CBGP
Centre de Biologie pour
la Gestion des Populations

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POPULATION SIZE, INCOMPLETE LINEAGE SORTING AND SELECTION IN ANIMAL GENOMES

par
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Understanding the causes and consequences of the variation of population size on adaptation, whether it be variation between species or variation between regions of the genome, is a central question in molecular evolution. During my PhD at ISEM in Montpellier and my first post-doc at BiRC in Aarhus, Denmark, I tackled two aspects of this question.

During my PhD, I analyzed how differences in population size between metazoan taxa influence the adaptive substitution rate, using a test derived from the Mc-Donald & Kreitman test in 40 species from 9 taxa. With my collaborators we revealed a negative relationship between the adaptive substitution rate and life-history traits representative of the long-term population size. This result is in contradiction with the widespread hypothesis that adaptation is more efficient in large populations.

During my post-doc in Denmark, I approached the question of the population size with the study of incomplete lineage sorting (ILS) in the primate phylogeny. Genomic levels of ILS depend on the time span between two consecutive speciation events, but also on the population size, which can vary along the genome. By reconstructing the coalescent topology along 4-ways alignments of primate genomes, my collaborators and I could on one hand infer speciation times and ancestral population sizes in 27 branches of the phylogeny, and on the other hand analyze the variation in population size along ancestral genomes and its determinants.