

OVERVIEW OF ECONOGENE, AN EUROPEAN PROJECT THAT INTEGRATES GENETICS, SOCIO-ECONOMICS AND GEO-STATISTICS FOR THE SUSTAINABLE CONSERVATION OF SHEEP AND GOAT GENETIC RESOURCES

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<http://lasig.epfl.ch/projets/ECONOGENE/>

Summary

ECONOGENE combines a molecular analysis of biodiversity, socio-economics and geostatistics to address the conservation of sheep and goat genetic resources and rural development in marginal agrosystems in Europe. To assist in situ conservation and address the relevant socio-economic factors, a co-ordinated approach was developed to define strategies of genetic management and rural development. Knowledge of sheep and goat genetic diversity has been greatly extended.

Keywords

Goat, sheep, biodiversity, GIS Science, genetics, molecular markers

Contribution

The ECONOGENE project is funded by the European Union within the Quality of Life V framework programme, a programme that comprises six Key actions aiming to enhance the quality of life of European citizens and to improve the competitiveness of European industry. The ECONOGENE Consortium comprises 12 Partners and 11 Subcontractors from 9 EU-25 Countries (among which 7 EU-15 Countries), 1 CEEC Country and 5 non EU Countries. In addition the Consortium includes many contributors that generously supported different phases or tasks of the project (the complete list can be found at the address <http://lasig.epfl.ch/projets/ECONOGENE/>).

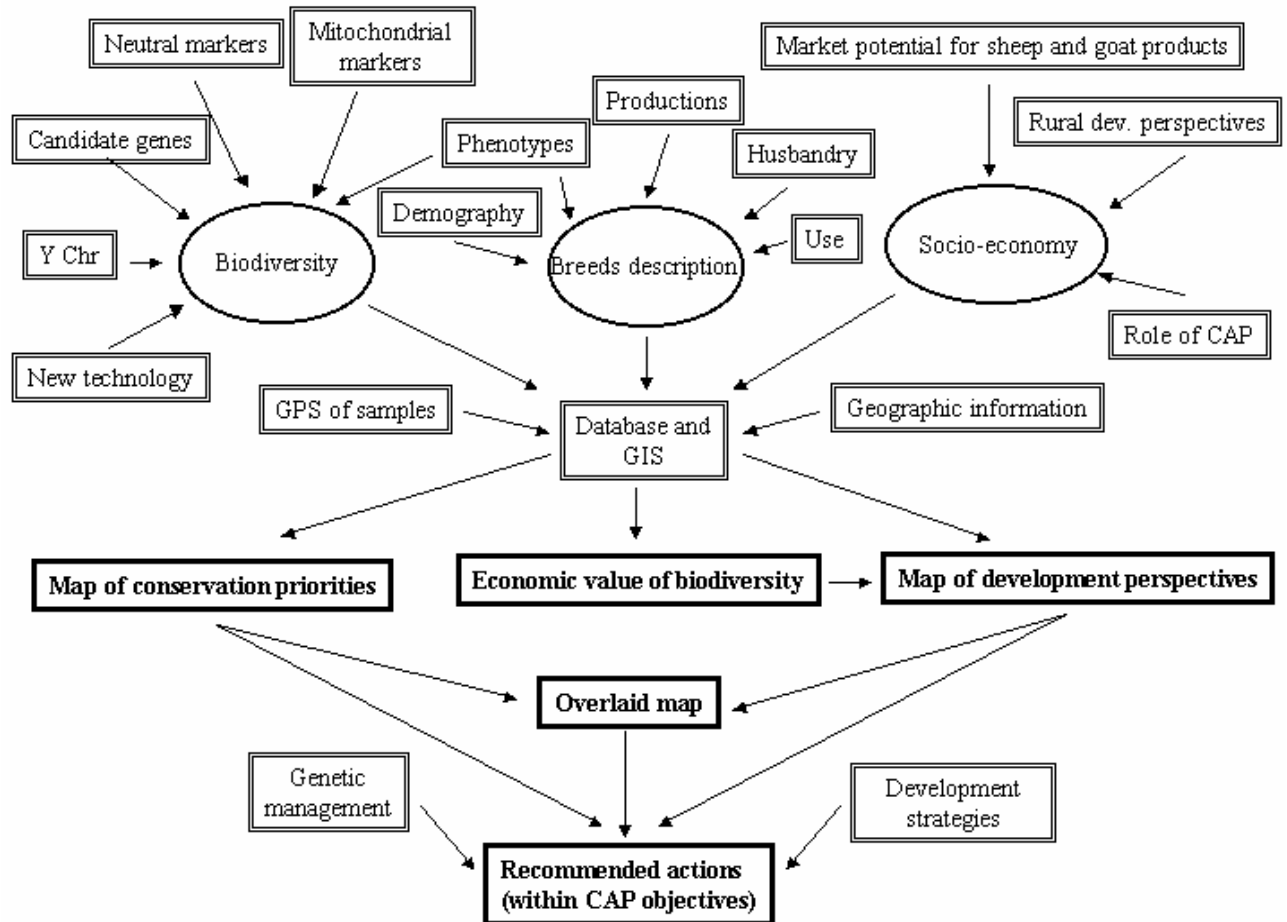
The overall objective of the project is to promote the sustainable conservation of genetic resources in sheep and goat by:

