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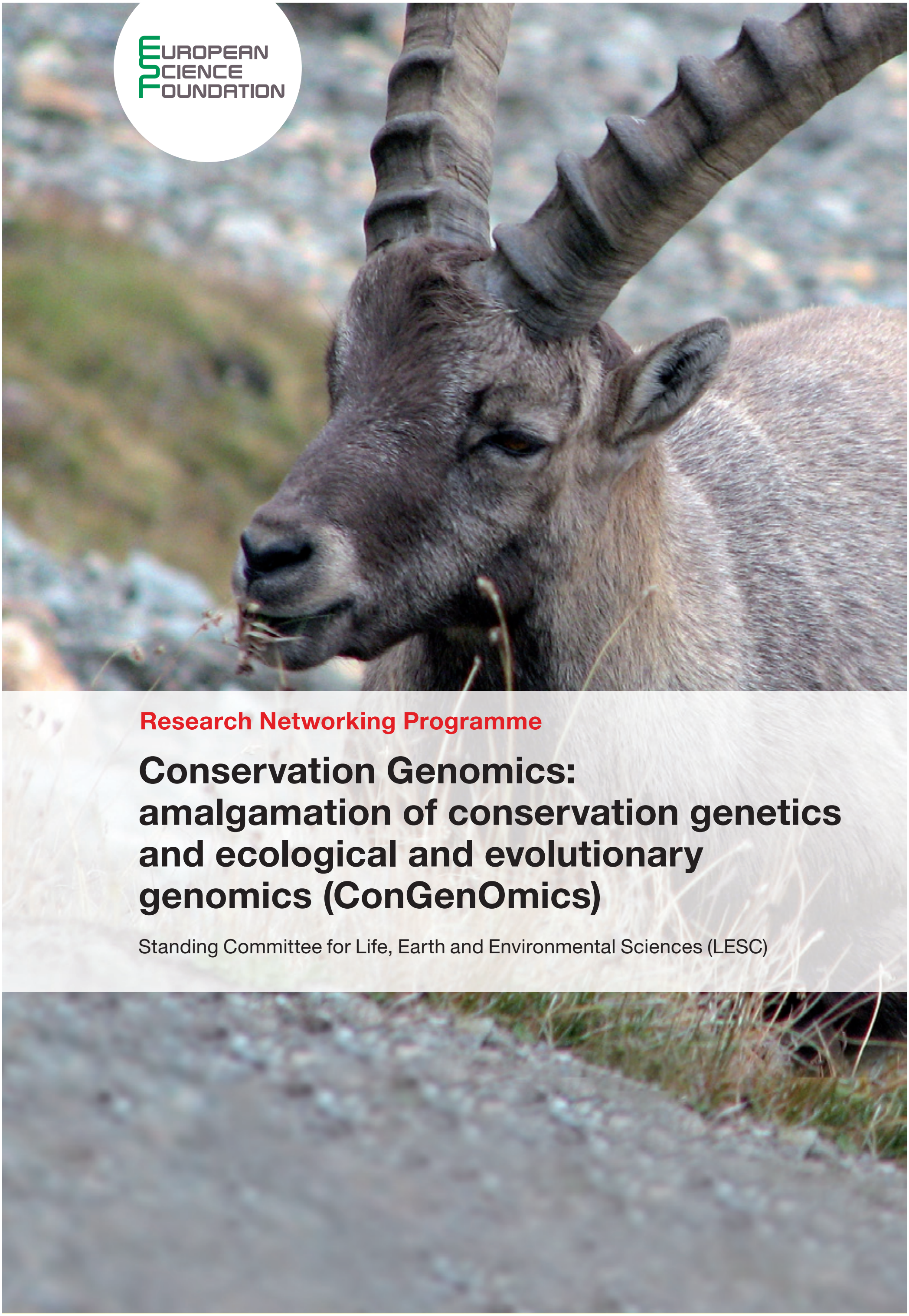


Research Networking Programme

Conservation Genomics: amalgamation of conservation genetics and ecological and evolutionary genomics (ConGenOmics)

Standing Committee for Life, Earth and Environmental Sciences (LESC)

There is little doubt that environments are changing rapidly, partly, if not primarily, due to human activity. The field of conservation biology has evolved from different scientific fields, economics and nature management and aims to protect species and their habitats from the negative effects of these changes. As the field has matured over the past decades, additional important future roles for conservation biology have been recognised. These include an increased focus on improving *predictions* about what changes are expected to occur in the future, what biodiversity needs to be preserved to maximise the chances of species to adapt to these changes, the rate at which these adaptations can occur, and understanding how species are expected to respond to these changes.

