GRCHESTNUT: GENETIC RESOURCES OF CHESTNUT IN EUROPE FOR THE FOOD CHAIN

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WHERE ARE THE MAIN GENETIC RESOURCES OF EUROPEAN CHESTNUT?

Conedera and Krebs, Chestnut in Fruit Breeding, 2012
What was behind our proposal?:


What have we proposed?: GRCHESTNUT

- Consortium: 18 partners from
  - Spain, Italy, UK, France, Portugal, Switzerland, Greece, Turkey, Morocco, Syria and Georgia
- Proposal: submitted at the EU Work programme, firstly on 2014 (invited to be completed at 2nd stage) and again on 2015.

- The project results provided: a) background information on neutral genetic diversity of C. sativa across its distribution range; b) adaptive diversity of natural populations (drought tolerance, phenology), and c) a C. sativa genetic map.

In addition, the CASCADE project provided valuable material which will be used in GRCHESTNUT project, i.e.:

- cryoconserved samples representative of 180 populations spanning the European distribution of C. sativa;
- one of the six comparative field trials established in three EU countries;
- one intraspecific C. sativa full-sib mapping progeny.

All of these results were obtained before the arrival of chestnut gallwasp in Europe, a new threat requiring reassessment of chestnut genetic and phenotypic diversity.
CASCADE

Securing gene conservation, adaptive and breeding potential of a model multipurpose tree species (*Castanea sativa*) in a dynamic environment

EU Environment Project
No. EVK2-CT-1999-00006

**Programme:** Energy, Environment and Sustainable Development

**Key Action:** Global Change, Climate and Biodiversity

**Thematic Priority:** Assessing and Preserving Biodiversity
CASCADE

Skills and contact details

11 PARTNERS - 5 COUNTRIES (Italy, Greece, Spain, UK, France)

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**EC OFFICERS:** Martin Sharman, Karin Zaunberger
BIOTA cluster: 23 projects

**Aims**

• Assess and predict the impact of major drivers of biodiversity

• Develop tools, such as biodiversity indicators, to promote the conservation and sustainable use of biodiversity

• Seek to identify and resolve conflicts between society, economy and biodiversity

• Support the conservation of biodiversity by creating databases on the taxonomy, biology and ecology of Europe’s plants and animals
**Context**

*Castanea sativa*: a model multipurpose tree species important for Mediterranean landscape and rural diversification

Its biodiversity at risk due to:

- domestication and silvicultural practices
- fungal attacks
- climatic changes

**Mission statement**

- to **assess** the genetic biodiversity of this model species in relation to major evolutionary factors and human impacts
- to **project** its future response under the expected changes of environmental conditions
- to **develop** optimized long-term strategies of conservation and sustainable management of forest tree resources
- to **develop a multidisciplinary study model** to be extended to other multipurpose species
Needs

- Rules for transfer of nuts for reforestation
- Gene conservation plan for the species
- Cost for a sustainable use and conservation of the species
Securing gene conservation, adaptive and breeding potential of a model multipurpose tree species (Castanea sativa) in a changing environment

CASCADe is a multidisciplinary research project aimed to integrate information from several research fields to devise long-term optimized strategies for the conservation of chestnut genetic resources.

**Molecular Genetic Analysis**
Molecular markers allow genetic profiles of single individuals, seeds or even pollen grains to be determined with high accuracy. Presence of rare bands/variants in the profiles allow conservation priority to be formulated. Comparison of profiles between seeds and adults may allow paternity of seeds to be attributed. Associations of profiles with ecological performances may lead to pick out genomic regions influencing the traits.

**Pathology Studies**
Material sampled from the various populations will be inoculated with strains of Phytophtthora in controlled conditions and assessed for response. In addition mature trees showing field resistance will be identified. The data will be used to clarify the genetics of resistance and to promising sources.

**Long-Term Strategies for Conservation of Genetic Resources**
Detailed information on the availability of chestnut resources will help in defining conservation priorities and optimal exploitation of extant breeding stocks.