- identifying the most diverse and distinctive populations in these species investigating gene and genome biodiversity at several levels (neutral markers, expressed sequences, maternal and paternal lineages) in sheep and goat breeds that are unstudied and locally important in marginal areas of Europe, Middle East and North-Africa;
- evaluating the economic value of genetic resources by integrating economic and demographic data (i.e. performance, management, product marketing and land use) with information on the degree of genetic distinctiveness of these breeds;
- identifying areas where actions for promoting rural development through the use and conservation of the most valuable populations have the highest chance of success.

We used Geostatistical systems to integrate geographic, genetic and socio-economic data, greatly increasing the value of each single specialised analysis.

From all this information, and from the identification of the factors that in the past caused the partial failure of specific actions of CAP in marginal areas, guidelines are being proposed for the development of rural areas. These are based on the breeding of valuable genetic resources, and on the correct management of these populations.

Figure 1. Graphical representation of project components



To achieve these objectives the workplan was organised into 6 work packages.

- Work package 1:
 - o preparation of databases for data collection from different sources;
 - o implementation of interfaces that permit easy access for partners to data input and analyses, exchange of information and real time monitoring of project progress.
- Work package 2:
 - o collection of biological samples for molecular analyses;
 - o recording of GPS position of samples;
 - o collection of information on breed management.
- Work package 3:
 - o collection of descriptive and economic data on the breeds investigated and of socio-economic data on rural areas;
 - o analysis of case studies on the effectiveness of the actual application of CAP measures;
 - o development of models for the economic evaluation of genetic resources.

- Work package 4:
 - o gene and genome analysis of genetic resources.
- Work package 5:
 - o analysis of all the genetic, socio-economic and geographic data collected using Geographic information science.
- Work package 6:
 - o proposal of specific actions capable of promoting sustainable sheep and goat farming in areas of high priority for conservation;
 - o indication of management systems suited to maintain originality and biodiversity in local populations.