Conservation genetics focuses on the survival of species, characterised by small populations, which are prone to extinction. During the last five years this field has expanded substantially as evidenced by a number of recently published text books and scientific papers. Conservation genetics approaches are also routinely used in practical conservation projects and, as such, contribute to minimise biodiversity loss worldwide. Within Europe, the ESF Research Networking Programme CONGEN has contributed to the success of this field.

The ESF ConGenOmics network builds on the advances from CONGEN and develops a conservation genomics programme that includes the latest technological advances of the genomics revolution. Genomics approaches, which have been revolutionising all fields of biology recently, can offer important insights into a number of challenges faced by conservation biology such as identification of functionally important genomic variation and an improved understanding of the mechanisms behind important conservation genetic processes such as inbreeding depression.

The running period of the ESF ConGenOmics Research Networking Programme is five years, from June 2011 to June 2016.

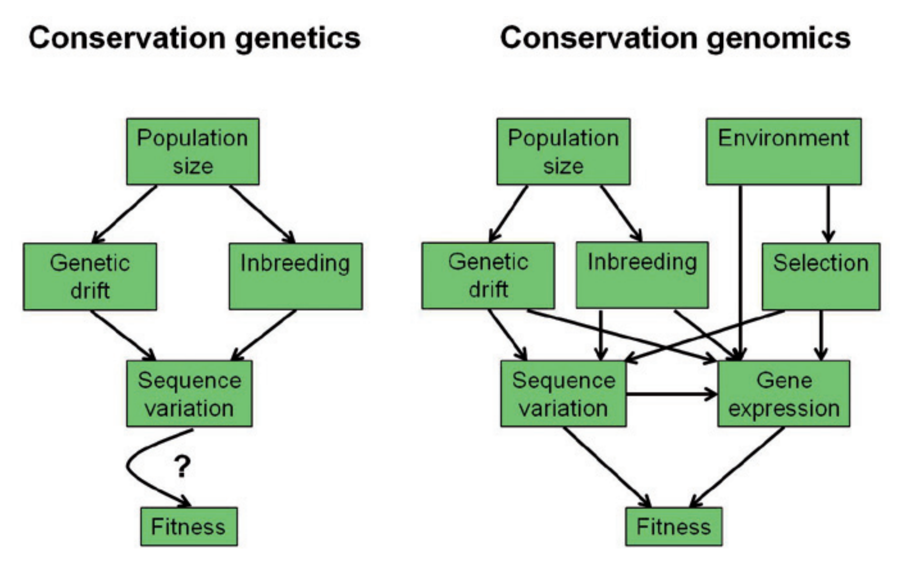
Scientific Background

Possibly the most noteworthy recent technological development of relevance for conservation biology is the emergence of the next generation of sequencing technologies. These “deep sequencing” or “ultra-high throughput sequencing” technologies have already demonstrated their potential by removing one of the main constraints of genomic approaches in non-model organisms, including many of conservation relevance: the lack of extensive genomic sequence information.

The genomics revolution brought about by technologies such as next-generation sequencing offer great possibilities but also present challenges. Much of the advance is technology-driven and expensive, which has the consequence that for many labs, currently working with more traditional methods, it will not be feasible, or even desirable, to update their scientific equipment. Instead, the most advanced equipment will be/is available in large outsourced commercial laboratories. This may in fact result in better possibilities to use these infrastructures. But what remains lacking is the necessary training in data analysis. In addition, genomics knowledge and facilities are very unevenly distributed across European countries.

