the preservation of the *Cynara* genetic biodiversity had been written down and subscribed by the network group which is now composed by GEVES (France), IGV-CNR (Italy), ENEA (Italy), ITGA (Spain) and UPCT (Spain) (For more details see point 3.2). CYNARES Charter describes the rules and the missions of each of the partners within the network to manage the core collections at regional, national and international levels. Additional organisations can join the network by submitting applications to any of the present network partners.

## Links

All information regarding the project and its results can be found at: [www.cynares.com](http://www.cynares.com)

## The database

By the end of the project, the database – contained 209 accessions, divided in 155 (92 from Italy, 35 from Spain, and 28 from France) for globe artichoke and 54 (10 from Italy, 39 from Spain, and 5 from France) for wild and cultivated cardoon. Pictures and, in some cases also maps, related to accessions have been loaded into the database. All the accessions characteristics are available in the database.

Every registered user can continue to add accessions, and thereby improves the database further.

The database is accessible on the Cynares web site and is an important tool to search for germplasm with particular characteristics. The database is also published in a booklet which could be download at <http://www.cynares.com/interna.asp?idPag=102>

Examples of the accessions are listed in the CYNARES DATABASE.



Post harvest processing:  
cutting, washing and warm  
lemon juice bath treatment  
to reduce oxidation

### List of publications made in the context of the CYNARES project

The CYNARES project produced:

- 16 papers on international journals;
- 32 papers published in national or international congresses proceedings;
- 25 oral or poster presented actions at national or international congresses;
- 13 articles presented into books;
- 1 document for the UPOV (International Union for the Protection of new Varieties of Plants) meeting;
- 14 papers are ready for publication;
- additional papers are being prepared for publication.

The list of publications is available at <http://www.cynares.com/interna.asp?idPag=87>

Picture of the fourth meeting



### Other publications and links

More information about the European Commission's Community Programme on the conservation, characterisation, collection and utilisation of genetic resources in agriculture can be found at: [http://ec.europa.eu/agriculture/envir/biodiv/genres/index\\_en.htm](http://ec.europa.eu/agriculture/envir/biodiv/genres/index_en.htm)

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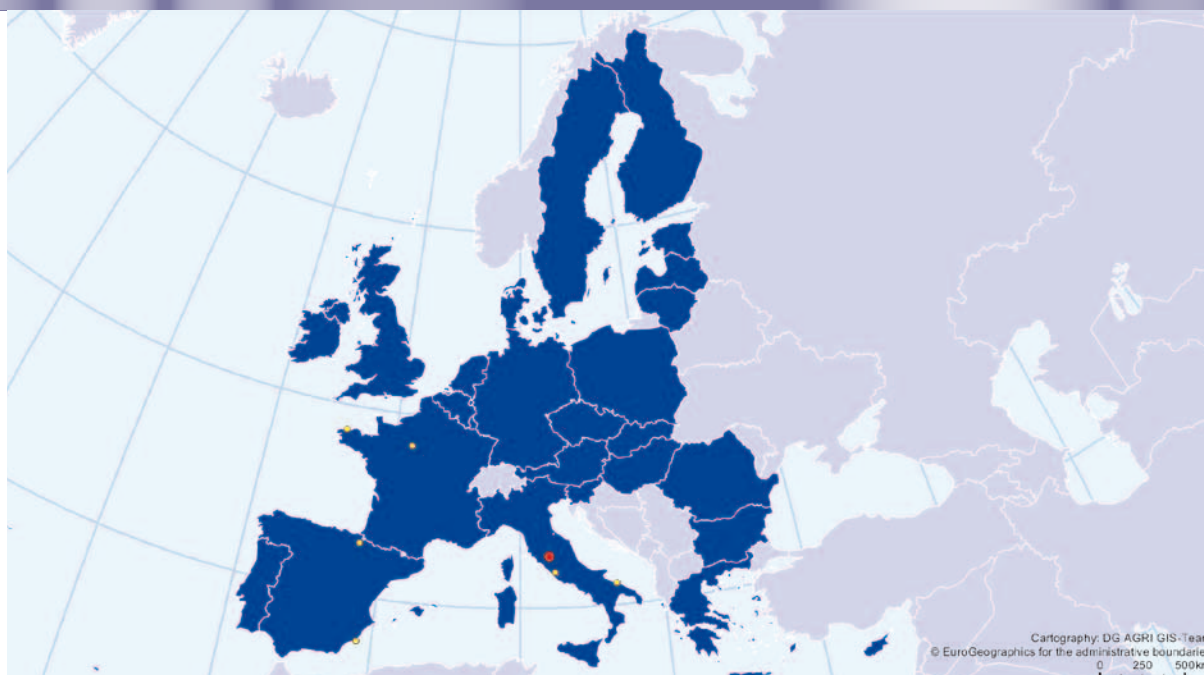
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## Nuts and almonds

