MASTER'S THESIS PROJECT: GENETIC AND EPIGENETIC ADAPTATION TO ENVIRONMENTAL UNPREDICTABILITY

Background

How do wild animals adapt to environments that differ dramatically in their predictability?

The Rufous-collared Sparrow (Zonotrichia capensis) occupies environments ranging from highly seasonal habitats to the exceptionally stable but climatically extreme river valleys of the Atacama Desert. This makes the species an excellent natural model for investigating how genetic and epigenetic mechanisms contribute to adaptation and phenotypic flexibility.

In a recently published study, we used GBS-MeDIP to characterize genetic and DNA methylation variation associated with life-history stages in birds from the Atacama Desert. The results indicated that DNA methylation is associated with regulatory variation linked to the expression of life-history stages in this weakly seasonal environment:

Pértille, F., Gonzalez-Gomez, P. L., Wingfield, J. C. & Guerrero-Bosagna, C. (2026). Epigenetic changes as regulatory mechanism for the expression of life history stages in Zonotrichia capensis inhabiting an aseasonal environment. Journal of Avian Biology, e03516. https://doi.org/10.1002/jav.03516

Building on this work, we have generated a new GBS-MeDIP dataset comparing birds from the Atacama Desert with birds from Fray Jorge, a more seasonal and environmentally predictable site in Chile. GBS-MeDIP enables genetic variants and DNA methylation profiles to be examined in parallel from the same individuals and genomic fraction.

Project aims

The project will investigate whether birds living under contrasting levels of environmental predictability differ in their genetic and epigenetic profiles.

Depending on the duration of the thesis and the student's interests, the project could address questions such as:

- Do the Atacama and Fray Jorge populations exhibit genetic differentiation?
- Which genomic regions show differential DNA methylation between the environments?
- Are the observed molecular differences associated with genes and biological pathways involved in environmental responses, metabolism, stress regulation, or life-history transitions?
- To what extent are differences in DNA methylation independent of, or associated with, the underlying genetic variation?

Tasks

The student will work primarily with bioinformatic and statistical analyses. Tasks may include:

- Quality control and processing of GBS-MeDIP sequencing data.
- Read alignment and assessment of sequencing coverage.
- Identification and analysis of SNPs and differentially methylated regions.

- Population structure and genetic differentiation analyses.
- Genomic annotation and functional enrichment analysis.
- Integration of genetic, epigenetic, environmental, and phenotypic information.
- Visualization and biological interpretation of the results.
- Scientific writing and presentation of the findings.

Opportunities

The project offers the opportunity to:

- Work with a novel dataset from wild populations inhabiting contrasting environments.
- Gain practical experience in evolutionary genomics, ecological epigenetics, and bioinformatics.
- Work with R, UNIX/Linux, and high-performance computing resources at UPPMAX.
- Participate in an international collaboration involving Uppsala University and the University of California, Davis.
- Contribute to an ongoing scientific study intended for publication in a peer-reviewed journal. Authorship will depend on the student's contribution to the analysis and manuscript.

Requirements

We are looking for a motivated Master's student with:

- A strong interest in evolutionary biology, genomics, epigenetics, or adaptation to changing environments.
- Previous experience with bioinformatics, R, UNIX/Linux, or analysis of sequencing data.
- An ability to work independently while participating actively in project discussions.
- Good scientific communication and writing skills in English.

Previous experience with population genomics or DNA methylation analysis is advantageous but not essential.

Practical information

Extent/credits: 30, 45, or 60 hp.

Start date: Autumn 2026 or spring 2027, according to agreement and data availability.

Location: Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University.

Supervision: Fábio Pèrtille and (co) Carlos Guerrero-Bosagna, Uppsala University, in collaboration with Paulina González-Gómez, University of California, Davis.

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To apply, please send a short statement describing your interest and relevant experience, together with your CV and transcript of records. Informal enquiries about the project are also welcome.