

**Scientific Meeting organised within the Research Networking Programme
ConGenOmics:
“Merging Conservation Genetics and Ecological Genomics”**

Summary

Title: Merging Conservation Genetics and Ecological Genomics

Date: 9-10-11 February 2012

Duration: 3 days

Participants: 65 participants originating from 15 countries

Budget: € 35,000

Claimed costs: € 29,516.02

Host: Carles Vilà from Estación Biológica de Doñana (CSIC)

Organizers: Carles Vilà, Gernot Segelbacher, Philippine Vergeer

The CONGENOMICS programme aims to deliver a European platform for exchange of knowledge and facilities in the context of conservation genomics. The meeting addressed 3 major research topics which were represented in 3 separate sessions. Each session was introduced by invited speakers who are experts in the scientific field. The invited speakers were asked to present their cutting edge work on ecological and conservation genomics and to give their view on the application of genomic techniques in conservation biology and how these can contribute to future studies. By means of their presentations, the invited speakers sketched the topical framework of each session. At the end of each day, there was a lively plenary discussion in which the current knowledge and the future direction of conservation genomics were discussed. We also discussed gaps in our current knowledge as well as how to deal with these. Furthermore, areas of high priority were identified. The information brought together in this meeting will be used to shape and define the upcoming network activities of the CONGENOMICS programme.

The meeting was attended by 65 registered participants originating from 15 countries. 14 speakers were invited to give a talk.

Detailed description of scientific content

The CONGENOMICS programme is a multinational research program within the ESF Research Networking Programme. The CONGENOMICS programme aims to deliver a European platform for exchange of knowledge and facilities in the context of conservation genomics. Conservation genomics is a new field that is developing out of the merging of conservation genetics with ecological and evolutionary genomics. By using the latest genomic technologies conservation genomics is concentrating on : i) applying genome-wide markers to reliably estimate demographic and genetic parameters in a conservation context, ii) applying gene-expression tools to study the mechanisms behind important conservation genetic processes, like inbreeding depression, and iii) using metagenomic approaches to develop from population level approaches to species and community level assessments.

The present meeting is the first scientific meeting organized within this networking programme. The goal of this first meeting was to discuss the latest knowledge and to identify gaps in our current knowledge in the field of conservation genomics. During this meeting, fields of research of high priority for conservation genomics were identified and applications of genomic technologies in conservation genomics were shared and discussed. In addition, topical questions in conservation genomics were addressed and it was discussed how to analyze these best. The information brought together in this meeting will be used to shape and define upcoming network activities within the ConGenOmic programme.

The meeting addressed 3 major research topics which were represented in 3 separate sessions. Each session was introduced by invited speakers who are experts in the scientific field. The invited speakers sketched the topical framework of each session by presenting their cutting edge work and their view on the application of genomic techniques in conservation biology and how these can contribute to future studies. This resulted in a lively discussion among all participants.

The following 3 research topics were addressed:

1. The experimental studies of (genomic) mechanisms behind important biological processes of relevance for conservation.

In this session we discussed research aiming 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.

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

This session focused on methods and techniques for data handling. New genomic technologies potentially allow deeper, higher resolution insights in important demographic and population genetic parameters and processes, and will allow disentangling the mechanisms involved in these processes. However these new techniques also result in large amounts of data, challenging traditional ways to deal with the data. We discussed standard experimental protocols, the use of limited research sources in the most efficient way, sharing genomic information and results at a European and/or global scale and data handling procedures.

3. The application of community and metagenomics in conservation biological 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, NGS) of microbial

communities. This new science provides access to organisms that cannot be cultured, as are 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 insight into the structure and function of ecosystems as diverse as a polluted habitat or the gastrointestinal tract of an endangered species. This session focused on the studies that incorporate metagenomic monitoring in a conservation genetic assessments, studies that aim to disentangle the relationship between genetic and genomic variation at population level and biodiversity and ecosystem functioning, studies that target the influence of species interactions on genetic variation and functional genomic activity, and studies that aim to disentangle the genomic interactions between pathogens, parasites and herbivores on one side and hosts on the other.

At the end of each day, there was an active plenary discussion in which the current knowledge, the future direction of conservation genomics and areas of high priority were discussed (see section “summary of the discussions”). The information brought together in this meeting is used to shape and define the upcoming network activities of the CONGENOMICS programme.

Summary of the discussions

In two plenary discussions the characteristics, priorities and future of Conservation Genomics were discussed with all attendants.

It was generally agreed that conservation genomics should be seen as a valuable expansion, not as a replacement, of conservation genetics. The questions to be addressed within a conservation genomic context vary from community screening (metagenomics) to detailed functional genomics of processes and phenomena that are relevant for conservation, like inbreeding depression. All these approaches share that they involve non-model species and the application of Next Generation Sequencing.

Roughly the goals were divided along two lines: on the one hand conservation genomics should apply genome-wide assessment of genetic variation, which should be done in as many species as possible, while on the other hand, for a restricted set of species, conservation genomics should try to elucidate general principles and mechanisms that are relevant for genetic management.