### Safeguard of hazelnut and almond genetic resources

The Hazelnuts and Almonds action studied hazelnut and almond genetic resources across 6 Member States, enhanced to retrieve and safeguard the acquired traditional knowledge of tree nuts and contributed to their conservation. A core collection was designed offering to the breeders an opportunity to work with accessions evaluated on traits of economic importance.

### Project details

<b>Duration</b>	36 months
<b>Start Date</b>	01/04/2007
<b>End Date</b>	30/09/2010
<b>Budget Total Cost</b>	1 120 610 €
<b>Budget EU Co-funding</b>	557 000 €
<b>Actual EU Co-funding</b>	531 143.65€
<b>Coordinator</b>	Agenzia Nazionale per le Nuove Tecnologie, l'Energia e lo Sviluppo Economico Sostenibile (ENEA)
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<b>E-mail</b>	loretta.bacchetta@casaccia.enea.it
<b>Coordinator's Website</b>	<a href="http://safenut.casaccia.enea.it">http://safenut.casaccia.enea.it</a>

### Background

Among dried fruit, almond (*Prunus dulci*) and hazelnut (*Corylus avellana*) have a relevant economic importance. In the last five years the world production of nuts has increased more than 20 %. Turkey and the United States are the main suppliers, respectively for hazelnut and almond, producing more than 80 % of the global production. Moreover, emerging markets such as China, India, the United Arab Emirates and Australia have increased their trade by more than 80 % in the last 5 years.

At the European level, Spain is the largest almond producer, followed by Italy and Greece. The Spanish production it is not expected to increase significantly in the long term. Based on the EU-27 Tree Nuts Annual 2010, Australia will surpass Spain by 2015 to become the second world largest almond producer. This situation is favoured by the decline in the EU agricultural support programs and mainly by the strong competition from the Californian almond production traded at low prices. The abandonment of plantations or a shifting towards more profitable crops is a consequence. Regarding hazelnuts, Italy is the second largest producer in the world just before the U.S. and behind Turkey whose huge supply largely affects the world market and prices.

As for the internal nuts market in Europe, the per capita consumption of nuts in Greece (17 Kg/year) is the highest in Europe – and one of the highest in the world – followed by Spain and Italy. The high consumption is due to the importance of the two crops in the Mediterranean diet. Nuts are the best source of proteins; they are rich in fibres, phytonutrients, antioxidants such as Vitamin E and are rich in polyunsaturated fats. In the past two decades, several biochemical and clinical studies have provided consistent evidence of the healthy properties of nuts. The EU domestic production supplies less than 40 % of the local demand and the rest is imported by Turkey and USA.

From this analysis some critical issues emerge at the European level:

- 1) the abandonment, particularly for almond orchards, is evident in many European Countries;
- 2) the problem of the decreasing number of cultivated varieties (genetic erosion);
- 3) the lower value of the imported supplies which affect the quality, the taste and the nutritional properties of the European traditional products. This issue could be worsen by the recent increase of the maximum level of aflatoxin in nuts based on the recent regulation of the Commission.

Another important issue to be considered is the social value and the role of hazelnuts and almonds in sustainable traditional agricultural systems: these crops are strongly intertwined with the territory and people who cultivated them for millennia. About 5 000 years before Christ a Chinese manuscript highlighted the medical properties of *Corylus avellana*, while Catone (234-149 a.C), the most ancient Latin writer, spurred

the cultivation of this specie indicated as '*...nucēs, calvas, avelanas, praenestinas et graeca*'. Almonds was known by Romans as 'Greek nuts'.