**Adaptive Traits Analysis**
Drought resistance of chestnut seedlings will be evaluated by applying different temperature and watering regimes, simulating the upcoming conditions under regional scenarios of climate change.

**Auto-Ecology, Management and Cost-Benefit Analysis**
Present and future dynamics of chestnut ecosystems will be inferred from studies on ecology and management (and their relationships with environmental conditions and local market demands), ecological background information of chestnut distribution area, typology of both environmental conditions (climatic, edaphic) and management types (including silviculture), annual rings growth analysis.
Stress index $x_i = 2\text{TM}-\text{RR} \ (2\text{TM}>\text{RR})$. 

WP1 – Distribution, autoecology, management
Sampling sites and collection of ecological data

<table>
<thead>
<tr>
<th>Site</th>
<th>Tree</th>
</tr>
</thead>
<tbody>
<tr>
<td>Climate</td>
<td>Height</td>
</tr>
<tr>
<td>Vegetation</td>
<td>Diameter</td>
</tr>
<tr>
<td>Management</td>
<td>Age (wood cores)</td>
</tr>
</tbody>
</table>

Naturalised

Orchard

Coppice
Germplasm resources

180 populations across Europe
- 124 naturalized
- 30 coppice
- 26 orchards

Comparative field trials
Spain, Italy, Greece

Provenance trial
F1 full sib progeny
Turkey

VI Convegno Nazionale sul Castagno - CASTANEA2014 - Viterbo, 22-25 settembre 2014
Tools

Molecular markers
- Neutral
  - Isozymes, ISSR, AFLP, SSR
- Gene specific
  - EST-SSR

Adaptive traits
- Growth
- Phenology
- Drought tolerance
- Pathogen resistance
WP2 - Gene dispersal and genetic make up of populations

- Population genetics of 78 populations (over 2000 individuals) originating from 5 European countries, using *isoenzyme* and *ISSR* markers.

- Gene flow & spatial genetic structure of 18 populations (over 4000 individuals) originating from 3 European countries, using *isoenzyme* and *SSR* markers.
Main gene pools of *C. sativa* natural populations in Europe

Population analyzed with SSR markers

Clustering surface map based on spatial interpolation (ArcGis 9.3) of population membership values according to STRUCTURE 2.3.3. for K=3.

Significant genetic barriers identified by BARRIER software using 100 bootstrapped Nei's genetic distance matrices and Monmonier’s maximum difference algorithm.
Spatial interpolation of Genetic Diversity indices

**Castanea sativa - Landscape and Population genetics**

**Indicators**

- Observed Heterozygosity ($Ho$)
- Expected Heterozygosity ($He$)
- Private allelic richness (pRs)
- Allelic richness ($Rs$)

**Legend**

- Colors represent different ranges of values for each indicator.
Genetic variation of Natural populations vs. Cultivated varieties
Original locations of *C. sativa* used as half sib families in phytotron and in 5 comparative field trials experiments.

