

Autumn school organised within the ESF Research Networking Programme
ConGenOmics:
“An Introduction to Conservation Genomics”

Summary

Date: 30 September – 5 October 2012

Duration: 6 days

Participants: 35 participants

Lecturers: 7 lecturers

ESF Budget: € 30,000

Host: Prof Craig Primmer, Department of Biology, University of Turku, Finland

Organizers: Craig Primmer, Philippine Vergeer, Ville Aukey

By using the latest genomic technologies conservation genomics can now concentrate for example on the application of genome-wide markers to reliably estimate demographic and genetic parameters in a conservation context. During this autumn school we specifically focussed on the application and technical aspects of genomic techniques and how these genomic techniques can be used to address topical questions in conservation biology.

The autumn school was aimed at early-career researchers with some background knowledge in basic genetics and conservation biology and a strong interest in learning more about topics that are related to the application of genomic technologies in conservation biology. Prospective participants had to send an application by email to the organizers containing a brief CV with a list of publications (if any) together with a one-paragraph statement of scientific interests and motivation (up to 250 words). We received ca. 75 applications. 35 participants from 8 countries were selected based on CV and letter of motivation.

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.

This autumn school was the first autumn school meeting organized within this networking programme. The goal of this autumn school was to focus on the use of genomics techniques, in particular next-generation sequencing (NGS) methodologies, in conservation biology specifically for non-model species. The autumn school aimed at early-career researchers who have some background knowledge in basic genetics and conservation biology but who have an interest in learning more about topics that are related to the application of genomic technologies in conservation biology.

During this autumn school, the application of NGS techniques and other genomic methods were discussed in different sessions. Each session was led by invited speakers who are experts in the scientific field and familiar with the pro's and con's of these techniques. 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. Some sessions included practical sessions with data analysis and computer exercises e.g. on the process of SNP discovery.

During the different sessions, the following topics were addressed:

On Sunday the topic was introduced, and arguments were provided for a role of genomic approaches in conservation. Also the current state of the field of conservation genomics in general was introduced and a number of tasks and questions laying ahead were discussed.

On Monday an overview was given of current and future NGS technologies, supplemented by a presentation of major NGS companies the latest NGS technologies (Life Technologies: Ion Torrent and SOLiD; Roche 454; Illumina (HiSeq, MiSeq, SNP genotyping) and Pacific Biosciences). In the afternoon, the experimental design of genomics studies was discussed.

On Tuesday we discussed how to go from NGS data to molecular markers. First, we focussed on the conditions of NGS use. Topics such as data cleaning, pre-processing data, software issues and data quality were discussed. Second, methods such as SNP analysis and SNP chips, targeted re-sequencing, genotyping by sequencing and allelotyping by sequencing were discussed. This session included a practical session with data analysis and computer exercises on the process of SNP discovery.

The session on Wednesday focussed on how to go from single reads to annotated sequences. During this session we discussed aspects of data cleaning, assembly and quality control. Like Tuesday afternoon, this session included practical sessions with data analysis and some more exercises on SNP discovery.

On Thursday, examples of conservation genomic studies were presented and discussed. During this last session, questions of Sunday evening were connected to the actual conservation interpretation, via the technical explanations given during the course.

Most speakers were present for discussions during the entire autumn school which provided an excellent opportunity for strong interaction and brainstorming on the application of genomic

techniques in conservation biology. At the end of the autumn school, a virtual folder on the ConGenOmics website was created with additional information, literature, excersises, software and datasets. In addition, all lectures were uploaded. This virtual website is available to all participants and is visited frequently.

Assessment of the results and impact of the event on the future directions of the field

The course gave a short, but full, introduction to the new aspects that are involved in genomic analyses in a conservation context. The students mostly worked with non-model species in their own research and were very interested in how NGS might help in case of a non-fully sequenced non-model species. In fact, this issue challenged the lecturers as well, as many techniques work more or less routinely in model species like *Arabidopsis thaliana* and fruit flies, but their transfer to rare or threatened species is by no means trivial. In that sense the course also was valuable for the lecturers.

At the end an internet questionnaire was designed and send to the students. We got 100% response and without exception all were very happy with the course. The course was seen as very helpful in further development of skills that are going to be applied in the respective research programs of the students. Several suggestions for a follow up course were given, and the steering committee of the ConGenOmics program will thankfully profit from these suggestions.

Annex 1: List of speakers/lecturers and participants

Speakers:

Dr. John Davey	Edinburgh, (UK)	Speaker
Professor Jacob Höglund	Uppsala, (SE)	Speaker
Dr. Erica Leder	Turku, (FI)	Speaker
Dr. Marjorie Oleksiak	Miami, (US)	Speaker
Dr. Joop Ouborg	Nijmegen, (NL)	Speaker
Dr. Anna Santure	Sheffield, (UK)	Speaker
Dr. Matthew Webster	Uppsala, (SE)	Speaker

Participants:

