



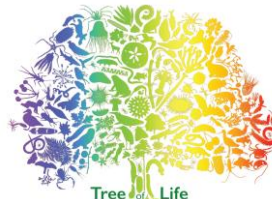
Welcome to the Biodiversity Genomics course!

Joana Meier, Karin Näsval, Nicol Rueda, Patricio Salazar
Tree of Life Programme, Wellcome Sanger Institute

THE
ROYAL
SOCIETY

The
Branco Weiss
Fellowship
Society in Science

W
wellcome

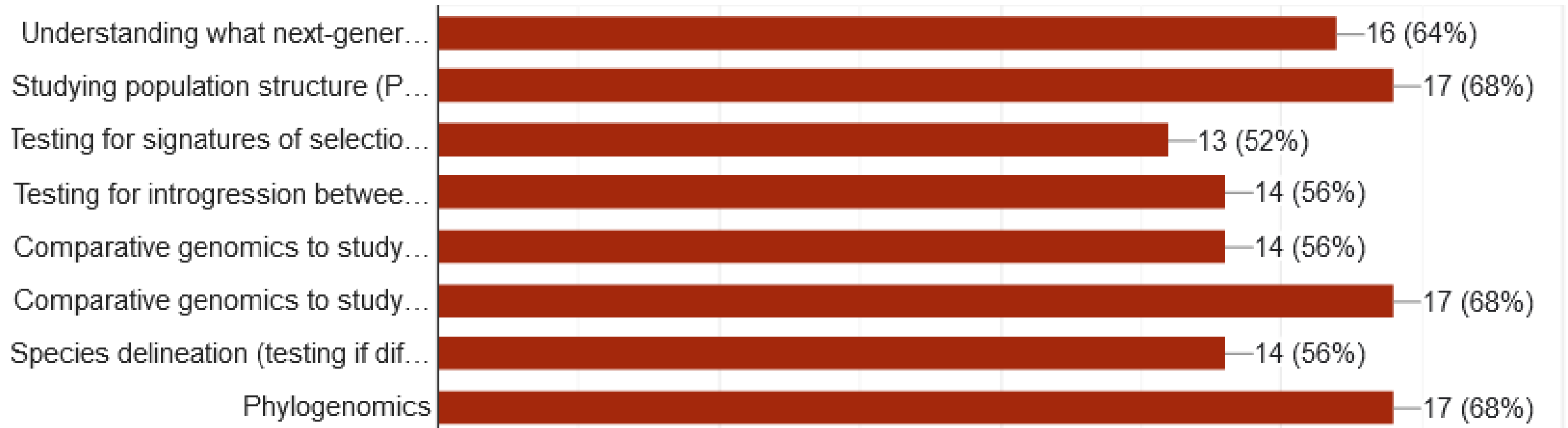


wellcome
sanger
institute



UNIVERSITY OF
CAMBRIDGE

What you wanted us to cover in the course



Basically everything we offered! We will thus give an introduction to each of these fields

Tentative schedule

- Saturday, 20 July:
 - introduction to biodiversity genomics, Linux, NGS data
 - Filtering and quality checks of Illumina data
- Sunday, 21 July:
 - Mapping reads to a reference genome
 - Variant calling and filtering vcf files
- Monday, 22 July:
 - Population structure with PCA and phylogenomics
 - Genome scans to identify regions under selection
- Tuesday, 23 July:
 - Detecting introgression
 - Comparative genomics
- Wednesday, 24 July:
 - Phylogenomics with reference genomes
 - Buffer, topics of interest & discussing own projects

Daily sessions:

- 9:00-10:30: First session (1.5 hours)
- 10:30-11:00: Coffee break (30 min)
- 11:00-12:30: Second session (1.5 hours)
- 12:30-1:30: Lunch break (1 hour)
- 1:30-3:30: Third session (2 hours)
- 3:30-4:00: Coffee break (30 min)
- 4:00-6:00: Fourth session (2 hours)

Researchers who contributed to organising this course and can help with questions about IKIAM / Tena



