The evolutionary significance of cryptic meiotic drive : a case study in the house mouse *Mus musculus*

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Research them : Natural selection can act at multiple levels. Numerous traits are obviously adaptive at the organism level, but others are beneficial only for some portions of the genome (Burt & Trivers, 2006). The evolutionary significance of these "Selfish Genetic Elements" is demonstrated by the wide abundance of their most conspicuous representatives, transposable elements, that constitute a never-ending source of co- evolution through conflict or domestication events. Yet, many other selfish strategies exist, and may leave less obvious signatures within genomes. Meiotic drive is one such strategy, involving genetic elements that increase their representation in the gametic pool of heterozygous individuals beyond the expected Mendelian ratio of 0.5. This may be achieved either by eliminating non-carrier gametes, as is usual in male gametogenesis, or by avoiding the polar bodies, that constitute dead end products of the female meiosis.

Although many cases of meiotic drive have been described to date, there are important theoretical reasons to suspect that these may only represent a small fraction of the existing cases (Lindholm *et al.*, 2016). The first reason is that meiotic drive may not induce any obvious phenotypic effects, except when it occurs on sexual chromosomes, where it induces a sex-ratio bias in the offspring. The second reason is that meiotic drivers, unless they are counter balanced by deleterious effects or repressors, can reach fixation and thus become inactive and invisible.

This project aims at exploring the hypothesis that such hidden meiotic drivers may be frequent in the house mouse *Mus musculus*, using the following principle: producing hybrids between two well isolated populations should reveal the presence of meiotic drivers that would otherwise remain hidden, because they have reached fixation in their own population. Precisely, such an experiment has previously been performed for other purposes, providing us with the appropriate genomic data: hybrid males have been obtained by crossing mice from two distinct subspecies, *Mus musculus domesticus* and *Mus musculus casteneus*, and their gametes have been subject to deep sequencing, targeting 1500 loci that constitute as many genetic markers distributed throughout the genome. With this data, it is possible to ask if some portions of the genome, from either of the two subspecies are over- or under-represented in the sperm pool. Moreover, by assessing how allelic frequencies vary across the genome, it should be possible to map the distorters and thus shed light on the putative mechanisms involved, thanks to the abundant annotation of the house mouse genome.

Tools and methods : The candidate will have to master the evolutionary concepts underlying the project and develop the appropriate bioinformatic and statistical tools to detect and interpret any significant deviation from the expected mendelian proportions along the genome.

Profile : We are seeking a highly motivated student, with a pronounced taste for approaching puzzling evolutionary biology questions through genomics and statistical thinking.

Funding : this internship is financed through the ANR Horizon

Scientific environment: the candidate will from the rich scientific life of two teams within the LBBE.

References:

Burt, A. & Trivers, R. 2006. *Genes in Conflict: The Biology of Selfish Genetic Elements*. Belknap Press, Harvard.

Lindholm, A.K., Dyer, K.A., Firman, R.C., Fishman, L., Forstmeier, W., Holman, L., *et al.* 2016. The Ecology and Evolutionary Dynamics of Meiotic Drive. *Trends Ecol. Evol.* **31**: 315–326. Elsevier Ltd.