



## Research Networking Programmes

Short Visit Grant  or Exchange Visit Grant

*(please tick the relevant box)*

### Scientific Report

The scientific report (WORD or PDF file – maximum of eight A4 pages) should be submitted online within one month of the event. It will be published on the ESF website.

**Proposal Title:** Deciphering genetics from epigenetics - local adaptation in marine three-spined sticklebacks

**Application Reference N°:** 7206

#### 1) Purpose of the visit

The project is embedded within a bigger framework of the EU-BONUS project (BAMBI, <http://bambi.gu.se>), in which we investigate the population structure of marine three-spined sticklebacks from the Baltic Sea with genome-wide markers such as RAD-sequencing and copy number variants (CNV). The overarching goal is to access the evolutionary potential of species to respond to climate change, here decreased salinity.

The precise aim of my visit in Ovidiu Paun's Lab under the guidance of Emiliano Trucchi was to intensify collaboration and apply innovative methods to decipher genetic and epigenetic processes of local adaptation in the three-spined sticklebacks. Particularly, focusing on DNA-methylation, we wanted to test a new method (Trucchi et al, under review), with which we later want to investigate genome-wide DNA-methylation of hundreds of individuals from locations with different salinity regimes.

As this is ongoing work, I will not go further to the details.

#### 2) Description of the work carried out during the visit

Under supervision from my Viennan hosts I learnt the standard RAD-sequencing protocol (e.g. Hohenlohe et al. 2010; Etter et al. 2011) and optimized each step with variations in used chemistry (e.g. for cleaning of genomic DNA with NucleoSpin gDNA clean-up kit, MN; for cleaning of library steps with Ampure SPRIselect beads and Qiagen MinElute PCR Cleanup Kit) or available equipment (e.g. Pippin Prep; Bioruptor). Following our freshly changed protocol I generated two libraries encompassing barcoded DNA of 20 individuals.

Additionally I executed a bisulfite conversion step to the same template DNA and managed to create functional libraries. The quality check for the libraries were done with Agarose gel, Qubit and Bioanalyzer.

As this is ongoing work, I will not go further to the details.

**3) Description of the main results obtained**

I managed to generate libraries (both Standard and bisulfite-converted), which we now will sequence on a NextSeq Illumina machine. After successful sequencing in late summer 2015 and some preliminary bioinformatic assessment, I can better evaluate the applicability of this method to a bigger scale.

**4) Future collaboration with host institution (if applicable)**

I plan to continue collaboration intensively: besides more labwork, I would like to co-develop bioinformatic pipelines and create new projects. The different kind of collaborations are in planning phase and discussed with the partners. It is also planned to invite our host to the GEOMAR to give a lecture or special seminar.

**5) Projected publications / articles resulting or to result from the grant (*ESF must be acknowledged in publications resulting from the grantee's work in relation with the grant*)**

Pending further analyses and extended experiments, we expect our results in a joined paper of Britta S. Meyer, Emiliano Trucchi, Christophe Eizaguirre and Thorsten Reusch, who all contributed to project development or conduction. Considering the results we target for subject specific journals within the field of Evolutionary Biology.

**6) Other comments (if any)**

Etter PD, Bassham S, Hohenlohe PA, Johnson EA, Cresko WA. 2011. SNP Discovery and Genotyping for Evolutionary Genetics Using RAD Sequencing. In: *Methods in Molecular Biology*. Vol. 772. *Methods in Molecular Biology*. Totowa, NJ: Humana Press. pp. 157–178.

Hohenlohe PA, Bassham S, Etter PD, Stiffler N, Johnson EA, Cresko WA. 2010. PLOS Genetics: Population Genomics of Parallel Adaptation in Threespine Stickleback using Sequenced RAD Tags. Begun DJ, editor. *PLoS Genet* [Internet] 6:e1000862. Available from: <http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1000862#abstract0>