OFFRE D'ALLOCATION DE THESE

ÉCOLE DOCTORALE SCIENCES EXACTES ET LEURS APPLICATIONS - ED 211
Avenue de l'université BP 1155 64 013 PAU Cedex – France

SUJET DE THESE

TITRE : **Co-evolution of traits and genome structure under sexual selection : demogenetics meet behavioural ecology.**

RESUME :
Evolution of traits under sexual selection has, up to now, been investigated through analytical models, usually assuming many simplifying hypotheses. Recently however, with the dramatic development of genomics and a renewed interest for sexual selection (in relationship with diversity dynamics or evolution of selective values in exploited species), the genetic architecture of sexually selected traits appears as much more complex than previously anticipated. Additionally, sexual selection is strongly interacting with natural selection to control traits evolution. We here propose to study the co-evolution of both sexually and naturally selected traits and their genomic architecture, using demogenetic models explicitly describing the genome structure (number of loci, their topology, allelic diversity, etc…), mutation and selection forces, while accounting for behavioural (intersexual preference, intrasexual competition, sampling strategies, mating systems) and demographic processes (partners availability, survival, resources). The central idea is that trait evolution is strongly constrained by genetic architecture – something that analytical models fail to account for. But conversely, evolution of traits will in time modify the genome structure through sexual selection, by favouring the genomic structures of the most efficient individuals in term of reproductive success. The individual based demogenetic model (already functional) is developed on the CAPSIS-4 modelling platform (hosted by INRA). Its predictions in terms of behavioural ecology, traits, or genomic patterns will be compared to current analytical models on the one hand, and with worldwide genomic database for sexually selected traits. Several collaborations are already envisioned to broaden the perspective of this proposal.

Mots clés: sexual selection, demogenetic model, genome structure, behavioural ecology, integrative biology

CONDITIONS D'EXERCICE

Laboratoire : UMR 1224 ECOBIOP UPPA/INRA

Site web : https://www6.bordeaux-aquitaine.inra.fr/st_pee/UMR-Ecobiop

Directeur de thèse : JACQUES LABONNE
Co-Directeur de thèse :

Lieu : AQUAPOLE INRA, Quartier Ibarron, 64310 Saint-Pée sur Nivelle

Date début : 01/09/2017 | **Durée : 3 ans**

Employeur : Université de Pau et des Pays de l'Adour (UPPA) ou INRA

Salaire mensuel brut : 1685 € *(pour contrat doctoral sur crédits UPPA et collectivités locales)*

SAVOIR-FAIRE DU LABORATOIRE

The applicant will be supervised by Jacques Labonne (UMR INRA ECOBIOP 1224) who has developed various demogenetic models in the past years for both theoretical and applied questions (Labonne et al. 2008, Labonne & Hendry 2010), while also developing *in natura* or experimental approaches around sexual selection (Labonne et al 2009, Gauthey et al 2016) . The lab has a strong experience of modelling demographic processes and genetic processes (Piou & Prevost 2012, 2013, Buoro et al. 2012), as well as in the field of behavioural ecology (Tentelier et al. 2016). The candidate will have access to local computing stations and high performance computing cluster (HPC, DSI-CCUB). Long-lasting visits in foreign labs for training and collaboration will be encouraged during the PhD.

MISSION - ACTIVITÉS PRINCIPALES

Le contexte scientifique

Behavioural ecology studies the animal behaviour with a Darwinian perspective, in the sense that it deals with the evolution of traits and species in space and time. Considered as a major evolutionary force, sexual selection occurs when variation in mating success (numbers of sexual partners) and reproductive success (number of offspring) are correlated to variation in traits (Andersson 1994). Such process strongly affects the distribution of genetic variation between generations. Mating success can be maximized by investing in traits that improves the access to a high quality partner such as, for instance, movement ability for partner sampling, sensory acuity for partner quality discrimination and sexual signalling (Baldauf et al. 2014). Reproductive success of both partners is affected by the individual fecundity, good genes, genetic or behavioural compatibility between partners and the ability to provide parental care (Royle et al. 2014). All these traits and behaviours are likely to be controlled by their underlying genetic architecture. The spectrum of polygeny, pleiotropy, spatial location in the genome (implying possible physical linkage), and chromosomes types affect the strength of selection, drift and mutation on the evolution of these traits. For instance, monogenic traits are more strongly affected by selection when located on a sexual chromosome. Pleiotropy generates conflict in the evolution of traits, since positive selection for one trait has also an effect on other traits through alleles sharing. Additionally, traits can be under antagonistic sexual selection, meaning that a trait that is benefiting one sex's fitness is hampering another sex's fitness.