Website and database

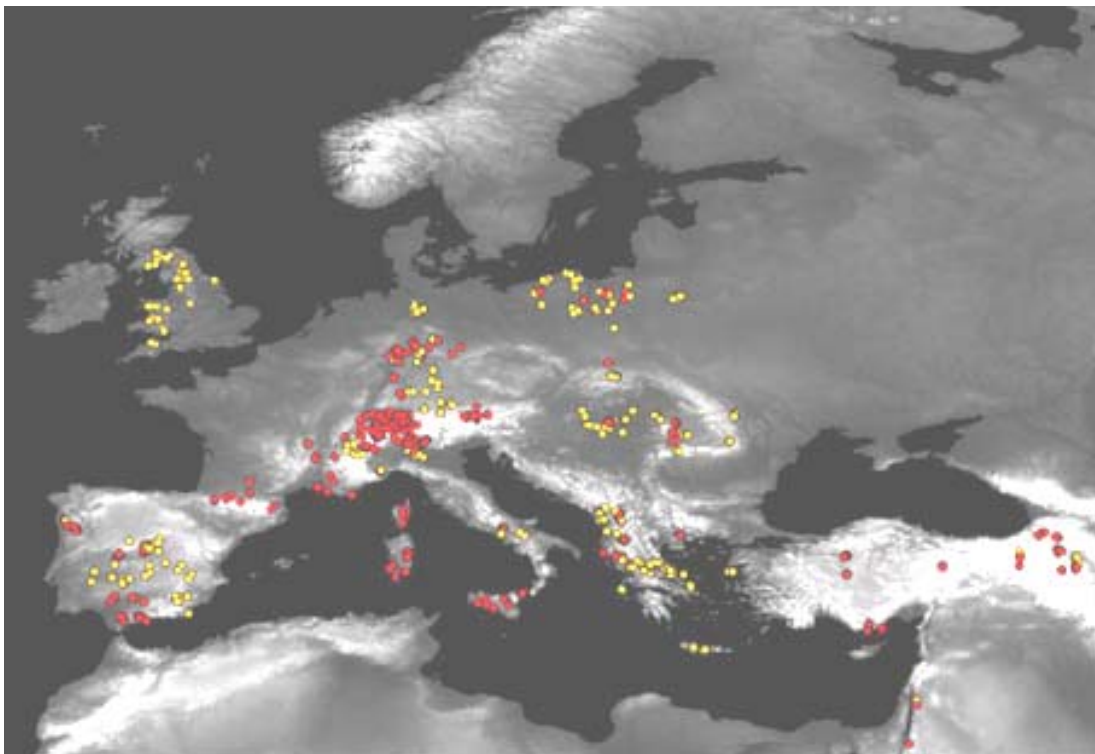
The ECONOGENE Website (<http://lasig.epfl.ch/projets/ECONOGENE/>) represented the core of the project. It was structured in two parts. The first part is public and designed to contain areas dedicated to general information about the project, the list of official participants and of members of the ECONOGENE Consortium, molecular markers and primer pairs used by the project and sheep and goat breeds analysed, the most important web links related to the topics of the project and the abstracts of papers published within the project.

The second part, restricted “to Partners only”, contains areas dedicated to meeting slides and reports, slides of invited lectures and open communications given during meetings, full text of papers published within the projects, protocols, questionnaires and guidelines, on-line tools for monitoring sampling progress, a discussion forum and databases.

Sampling

ECONOGENE collected a total of 3401 animals from 885 sampling sites (Figure 2) across Europe, Middle East and Egypt.

Figure 2. Geographical location of the 885 ECONOGENE sheep and goats sampling sites.



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These belong to 104 populations (57 sheep and 47 goats; see Table 1). Among these are 95 autochthonous breeds (52 sheep and 43 goats). In addition Merino sheep and Alpine were double sampled in the site of origin (Spain and Switzerland respectively) and sampled in multiple locations (Merino sheep in Spain, Germany, Hungary, Poland and Romania; Alpine goat in Switzerland, Germany, Italy and France) as check for sampling bias.

Sampling criteria were to collect at most three unrelated animals (one male and two females) per flock from 11 farms covering the traditional rearing area of the breed.