In conclusion, as stated in the Commission report on nut sector (SEC 2002 797): 'nut production plays a fundamental part in protecting and maintaining the environmental, social and rural balance in many regions'. These aspects are key factors in favouring sustainability in rural areas according to a multifunctional concept of agriculture.

Recovery and conservation of various types of almonds and hazelnuts represent a resource for future generations: people who want to benefit from high-quality products, will need to turn to a life-style more respectful of the environment by safeguarding traditional knowledge.

On these premises, the European SAFENUT Action, elaborated within the Council Regulation (EC) N° 870/2004 AGRI GEN RES, represents a resourceful strategy for re-organizing and sharing, in a more efficient manner, the hazelnut and almond genetic resources by upgrading the knowledge on their value as well as the precious cultural meaning related to traditional and historical uses of people who conserved and, in some cases, improved them.

### The preservation of almonds and hazelnuts: how the SAFENUT Project meets the problem

The progressive impoverishment of agro-biodiversity, due to renowned cultivars, has determined a reduction of local varieties that were selected over millennia in traditional agricultural systems and that are now seriously endangered (2). Nowadays, in Italy for instance, the traditional almond crops are represented by only a few new varieties with unrecoverable losses of genotypes

which are appreciable for their organoleptic characteristics. In fact, improvement in almond cultivars for late blooming, high yield, adaptability to intensive agriculture have widely reduced the number of cultivated varieties. Although plant exchange and plant introduction have sporadically occurred for centuries, aimed efforts started only in 1920s. During the seventies, taking into account the concept of genetic erosion, surveys have been carried out and collections have been established often with different techniques and approaches. In some Countries, for instance, programmes promoted at Regional level have generated a proliferation of unknown small repository collections. The first step of the SAFENUT Action was the data acquisition on the *in situ* and *ex situ* European collections. The survey was performed in order to share information on the number and the kind of nut plants conserved in the partners' collections. A list of 209 and 58 selections of hazelnuts existing in 13 collections and a list of 180 almond cultivars present in 4 partner Countries were released, amending the spelling mistakes. Moreover the exploitation of 'ecotypes' present in low frequency, usually well adapted to the local conditions, represents a tool for cultural diversification preserving the greatest genetic variability. Many interesting tree nuts are conserved on farm, which means the maintenance of traditional crop varieties within traditional agricultural system where the farmer is one of the actors who creates and maintains the present diversity. In particular, organic farmers, and other farmers using methods that do not heavily rely on fertilisers and pesticides, require selected crops for their specific growing conditions. During the SAFENUT Project the survey was carried out in Italy, Slovenia, Spain and Greece in order to recover the on farm endangered cultivars: 88 new hazelnuts and 122 almond cultivars, confirmed by DNA analysis, were selected and evaluated. The following step for the re-organization of the genetic resources' conservation was the long term storage; the DNA bank was organized in Spain where more than 200 almond cultivars were maintained.

Hazelnut and Almond variability



### The importance of the knowledge of the almonds and hazelnuts traits: progresses in the SAFENUT Project.

The limited number of cultivars grown as monoculture over vast areas, get them highly vulnerable to the rapid spread of insects, pests, and pathogens. Plant breeders are therefore dependent on the diverse genes to continue developing new cultivars to keep ahead of such calamities. The same consideration is for the recent climatic change issues related to crops. Moreover, the knowledge of the tree nuts maintained in the collections, with a special attention to nutritional and nutraceutical aspects, meets the demand of the consumers towards high quality food, favouring new agro-industrial opportunities. During the SAFENUT Action, traditional hazelnuts and almonds were evaluated using harmonised morphological descriptors. Furthermore, the most important nutritional traits of nuts were considered and the fatty acids, mineral, protein and phenolic compounds contents were evaluated in traditional and valuable cultivars (3).

In addition, the lack of nursery activities or certified material for the propagation in the new orchards as well as the great number of varieties, have increased the chance of mistakes or caused some confusion among local populations. The consequence is a waste of human and financial resources for conservation and duplication of useless materials. In this regards, 305 hazelnut and 240 almond samples were evaluated by DNA analysis during the three year of the project, with the aim to verify the identity of the plants maintained in the European collections as well as the rescued ones (4, 5, 6). Moreover, two hundred and seventy five almond accessions were analysed for self-incompatibility genes: an important outcome for almond productivity. On the basis of these results, the identification of 'core collections', a selected and smaller group of plants representative of species' genetic diversity, has represented the final step. Designing a core collection involves an appropriate use of diversity, offering to the breeders an opportunity to work with a quite manageable number of accessions evaluated on traits of economic importance. This goal meets the crucial point stressed by the Commission: 'improved quality is one of the key factors in improving the international competitiveness of the tree nut sector' (Report Analysis of the nut sector, 2010).

