Faculté des Sciences
Aix*Marseille Université

A envoyer au secrétariat du master BBSG :
Aurelie.glowacz@univ-amu.fr

FORMULAIRE STAGE Recherche-M2 BBSG
(période de stage : du 5 janvier 2016 au 3 juillet 2016)

Titre du stage : Analysis of non-coding genetic variants involved in adult heart performance in a natural population of Drosophila flies

Laboratoire (intitulé, adresse, site web) : TAGC/INSERM U1090 163, avenue de Luminy - case 928 13288 Marseille cedex 09 Tel +33 (0)491 82 87 48 Fax +33 (0)491 82 87 01
https://aitgon.bitbucket.org

Equipe :

Maitre de stage : Altor GONZALEZ

E-mail : aitor.gonzalez@univ-amu.fr

Téléphone : 04 91 82 87 41

Descriptif du stage :

The TAGC laboratory is interested in the genetics of cardiac aging in adult Drosophila flies and we would like to find new genes and mechanisms related to this process. To this aim, Laurent Perrin (TAGC) and collaborators are screening different heart parameters (heart frequency, diastolic opening, etc) in clonal fly lines derived from a natural population (DGRP, Drosophila Genetic Reference Panel) [1,2]. The genome of these fly lines are fully sequenced and therefore, we are able to associate single nucleotide polymorphismes (SNPs) to heart phenotypes using genome-wide association study (GWAS). Around 90 % associated SNPs fall in non-coding regions (regulatory SNPs, rSNPs).

In addition to a strong interest in GWAS (P. Rihet, TAGC) [3], our laboratory is also involved in developing methods for the analysis of the non-coding genome (B. Ballester, J. van Helden, TAGC) [4]. In a different by complementary human project, A. González (TAGC) and collaborators are also developing a method based on supervised classification to analyse non-coding SNPs (Unpublished).

At the methodological level, we would like the student to further develop the supervised classification method for the Drosophila project. At the biological level, we would like to analyse associated non-coding SNPs to gain insights into the biology of adult heart and answer this kind of questions:
- What are the molecular function of associated non-coding SNPs.
- What are the differences of non-coding SNPs between different cardiac phenotypes.

[1] http://dgrp2.gnets.ncsu.edu/
[2] Tissue specific RNA isolation in Drosophila embryos: a strategy to analyze context dependent transcriptome landscapes using FACS. Defaye A, Perrin L. Methods Mol Biol. 2014;1196:183-95. doi: 10.1007/978-1-4939-1242-1_11.

[3] A genome scan for Plasmodium falciparum malaria identifies quantitative trait loci on chromosomes 5q31, 6p21.3, 17p12, and 19p13. Brisebarre A, Kumulungui B, Sawadogo S, Atkinson A, Garnier S, Fumoux F, Rihet P. Malar J. 2014 May 28;13:198. [4] Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. Griffon A, Barbier Q, Dalino J, van Helden J, Spicuglia S, Ballester B. Nucleic Acids Res. 2015 Feb 27;43(4):e27.