**Adaptive genomics of pangolins applied to their conservation**

Pangolins have become a central part of conservation action due to their notorious label of being the most trafficked wild mammal in the world. Novel comparative and population genomic research on all eight species across their global distributions are starting to shed light on their risk of extinction, evolution and population dynamics. These pieces of evidence through neutral markers are being put together to develop best conservation genetic practices for protecting these Evolutionarily Distinct and Globally Endangered (EDGE) species and their populations, including the identification and management of conservation units (CUs). However, to truly understand pangolin evolution and support conservation genetic practices (i.e. translocations and identification of CUs or admixed species) that are robust, studies on the adaptive genomic signature in pangolins are paramount. Here we propose a project with the aim of understanding the adaptation of pangolin species and their populations using both phylogenomic and population genomics approaches. The candidate will have access to already sequenced full genomes, extracted and aligned ± 3 200 orthologous genes, and mapped gene-capture data (670 loci at ± 35x depth) of around 900 individuals across the eight species. Gene-capture data include around 250 loci directly linked to genes found to be of adaptive importance in other species to environmental and biological variation. The candidate will use this already produced genomic data to identify and categorize genes and SNPs under selection at (i) a species level using shifts in substitutions of gene alignments (e.g. dN/dS ratios) and phylogenetic approaches (substitution rate variation) from genomes and orthologous genes, as well as (ii) a population level using outlier detection (e.g., Fst and association to gene characteristics) and genotype-environment associations (GEAs) from gene-capture data. The candidate will then explore the adaptation of key genes and provide conservation genetic guidelines for these EDGE species and their populations following these results.

Key skills we are looking for:
•        Background or experience in bioinformatics
•        Ability to work in Linux bash and/or R environments
•        Previous experience in analyses of selection and python scripting is advantageous

Key publications:
Heighton, S.P., Allio, R., Murienne, J., Salmona, J., Meng, H., Scornavacca, C., Bastos, A.D., Njiokou, F., Pietersen, D.W., Tilak, M.K. and Luo, S.J., 2023. Pangolin genomes offer key insights and resources for the world’s most trafficked wild mammals. Molecular Biology and Evolution, 40(10), p.msad190.
Choo, S.W., Rayko, M., Tan, T.K., Hari, R., Komissarov, A., Wee, W.Y., Yurchenko, A.A., Kliver, S., Tamazian, G., Antunes, A. and Wilson, R.K., 2016. Pangolin genomes and the evolution of mammalian scales and immunity. Genome research, 26(10), pp.1312-1322.
Flanagan SP, Forester BR, Latch EK, Aitken SN, Hoban S. Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. Evol Appl. 2017 Dec 2;11(7):1035-1052. doi: 10.1111/eva.12569. PMID: 30026796; PM[CID](https://synergies.univ-tlse3.fr/CID%22%20%5Ct%20%22_blank): PMC6050180.
Latrille, T., Rodrigue, N. and Lartillot, N., 2023. Genes and sites under adaptation at the phylogenetic scale also exhibit adaptation at the population-genetic scale. Proceedings of the National Academy of Sciences, 120(11), p.e2214977120.
Forester, B.R., Landguth, E.L., Hand, B.K. and Balkenhol, N., 2021. Landscape genomics for wildlife research. Population genomics: wildlife, pp.145-184.

Period of internship:

Jan - Jun 2024

Contact:
Philippe GAUBERT (Laboratoire Évolution et Diversité Biologique, UPS Toulouse): philippe.gaubert@ird.fr
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[Philippe GAUBERT](https://philippe-gaubert.eu/)
***DR IRD****(Director of Research at Institut de Recherche pour le Développement)*
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Address:

Laboratoire Évolution et Diversité Biologique ([EDB](https://www.google.com/url?sa=t&rct=j&q=&esrc=s&source=web&cd=&cad=rja&uact=8&ved=2ahUKEwjPl9DuirGAAxVLT6QEHeAlBtwQFnoECA4QAQ&url=https%3A%2F%2Fedb.cnrs.fr%2F&usg=AOvVaw3FwplI992xvjlGlQ_OfsLY&opi=89978449))
Université Toulouse III Paul Sabatier
118, route de Narbonne
Bâtiment 4R1
31062 Toulouse cedex 9
FRANCE
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*Associate Researcher*
[CIIMAR](https://www.google.com/url?sa=t&rct=j&q=&esrc=s&source=web&cd=&cad=rja&uact=8&ved=2ahUKEwiFlLeBi7GAAxX6TaQEHaEvBZAQFnoECA4QAQ&url=https%3A%2F%2Fwww2.ciimar.up.pt%2F&usg=AOvVaw1u0DqbN5ym8VQxZQi9HU3A&opi=89978449) - Evolutionary Genomics and Bioinformatics
Terminal de Cruzeiros de Leixões
Av. General Norton de Matos s/n
4450-208 Matosinhos
PORTUGAL

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