



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: LANDSCAPE GENOMICS IN THE WATER FLEA, DAPHNIA

Application Reference N°: 4810

1) Purpose of the visit

As it was indicated in the application form, the current proposal for the ESF Exchange visit grant 2014 was awarded to facilitate two main tasks. Firstly, starting from genomic raw data generated for *Daphnia pulex* during the current postdoctoral position of the applicant, he would develop a pipeline to filter those highly confident and biallelic SNPs markers to analyze the effect of ‘cultural eutrophication’ on natural populations. Second, the results compiled would be discussed with the host researcher Prof. De Meester and his team in order to prepare a proposal for the European International Fellowship-PEOPLE (IF-MSCA-H2020). In particular, the aims of this proposal were: a) Development and transfer of genomic knowledge (e.g., genomic software); b) Preparation of future collaborations of the applicant with the team of Prof. De Meester; and c) Application and development of data handling related to (adaptive) evolution of natural populations using *Daphnia pulex* as model organism.

2) Description of the work carried out during the visit

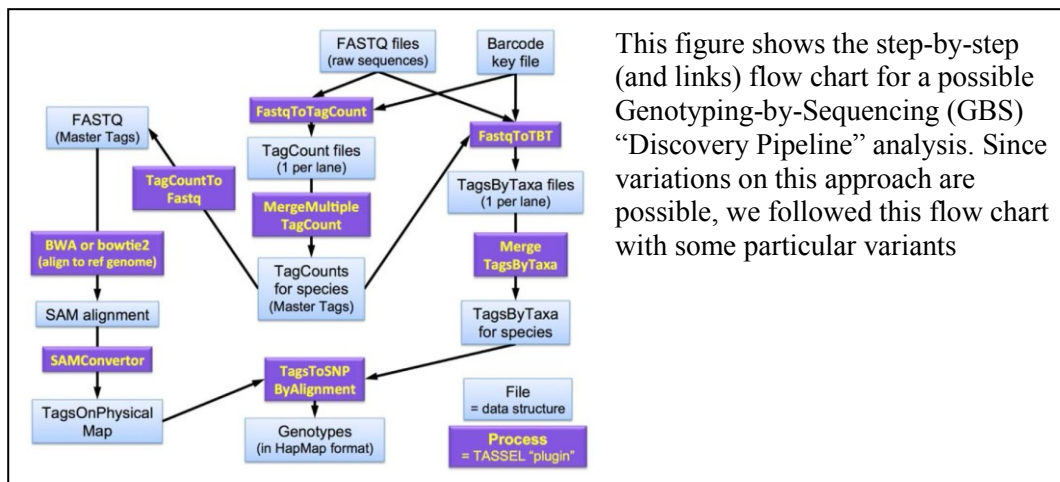
During the Exchange visit to KU Leuven, Leuven, Belgium (five weeks in total), the host researcher (Prof. Luc De Meester), his team and the applicant have been discussing and working very closely with the Next-Generation-Sequencing raw data generated by the applicant along his current IOF-Marie Curie (the University of Oklahoma [OU] – USA, and the Spanish National Research Council [CSIC]). All the purposes of this visit have been successfully covered, and two major tasks were carried out:

A) Acquiring the conceptual basis, skills and handling for several bioinformatics software such as TASSEL, BWA, and VCFtools under Linux platform (see figures in the next page).

Preparing and applying for an Individual Fellowship (IF) from the Marie Skłodowska-Curie Action proposal within the new European framework programme HORIZON 2020 to be hosted in KU Leuven (Leuven, Belgium) under the supervision of Prof. De Meester.

Bio-Linux is a bioinformatics easy way to use and access to a variety of projects involved the following methods:

- Provision of complete systems
- Provision of bioinformatics software repositories
- Addition of bioinformatics packages to standard distributions
- Community building and support systems



This figure shows the step-by-step (and links) flow chart for a possible Genotyping-by-Sequencing (GBS) "Discovery Pipeline" analysis. Since variations on this approach are possible, we followed this flow chart with some particular variants

3) Description of the main results obtained

The applicant consider this Exchange visit as very productive to the applicant and the host institution. Results obtained are in concordance with the objectives and the work indicated in the initial application. The main results have been the transference of knowledge regarding to genomic tools and the preparation of a draft project to be submitted for a European International Fellowship-PEOPLE (IF-MSCA-H2020).