### The SAFENUT Project and the safeguard of traditional knowledge from elder to young generation

By turning its attention on genetic resources as a pool of useful genes as well as gathering information on traditions and local uses, this project adds a plus value for future generations and for historical memory. The purpose is to describe genetic resources from different point of views: morphological, biochemical, molecular as well as ecological and traditional for people that have conserved them and, in same case, improved them.

The aim of this approach is to built a strong link between genetic resources and the eco-geographical areas they belong to.

The genetic resources represent the useful pool of genetic background utilized for different purposes in the breeding programme while containing a precious cultural meaning related to traditional and historical uses. The safeguard of the traditional memory is indispensable for the cultural heritage of future generations. Important implications are related to the recovery of local uses which can be potentially useful for novel agro industrial applications.

In order to recover the historical memory, the students of 11 European high schools have been involved through a questionnaire on the tree traits and use of the species in the diet in which specific questions concerned the students' parents and grand parents. This methodology allowed to collect information from a large platform of users: as a result, 2097 questionnaires were collected and elaborated; two booklets were published, one on the main results of the interviews [1] and the other on traditional recipes [2]. Besides, 75 farmers from partner Countries were involved in collecting data on traditional practices. A practical example was provided by the French partner who took 5 farmers on to use old endangered varieties for the renewal of orchards. A survey on the most important almond and hazelnut exhibitions at the European level was carried out and a publication was released with information on local and English languages.

In this frame, it was also looked at different ways of promoting the recovered endangered varieties in the different Country partners by analysing the crucial aspects for a common way to succeed.

### Communicating value

The SAFENUT Project has enabled us to study hazelnut and almond genetic resources across the Countries' partner, enhance

#### 'On-farm' conserved hazelnuts – Spain





to retrieve and safeguard the tree nuts traditional knowledge and contribute to a long term objective of conservation. Nevertheless, all this information would have a limited importance if not adequately disseminated. The purpose of communications is to increase the overall outputs of the project. The added value of communication can be found in reaching out to an identified target groups and make them feel important. It needs to look at making the relevant issues attractive enough to engage the audience. Information is about making things available, while communication is about making the audience understand the importance of it and the value it contains. Conscious of the strategic value of communication, a great effort and involvement was spent, particularly on the website: <http://safenut.casaccia.enea.it/>

In the light of the above, communicating is equally important, both with the experts' community and with the public. In the first case, the establishment of a database ([safenut.casaccia.enea.it/db](http://safenut.casaccia.enea.it/db)) – particularly in connection with other similar ones previously established – e.g. Prunus database, helps to build strong relationships and potential partnerships. In the second case, the aim was to reach the general public, besides stakeholders, through simple and direct articles. In particular, for this purpose, the SAFENUT project was linked to the RELATE (REsearch LABs for TEaching journalists – <http://relateproject.eu/>) project [3]. Funded by the European Union with the aim to bring scientists face to face with next generation journalists who will then 'relate' their experiences, producing balanced accounts of the benefits and impacts of various scientific fields, from which this same brochure benefited.

## More information

### Project details

The project started on 1 April 2007 and ended on 30 September 2010, following an extension of six months mainly due to the problems caused by the earthquake in Abruzzo which changed

the agenda for the chemical evaluation. ENEA, the Italian National Agency for New Technologies, Energy and Sustainable Economic Development, coordinated the Action, benefiting from the partnership of outstanding scientists from eleven organizations located in six European Member States – Italy, France, Spain, Greece, Slovenia, Portugal.

