

A **PhD position** is available at the Centre of Biology for the Management of Populations (CBGP) in Montpellier (France), co-funded by the French National Institute for Agricultural Research (INRA) and the European network BiodivERsA. **Analysing genetic differentiation to identify genomic signatures of**

selection

The rapid development of high throughput sequencing and genotyping technologies (Next Generation Sequencing, NGS) permits the comparison of patterns of polymorphisms at a very large number of molecular markers, which allows a detailed characterization of the genomic regions involved in the adaptation of organisms to their environment. However, most of the statistical methods developed so far to identify signatures of selection in the genomes rely on over-simplified demo-genetic models, and generally ignore the information brought by linkage disequilibrium (LD) between genetic markers. The aim of this PhD project is to propose and evaluate new model-based methods to identify signatures of selection using allele frequency data in a Bayesian framework, along two main axes: (i) improving the underlying demo-genetic models, by extending existing approaches based on a migration-drift equilibrium model (Vitalis et al. 2014), or the explicit modelling of the divergence history of populations (Gautier et Vitalis, 2013). An alternative approach will consist in estimating the correlation structure of allele frequencies between populations (Guillot et al., 2014). (ii) using the information brought by the spatial organization of markers (LD). This might be achieved, e.g., by integrating the correlation of gene frequencies at neighbouring SNPs in the models, using hidden Markov models or autoregressive models; or by analysing phased data (obtained by haplotype reconstruction using unsupervised classification techniques) and considering haplotype blocks as multi-allelic loci. These new methods will be directly applied on NGS (pool-seq) data obtained within the European (BiodivERsA) programme EXOTIC, which aims at characterizing the genetic bases of adaptation during the invasion of an iconic species: the Harlequin ladybird *Harmonia axyridis* (Lombaert et al. 2014). These data, which are already available, will be used to contrast the genomic characteristics of native and invasive populations, at a worldwide scale. We seek a highly motivated candidate with a Master degree, trained in mathematical modelling and/or biostatistics, with a strong interest for evolutionary biology and the analysis of data (NGS in particular). A good knowledge of population genetics principles and likelihood-based inference techniques will be appreciated. Advanced programming skills in one programming language (e.g., C, C++, Fortran), and the statistical software R, are required. This PhD will be co-supervised by Renaud Vitalis and Mathieu Gautier, at the Centre of Biology for the Management of Populations (CBGP), in Montpellier, France. The application of the new methods developed on the Harlequin ladybird will benefit from a close collaboration with Arnaud Estoup and Benoit Facon. We invite the interested candidates to send us a detailed CV, a motivation letter and the e-mail address of one referee, at:

renaud.vitalis@supagro.inra.fr

and

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before July 1st 2015

. A first selection round will be done based on this information, and the successful candidates will be interviewed through Skype before July 10th 2015. Funding: ca. 1 757 euros (gross)

per month (for 3 years), starting October 1st 2015. Montpellier is located in Southern France, and benefits from a vibrant scientific community, in particular in the fields of Ecology and Evolution. Selected publications in relation to the subject: Gautier M and Vitalis R (2012) rehh : An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Bioinformatics*, 28: 1176-1177 Gautier M and Vitalis R (2013) Inferring population histories using genome-wide allele frequency data. *Molecular Biology and Evolution*, 30: 654-668 Guillot G, Vitalis R, le Rouzic A and Gautier M (2014) Detecting correlation between allele frequencies and environmental variables as a signature of selection. A fast computational approach for genome-wide studies. *Spatial Statistics*, 8: 145-155 Lombaert E, Guillemaud T, Lundgren J, Koch R, Facon B, Grez A, Loomans A, Malausa T, Nedved O, Rhule E, Staverlokk A, Steenberg T and Estoup A (2014) Complementarity of statistical treatments to reconstruct worldwide routes of invasion: the case of the Asian ladybird *Harmonia axyridis*. *Molecular Ecology*, 23: 5931-5962 Vitalis R, Gautier M, Dawson KJ, and Beaumont MA (2014) Detecting and measuring selection from gene frequency data. *Genetics*, 196: 799-817 -- Renaud Vitalis Centre de Biologie pour la Gestion des Populations 755 avenue du campus Agropolis CS 30016 34988 Montferrier-sur-Lez cedex France Tel : +33 (0)4 99 62 33 42 Fax : +33 (0)4 99 62 33 45 E-mail :

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