Integrating ecological and evolutionary genomics in conservation genetics will revolutionise conservation genetics, compared to the concepts that prevailed in the ESF-CONGEN programme, in three important ways: 1) high throughput sequencing techniques will result in markers at high genome-wide density, allowing insight into genome-wide genetic variation, including sequence variation in functional genes and their regulators at extremely high detail; 2) the step from analyses of sequence diversity to

Figure 1. The conceptual difference between a conservation genetics and conservation genomics research approach (modified after Ouborg *et al*. 2010, *Trends in Genetics* **26**: 177–187).



transcriptional analyses of gene activity will facilitate the study of mechanisms that are involved in (mal)adaptation in threatened populations; and 3) new genomics technologies will allow a step up from the population level, the focus of conservation genetics, to community and species levels, the realm of metagenomics. The challenges that accompany this transformation of conservation genetics into conservation genomics should ideally be addressed at a European, or even global, multidisciplinary scale.

The principal scientific objective of this network programme is to aid knowledge transfer of the technological advances and challenges among European research groups focusing specifically on applications of genomic technologies in conservation biology. By promoting activities such as organising workshops and summer schools, expert meetings and the exchange of early-career researchers at European and pan-European levels, we will guide European conservation genetics into the genomics era. Researchers interested in the interface between genomics and conservation will benefit by being able to attend these activities to expand their knowledge on how to use genomics in conservation. We are convinced these activities will benefit conservation genomics as a research field and the application of genomics approaches in practical conservation.

Scope of the Programme

The founding ideas of conservation genetics in the 1980s largely concerned the impact of genetic drift and inbreeding on population persistence. Although the issue of genetic erosion has remained central, the field has since then greatly expanded. Ample empirical evidence has been found for an association between population size, genetic variation within populations, and level of inbreeding, in studies using supposedly neutral genetic markers, such as microsatellites and AFLPs (amplified fragment length polymorphisms).

Recently, new technical developments have opened the way to ask and answer new questions. The invention of next generation sequencing (NGS) techniques enables the collection of genome-wide information on genetic variation. NGS also facilitates genomic studies of non-model species that lack data on the genome and transcriptome. This revolutionises the field of conservation genetics in the following ways:

- Applying NGS techniques will give estimates of genetic variation across the entire genome, instead of estimates of variation based on a limited set of markers.
- Information on variation in thousands of single nucleotide polymorphism (SNP) markers allows a population genomic approach, which enables signals of selection and adaptation to be identified. SNP markers associated with selection can be investigated in small populations, which may lead to evaluations of the balance between genetic drift and selection.
- NGS allows the study of gene expression rather than the study of sequence variation. Transcriptomic studies will aid in identifying genes of adaptive importance, and will help considerably in investigating the mechanisms of

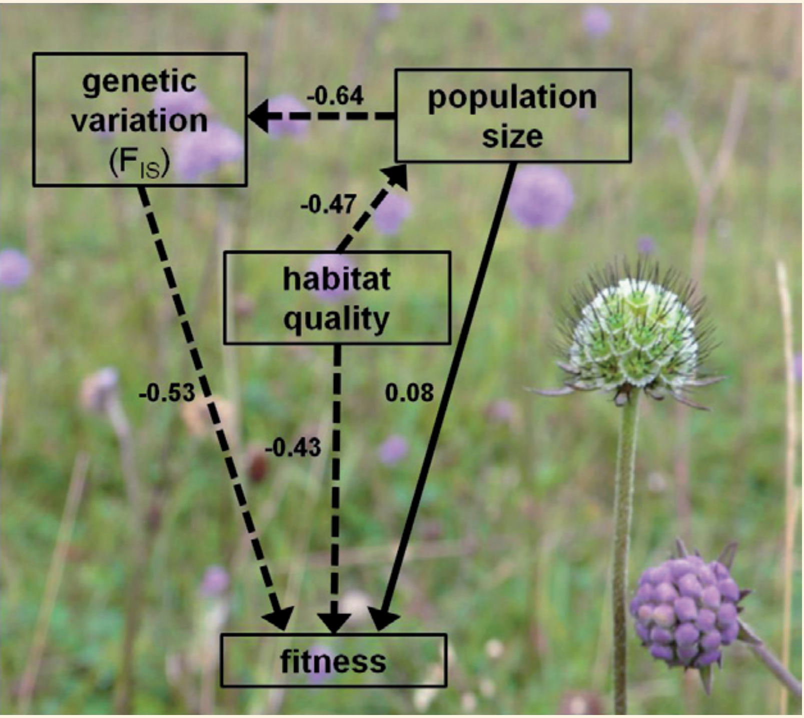


Figure 2. Combining environmental and genetic processes is one of the main research fields of conservation genomics.
The importance of combining environmental and genetic processes is illustrated in this diagram. Shown are the direct and indirect effects of genetic variation (F_{IS}), habitat quality and population size on plant fitness of the perennial plant Devil's-bit scabious, measured in 17 Dutch populations. Effect sizes are indicated next to the arrows (modified after Vergeer *et al*. 2003, *Journal of Ecology* **91**: 600-609).