## Links

### The SAFENUT website

The SAFENUT web site (<http://safenut.casaccia.enea.it>) [4] has been constantly updated on the basis of the follow up of the project. It has also served the purpose of providing a window on events and news related to the topic of the project. The project activities are thus constantly reported and are made available at the public as well as syntheses of the technical reports. During the project, the website was also moved from a static HTML-only website, to a database-driven dynamic application. This improvement allowed the partners to include relevant information in the news section of the website by means of a user-friendly interface that easily allows also non-technical persons to create pages, photo galleries and news on the website. Therefore, the SAFENUT web site has represented a virtual place of interaction, exchange of information among partners as well as a tool to operate directly on the project that will help to communicate the work through the project life cycle and beyond.

### The SAFENUT Database

The management of plant genetic resources spans from collection and conservation of germplasm to its distribution and use. The development of a virtual germplasm collection using the standard descriptors makes efficient and timely the dissemination of germplasm information and therefore its utilization. The SAFENUT DB, web interface available at the address: [safenut.casaccia.enea.it/db](http://safenut.casaccia.enea.it/db) [5], was organised in order to



Almond and hazelnut flowers and fruits

provide users driven on-line interrogation of search-queries, across multi-trait data based on characteristics of hazelnuts and almonds with Photos and related documents.

### List of publications

We are writing technical and scientific reports and publications: Publications that were already available at the time of writing are listed in the below.

An article on the SAFENUT Project was published in the 'Parliament Magazine' [6]. These tools, which deal with affairs of the European Parliament, Commission, and Council, were useful to enlarge the knowledge on the SAFENUT Project at European level. A paper on the enhancement of local hazelnut traditional varieties by *in vitro* culture was published during the first year of the project. In the last year of the Project three scientific papers were published on the use of DNA analysis to verify the identity of the tree nuts as well as their origins.

Furthermore, the SAFENUT project found its dissemination also through:

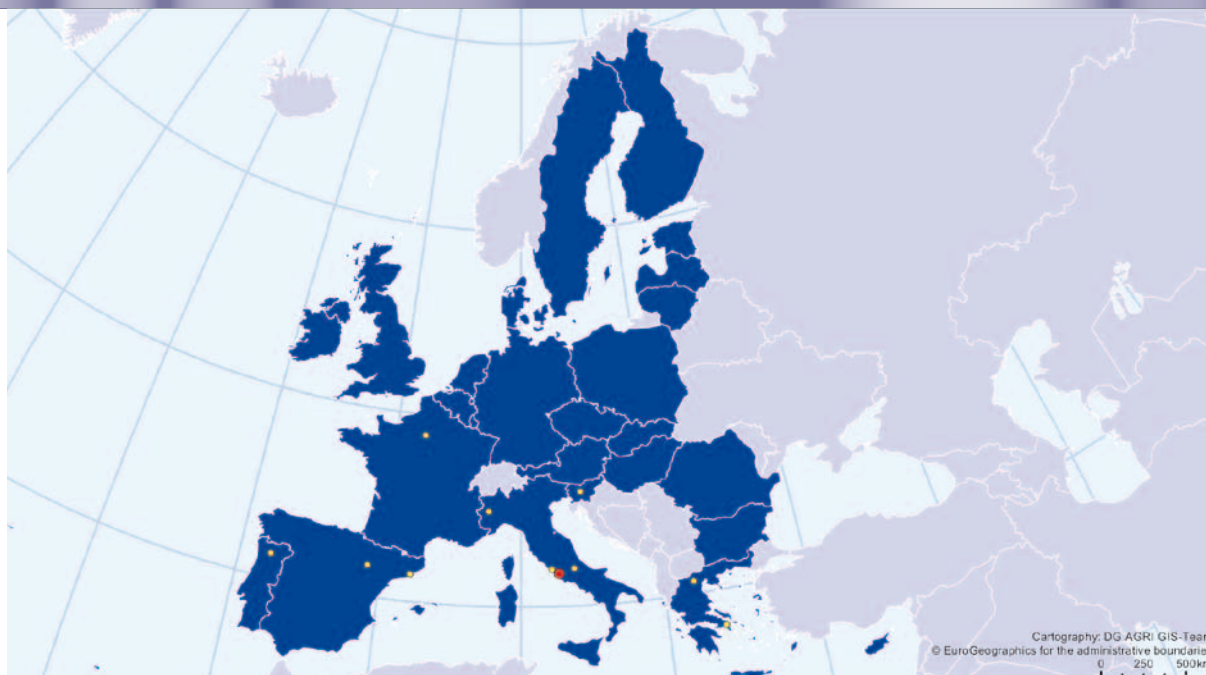
- project were also taken to inform and involve the scientific community as well as the general public through a report showed on the ENEA web television (see: ENEA News 24/11/2008);
- the article 'How many millennia can the hazelnut survive?' by Mr. Abdulsamet Gunek 2009: <http://goo.gl/0jV7b> (Annex 6.VII). The article was the outcome of the RELATE (REsearch LABs for TEaching journalists) project, carried out in ENEA from 9 to 13 November 2009;
- video interview with SAFENUT Project coordinator on New Science Journalism: <http://safenut.casaccia.enea.it/node/87>. This is a video that explains the dangers of genetic erosion and how it can be stopped.