<table>
<thead>
<tr>
<th>EU code</th>
<th>Population name</th>
<th>Village name</th>
<th>Region</th>
<th>Country</th>
<th>Longitude</th>
<th>Latitude</th>
<th>Xerothermic index</th>
</tr>
</thead>
<tbody>
<tr>
<td>ES 7</td>
<td>Málaga</td>
<td>Gaucín</td>
<td>Málaga</td>
<td>Spain</td>
<td>5°18′21″ W</td>
<td>36°32′10″ N</td>
<td>118.2</td>
</tr>
<tr>
<td>ES 11</td>
<td>Coruna</td>
<td>Cambre</td>
<td>Coruna</td>
<td>Spain</td>
<td>8°22′25″ W</td>
<td>43°17′15″ N</td>
<td>10.6</td>
</tr>
<tr>
<td>IT 37</td>
<td>Sicily</td>
<td>Petralia Sottana</td>
<td>Sicily</td>
<td>Italy</td>
<td>14°05′20″ E</td>
<td>37°49′22″ N</td>
<td>77.4</td>
</tr>
<tr>
<td>IT 56</td>
<td>Pellicc</td>
<td>Villar Pellicc</td>
<td>Piemonte I</td>
<td>Italy</td>
<td>7°09′00″ E</td>
<td>44°49′00″ N</td>
<td>0</td>
</tr>
<tr>
<td>GR 68</td>
<td>Hortiatis</td>
<td>Hortiatis</td>
<td>Central Mac.</td>
<td>Greece</td>
<td>23°09′52″ E</td>
<td>40°22′43″ N</td>
<td>93.6</td>
</tr>
<tr>
<td>GR 65</td>
<td>Paiko</td>
<td>Griva</td>
<td>Northern Mac.</td>
<td>Greece</td>
<td>22°22′18″ E</td>
<td>40°57′42″ N</td>
<td>38.8</td>
</tr>
</tbody>
</table>
Phytotron experiment

- Provenances: 6 (Spain, Italy, Greece)
- Each site: 6 provenances x 26 trees x 20 half-sib progenies
- Traits: Growth, Bud set, Leaf fall, Bud burst, Drought tolerance, Pathogen resistance

Comparative provenance/progeny field

- Year 2001
- Year 2014

Adaptive variation
Additive genetic coefficient of variation (CV_A%) of height of one-year-old Castanea sativa progenies grown in climatic chambers with different temperature and watering treatments.

Phenotypic plasticity correlates with Xerothermic index

*Phenotypic plasticity estimated according to Schlichting and Levin (1986) as the difference between the highest and lowest mean in a population divided by the trait mean value for this population

Lauteri et al. (2004). Journal of Evolutionary Biology
Adaptive variation

Phytophthora cambivora resistance tests

After excised shoot inoculation of adults/5 countries

After root inoculation of seedlings/5 countries

Table 6
Analysis of variance of the percentage of infected taproot for different chestnut families, after root inoculation with Phytophthora, and estimates of variance components for this parameter

<table>
<thead>
<tr>
<th>Families</th>
<th>d.f.</th>
<th>MS</th>
<th>F</th>
<th>P</th>
<th>Variance components</th>
</tr>
</thead>
<tbody>
<tr>
<td>French and English</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Population</td>
<td>7</td>
<td>0.4053</td>
<td>2.22</td>
<td>0.0322</td>
<td>0.0003</td>
</tr>
<tr>
<td>Family</td>
<td>39</td>
<td>0.2956</td>
<td>1.662</td>
<td>0.0132</td>
<td>0.0287</td>
</tr>
<tr>
<td>Greek</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Population</td>
<td>4</td>
<td>0.4242</td>
<td>2.89</td>
<td>0.0222</td>
<td>0.0020</td>
</tr>
<tr>
<td>Family</td>
<td>26</td>
<td>0.5381</td>
<td>3.67</td>
<td>&lt;0.0001</td>
<td>0.0131</td>
</tr>
<tr>
<td>Italian and Spanish</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Population</td>
<td>9</td>
<td>0.6890</td>
<td>4.22</td>
<td>&lt;0.0001</td>
<td>0.0028</td>
</tr>
<tr>
<td>Family</td>
<td>71</td>
<td>0.3351</td>
<td>2.05</td>
<td>&lt;0.0001</td>
<td>0.0105</td>
</tr>
</tbody>
</table>

