

Master project 2020-2021

Personal Information

Supervisor	Carlos Barata Martí
Email	cbmqam@cid.csic.es
Institution	IDAEA-CSIC
Website	www.idaea.csic
Group	Toxicology Group

Project

Computational systems biology

Project Title:

Functional transcriptomic analysis in the crustacean *Daphnia magna*

Keywords:

functional gene annotation, genome, *Daphnia*, curate

Summary:

Developing a friendly use pipeline for processing RNA seq data in *Daphnia magna* which involves assembling reads, mapping, quantifying counts and functional annotation and interpretation using Blast, KEGG and other bioinformatic databases. In addition the student will work on the annotation of the probes of a 8 x 60 K Agilent eArray containing the full set of the 41317 gene models representing the full transcriptome of *Daphnia magna*. Three years ago we developed this array and we were able to annotate 50% of its probes. However, the genome of *Daphnia* is changing continuously and hence it has to be re-annotated using the existing gene Banks. The idea is to use the *Daphnia magna* genome (wleabase) for a primary annotation of probes and then using NCBI Blast tools using translated proteins or genes across taxa (mainly arthropods). The end product is to provide gene names associated to each probe and its homologous in *Drosophila*, humans and other species. We also intent to annotate the gene codes to perform GENE ONTOLOGY, KEGG and other functional analyses

References:

Campos B, Fletcher D, Piña B, Tauler R, Barata C. Differential gene transcription across the life cycle in *Daphnia magna* using a new all genome custom-made microarray. BMC Genomics 2018; 19. Campos B, Garcia-Reyero N, Rivetti C, Escalon L, Habib T, Tauler R, et al. Identification of metabolic pathways in *daphnia magna* explaining hormetic effects of selective serotonin reuptake inhibitors and 4-nonylphenol using transcriptomic and phenotypic responses. Environmental Science and Technology 2013; 47: 9434-9443. Campos B, Rivetti C, Tauler R, Piña B, Barata C. Tryptophan hydroxylase (TRH) loss of function mutations in *Daphnia* deregulated growth, energetic, serotonergic and arachidonic acid metabolic signalling pathways. Scientific Reports 2019; 9. Fuertes I, Campos B, Rivetti C, Piña B, Barata C. Effects of Single and Combined Low Concentrations of Neuroactive Drugs on *Daphnia magna* Reproduction and Transcriptomic Responses. Environmental Science and Technology 2019a; 53: 11979-11987. Fuertes I, Jordão R, Piña B, Barata C. Time-dependent transcriptomic responses of *Daphnia magna* exposed to metabolic disruptors that enhanced storage lipid accumulation. Environmental Pollution 2019b; 249: 99-108. Piña B, Barata C. A genomic and ecotoxicological perspective of DNA array studies in aquatic environmental risk assessment. Aquatic Toxicology 2011; 105: 40-49.

Expected skills::

knowled in r, pyton, automatic functional annotation, gerontaology, KEGG

Possibility of funding::

No

Possible continuity with PhD: :

To be discussed