In particular, the time dedicated to genomic dataset has resulted in a first manuscript draft, which will be co-authored by the applicant, the host researcher (Prof. De Meester), part of his team (i.e., Anurag Chaturvedi), and the scientific-in-charge (Prof. Weider, Univ. Oklahoma, USA) from the IOF grant that the applicant is currently enjoying. Here you can read the resulting tentative title and abstract:

Tentative title: Characterization of genome-wide SNPs for the water flea *Daphnia pulex* generated by genotyping-by-sequencing (GBS)

Joaquín Muñoz 1,2, Anurag Chaturvedi 3, Luc De Meester 3, Lawrence J Weider 2

1 - Doñana Biological Station (CSIC), Isla de La Cartuja, Av. Américo Vespucio S/N, 41008-Seville, Spain

2 - Department of Biology, Program in Ecology and Evolutionary Biology, The University of Oklahoma, 730 Van Vleet Oval, Norman, OK 73019, USA

3 - Laboratory of Aquatic Ecology, Evolution and Conservation, University of Leuven, Ch. Deberiotstraat 32, Leuven 3000, Belgium

Running title: SNP characterization in *Daphnia pulex*

Abstract: Water flea *Daphnia* – a keystone aquatic herbivore – has been studied for more than 150 years in the context of evolution, ecology and ecotoxicology. Although it is rapidly becoming an emergent model for environmental and population genomics, has not been yet explored at genome-wide level in natural populations. Next generation sequencing provides a useful approach to link ecological and genetic information. In this work we report a unique resource of novel SNP markers for *Daphnia pulex* using the reduction in genomic complexity with restriction enzymes approach genotyping-by-sequencing (GBS). SNPs were scored in a genome-wide scan of 64 different clones from five different populations using the *D. pulex* genome as reference. Our analyses resulted in >40,000 putative SNPs, which after applying stringent filtering criteria using bioinformatics pipelines were reduced up to 8,490 highly confident and bi-allelic SNP markers. A total of 908 outlier SNPs were detected identifying 1,705 annotated genes into *D. pulex* genome, including 453 SNPs within gene. Out of 678 EuKaryotic Orthologous Groups (KOG) we found from outlier SNPs, 240 were involved mainly in three metabolic (lipid, nucleotide and amino acid metabolism) and four regulatory pathways. The generated SNP resource provides a valuable tool for future population genomics surveys targeting specific and interesting loci/regions for *Daphnia*.

On the other hand, this Exchange visit was used to prepare and submit a proposal for a European International Fellowship-PEOPLE (IF-MSCA-H2020) to be hosted by KU Leuven being the responsible researcher Prof. De Meester. It was submitted in time and currently is under evaluation of the European Commission. Final evaluation should be

ready by about March-April 2015. Here you can read a summary of the resulting proposal/project:

Title of the project: Ecological generalism and regional coexistence of different reproduction modes in *Daphnia* as a the model organism

Acronym: ECOGEN-REPRODUCTION

Summary: Many species have both sexual and asexual lineages. However, asexuals tend to occur more in predictable, marginal and high altitude environments; and in most cases both reproduction modes do not coexist regionally. Which factors would explain a generalist success of asexual genotypes, and how could sexual and asexual lineages coexist? We will tackle these questions using two model systems where a single asexual lineage of water fleas of the *Daphnia pulex* species complex shows a broad ecological niche. In Finland, an asexual hybrid regionally, but not locally, coexists with its sexual relative, the European *D. pulex*. I will quantify (1) the fitness and the capacity to colonize different ecological niche of both sexual and asexual, (2) the stability of genotypic composition of populations through time using dormant egg banks in sediment cores, (3) the importance of priority effects through in situ transplant experiments, and (4) the mechanisms of adaptation using epigenomic approaches. The second model system involves the asexual hybrid lineage that invaded nearly the whole African continent and occurs in a wide variety of habitats. Here, I (1) will test the hypothesis that the asexual lineage is successful thanks to an increased resistance to parasites, and (2) will investigate its ecological versatility related to epigenetic control. The inter-disciplinary perspective adopted by this study is aimed to contribute to critical enquiry into the interaction of asexual and sexual relatives, and the evolution of ecological generalism in asexual species. This fellowship will have an invaluable importance for the applicant's training receiving both conceptual and technical skills in evolutionary biology of sexual reproduction, spatial statistics, and epigenetic analyses. In addition, it will allow strengthening the applicant's career through establishing new collaborations, networking, teaching and mentoring through the KU Leuven's Young Researchers' Careers program.

4) Future collaboration with host institution (if applicable)

There is an intention to further collaboration between the host researcher at the KU Leuven and the applicant. Both the manuscript draft and the submission for an IF-MSCA-HORIZON 2020 give clear evidence of this idea (please, see section 1.3). In addition, research lines of the applicant and Prof. De Meester match in a perfect way to continue developing future projects and collaborations. Obviously, such future collaborations with the host institution will depend on the funding.

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*)

As it has been described in section 1.3, this grant has enabled the production of a manuscript dealing with the characterization of a set of SNPs at a wide-genome scale for one species of the model organism *Daphnia*, *D. pulex*. The current draft will take time in became a submitted manuscript, but once it is accepted there is an additional projected publication addressing with the role of 'cultural eutrophication' of lakes (i.e., increase of phosphorus loading on water bodies) on local adaptation by analysing genetic changes at

wide-genome scale. Furthermore, it is noteworthy that the results generated thanks to this Exchange grant have been those who have brought new ideas to develop on future projects/manuscripts. If these results became published, ESF would be acknowledged in the scientific paper in relation with the grant.

6) Other comments (if any)