# Dk resistance

## C. sativa resistant to Drycosmus kuriphylus

<table>
<thead>
<tr>
<th>Populations</th>
<th>No. (fam. size)</th>
<th>HS</th>
<th>av.</th>
<th>r</th>
<th>% r</th>
<th>r distrib.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coruna (ES), wet</td>
<td>250 (26.9.6)</td>
<td>26</td>
<td>9.6</td>
<td>11</td>
<td>2.4</td>
<td>scattered</td>
</tr>
<tr>
<td>Malaga (ES), dry</td>
<td>150 (23.6.5)</td>
<td>23</td>
<td>6.5</td>
<td>6</td>
<td>7.3</td>
<td>scattered</td>
</tr>
<tr>
<td>Pellice (IT), wet</td>
<td>184 (27.6.8)</td>
<td>27</td>
<td>6.8</td>
<td>8</td>
<td>4.3</td>
<td>scattered</td>
</tr>
<tr>
<td>Petralia Sottana (IT), dry</td>
<td>295 (26.11.3)</td>
<td>26</td>
<td>11</td>
<td>14</td>
<td>4.7</td>
<td>scattered</td>
</tr>
<tr>
<td>Paiko (GR), wet</td>
<td>81 (18.4.5)</td>
<td>18</td>
<td>4.5</td>
<td>24</td>
<td>29.6</td>
<td>scattered</td>
</tr>
<tr>
<td>Hortiatis (GR), dry</td>
<td>133 (23.5.7)</td>
<td>23</td>
<td>5.7</td>
<td>66</td>
<td>49.6</td>
<td>not scattered</td>
</tr>
<tr>
<td><strong>Tot.</strong></td>
<td><strong>1093 (143.7.6)</strong></td>
<td>143</td>
<td>7.6</td>
<td>128</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Construction of a full-sib *C. sativa* progeny for mapping

High genetic (molecular markers), morphological (fruit), physiological (WUE) differentiation among Turkish populations

Genetic Mapping

**BURSA × HOPA**

Full-sib progeny

186 F1 trees

**Tot. Genetic distance:** 865 (cM)

**Genome saturation:** 82 %

**Total size:** 1050 (cM)

**Molecular markers:**
RAPD, ISSR, AFLP, SSR, STS, isozymes, EST-SSR

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*VI Convegno Nazionale sul Castagno - CASTANEA2014 - Viterbo, 22-25 settembre 2014*
Phenotypic assessment was performed during three growing seasons on 135-174 offsprings.

The traits analyzed and QTL detected were:

- **Growth** (Height and diameter) → 10 QTL
- **Water Use Efficiency** (WUE) → 7 QTL
- **Phenology**
  - Bud burst → 9 QTL
  - Bud set → 3 QTL

C. sativa genetic map

Comparative Genetic and QTL Mapping: Q. robur vs. C. sativa

- 55 orthologous molecular markers
- Colocation of the QTL for bud burst timing
- Identified putative candidate gene for bud burst

Casasoli et al. (2006) Comparison of Quantitative Trait Loci for Adaptive Traits Between Oak and Chestnut Based on an Expressed Sequence Tag Consensus Map Genetics 172: 533–546
WP4 – Variation in disease resistance

Field survey

78 selected sites
Specific actions

- use general public surveys (1025 questionnaires) in Italy, Greece and France to examine at consumption of chestnut related goods for food, timber and recreation;

- estimate production costs and revenue in Italy;

- investigate local preferences for possible policy solutions that can support development;

- use choice experiments to investigate the costs and benefits of maintaining the species.
WP6 – Strategy for Integrated conservation and utilization

Castanea sativa gene conservation

Prime objective: Safeguarding the potential for adaptation

Utilise existing genetic variation: Capture existing variation in adaptedness as starting material for gene conservation, free from pollen contamination

Selected populations must have sufficient additive variance

First step: Utilise traits of assumed adaptive significance

Second step: Select among these based on marker variation

Third step: Selection based on ecogeographic principles, including xerothermic index
Marker based conservation value, MBCV

Additive trait conservation value, ATCV

Pathogen tolerance conservation value, PTCV

CASCADE Project
Network of conservation units

Figure 21. The suggested network of gene resource populations for sweet chestnut in the countries involved in the CASCADE project (green circles).
WHAT ARE THE MAIN POINTS TO BE SOLVED FOR NEXT GENERATIONS?

