

BENOÎT ALIAGA

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EDUCATION

University of Perpignan Via Domitia Ph.D., Epigenetics	Perpignan, France May 2018
University of Perpignan Via Domitia M.Sc., Environmental Genomics	Perpignan, France June 2014
University of Perpignan Via Domitia B.Sc., Biology-Ecology	Perpignan, France June 2011

FELLOWSHIPS

National Ph.D. grant for disabled graduate students (French Ministry of Education and Research) 2014-2018

RESEARCH EXPERIENCE

University of Perpignan Via Domitia Perpignan, France
Graduate Student with Dr. David Duval and Prof. Christoph Grunau 2014-2018
Dissertation: Epigenomics comparison of non-model species

- The main aim was to identify several epigenomic patterns in various species living in different environments and throughout evolution.
- Developed a bioinformatic tool called Notos and validated it with DNA methylation patterns in gene bodies described in very well know species in the literature.
- Used Notos results to identify the evolution of DNA methylation patterns in gene bodies in a pan-species study.
- Compared the epigenome (ChIP-seq) of two different *Schistosoma mansoni* life cycle stages: miracidia and sporocysts which live in different environments (freshwater for miracidia and intra-molluscan for sporocyst).
- Tested the effect of an epidrug (Trichostatine A) on *Schistosoma mansoni* larvae and observed their plasticity during infestation and development inside their intermediate host *Biomphalaria glabrata*.

University of Perpignan Via Domitia Perpignan, France
Intern with Prof. Jan Bulla and Prof. Christoph Grunau (6 months) 2014
Dissertation: Pan-species analysis of DNA methylation with bioinformatic tools

- The objective was to develop a bioinformatic tool (based on CpGo/e ratios) to study DNA methylation patterns in the gene bodies with only the sequences present in databases.
- Used three statistical approaches (Silvermann test, Gaussian and non-Gaussian distributions) to define DNA methylation patterns.

University of Lausanne Lausanne, Switzerland
Intern with Dr. Pierre Bize (8 months) 2013
Dissertation: Telomeres length, individual quality and fitness

- The goal of this work was study the aging plasticity in natural population of bird.
- Extracted DNA from bird blood and measured telomere length by qPCR.
- Searched some statistical relations between aging, dispersal, habitat quality, life history traits and telomere length.

University of Rennes I

Rennes, France

Intern with Dr. Armel Salmon and Prof. Malika Ainouche (3 months)

2012

Dissertation: Reconstruction and assembly of ribosomal DNA (45S rDNA) in Spartines polyploidy

- The aim was to validate the 45S rDNA haplotypes present in *Spartina maritima* (Poaceae), and detected by bioinformatic tools, for pyrosequencing and illumina.
- Amplified by PCR the different regions of 45S rDNA containing the previously identified SNPs (Single Nucleotide Polymorphisms), which are necessary to differentiate the haplotypes.
- Cloned and sequenced the PCR products.
- Assembled the different sequenced regions and reconstructed the different haplotypes.

University of Perpignan Via Domitia

Perpignan, France

Literature study work with Dr. Eric Lasserre (5 months)

2011

Dissertation: LTR retrotransposons in plants

- The goal of this work was to write a review of LTR retrotransposons in plants (structure, transposition mechanisms, epigenetics, role and impact ...).

SKILLS AND TECHNIQUES

- Epigenetics: gene positioning
- Bioinformatics: Galaxy
- Biostatistics: R, JMP
- Molecular Biology: DNA extraction, PCR, qPCR, molecular cloning, Tecan freedom evo
- Parasitology: familiarized with the *Schistosoma mansoni* techniques (recovering eggs from liver and feces, miracidia and cercaria larva, infestation of mice or hamsters, *in vitro* sporocyst transformation).
- Microbiology: general techniques
- Programming languages: Bash, HTML5, CSS3 and I am learning Python
- Text processing softwares: Word, Excel, Powerpoint, LibreOffice and Latex
- Languages: French (mother tongue), English (B1 level), French Sign Language (fluent)

LEADERSHIP EXPERIENCE

II Joint Congress on Evolutionary Biology (volunteer)	2018
Models in Ecology and Evolution seminar (scientific committee)	2018
Member of the IHPE (Interaction Host Pathogen and Environment) lab group communication.	2015-2018
I taught during 64 hours:	2015-2016
• Introduction to microbiology (practical works for 1 st year undergraduates)	
• Animal physiology (practical works for 2 nd year undergraduates)	
Yearly participation in science popularization days	2011-2018
UPVDoc congress (scientific committee)	2015
Vice-President of a local association for deaf and hearing-impaired people (APIDA 66)	2011-present