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- [2]. Booklet on Traditional Recipes (<http://safenut.casaccia.enea.it/node/108>)
- [3]. RELATE project (REsearch LABs for TEaching journalists) <http://relateproject.eu/>
- [4]. The SAFENUT web site (<http://safenut.casaccia.enea.it>)
- [5]. The SAFENUT Database (<http://safenut.casaccia.enea.it/db>)
- [6]. SAFENUT Advertisement on The Parliament Magazine (issue 3/2007) <http://www.e-pages.dk/dods/16/2>

SAFENUT Partner – Final meeting, Avezzano (Italy) Settembre 22, 2010





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## Currents and gooseberry

### Core collection of Northern Europe gene pool of *Ribes*

The Currant and Gooseberry action across 9 Member States in Northern Europe contributed to European small fruit germplasm collections, found the germplasm's most valuable characteristics that may be useful for breeding purposes, established the core collection, and discovered means of conserving and protecting the collections for future use by developing *in vitro* culture and cryopreservation.

### Project details

Duration	48 months
Start Date	01/04/2007
End Date	31/03/2011
Budget Total Cost	1 068 620 €
Budget EU Co-funding	534 310 €
Actual EU Co-funding	526 106.99€
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Coordinator's Website	<a href="http://www.mtt.fi/ribesco">http://www.mtt.fi/ribesco</a>

### Background

Black currant, red currant and gooseberry (Latin name: *Ribes*) have a long cultivation history in Northern Europe. The plants provide voluminous crops at reasonable costs. The berries are used for producing juice, liquor and jam, both at household and industrial levels. They are also good for consumption as fresh. Thanks to their high contents of vitamin C and antioxidants, currants are particularly valuable in terms of human health, and are exploited in functional foods and cosmetics as well.

In Northern Europe, both black and red currant species grow wild. The region is the leading production area of currants worldwide. There are valuable genetic resources worth preserving in the Northern European countries.

The local currant and gooseberry types are adapted to the hard winter conditions and a short growing season. These characteristics are important for the purposes of breeding new varieties, and the traditional plant material is thus very valuable. Collections of old and more modern currant and gooseberry types have been established by several institutes, often to support plant breeding. Costs for keeping these collections are high, however, and efforts to reduce the costs are much needed.

Modern currant cultivation is characterised by large areas and the use of few cultivars. The on-farm conservation of clonally propagated material is thus risky because the plants may be replaced by other, newer varieties.

The aim of the RIBESCO project was to establish cooperation between national collections in different countries in order to find the most valuable part of each collection and organise a decentralised core collection for the safe and recognised conservation of edible currants and gooseberry [1].

'Venny' is a modern green-fruited black currant variety with very high content of vitamin C

Black currant foliage expressing the symptoms of reversion virus (BRV)



## The existing collections and their potential threats

At present, the European agricultural research is facing a pressure to rationalise germplasm preservation, especially as regards the collections of those plants that cannot be conserved as seeds but must be maintained as plants, mainly in field collections. For sustainable future production and development of new varieties, it is necessary to keep the genetic variability safe.

The first stage of the RIBESCO project was to gather information about the currant and gooseberry varieties and strains in the existing collections. It was found that more than 600 black currant, 300 red currant and 400 gooseberry varieties and strains were kept in collections in eight Baltic Sea countries participating in the project.

The project revealed the poor state of some currant collections in field conditions. This is due to the spreading of a pest, gall mite, and the viral disease caused by black currant reversion virus (BRV), which is transmitted by the mite. The project thus showed that we must prioritise efforts on virus-cleaning of currants and saving the most valuable ones in safety collections, as long as they still are available.