Table 1. Sheep and goat breeds collected in ECONOGENE

Country	Goat breed	Sheep breed
Albania	Liqenasi, Mati, Capore, Muzhake, Hasi, Dukati	Bardhoka, Ruda, Shkodrane
Austria	Pintzgauer, Tauernschecken	
Cyprus	Cyprus Makeras goat	Cyprus fat tail
Egypt		Ossimi
France	Rove, Pyrenean, Corsican, French Alpine	Thone et Marthod
Jordan	Jordan Mountain	
Germany	Thuringian forest goat, German Alpine goat	Grey Heath, German merino, Rhöensheep, Brown/White Mountain Sheep
Greece	Skopelos goat, Greek goat	Orino, Sfakia, Anogeiano, Kalarritiko, Pilioritiko, Kefalleneas, Karagouniko, Lesvos, Kymi, Skopelos
Hungary		Racka (black and white), Tsigaja, Cikta, Hungarian merino
Italy	Girgentana, Grigia Molisana, Maltese, Bionda dell'Adamello, Orobica, Valdostana, Camosciata (It. Alpine), Girgentana, Argentatat dell'Etna, Sarda	Gentile di Puglia, Laticauda, Altamura, Bergamasca, Delle Langhe
Portugal	Brava	Churra Bragançana
Poland	Polish Fawn improved goat	Zelazna (Polish lowland), Pomorska, Kamieniec, Polish mountain, Polish heat, Polish Merino
Romania	Carpathian	Turcanà, Tsigai, Transilvanian Merino, Black Karakul
Saudi Arabia	Beeshi, Najrani	Naemi, Najdi, Heri
Spain	Verata, Florida, Guadarrama, Payoya, Malagueña	Merinos, Merinos2, Manchega, Colmenareña, Segureña, Rubia del Molar
Switzerland	St. Gallen booted Goat, Peacockgoat, Swiss Alpine, Swiss Alpine 2, Grisons striped	
Turkey	Angora, Hair, Gurcu, Abaza	Daglic, Akkaraman (White Karaman), Morkaraman (Red Karaman), Karayaka
UK		Scottish Blackface, Swaledale, Welsh Mountain, Exmoor Horn

Molecular data

AFLPs

Following a screening of primer pairs, three combination per species were selected: E35/T32 (selective nucleotides: ACA/AAC in *EcoRI* and *TaqI* primers respectively), E35/T38 (ACA/ACT) and E45/T38 (ATG/ACT) in sheep and E32/T38 (AAC/ACT), E43/T33 (ATA/AAG) and E45/T32 (ATG/AAC) in goats. These produced 104 AFLP markers in goats [1] and 98 in sheep [2].

Microsatellites

In each species 30 microsatellite markers were selected with the aim of: i) covering most chromosomes; ii) maximising the overlap between ECONOGENE list and markers employed in other large scale projects; iii) optimising the experimental effort (e.g. selecting markers suited to the set up of multiplex amplification and run).

The list of ECONOGENE microsatellites has become the FAO list of recommended markers (<http://dad.fao.org/en/refer/library/guidelin/marker.pdf>) for the investigation of biodiversity in sheep and goats. Loci were ranked by quality [3], robustness, informativeness and suitability to multiplexing. Ranked markers should maximise overlapping among independent investigation using variable number of loci. Link to public sequence database, mapping information and references on the discovery and use of each locus was also provided.

Mitochondrial DNA

Mitochondrial DNA analysis was conducted partially by direct sequencing and partially by genotyping. In sheep the control region for all the individuals was analysed using RFLPs and a subset of these individuals (approximately 400) were sequenced, to cover all the breeds involved in the study and all the different haplogroups revealed during RFLP screening in the most balanced way possible.

In goat on average 8 males per breed (approximately 350) were sequenced a 481bp fragment from the HVI mtDNA fragment

DNA arrays

The use of DNA arrays for the analysis of sheep and goats genetic diversity has been explored testing the Diversity Arrays™ Technology developed in 2001 at the Center for the Application of Molecular Biology to International Agriculture (CAMBIA) on rice plants [4]. This task of new technology development represented the "high risk" task of the project and indeed caused some difficulties that are presently addressed.

SNPs in candidate genes

A concerted list of thirty genes per species have been selected for SNP discovery. These are involved in key metabolic pathways influencing production, disease resistance and morphological traits. All these genes are candidate to have high adaptive value and to be under strong natural or artificial selection.

SNP discovery was originally conducted analysing individuals from two reference panels including individuals from 8 different breeds per species (3 males per breed), representing the most of the variation across a wide geographic area. This strategy has recently been challenged by new theoretical advances in SNP analysis [5], [6]. Additional individuals (preferentially belonging to breeds original from domestication sites) were therefore added to the standard panels for SNP discovery to circumvent possible "ascertainment bias" in the number and distribution of SNPs within and between breeds due to the choice of the individuals we included in the panels.