- Chestnut decline due to:
  - Abandon
  - Pest and diseases
  - Reduced scientific knowledge in comparison to other species
  - Complexity of this multipurpose species
  - Disconnected sector: producers, industry, researchers, academics, enterprises, tourism, ..
WHAT HAVE WE PROPOSED?: GRCHESTNUT

- **Consortium**: 18 partners from
  - Spain, Italy, UK, France, Portugal, Switzerland, Greece, Turkey, Morocco, Syria and Georgia
- **Proposal**: submitted firstly on 2014 (invited to be completed at 2nd stage) and again on 2015.
2014

- INRA
- EMR
- CEH
- UEDIN
- WSL
- UNITO
- CNR-IBAF
- UNITUS
- OMU
- Santiago de Compostela University
- UCO
- INIAV
- UTAD
- UTHESS
<table>
<thead>
<tr>
<th>Participant No *</th>
<th>Participant organisation name</th>
<th>Country</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (Coordinator)</td>
<td>S. Pereira-Lorenzo, Universidad de Santiago de Compostela (USC)</td>
<td>Spain</td>
</tr>
<tr>
<td>2</td>
<td>R. Botta, Università degli Studi di Torino (UNITO)</td>
<td>Italy</td>
</tr>
<tr>
<td>3</td>
<td>F. Villani, National Research Council (CNR-IBAF)</td>
<td>Italy</td>
</tr>
<tr>
<td>4</td>
<td>R. Harrison, East Malling Research (EMR)</td>
<td>UK</td>
</tr>
<tr>
<td>5</td>
<td>K. Schönrogge, Centre for Ecology &amp; Hydrology (CEH)</td>
<td>UK</td>
</tr>
<tr>
<td>6</td>
<td>L. Martín, Universidad de Córdoba (UCO)</td>
<td>Spain</td>
</tr>
<tr>
<td>7</td>
<td>C. Robin, INRA-Bordeaux</td>
<td>France</td>
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<td>8</td>
<td>R. Costa, INIAV</td>
<td>Portugal</td>
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<td>9</td>
<td>J. Laranjo, University of Tras-Os-Montes (UTAD)</td>
<td>Portugal</td>
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<tr>
<td>10</td>
<td>M. Conedera, Swiss Federal Institute for Forest, Snow and Landscape Research (WSL)</td>
<td>Switzerland</td>
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<td>11</td>
<td>P. Madesis, National Center for Research and Technology, Institute of Applied Biosciences (INAB)</td>
<td>Greece</td>
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<td>12</td>
<td>U. Serdar, Ondokuz Mayıs University</td>
<td>Turkey</td>
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<td>13</td>
<td>A.M. Vettraino, Università degli Studi della Tuscia (UNITUS)</td>
<td>Italy</td>
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<td>G.N. Stone, University of Edinburgh (UEDIN)</td>
<td>UK</td>
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<td>15</td>
<td>J. Dasque, AREFLH, Assemblée des Régions Européennes Fruitières, Légumières et Horticoles</td>
<td>France</td>
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<tr>
<td>16</td>
<td>M. Ater, Abdelmalek Essaâdi University</td>
<td>Morocco</td>
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<td>17</td>
<td>T. Wardeh, Aleppo University</td>
<td>Syria</td>
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<td>18</td>
<td>Z. Bobokashvili, Scientific-research Center of Agriculture</td>
<td>Georgia</td>
</tr>
</tbody>
</table>
USA, Professor J. Carlson from USA. Molecular Genetics. Director, Schatz Center for Tree Molecular Genetics. Department of Ecosystem Science and Management Pennsylvania State University.

Japan, Dr. S. Nishio, Laboratory of Japanese Pear and Chestnut Breeding, NARO Institute of Fruit Tree Science. Fujimoto 2-1, Tsukuba Japan.

China, Professor Qin Ling, Department of Horticulture, Beijing Agricultural College, Beijing 102206, China Q. Ling, Beijing University
GRCHESTNUT OBJECTIVES

- To evaluate the representativeness of existing ex-situ and in-situ genetic resources and databases, seeking to harmonise, rationalise and improve their management and usefulness.