Miss Heidi Aisala	Oulu, (FI)	Participant
Dr. David Canal	Seville, (ES)	Participant
Dr. Joanne Chapman	Kalmar, (SE)	Participant
Mr. Luca Cornetti	S. Michele, (IT)	Participant
Mr. Joost De Jong	Wageningen, (NL)	Participant
Miss Hanne De Kort	Heverlee, (BE)	Participant
Mr. Chris Eberlein	Helsinki, (FI)	Participant
Dr. Leanne Falks	Uppsala, (SE)	Participant
Dr. Joana Ferreira Marques	Lund, (SE)	Participant
Dr. Carmelo Fruciano	Konstanz, (DE)	Participant
Mr. Konstantinos Gkagkavouzis	Thessaloniki, (GR)	Participant
Dr. Delphine Grivet	Madrid, (ES)	Participant
Dr. Philippe Helsen	Antwerpen, (BE)	Participant
Miss Aino Kalske	Turku, (FI)	Participant
Miss Hanna Laakkonen	Helsinki, (FI)	Participant
Miss Veronika Laine	Turku, (FI)	Participant
Dr. Christophe Lejeusne	Seville, (ES)	Participant
Miss Elena Marmesat	Seville, (ES)	Participant
Miss Tiina Mattila	Oulu, (FI)	Participant
Mr. Kevin Mulder	Uppsala, (SE)	Participant
Dr. Violeta Muñoz-Fuentes	Seville, (ES)	Participant
Miss Alina Niskanen	Oulu, (FI)	Participant
Dr. Sanna Olsson	Helsinki, (FI)	Participant
Dr. Ferran Palero	Valencia, (ES)	Participant
Dr. Paolo Ruggeri	Ancona, (IT)	Participant
Dr. Irene Salicini	Sevilla, (ES)	Participant
Mr. Juan-Diego Santillana-Ortiz	Düsseldorf, (DE)	Participant
Miss Katharina Steyer	Frankfurt, (DE)	Participant
Dr. Gonçalo Themudo	Vairão, (PT)	Participant
Miss Sibelle Torres Vilaça	Ferrara, (IT)	Participant
Miss Veera Tuovinen	Uppsala, (SE)	Participant
Dr. Silva Uusi-Heikkilä	Berlin, (DE)	Participant
Miss Heidi Viitaniemi	Turku, (FI)	Participant
Dr. Eugenia Zarza	Frankfurt am Main, (DE)	Participant
Miss Ksenia Zueva	Turku, (FI)	Participant

Annex 2: Programme

Lecturers: AS- Anna Santure; CP- Craig Primmer; EL- Erica Leder; JD- John Davey; JH- Jacob Höglund; JO- Joop Ouborg; MO- Margie Oleksiak; MW- Matthew Webster

Note- both morning and afternoon sessions include a coffee break, even if not listed

Sunday 30 Sept -- Arrival plus introductory lectures

16:00-18:00 Arrival and Welcome
18:00-19:00 Dinner
19:00-21:00 Introduction evening session
Why Conservation genomics? (JO)
Next generation sequencing methodologies- an overview (EL)
21:00-23:00 Welcoming reception

Monday 1 Oct -- Introduction to Conservation Genomics

8:00-9:00 breakfast
9:00-12:00 Overview of current and future NGS technologies
9:00-9:40 Life Technologies: Ion Torrent, SOLiD (Peter Karlberg)
9:40-10:20 Roche 454 (Lars Paulin)
10:20-10:40 Coffee
10:40-11:20 Illumina: HiSeq, MiSeq, SNP genotyping (Golden Gate, Infinium)- Reija Lahtinen
11:20-12:00 Pacific Biosciences- Jenny Ekholm
12:00-13:00 lunch
13:00-17:00 Experimental design (MO)
18:00-19:00 dinner
19:00-21:00 Slots for extra teaching discussion sessions and/or personal advice
21:00 light evening snack
21:00 → Hostel sauna (fits 8-10 people at a time)

Tuesday 2 Oct -- From NGS data to molecular markers and annotated sequences

8:00-9:00 breakfast
9:00-12:00 Data cleaning, assembly and quality control (MW)
12:00-13:00 lunch
13:00-17:00 Sequence annotation, ortholog identification and associated data analyses (MO)
SNP discovery and analysis (AS)
18:00-19:00 dinner
19:00-21:00 Slots for extra teaching discussion sessions and/or personal advice
21:00 light evening snack
21:00 → Hostel sauna (fits 8-10 people at a time)

Wednesday 3 Oct -- From NGS data to molecular markers and annotated sequences (cont.)

8:00-9:00 breakfast
9:00-12:00 SNP discovery and analysis (cont.) (AS)
12:00-13:00 lunch
13:00-17:00 Genome complexity reduction methods (JD)
18:00-19:00 dinner, possibly in city centre (at own cost) or else at Tuorla as normal
19:00-... Expedition into town centre to experience local night life (optional)
21:00 light evening snack

Thursday 4 Oct – Molecular markers (cont.) and examples of conservation genomic studies

- 8:00-9:00 breakfast
- 9:00-12:00 Genome complexity reduction methods (cont)(JD)
- 12:00-13:00 lunch
- 13:00-17:00 Examples of conservation genomic studies
- 13:00-13:40 Heidi Aisala- Gyrodactylus salaris genome sequencing
- 13:40-14:20 Anna Santure- Great tit genomics
- 14:20-14:45 Coffee
- 14:45-15:25 Jacob Höglund- Black grouse MHC characterisation using NGS
- 15:25- 16:05 Susan Johnston- SNP analyses using degraded DNA: experiences with archived Atlantic salmon scales
- 17:00-23:30 Farewell Dinner, Finnish sauna (fits 20 people), Finnish sausage, and swimming in the Baltic (private bus transport to and from)
- 23:50 arrival back to Tuorla

Friday morning 5 Oct – Departure

- 8:00-9:00 breakfast
- 9:00-... Departure