PROFESSIONAL ASSOCIATIONS

- Member of the European Society for Evolutionary Biology (ESEB)
- Member of the Société Française de BioInformatique (SFBI)
- Member of the Jeunes BioInformaticiens de France (JeBIF)

PUBLICATIONS

Aliaga B., Bulla I., Mouahid G., Duval D., Grunau C. (2018) The universality of gene body DNA methylation. Scientific Reports. Accepted

Roquis D., Taudt A., Geyer K. K., Padalino G., Hoffmann K. F., Holroyd N., Berriman M., **Aliaga B.**, Chaparro C., Grunau., Augusto R. (2018) Histone methylation changes are essential for life cycle progression in the human parasite *Schistosoma mansoni*. PLOS Pathogens.

Bulla I., **Aliaga B.**, Lacal V., Bulla J., Grunau C., Chaparro C. (2018) Notos - a Galaxy tool to analyze CpN observed expected ratios for inferring DNA methylation types. BMC Bioinformatics.

Fneich S., Theron A., Cosseau C., Rognon A., **Aliaga B.**, Buard J., Duval., Aranciabla N., Boissier J., Roquis D., Mitta G., Grunau C. (2016) Epigenetic origin of adaptative phenotypic variants in the human blood-fluke *Schistosoma mansoni*. Epigenetics & Chromatin.

Boutte J., **Aliaga B.**, Lima O., Ferreira de Carvalho J., Aïnouche A., Macas J., Rousseau-Gueutin M., Coriton O., Aïnouche M., Salmon A. (2016) Haplotype detection from next generation sequencing in high ploidy-level species: 45S rDNA genes copies in the hexaploid *Spartina maritima*. G3: Genes, Genomes, Genetics.

CONFERENCE PRESENTATIONS

B. Aliaga, I. Bulla, V. Lacal, J. Bulla, D. Duval, C. Grunau, C. Chaparro*. Predicting DNA methylation by means of CpGo/e ratios in the case of a pan-species study. CEMEB Workshop Epigenetics in Ecology and Evolution, April 4th 2016, Montpellier, France. * presented by Chaparro in my absence

B. Aliaga, D. Duval, C. Grunau. How to correlate the prediction of DNA methylation with experimental data: a statistical approach. Brainstorming Workshop: Epigenetics & Mathematics, October 28th-31th 2015, Berlin, Germany.

B. Aliaga, D. Duval, K. Brehm, C. Grunau. Genome-wide comparison of chromatin structure changes in infective forms of parasitic flatworms. Interaction Micro-organismes Hôtes (IMH), November 19th 2014, Montpellier, France.

POSTER PRESENTATIONS

B. Aliaga, I. Bulla, G. Mouahid, D. Duval, C. Grunau. DNA methylation prediction in the gene body by means of CpGo/e ratios in a eukaryotic pan-species study. II Joint Congress on Evolutionary Biology, August 19th-22th 2018, Montpellier, France.

B. Aliaga, I. Bulla, V. Lacal, D. Duval, J. Bulla, C. Chaparro, C. Grunau. Predicting DNA methylation by means of CpGo/e ratios in the case of a pan-species study. Journées Ouvertes de Biologie, Informatique & Mathématiques (JOBIM), June 28th-30th 2016, Lyon, France.

B. Aliaga, V. Lacal, I. Bulla, D. Duval, J. Bulla, C. Grunau. A pan-species study of DNA methylation patterns by means of distributions of CpG o/e ratios. European Society for Evolutionary Biology (ESEB), August 10th-14th 2015, Lausanne, Switzerland.

J. Boutte, **B. Aliaga**, J. Ferreira de Carvalho, O. Lima, S. Coudouel, D. Naquin, P. Wincker, J. Poulain, C. Da Silva, M. Aïnouche and A. Salmon. Automated detection of duplicated copies from NGS data: application to 45S rDNA and coding genes in hexaploid *Spartina* species (Poaceae). International Conference on Polyploidy, Hybridization, and Biodiversity (ICPHB), May 7th-10th 2012, Průhonice, Czech Republic.

REFERENCES

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