There was consensus about the statement that within conservation genomics research questions should be leading and techniques should follow question.

Although much variation in topics and questions was evident, general priorities were formulated on:

- The clear need for case studies that illustrate the value of a conservation genomic approach.
- The simultaneous study of drift and selection, aiming to investigate the balance between local adaptation and genetic erosion.

Impacts on future directions of Conservation Genomics

The information brought together in this meeting will be used to shape and define the upcoming network activities of the ConGenOmics programme. For the ConGenOmics program we feel that this results in the following priorities:

- Training the conservation (genetic) community in the application of NGS, with special attention for how to apply the techniques in non-model species that lack most of the genomic resources. An introductory summer school, and a NGS technique meeting were considered to be most helpful.
- Organising a meeting on how to deal with the immense amount of data that result from an NGS experiment. Focus should lie on how to manage and handle the data, and how to perform initial

analyses, like assembly of NGS reads. Focusing on the bioinformatics aspects of conservation genomics was considered to have high priority.

- Organising meetings on specific topics that illustrate and work out the value of conservation genomics for the broader community. An open call procedure, based on a bottom-up approach, was embraced by all attendants.

Conclusion

Held in an informal but stimulating scientific atmosphere, with a limited number of 65 participants, this meeting provided an excellent opportunity for knowledge transfer and establishments of interactive collaborations in the field of conservation genomics with a lot of interaction between participants from different countries. There was a good mixture of top-ranked invited speakers and senior and junior researchers for fruitful discussions focusing on major challenges in conservation genomics, future directions, gaps in our current knowledge, as well as on what topics should be addressed and discussed in future workshops and summer schools.

Programme

Thursday 9 February 2012

(Location: Foro de la Biodiversidad, Patio de Banderas 16, Seville)

- 9:00-9:30 Registration
- 9:30-9:45 Welcome by **Carles Vilà** (*Estación Biológica de Doñana, Sevilla, Spain*)
- 9:45-10:15 Introduction to Conservation Genomics by **Joop Ouborg** (*Molecular Ecology, Radboud University of Nijmegen, Netherlands*)
- 10:15-10:45 coffee/tea
- 10:45-11:35 **Alex Widmer** (*ETH Zurich Plant Ecological Genetic, Institute of Integrative Biology, Zürich, Switzerland*) -- Developing a genome-wide perspective on genetic variation.
- 11:35-12:25 **Mike Bruford** (*School of Biosciences, Cardiff University, United Kingdom*) -- The falcon genome project: first results.
- 12:25-13:15 **Leif Andersson** (*Department of Medical Biochemistry and Microbiology, Uppsala University, Sweden*) -- Detecting signatures of selection in the Atlantic herring using whole genome resequencing.
- 13:15-14:45 lunch
- 14:45-15:35 **Simone Sommer** (*Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany*) -- Evolutionary adaptations and biodiversity conservation
- 15.35-16.00 **Ilik Saccheri** (*School of Biological Sciences, University of Liverpool, United Kingdom*) -- Genomic hotspots for inbreeding depression and the maintenance of genetic load.
- 16.00-16.25 **Raj Whitlock** (*School of Biological Sciences, University of Liverpool, United Kingdom*) - Lineage mixing and outbreeding depression - a systematic review of the evidence.
- 16:25-17:00 coffee/tea
- 17:00-17:50 **Staffan Bensch** (*Molecular Ecology and Evolution Lab, Lund University, Sweden*) – Finding genetic differences when small: examples from a very abundant songbird with implications for conservation genomics.
- 17:50-19:30 Plenary discussion Day 1: Future and prospects of conservation genomics
- 20.30- 22.30 Dinner (in the restaurant of hotel Casa Romana)
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Friday 10 February 2012

(Location: Foro de la Biodiversidad, Patio de Banderas 16, Seville)

- 9:00-9:30 **Loretta Johnson** (*Ecological Genomics Institute, Kansas State University, Manhattan, USA*) -- Ecotypic and genetic variation in a dominant prairie grass: Implications for grassland conservation in a changing climate.
- 9.30-10.20 **Joachim Mergeay** (*Research Institute for Nature and Forest, Scientific Institute of the Flemish government, Belgium*) -- Conservation genomics: more than genomic conversations?

- 10:20-11:00 coffee/tea
- 11.00-11.50 **Oscar Gaggiotti** (*Laboratoire d'Ecologie Alpine (LECA), Universite Grenoble I, Grenoble, France*) -- Environmental and ecological drivers of intra-specific biodiversity: the role of theoretical and statistical modeling in population genetics.
- 11:50-12.40 **David Pollock** (*Department of Biochemistry and Molecular Genetics, University of Colorado, Denver, USA*) -- Evolutionary genomic sampling: Microsatellites, transposable elements, variation and the future of conservation genomics.
- 12:40-13:00 Photo
- 13:00-14:30 lunch
- 14:30-15:20 **Eric Coissac** (*Laboratoire d'Ecologie Alpine (LECA), Universite Grenoble I, Grenoble, France*) -- DNA Metabarcoding: High-throughput biodiversity assessment.
- 15:20-16:20 Plenary discussion Day 2: Future and prospects of conservation genomics
- 16:20-17:00 coffee/tea