Dr Patricio Salazar

Lead organiser



Franz Chandi

**Chief of
lunch breaks**



**Kimberly
Gavilanes**

**Chief of coffee
breaks
& facilities**



Alex Arias

**Chief of class
room
infrastructure**



**María José
Sánchez**

**Jack of all
trades**



**Prof Caroline
Bacquet**

Key facilitator

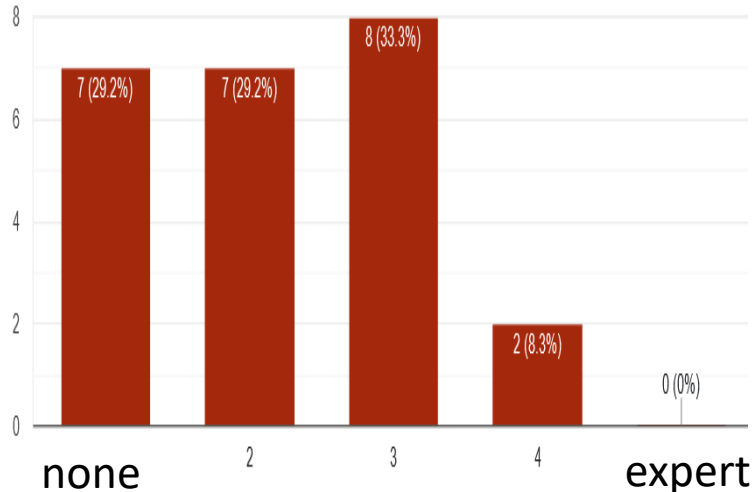
A few tips and housekeeping rules

- Be kind to each other
- Sexism, racism, or any other kind of unfair behaviour is not tolerated. Please let me, Patricio, Nicol or Karin know if you experience or see anything like this.
- To ask questions, please raise your hand. Questions are very much encouraged. If you do not understand something, just ask!
- If you struggle with something, put the green card on your desk and someone will come to help you.
- All course materials (including slides) can be found here:
github.com/rapidspeciation/biodiversity_genomics_course

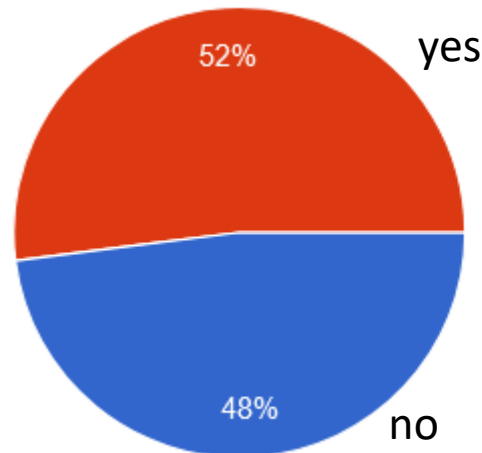
We are a very diverse group, which is great!

- Always feel free to ask questions at any time. It is likely that at least one other person is sooo happy that you asked.
- Our diversity is a big advantage. Let's learn from each other!