SNPs have been discovered in exon and intron sequences following direct sequencing, SSCP and DHPLC analyses. A total of 31 genes in sheep and 20 in goats have been fully typed in all samples collected for SNP characterisation.

Y Chromosome

Direct sequencing of SRY, ZFY, DBY, SMCY and UBRY genes permitted the investigation of goat and sheep Y chromosomes in search for SNPs. Interestingly while 10 SNPs have been identified and further used in goats to characterise male animals from different breeds, not a

single polymorphism was found in sheep in which all genes have been tested, with the exception of region 3 of SRY.

Socio-economic data.

Socio-economic data on sampling sites have been collected through three questionnaires addressed to:

- farmer, containing sections on the identification of interviewer, his/her family and farm; on general information about the farm; on sheep and goat breeds present in the farm and on breeding system. Complete data on 633 farms in EU and other European Countries are in the database;
- region, containing socio-economic information on sampling regions. The questionnaire was substituted by direct retrieval of data from public sources.
- breeds, describing the characteristics of the breeds analysed in the project. Data on 30 sheep and 23 goat breeds autochthonous from 7 EU-15 Countries are in the database;
- information on farms where the breeds are raised have been also collected. Information has been obtained for 30 sheep and 23 goat breeds in 7 participating EU-15 Countries.

Analysis of current CAP, structural funds programs and Case studies

A critical analysis of current CAP policy programs was conducted with the aim to provide a description of economic and social issues related to actual and potential socio-economic development of rural areas [7].

Also, the project has prepared an handbook on 6 case studies in France, Italy and the UK. The breeds selected for case studies were Rove goat and Thone et Martod sheep in France; Valdostana goat and Gentile di Puglia sheep in Italy; Swaledale and Scottish Blackface in UK [8].

Evaluation of biodiversity for agricultural production

An handbook was conceived to review and design methods that can serve as a basis to guide conservation policies for livestock breeds at risk of extinction [9]. It reviews the principal issues of natural resources evaluation as they apply to biodiversity conservation. Concentrating on issues of livestock biodiversity, this review illustrates the key points relating to livestock biodiversity using a number of examples taken from the literature.

Integrated analyses and creation of maps

The integration of molecular, geographic, environmental and socio-economic analysis represented a real challenge to ECONOGENE participants. Tools have been developed to perform analysis in a Geographic Information System. Geographic level of data analysis was set at:

- the individual animal level, to describe geographic patterns of genetic variation and identify clines in allele and genotype frequencies;
- the farm level, to combine genetics, socio-economic data collected on farm and environmental variables, also collected on farm. A specific model for spatial analysis has been implemented at the farm level;
- the breed level. In this case the breed geographic location is represented by the centroid of the ECONOGENE sampling area for that specific breed. A specific model for spatial analysis has been implemented at the breed level;
- The NUTS III level. NUTS III is a regional unit that has some significance for EU that in addition to breed priorities may also be interested in regional priorities.

In addition, to implement the estimation of biodiversity, a questionnaire was submitted to breeding associations in all participating EU-countries that evaluates the characteristics of the breed and the importance of breed characteristics on a ranked scale. A final expert survey has been conducted to establish a utility weighting of different breed characteristics. These concern: intrabreed diversity, interbreed diversity (genetic distinctiveness), cultural value, market value and environmental value. Data were obtained from 137 experts (extension, university, breeding societies) and have been analysed using contingent choice models. The so estimated utility function is being implemented in the Weitzman model [10], [11], modified to consider the complexity and variety of data collected and to identify conservation priorities in different scenarios.

Guidelines for the sustainable conservation of genetic resources are being prepared on the basis of ECONOGENE results.

Conclusions

ECONOGENE is just finished, however data analysis and dissemination of results is only beginning. The issue of integrating data from different sources is addressed but not completely explored. A vast amount of novel information is organised and stored and represents a long lasting resource to be revisited whenever new methods become available.

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