Cultural visit

- 19.00-20.00 Visit the to the Royal Alcazar
(<http://www.patronato-alcazarsevilla.es/index.php>)
- 20.00-21.30 Dinner (cocktail in the gardens of the Royal Alcazar)

Saturday 11 February 2012

- 9:00-19:30 Excursion to Doñana National Park. Gather at 9.00 in front of hotel Casa Romana
- 20.30- 22.30 Dinner (in the restaurant of hotel Casa Romana)

Full list of registered participants

Title	Name	City	Country	Function
Prof	Carles Vilà	Seville	ES	Convenor
Dr	Gernot Segelbacher	Freiburg	DE	Convenor
Dr	Philippine Vergeer	NIJMEGEN	NL	Convenor
Prof	Alex Widmer	Zürich	CH	Speaker
Prof	David Pollock	Aurora	US	Speaker
Prof	Eric Coissac	Grenoble	FR	Speaker
Dr	Ilik Saccheri	Liverpool	UK	Speaker
Dr	Joachim Mergeay	Leuven	BE	Speaker
Prof	Joop Ouborg	NIJMEGEN	NL	Speaker
Prof	Leif Andersson	Uppsala	SE	Speaker
Prof	Loretta Johnson	Manhattan	US	Speaker
Prof	Mike Bruford	Cardiff	UK	Speaker
Prof	Oscar Gaggiotti	Grenoble	FR	Speaker
Dr	Raj Whitlock	Liverpool	UK	Speaker
Prof	Simone Sommer	Berlin	DE	Speaker
Prof	Staffan Bensch	Lund	SE	Speaker
Prof	Terry Burke	Sheffield	UK	Speaker
Dr	Alfredo García Fernández	Móstoles	ES	Participant
Dr	Adrian Brennan	Seville	ES	Participant
Mr	Alvaro Dugo	Seville	ES	Participant
Ms	Anna Cornellas	Seville	ES	Participant
Dr	Camila Mazzoni	Berlin	DE	Participant
Dr	Celia Schunter	Barcelona	ES	Participant
Dr	Chris Creevey	Grange	IE	Participant
Dr	Christine Grossen	Zurich	CH	Participant
Mr	Christophe Lejeusne	Seville	ES	Participant
Dr	Christopher Wheat	Helsinki	FI	Participant
Dr	Claudia Brandariz Fontes	Seville	ES	Participant
Prof	Domenico Fulgione	Naples	IT	Participant
Dr	Eaaswarkhanth Muthukrishnan	Seville	ES	Participant
Ms	Elena Marmesat	Seville	ES	Participant
Dr	Esperanza Manzano	Seville	ES	Participant
Prof	Ettore Randi	Ozzano Emilia	IT	Participant
Dr	Fernando Cruz	Seville	ES	Participant
Dr	Ferran Palero	Valencia	ES	Participant
Prof	Giorgio Bertorelle	Ferrara	IT	Participant

Dr	Guy Colling	Luxembourg	LU	Participant
Prof	Iosune Uriz Lespe	Blanes	ES	Participant
Dr	Irene Salicini	Seville	ES	Participant
Prof	Jacob Höglund	Uppsala	SE	Participant
Dr	Jennifer Leonard	Seville	ES	Participant
Prof	Jesús Fernández Martín	Madrid	ES	Participant
Dr	José Antonio Godoy	Seville	ES	Participant
Prof	Luc de Meester	Leuven	BE	Participant
Dr	M ^a Angeles Rodríguez de Cara	Madrid	ES	Participant
Prof	Marta Pascual	Barcelona	ES	Participant
Mr	Miguel Camacho	Seville	ES	Participant
Dr	Miguel Carneiro	Vairão	PT	Participant
Mr	Pablo Burraco Gaitán	Seville	ES	Participant
Prof	Paulo Celio Alves	Vairão	PT	Participant
Prof	Per J	Groningen	NL	Participant
Dr	Peter Galbusera	Wilrijk	BE	Participant
Mr	Peter Halvarsson	Uppsala	SE	Participant
Dr	Pim Edelaar	Seville	ES	Participant
Prof	Rafael Zardoya	Madrid	ES	Participant
Dr	Ramón Casimiro-Soriguer	Seville	ES	Participant
Dr	Ricardo Jorge Lopes	Vairão	PT	Participant
Dr	Robert Kraus	Frankfurt	DE	Participant
Dr	Rosa Agudo	Seville	ES	Participant
Prof	Salvatore Cozzolino	Naples	IT	Participant
Dr	Sanna Olsson	Madrid	ES	Participant
Dr	Tania Walisch	Luxembourg	LU	Participant
Dr	Violeta Munoz-Fuentes	Seville	ES	Participant
Dr	Xavier Turon	Blanes	ES	Participant
Prof	Zisis Mamuris	Larissa	GR	Participant