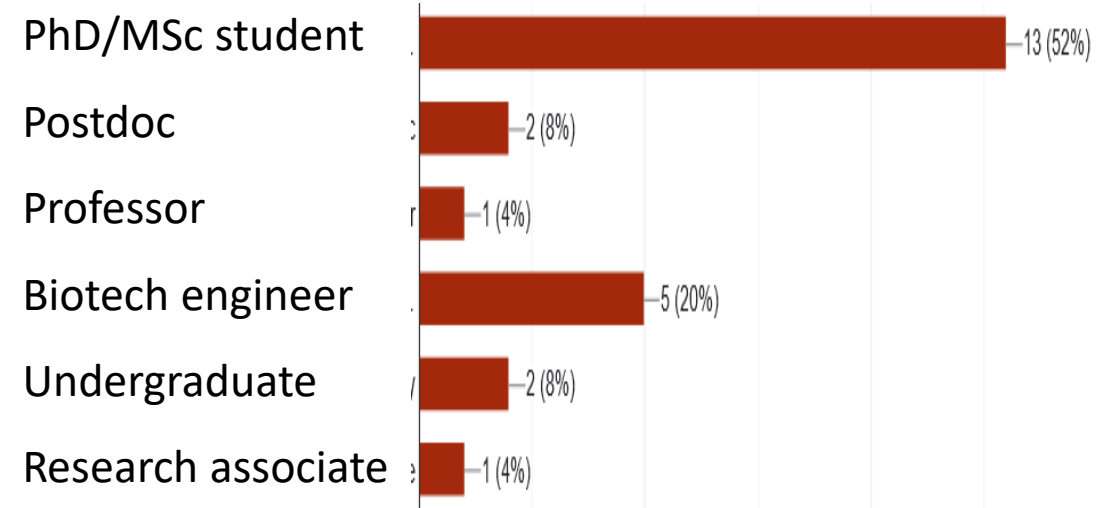
Linux experience



Prior experience with NGS data



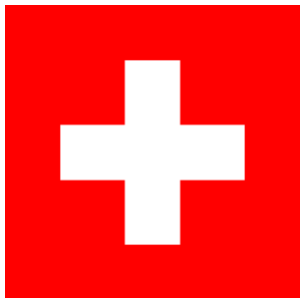
Current academic level/job



**Please, introduce yourself with your
name and if you wish also your country,
study organism or research question**

Joana Meier

Childhood



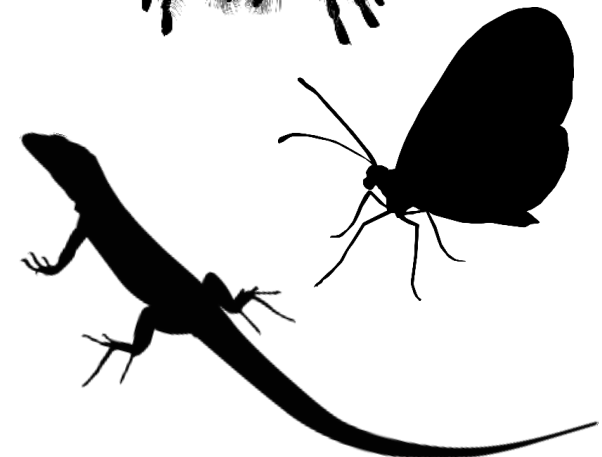
**PhD on cichlid fish
Speciation in Bern,
Switzerland**

