

The genomic architecture of a continuous color polymorphism in the European barn owl (*Tyto alba*)

Tristan Cumer^{1,2*}, Ana Paula Machado^{1,2*}, Luis M. San-Jose^{3*}, Alexandre Roulin¹, Jérôme Goudet^{1,2}

1 Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland

2 Swiss Institute of Bioinformatics, Lausanne, Switzerland

3 Laboratoire Évolution & Diversité Biologique, Université Toulouse III, Toulouse, France

Underline: speakers

*: Co-first authors, sorted alphabetically

Color polymorphism, and the mechanisms that allow its maintenance in populations, have fascinated evolutionary biologists for decades. Studies of the variation of coloration in wild populations often focus on discrete color traits exhibiting relatively simple inheritance patterns, while studies on continuously varying traits remain rare. Here, we studied the continuously varying white to red color polymorphism in the Western palearctic barn owls (*Tyto alba*), ranging from pale white in the south to reddish dark in the north of its distribution. By using a Genome Wide Association approach on whole genome data of 75 barn owl individuals sampled across Europe, we identified, on top of the previously known MC1R mutation, two other regions involved in this color polymorphism. We estimated the amount of variation linked to these QTL variants, and show the combination of the tree variants explain about 80% of the color variation. Among the two newly identified regions, a region on the sexual chromosome (Z) shows a large signal of differentiation on the Swiss populations when controlling for the MC1R genotype, and we suggest it may play a role in the sexual dimorphism observed in the species. These results uncover two new genomic regions and provide keys to better understand the molecular bases of the color polymorphism as well as the mechanisms responsible of the maintenance of the color polymorphism in the European barn owl at both continental and local scales.