

### Encadrement :

Nom : **Roulin** Prénom : **Alexandre** Qualité : **Professeur** Tel : 0041 21 692 41 89  
Laboratoire /Entreprise : **University of Lausanne**  
Adresse : Le Biophore, CH-1015, Lausanne, Switzerland  
Courriel : **alexandre.roulin@unil.ch**

### Titre du stage :

**Mutation rates at the MC-1R locus: implications for the evolution of melanin-based colorations**

### Mots clés :

Animal coloration, melanocortin system, MC1R, melanins, pigmentation

### Résumé (150 mots maximum) :

The expression of black or reddish melanin-based colorations is controlled by the melanocortin system; a complex network of hormonal peptides and membrane receptors. Variation in melanin-based coloration naturally occurred between individuals of the same or different species is based on the existence of variants of the melanocortin genes. Particularly, mutations at the melanocortin 1 receptor (MC-1r) gene have been repeatedly shown to explain variation in coloration. It has been proposed that colour variation is so recurrently based on the MC-1r gene because this gene may have a high mutation rate, a hypothesis that has never been tested. Using data from different animal species, the student will test whether the mutation rate at the MC-1r gene is higher than at the other genes of the melanocortin system and/or than at neutral genes. The project is a good opportunity to understand the genetic determination of phenotypic traits, a cutting-edge field in evolutionary biology.

### Deux références bibliographiques:

Rosenblum, E. B., H. E. Hoekstra, and M. W. Nachman. 2004. Adaptive reptile color variation and the evolution of the Mc1r gene. *Evolution* 58:1794–1808.

Mundy, N. I. 2005. A window on the genetics of evolution: MC-1R and plumage colouration in birds. *Proceedings of the Royal Society B: Biological Sciences* 272:1633–1640.

### Techniques mises en œuvre:

Calculate the number of synonymous substitutions at different loci (MC1R, POMC, ASIP, TYR, and control nuclear genes) in order to estimate mutation rate.

Statistical comparisons among genes in a phylogenetic framework.