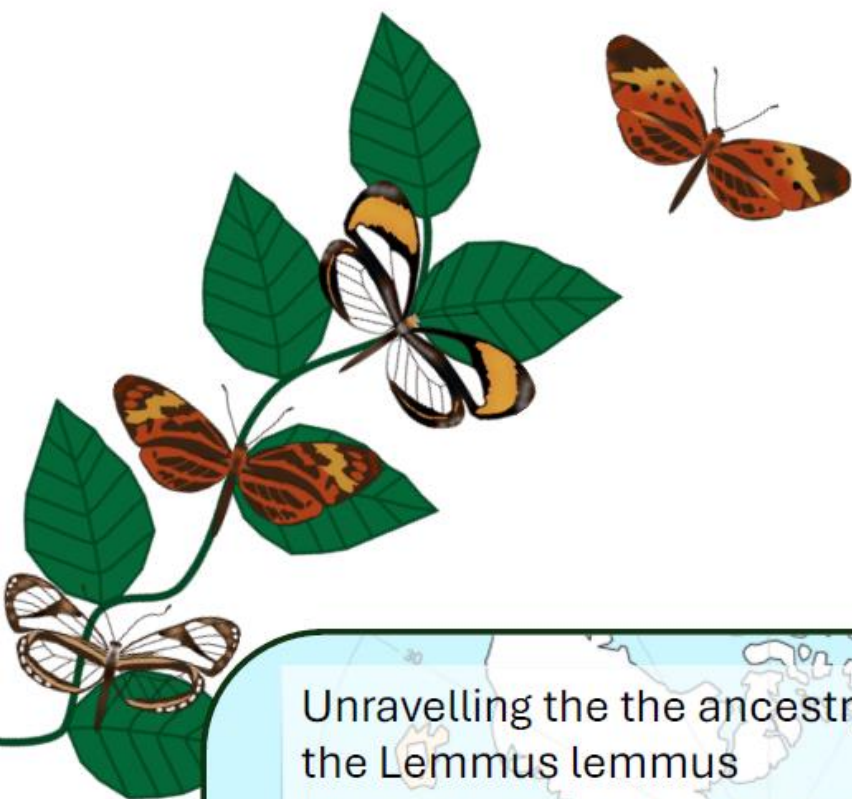


**Postdoc at the
University of
Cambridge, UK**



**Group leader at the
Wellcome Sanger
Institute**





Karin Näsval, PhD

Postdoctoral fellow

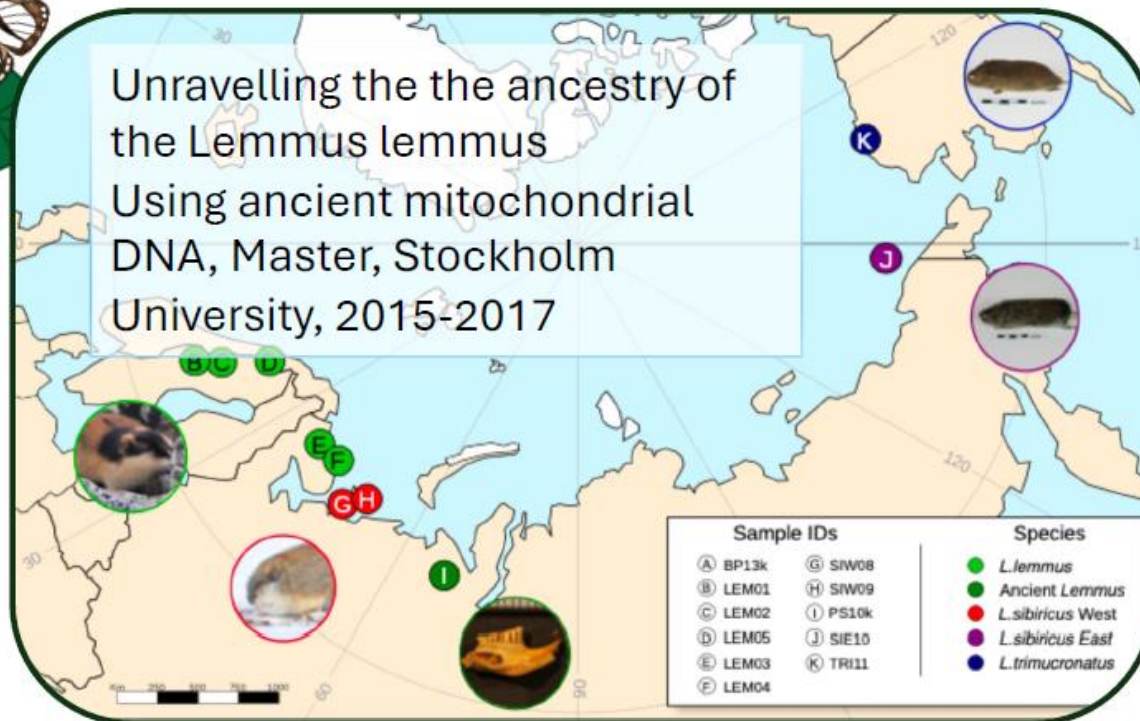
Rapid speciation group, Tree of Life

Wellcome Sanger Institute, UK

Unravelling the the ancestry of
the Lemmus lemmus

Using ancient mitochondrial
DNA, Master, Stockholm