- To acquire, conserve, characterise and enhance the use of chestnut genetic resources in breeding and forestry by close linking of novel research to the needs of stakeholders (e.g. breeders, producers, conservationists) and policy makers.

- To establish the combined impact of a diversity of pests and diseases that increasingly threaten European chestnut and associated industries, and develop methods for their management.

- To enhance the use of specific genetic resources in sustainable chestnut-related activities by assessing the economic impacts of current and improved management practises.

- To develop measures to disseminate information, to improve the status and use of collections and enhance awareness of environmentally and economically sustainable production schemes.
THE EFFECT OF GRENCHESTNUT ON EUROPEAN CHESTNUT PRODUCTION

EFFECT 1. REDUCTION OF THE DECLINE OF EUROPEAN CHESTNUT PRODUCTION.

VARIATION OF EUROPEAN PRODUCTION ACROSS YEARS (FAOSTAT, 2010; LIVRE BLANCHE DU CHÂTAIGNE, 2012).

Decline after first report of ink disease at the end of the 19th century in France. First report blight in Italy 1938.

First report of gallwasp in Italy.

Next decline 50% due to gallwasp?
THE EFFECT OF GRCHESTNUT ON THE IMPORT OF CHESTNUTS AND LACK OF ORIGIN. TRACEABILITY

EFFECT 2. INCREASED PRICES OF EUROPEAN CHESTNUT CROPS DUE TO EU PROTECTION: PDOS AND PGIS

- EU imports 7300 t of chestnuts (2010), value of €10.05 million.
- Traceability of origin will improve product value (protected denominations of origin, PGI; Denominations of Origen, PDO).
  + 5 PGIs and 2 PDOS in Italy,
  + 2 PDOS in France
  + 2 PDO’s in Portugal
  + 1 PGI in Spain
- PGIs can increase in the price per kg between 27%-56% when the production is commercialized under the PGI.
- In European terroirs enrolled in a larger network of PDOS and PGIs: crop value could increase from an EU total of €244.5 million (163,000 t sold at €1.5/kg) to €570 million if sold at €3.4/kg.
THE EFFECT OF GECHESTNUT ON SOCIAL IMPACTS AND EFFECT ON SOCIAL HERITAGE

EFFECT 3. JOB CREATION DERIVED FROM THE CHESTNUT INDUSTRY

- More than 100,000 chestnut growers active in Europe.
- Organic chestnut production is growing,
  - 3000 ha registered in more than 460 French orchards.
  - In Galicia (Spain), 98 chestnut growers (close to 1500 ha) are registered as organic (www.craega.es).
- Job opportunities
  - 50% of the European production of chestnuts is based on medium and small enterprises: 54,800 t, with an estimated value of €414 million.
THE EFFECT OF GRCHESTNUT ON EUROPEAN CHESTNUT RESOURCES

EFFECT 4. PROTECTING CHESTNUT GENETIC RESOURCES

- There is no common EU standards and the information is fragmented about collections and giant trees across countries.
- There are many examples of relevant giant trees disappearing because they are not recognizable as untapped resources by the general public.
- Giant trees have an economic impact as characteristic marks in the landscape through tourism (“Castagno dei Cento Cavalli”, Sant’Alfio, CT, Sicily), but their genetic relevance is not well understood.
- With GRCHESTNUT we propose the first central inventory and assessment of giant trees as a resource in management and breeding.
The response in USA in terms of public funds and research activities has been more robust than in Europe, with the consequence that leadership in chestnut conservation and genetics has steadily moved away from Europe.

The genomes of *C. dentata* and Chinese chestnut, *C. mollissima* have been sequenced in the US.

- These resources allowed identification of desirable phenotypic traits, even though American chestnut has no production industry.

The US currently implements a continuous breeding program supported by molecular intervention, while trying to preserve the native genome.