The currant and gooseberry plants in the existing collections were evaluated by their growth habit and characteristics that may be useful for future breeding purposes. For instance, they were observed for their tolerance to six different diseases and six different pests. Also various chemical analyses were conducted, including fruit sugar content, fruit acidity, fruit total anthocyanin, and fruit vitamin C assessments.

The varieties and strains were also documented by means of photographing, and information of their origin was recorded, when available.

## Establishing a core collection

In order to establish the core collection, we selected about 300 currant and gooseberry varieties and strains to be maintained with highest priority and with special efforts. This means that one quarter of the original collections were found to possess special value for future needs. The selection was based partly on agronomic, historical or other cultural values. The quality of berries was one selection criterion.

In addition, varieties and strains representing a high level of variance in both outward appearance and genetic properties were selected. We utilised DNA fingerprint markers to see the genetic relationships between the varieties and strains. This method also revealed several duplicate and even some mislabelled varieties in the existing collections. Some previously unnamed strains were identified as known varieties.

The original idea was to propagate the selected varieties and strains vegetatively and to maintain the core collection mainly in field collections. Because plant health is an important aspect in making such collections, we had to pay particular attention to freeing the plants from blackcurrant reversion virus, and keeping them in a mite safe environment. The work for cleaning of plants from viruses is still going on.

In the meantime, part of the varieties are being grown as micro-plants in laboratory conditions. One advantage of establishing these *in vitro* cultures through shoot apex culture is virus elimination, at least, in some degree [2].

Cryopreservation is a new method for conserving vegetative plant material. In cryopreservation, specific pieces of plants, in this case buds, are stored deep-frozen. Different methods for the cryopreservation are in use at the project coordinating institute, MTT Agrifood Research Finland [3]. We utilised this technique to save

‘Slivovyi’, the gooseberry variety of Russian origin selected to the core collection



An unknown Finnish red currant strain with very high content of anthocyanin



A part of RIBESCO core collection is conserved deep-frozen in a cryopreservation tank



the most urgent part of varieties before virus elimination. Dormant buds of the selected 55 black currant varieties were transferred to the gas phase of liquid nitrogen below  $-150^{\circ}\text{C}$  using the protocol developed for silver birch and aspen [4]. Pieces of microplants of five varieties were cryopreserved as well.

Experience of the use of cryopreservation is still limited, but a number of studies using different techniques have indicated that varieties keep their genetic properties when cryopreserved [5]. The method might be helpful even in getting rid of viruses through 'cryotherapy', as shown in some other species [6].

### Communication value

The RIBESCO project has enabled us to critically study and evaluate the currant and gooseberry collections in different partner countries, and to find their most valuable parts. Thus, we have been able to contribute to European small fruit germplasm collections and discover means of conserving and protecting them for further use in the future. Scientific information regarding the collections was accumulated with documented data of external appearance, fruit chemical properties and genetic relationships.

The improved availability of data in the database will ensure easier access to and utilisation of the collections. This will be of particular benefit for breeding and product development, for instance, to serve the food processing industry. Furthermore, the keeping security was improved: virus elimination and transferring to a virus-free environment will assure the availability of the varieties and strains for future needs.

The outcome of the RIBESCO project will be utilised, together with DG AGRI GEN RES action O36 GenBerry, in a new EU research project, EUBerry, that was launched in May 2011. The results of the two actions will provide knowledge to facilitate the development of high quality fresh berry fruits for European consumers.

Reports on the project have been published in several technical and scientific journals, and we have given presentations

at congresses and several other public events to disseminate information. The publications are listed at our website <http://www.mtt.fi/ribesco>, and through the links you can easily read, at least, the summaries of many of our articles. More articles are in preparation. The database at <http://www.ribes-rubus.gf.vu.lt> contains plenty of information accumulated in this project.

### More information

There were nine partners in eight EU countries within the Baltic Sea Region: Denmark, Estonia, Finland, Germany, Latvia, Lithuania, Poland and Sweden.