University, 2015-2017



Doctoral student

2018-2023

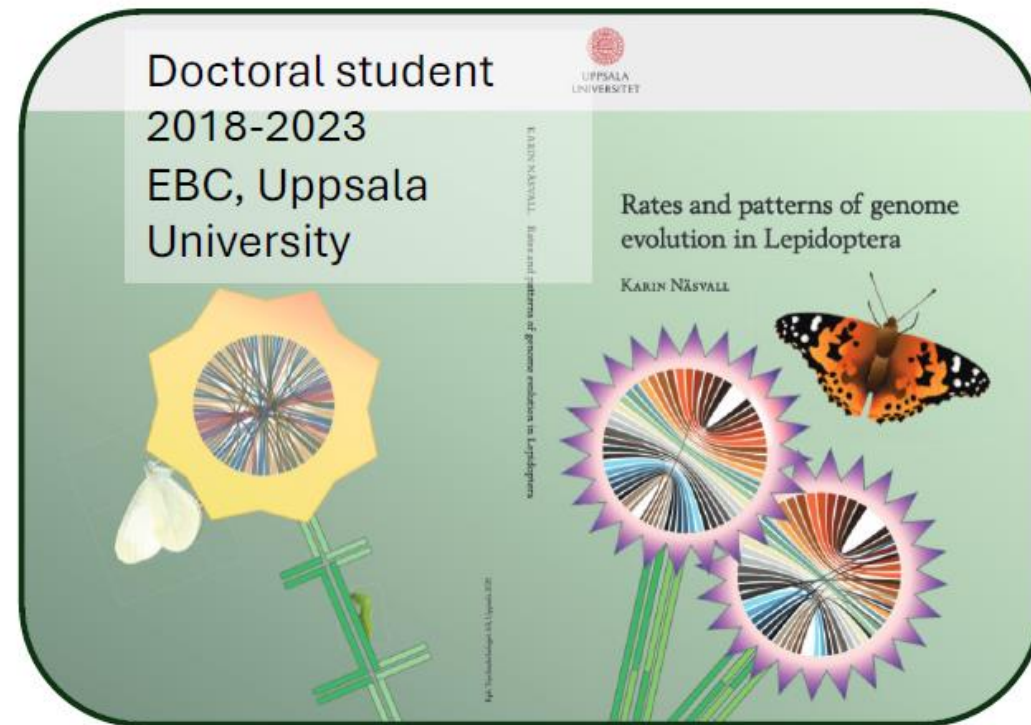
EBC, Uppsala

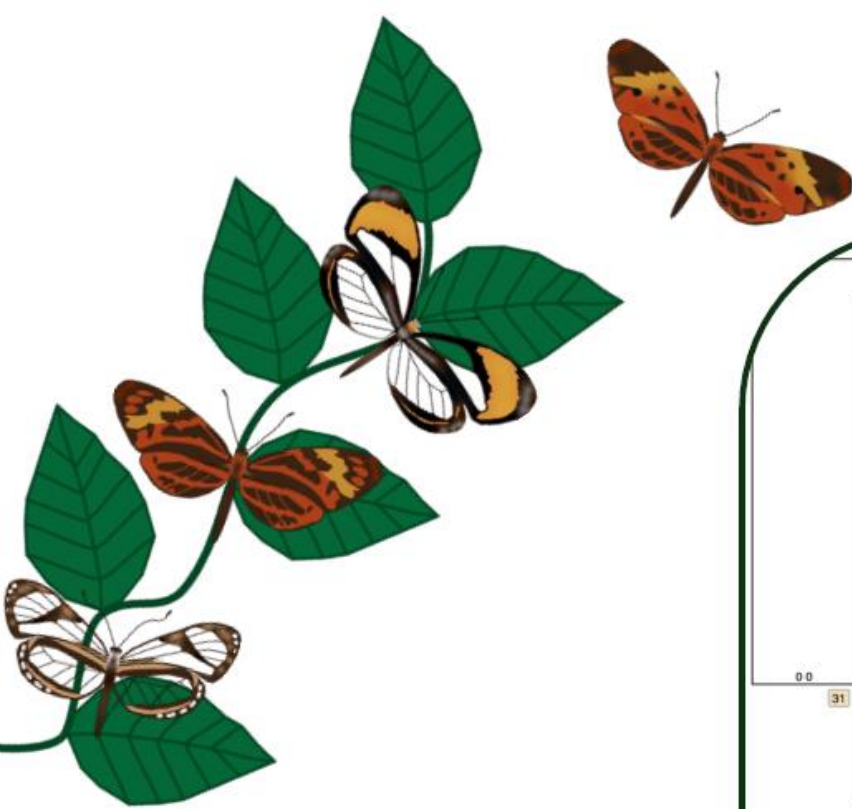
University



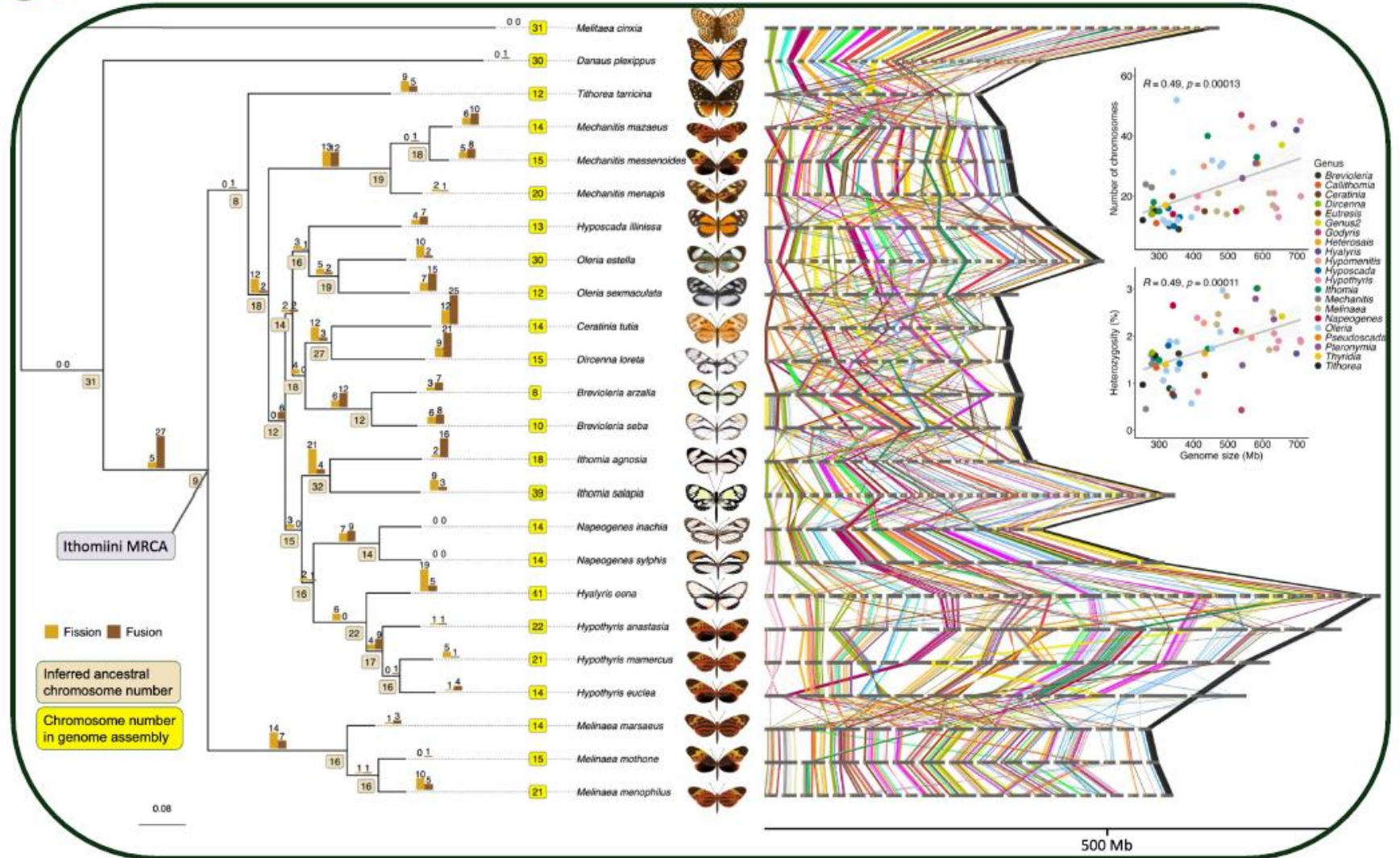
Rates and patterns of genome
evolution in Lepidoptera

KARIN NÄSVALL





Association between
speciation rate
And chromosomal
rearrangements in
Ithomiini butterflies



Nicol Rueda

Colombia

- **BSc in Biology - Colombia**
- **Master in Species Conservation in trade (CITES)**
Universidad Internacional de Andalucia - Spain
- **Master of Science in Biology**
Universidad Nacional de Colombia
- **PhD candidate in Biology**
Universidad del Rosario - Colombia

Master of science in Biology



Population monitoring for 7 months in two forests of different conservation status.