processes that are important in a conservation genetic context (such as inbreeding depression and local adaptation).

The integration of genomic approaches into conservation genetics is still in its infancy. Both technical and methodological incorporation is emerging in the literature. However, the expansion of conservation genetics towards conservation genomics requires increased technical, methodological and data handling skills. One of the priorities of the ConGenOmics network is to facilitate the transfer of these skills from the (ecological) genomic community to the conservation genetic community.

Scientific knowledge and research facilities are not evenly distributed across Europe. Some disciplines are particularly strong in certain countries and less developed in other countries. The ConGenOmics Research Networking Programme therefore specifically aims at facilitating transfer of knowledge and skills across European research groups in order to build an integrated European network in conservation genomics. The network will contribute to the further development of the field in terms of the development of new concepts and translation of results into conservation practices.

Specific Aims and Objectives

The development and transfer of genomics knowledge and approaches in a conservation genetic context

ConGenOmics aims to develop population genetic approaches in model and non-model species, taking advantage of next generation sequencing techniques, that will lead to: (i) deeper inferences on demographic history, (ii) higher resolution inferences of population structure, (iii) opportunities to identify genomic regions under selection, (iv) greater coverage and more representative estimates of genetic variation, and (v) application to the management of wild and captive populations. At the same time the specific challenges of SNP approaches (the most likely molecular marker of choice in the future) will be taken up, including: (i) *de novo* development of SNPs or comparative approaches, (ii) how to deal with ascertainment bias, (iii) technical challenges of screening for SNPs, and (iv) how to manage and store the vast amounts of SNP data in an efficient way.

The experimental study of the (genomic) mechanisms behind important biological processes of relevance for conservation

Networks will be developed which will allow design of research programmes that aim to disentangle the genomic aspects of population genetic processes, and fitness, in a conservation context, including: (i) transcriptomic, proteomic and metabolomic analyses of inbreeding and outbreeding depression, (ii) genomic mechanisms of genotype-by-environment interactions, (iii) the genomic signature and mechanisms of local adaptation, (iv) genomic mechanisms behind phenotypic plasticity, (v) epigenetic mechanisms of adaptation and evolution, and (vi) the dynamics of functional gene variation in small populations, likely to be dominated by genetic drift.

The application and development of data handling and processing strategies in conservation genomics

While the new genomics technologies potentially allow deeper, higher resolution insights in important demographic and population genetic parameters and process, and will allow the mechanisms involved in these processes to be disentangled, they also present the challenge of how to deal with these large amounts of data. Developing bioinformatics approaches and training (young) researchers in their application will be an essential part of boosting the scientific and applied relevance of conservation genomics. It is important to: (i) design standard experimental protocols, (ii) use limited

Figure 3. ConGenOmics focuses on a wide variety of organisms including livestock, wild animals and plants. Photos by C. Aa. Sørensen (livestock), G. Segelbacher (alpine ibex) and P. Vergeer (northern rock-cress).

research sources in the most efficient way, (iii) share genomic information and results at a European and/or global scale, (iv) design and develop data handling procedures to efficiently and accurately extract relevant information from genomic experiments.

The application of community and metagenomics in a conservation biology context

Conservation genetics has traditionally focused on processes at the population level, but at the same time acknowledged that genetic variation at population level and processes at species and community level are intricately related. Metagenomics is the genomic analysis (most commonly by means of next generation sequencing technologies) of microbial communities. This new science provides access to organisms that form the vast majority of microorganisms on Earth. Metagenomics thereby offers a first peek at the wide variety of life that has never been studied, thus providing new insights into the structure and function of ecosystems as diverse as a polluted habitat or the gastrointestinal tract of an endangered species. A specific aim of this networking programme is to integrate species and community level genomic assessments in conservation genetics approaches. Therefore we will develop network activities that target: (i) studies that incorporate metagenomic monitoring in conservation genetics assessments, (ii) studies that aim to disentangle the relationship between genetic and genomic variation at population level, biodiversity and ecosystem functioning, (iii) studies that target the influence of species interactions on genetic variation and functional genomic activity, and (iv) studies that aim to disentangle the genomic interactions between pathogens, parasites and herbivores on one side and hosts on the other.