A number of theoretical models have been developed for sexual selection (Kokko and Jennions 2008, Etienne et al. 2014, see Kuijper et al. 2010 for a review). These different approaches share, to some extent, several weaknesses: 1/ most of them neglect the interaction between traits and their genetic architecture, and when they do, this architecture is overly simplistic and unrealistic compared to available knowledge (Qvarnström et al 2006, Chenoweth and McGuigan 2010), 2/ nearly all of them assume sexual genders to be a given characteristic of sexual selection, 3/ most of them assume sex-dependent unrealistic asymmetrical systems for reproduction, in which males compete for choosy females and not the other way around (Royle et al. 2014), or in which anisogamy is not evolving whereas it should be (Cunningham & Birkhead 1998), 4/ consequently none of them accounts for a mechanism that should be at the core of sexual reproduction: mutual choice (Myhre et al. 2012), 5/ traits can be costly, therefore coding genes are costly: no model accounts for the cost of cellular activity in gene expression, whereas this can be a strong driver for genomic evolution (Lang 2008).

We therefore believe that some of these shortcomings and simplifying assumptions can be relaxed, by explicitly representing the genetic architecture of traits, by explicitly letting sex evolve per se in models of sexual selection, by considering competition and choosiness for all individuals (and therefore potentially all sexual genders), and by explicitly resolving mutual choice dynamics into models. It is also expected that the genetic architecture will evolve as a response to sexual selection, and in return shape the direction of the sexual selection.

Les objectifs

We propose to investigate this question through individual based simulation complemented by analytical approaches. The very base of the subject will be to complete the construction of a reference model of sexual selection able to tackle the above mentioned limitations of previously published models. This implies to

represent the genetic architecture of traits in a realistic/non-trivial genome structure (i.e. assuming chromosomes, physical distance between genes, mutation, recombination, pleiotropy), and to define a framework for evolution of traits and behaviours.

In order to adopt a parsimonious approach, the model will be made of several simpler sub-models. Each sub-models will take into account a limited number of the assumptions listed above and will first be analysed separately, with a strong focus on its behaviour in relationship with already published analytical models. Sensitivity analyses will be undertaken for each sub-model, and we will then progressively build back the full model, checking at each stage the behaviour of the intermediate models, so to understand how the different assumptions influence the course of evolution.

The first year will be dedicated to training and advertising about the models in targeted labs, so to ensure a maximum consensus regarding its assumptions and mechanisms. The second year will mainly serve to run the simulations and analyses the various results of our models : first, the relationships between initial conditions (for demography, genetic architecture, behavioural routines) and the evolution of traits; second the effect of trait evolution on genetic architecture (pleiotropy level, number of genes coding for traits, linkage groups dynamics). We anticipate new results in several areas: co-evolution between traits and genome of course, but also evolution of mate choice, evolution of sex-roles and genders, etc. The third year will be dedicated to finish scientific publications and to produce the PhD document.

Les résultats attendus

We expect new results in the field of sexual selection and life history traits evolution, wherein traits are simultaneously controlled by evolution of fitness and genomic structure. More precisely, we expect to challenge the generality of previous results obtained by analytic approaches that usually encompass less mechanisms and complexity. Additionally, we also aim at providing testable assumptions on the genes under sexual selection (genomic location, numbers and effects).

Les collaborations de recherche

The behavioural ecology part of the model will be improved through a collaboration with François-Xavier Dechaume-Moncharmont (UMR 6282 Biogéosciences, University of Bourgogne), an expert in behavioural ecology and modelling of mate choice processes. We have further identified some collaborations in labs covering either theoretical sexual selection topics (Dr. A. Courtiol in Berlin, Pr H. Kokko in Zurich, Pr. A.P. Hendry in McGill University, Montreal) or behavioural ecology (Dr T. Fawcett, University of Bristol). Finally, we aim at testing some predictions against the Tree of Sex database (http://treeofsex.org/ , a consortium supported by Berkeley, Doris Bachtrog's lab).

Littérature citée

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COMPETENCES REQUISES

Candidates should display a strong motivation for theoretical biology and skills in modelling and coding. Ability to analyse core publications in the field of evolutionary biology will be crucial. Fluency in English language is a plus as well as team working skills, since the candidate will probably have to interact with collaborators in other countries, in order to strengthen and validate the modelling approach. The candidate will attend to summer schools on individual-based modelling and on adaptive dynamics modelling.

CRITERES D'EVALUATION DE LA CANDIDATURE

Traitement du dossier :   Jury de sélection

Les candidats seront sélectionnés d'abord sur dossier. Un entretien sera organisé après la première phase de sélection du dossier de candidature.

- Adéquation entre le diplôme de Master (ou équivalents) et le sujet de thèse
- Notes et classements en Master, et régularité dans le cursus universitaire
- Maîtrise de l'anglais

- Capacité du candidat à présenter ses travaux
- Expériences professionnelle de type stage(s) en laboratoire ou autre ; éventuels travaux de recherche déjà réalisés (rapports, publications).

CONSTITUTION DU DOSSIER DE CANDIDATURE, DATE LIMITE DE DEPOT

Envoyer par email un dossier de candidature comprenant :
- CV
- lettre de motivation
- relevé de notes et classements en Master
- lettres de recommandation
- coordonnées des personnes du milieu professionnel (minimum deux) à contacter

DATE LIMITE DE DEPOT DU DOSSIER :	24/05/2017

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