Capture-Mark-recapture technique

Rev. Acad. Colomb. Cienc. Ex. Fis. Nat. 49(157):653-663, noviembre-diciembre de 2016
doi: <https://doi.org/10.15445/racyn.792>

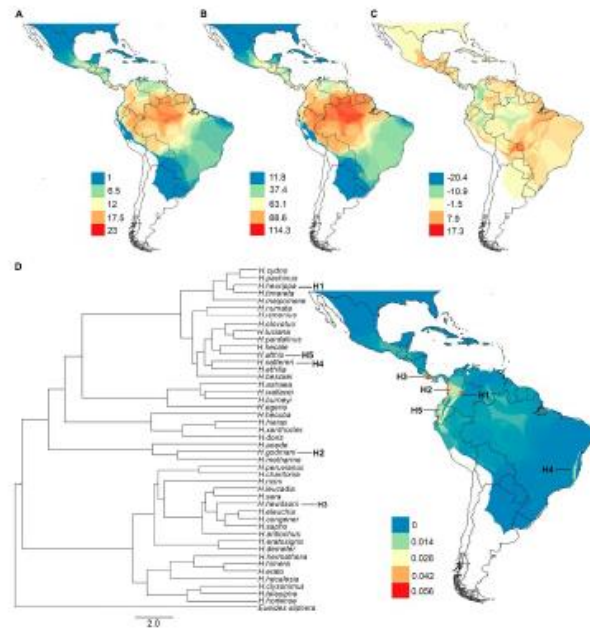
Artículo original

Ciencias Naturales

El género *Heliconius* Kluk, 1708 en dos habitats de diferente grado de conservación en la Amazonia colombiana y aportes para su conservación

Nicol Rueda-M¹*, M. Gonzalo Andrade-G²

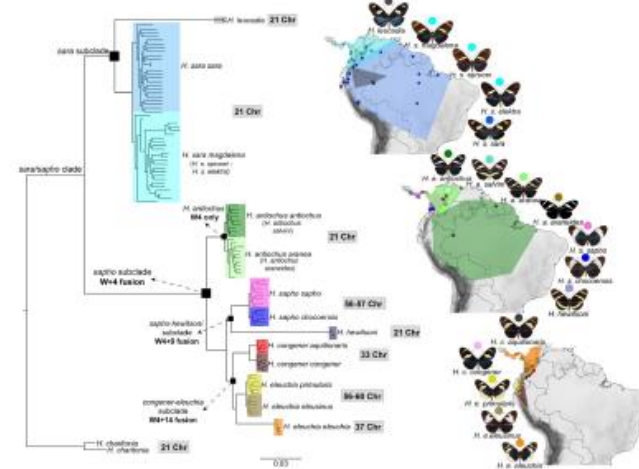
Drivers of diversification in *Heliconius*, with special focus on the *sara/sapho* clade



2021

Environmental Drivers of Diversification and Hybridization in Neotropical Butterflies

Ricor Rueda-Morales, Fabian C. Salazar-Alvarez, Carlos R. Salazar-Gil, Carolina Parla-Diaz, and Carlos Salazar

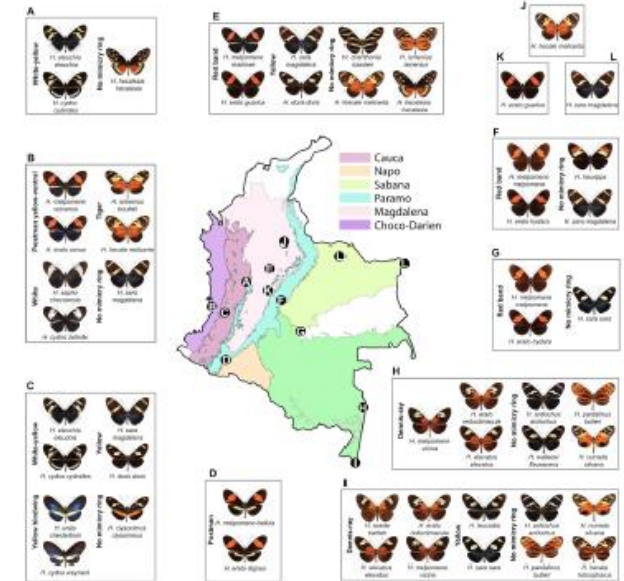


PLOS GENETICS

2024

Genomic evidence reveals three W-autosome fusions in *Heliconius* butterflies

Ricor Rueda-Morales^{1,2}, Carolina Parla-Diaz¹, Gabriela Montoya-Kovachovich¹, W. Owen McMillan³, Koyatol M. Kuzak^{4,5}, Carlos F. Arce^{1,6}, Jonathan Ready^{1,7}, Shane McCarthy⁸, Richard Durbin⁹, Chris D. Jiggins¹⁰, Joana I. Meier^{11,12}, Camilo Salazar^{1,13}



WORK IN PROGRESS