Programme Activities

During its five year running period the programme will aim to:

- Educate and train young scientists in interdisciplinary and collaborative research in the complex field of conservation genomics and familiarise young researchers with the European scientific community in this field.
- Review and standardise research approaches and evaluate procedures across Europe.
- Facilitate implementation and development of new and recent molecular tools as well as appropriate bioinformatics and analytical software and support access to biotechnological platforms.
- Detect and evaluate new developments in the field of conservation genomics and effectively disseminate the implications to the European scientific community, and make these accessible to other social actors such as nature managers and policy makers. This will undoubtedly promote development of adequate conservation management programmes for endangered species at a European scale.
- Establish a scientific network facilitating access to and exchange of sample material of endangered species across Europe.

These objectives will be pursued by carrying out the following activities.

Science workshop, conferences and summer schools

One of the main pillars of the programme will be to organise and/or support the organisation of workshops and summer schools. During its five year running period, different calls will be announced for the organisation of workshops, conferences and/or summer schools within the field of conservation genomics.

Supporting short and longer exchange visits

Another target of the programme is to promote exchange of practical knowledge and to initiate a network in conservation genomics and collaborative projects between laboratories at the European level. The exchange of researchers will be supported, ideally focusing on early careers researchers such as PhD students and postdocs. Open calls for short visits (1-2 weeks) as well as longer exchange visits (up to 6 months) will be made to foster scientific interactions between institutions from different countries. The planned visits should be directly relevant to the scope of the ConGenOmics network, which include topics such as development and transfer of genomics knowledge and approaches in a conservation context, experimental study of the (genomic) mechanisms behind important biological processes of relevance for conservation, application and development of data handling and processing strategies in conservation genomics, and application of community and metagenomics in a conservation biology context.

Building means of communication with researchers and end users in the field

Favourable Conservation Status is a central concept in the biodiversity conservation legislation of the European Union, e.g. in the Habitats directive. Conservation genomics approaches can provide critical information on the conservation status of species, for example whether populations and habitats meet the criteria deemed to be favourable, estimation of effective population size, and detection of effects

Figure 4. In the Netherlands, the perennial plant small scabious is an endangered species with highly fragmented and genetically eroded populations. The genomic aspects and differences in fitness are currently analysed in a conservation context, including transcriptomic and epigenetic analyses of inbreeding and inbreeding depression.
Photos by P. Vergeer.

of habitat fragmentation. ConGenOmics aspires to make genomics tools and knowledge available to a larger group of people, to transfer knowledge from genomics labs to conservation oriented labs, and from model organisms to threatened (non-model) species, from plants to animals.

ConGenOmics will also contribute to an acceleration of transfer from pure fundamental research to applied research, something that is very much needed given the pace of global changes. A further ambition is to put management recommendations on more scientifically solid ground.

To facilitate communication between various stakeholders the ConGenOmics programme has a central website (http://www.ru.nl/congenomics) where activities within the programme can be followed. ConGenOmics organises regular workshops and training courses to share concepts and methods between researchers. In the last stage of the network a conference will be organised that specifically aims to share concepts and achievements of the conservation genomics approach and the participating scientific community with potential end users.

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- **ΕΘΝΙΚΟ ΙΔΡΥΜΑ ΕΡΕΥΝΩΝ (NHRF)** *National Hellenic Research Foundation,* Greece
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The ConGenOmics network is officially associated with the Kansas (USA) ecogenomics initiative (http://ecogen.ksu.edu/index.html).

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For the latest information on this Research Networking Programme consult the ConGenOmics websites:
www.esf.org/congenomics
http://bit.ly/pgShrG
http://www.ru.nl/congenomics

The programme activities can also be followed via: twitter @ConGenOmics

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