### Links

We have made plenty of efforts to make our results and work description available to the public. At our website <http://www.mtt.fi/ribesco>, you can find more information of the research and achievements, as well as the contact persons in different partner countries. You can also contact the coordinating partner MTT directly by e-mailing to [mttpiikkio@mtt.fi](mailto:mttpiikkio@mtt.fi)

### The genetic resources

The RIBESCO project interfaces with several national and international bodies and programmes on genetic resources of horticultural plants. More information of one of the most important in the Northern Europe, NordGen – the Nordic Genetic Resource Center, can be found at <http://www.nordgen.org/index.php/en>

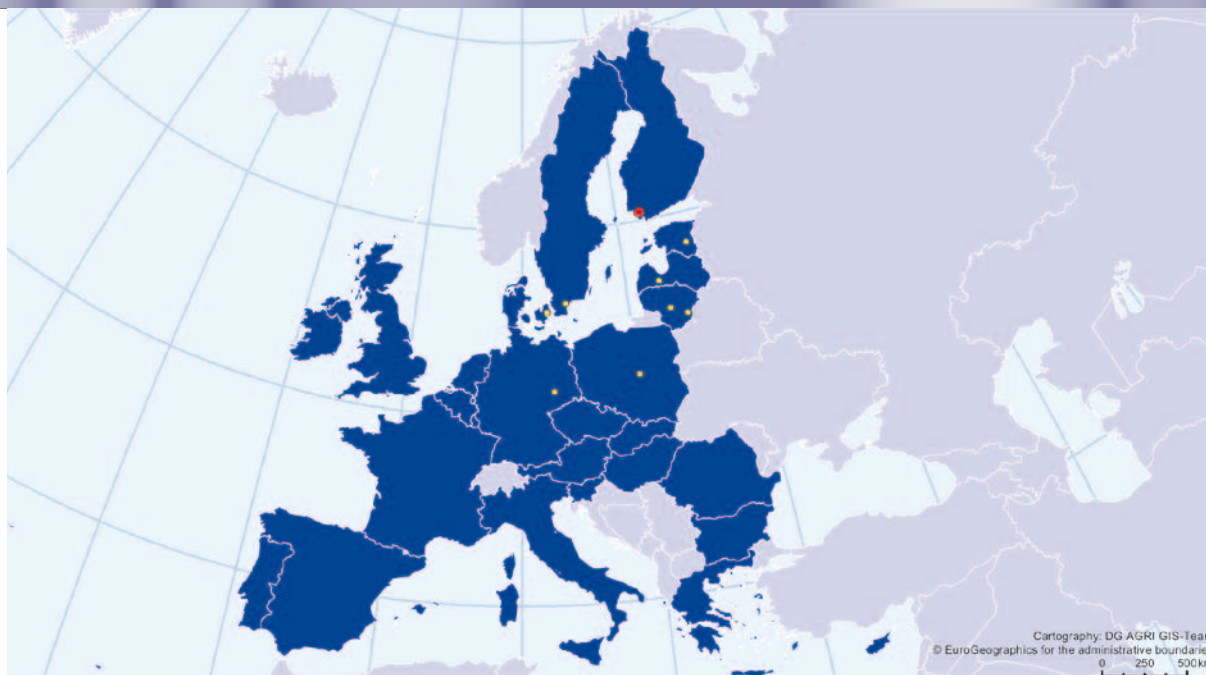
### The database

During this project, we utilised and completed the existing European Central Ribes/Rubus Database that is managed by the Lithuanian partner, Vilnius University. The database integrates information on the origin and characteristics of various currant and raspberry species. You are welcome to visit the database and find the collected information and photographs of the different currant varieties and strains at <http://www.ribes-rubus.gf.vu.lt>



The partners acquainting themselves with the currant collection at the University of Vilnius, Lithuania





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## List of publications

We are writing scientific and technical reports and publications. At our website <http://www.mtt.fi/ribesco>, you can find the list of our publications that are already available.

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- [1] Karhu, S., Antonius, K., Kaldmäe, H., Pluta, S., Rumpunen, K., Ryliskis, D., Sasnauskas, A., Schulte, E., Strautina, S. and Grout, B. 2007. The core collection of the Northern European gene pool of *Ribes* created by RIBESCO project. *Sodininkyste ir Darzininkyste* 26:179-186.
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European Commission

**Preserving genetic resources in agriculture**

Achievements of the 17 projects of the Community Programme 2006-2011

2013 — 124 pp. — 21 x 29.7 cm

ISBN XXXXXX



