

Encadrement :

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Titre du stage :

Meta-analysis on the effects of MC-1r on melanin-based colorations

Mots clés :

Animal coloration, MC-1R, melanins, meta-analysis, genetically-based colour variation

Résumé (150 mots maximum) :

The gene codifying for the melanocortin 1 receptor (MC-1r) is a widely used candidate gene for the study of natural variation in animal coloration. The product of this gene, the MC-1r, is a membrane protein that is vital for the regulation of the synthesis of eumelanins and pheomelanins, responsible for grey-to-black and brown-to-red animal colorations. Gene variants at the MC-1r have been observed to be associated with variation in coloration in different vertebrate taxa, including humans and other mammals and birds. However, the impact of MC-1r mutations on coloration is quite variable, with some species where the association between MC-1r gene variants and coloration is not complete or it is even absent. A potential explanation is that mutations occurring at some specific regions of the MC-1r gene can have more important effects on coloration, a hypothesis that remains untested.

Deux références bibliographiques:

Manceau, M., V. S. Domingues, C. R. Linnen, E. B. Rosenblum, and H. E. Hoekstra. 2010. Convergence in pigmentation at multiple levels: mutations, genes and function. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences* 365:2439–50.

Meunier, J., S. Figueiredo Pinto, R. Burri, and A. Roulin. 2010. Eumelanin-based coloration and fitness parameters in birds: a meta-analysis. *Behavioral Ecology and Sociobiology* 65:559–567.

Techniques mises en œuvre:

We propose to test this hypothesis using a meta-analytic approach. Meta-analyses combine results from several studies to test if there exist a general support of a given hypothesis. More importantly, they allow to statistically discern among factors that could explain the observed variation on effect sizes.