**GRCHESTNUT will work closely with American colleagues to develop resources for European chestnut to a similar standard, including a genome sequence.**
RELATION TO THE WORK PROGRAMME: WHERE HAVE WE APPLIED?

- Work programme: Food security, sustainable agriculture and forestry, marine and maritime and inland water research and the bioeconomy
- Topic SFS-07b-2015: Management and sustainable use of genetic resources
CONCEPT

**Step 1**  
*In situ* (2400 local cultivars and giant trees, 24 hotspots) and *ex situ* genetic resources

**Step 2**  
**Analysis:**  
1. With existing markers (SSR, EST-SSR) and newly developed markers, sequencing, transcriptome  
2. Heritage and production systems  
3. Community genetics

**Step 3**  
**4. Socio-economic**  
EVALUATION to chestnuts: stakeholders, food chain, and networks

**5. Measures to span from research to demonstration and dissemination**  
Development of (environmentally and economically) sustainable production schemes

Enhance local varieties and breeds with improved production systems

**GRCHESTNUT Database sustainability beyond the project**
| Phase 1: Gathering European chestnut genetic resources | WP0. Coordination | Task 0.1 Project Coordination and Management  
Task 0.2 Reporting and Financial Management |
|---|---|---|
| Phase 2: Analyzing the genetic information | WP1. Genetic Resources | Task 1.1 Definition and evaluation of chestnut resources  
Task 1.2 Definition of common molecular markers for characterization of chestnut genetic resources  
Task 1.3 Phenotyping of the selected genetic resources  
Task 1.4 Genetic characterization of *C. sativa* plant material  
Task 1.5 Identification of new and unexplored genetic resources for core collection and innovative breeding programmes |
| | WP2. Description, evaluation and management | Task 2.1 Description and characterization of the varieties and chestnut production systems  
Task 2.2 European inventory of giant chestnuts  
Task 2.3 Collecting and describing the European chestnut cultural heritage  
Task 2.4 Definition and proposition of innovative products that add value to existing and future chestnut systems |
| | WP3. Community genetics | Task 3.1 Compiling and evaluating data on potential resistance for two *C. sativa* pests and diseases  
Task 3.2 Legacy datasets of pests and diseases throughout the European native range of *C. sativa*  
Task 3.3 Endophytic fungal communities associated with *C. sativa*  
Task 3.4 Assessing how components of the *C. sativa* microbiome interact with pathogens, pests and disease |
| Phase 3: Exploitation and dissemination of results | WP4. Economic Impacts | Task 4.1 Definition of stakeholders related to chestnut  
Task 4.2 Definition of networks between regions and countries  
Task 4.3 Definition of the market chain from production to market  
Task 4.4 Definition of other threats to chestnut  
Task 4.5 Evaluation of Protected Origin Denominations  
Task 4.6 Modelling European chestnut production  
Task 4.7 Economic evaluation |
| | WP5. Dissemination and Exploitation | Task 5.1 GRCHESTNUT website – a complete database of European genetic resources of chestnut  
Task 5.2 Definition of best practices for chestnut management  
Task 5.3 Preparation of demonstration, dissemination and communication videos, brochures and publications  
Task 5.4 Promotion of cultural heritage of European chestnut |
WP 0. PROJECT MANAGEMENT, COORDINATION AND EVALUATION

- 0.1. Project Coordination and Management
- 0.2. Reporting & Financial Management
  - Define the Financial Management procedures.
  - Provide periodic project progress reports and the Final report.
- 0.3. Quality Assurance and Risk Assessment
WP 1. INVENTORY OF EXISTING EX-SITU AND IN-SITU GENETIC RESOURCES AND DATABASES, DEVELOPING TOOLS TO HARMONISE, RATIONALISE AND IMPROVE THEIR MANAGEMENT AND UTILITY.

❖ 1.1. Defining chestnut resources (orchards, coppices, natural populations)
❖ 1.2. Defining chestnut phenotypic descriptors (to harmonise)
❖ 1.3. Developing and selecting genetic molecular markers (SSRs, GBS, MRAD, SNPs)
❖ 1.4. Development of a comprehensive database of chestnut genetic resources (live website)
WP 2. ACQUIRE, CONSERVE, CHARACTERISE AND ENHANCE THE USE OF CHESTNUT GENETIC RESOURCES IN BREEDING AND FORESTRY BY CLOSE LINKING OF NOVEL RESEARCH TO THE NEEDS OF STAKEHOLDERS AND POLICY MAKERS.

2.1 Genetic characterisation of *C. sativa* resources, specially to pests (wall gasp, *D. kuriphilus*), other insects and diseases (ink disease, *Phytophthora* spp.; blight, *Cryphonectria parasitica*).

2.2. Development of legacy core collections
WP 3. ESTABLISH THE COMBINED IMPACT OF A DIVERSITY OF PESTS AND DISEASES THAT INCREASINGLY THREATEN EUROPEAN CHESTNUT AND ASSOCIATED INDUSTRIES, AND DEVELOP METHODS FOR THEIR MANAGEMENT.

- 3.1. Compile and evaluate data on genetic diversity related to chestnut pests and diseases.
- 3.2. The chestnut microbiome.
- 3.3. Interactions between components of the chestnut microbiome and pathogens and pests.
WP 4. ENHANCE THE USE OF SPECIFIC GENETIC RESOURCES IN SUSTAINABLE CHESTNUT-RELATED ACTIVITIES BY ASSESSING THE ECONOMIC IMPACTS OF CURRENT AND IMPROVED MANAGEMENT PRACTISES

- 4.1. Collecting and description of chestnut heritage
- 4.2. Definition of stakeholders (Operational groups) related to chestnut: growers, industries, enterprises, NGOs, cultural groups, musical groups
- 4.3. To define possible networks between regions and countries
- 4.4. To define the market chain, from production to market
- 4.5. To define threats to chestnut in addition to pests and diseases
- 4.6. Evaluation of Protected Denominations of Origin (PDO) and Geographic Protected Indications (PGI).
- 4.7. Modelling European chestnut production
- 4.8. To contrast economic benefits provided by chestnut biodiversity (material and immaterial) with the consequences of loss of this income
WP 5. DEVELOP MEASURES TO DISSEMINATE INFORMATION, TO IMPROVE THE STATUS AND USE OF COLLECTIONS AND ENHANCE AWARENESS OF ENVIRONMENTALLY AND ECONOMICALLY SUSTAINABLE PRODUCTION SCHEMES.

- **5.1.** GRGHESTNUT WEBSITE.
- **5.2.** Definition of the best practices for the management of chestnut orchards and forests.
- **5.3.** Preparation of demonstration, dissemination and communication videos, brochures and publications.
- **5.4.** To promote cultural heritage of European Chestnut stands and landscapes, involving gastronomy.
WP0. Coordination
WP1. Genetic resources
WP2. Description, evaluation, and management
WP3. Community genetics
WP4. Economic impacts
WP5. Dissemination and exploitation

STEP 1: CHESTNUT GENETIC RESOURCES

STEP 2: ANALYSIS OF GENETIC RESOURCES

STEP 3: EXPLOITING THE GATHERED RESOURCES AND DISSEMINATING
MAIN PROBLEMS TO SUCCEED AT EU FUNDS

- Reduced impact of chestnut in comparison to other species: fruit trees, horticultural crops, even domesticated animals.
- Topics of CALLS at the UE are general, opened to competitiveness among species and consortiums.
- Difficulty to explain the complexity of chestnut: crop, forest, landscape, heritage,...
- A more connected Scientific Consortium and stakeholders is needed.
WHAT DO WE EXPECT?

- Reinforce this Consortium to be more competitive.
- To ask for specific topic(s) at the EU program related to chestnut (if chestnut is included in a long list of shell trees, it will be the last).
- To apply to future Calls.
- To develop present research and dissemination as a legacy for future generations.