



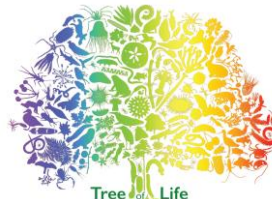
# Welcome to the Biodiversity Genomics course!

**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

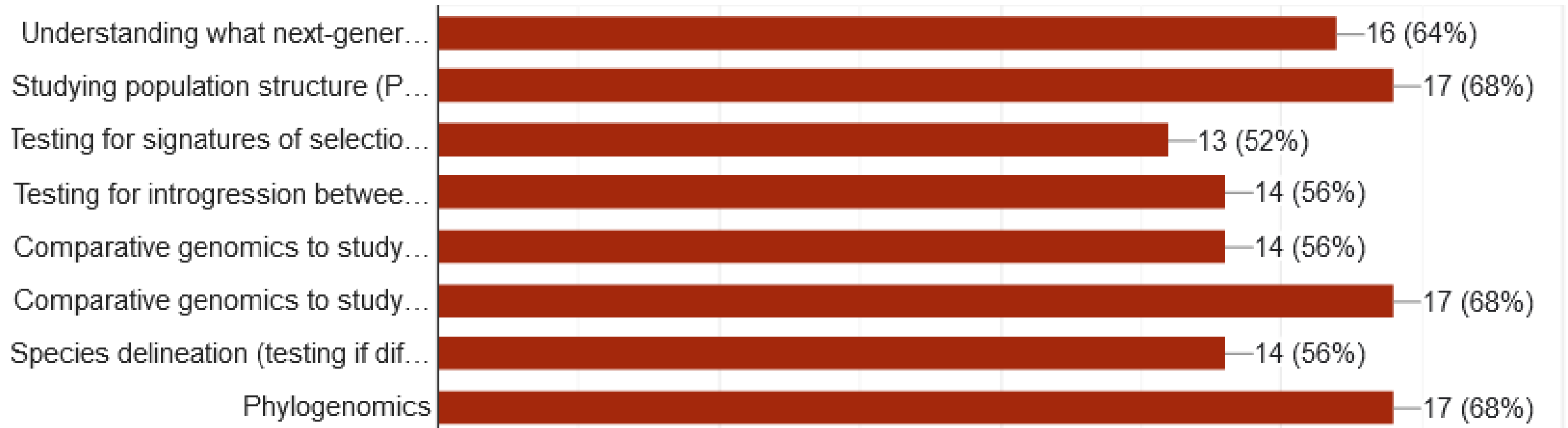


wellcome  
sanger  
institute



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 phylogenetics
  - Genome scans to identify regions under selection
- Tuesday, 23 July:
  - Genome scans to identify introgressed regions
  - Comparative genomics
  - Phylogenomics with reference genomes
- Wednesday, 24 July:
  - 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**

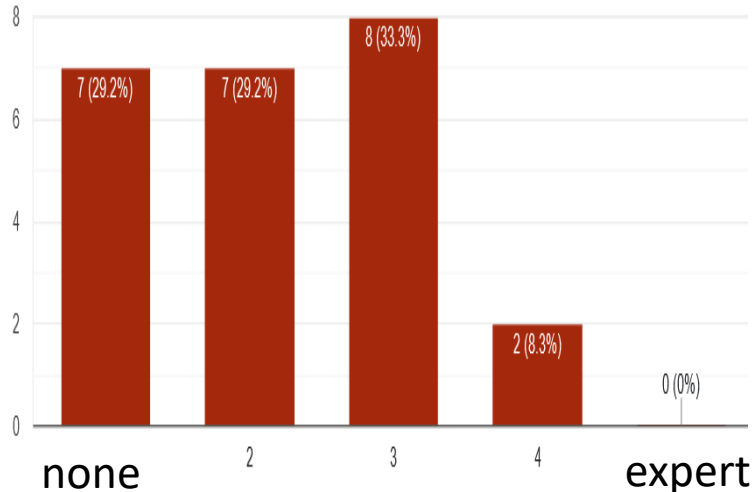
# A few tips and housekeeping rules

- 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](https://github.com/rapidspeciation/biodiversity_genomics_course)

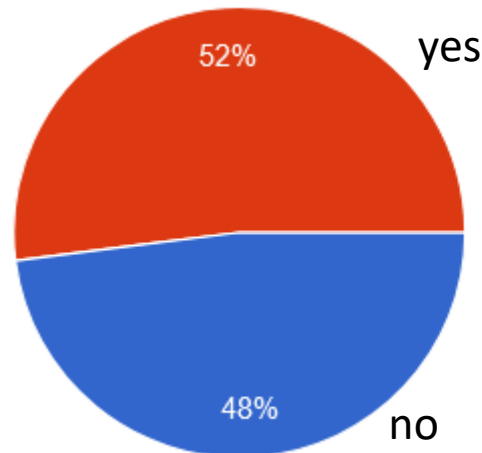
# We are a very diverse group, which is great!

- 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!

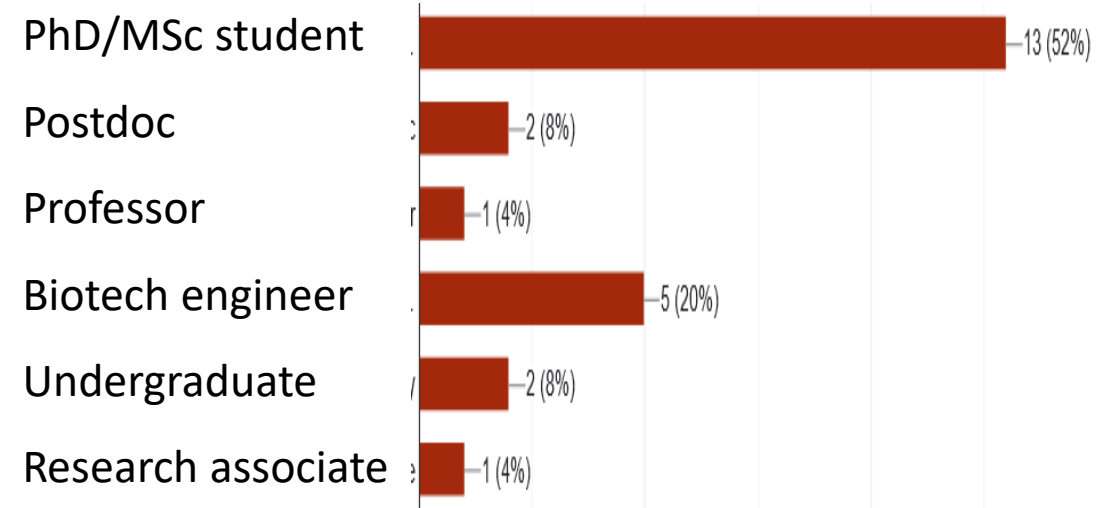
## Linux experience



## Prior experience with NGS data



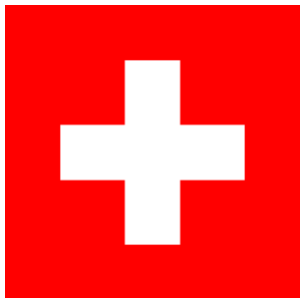
## Current academic level/job



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

# Joana Meier

## Childhood



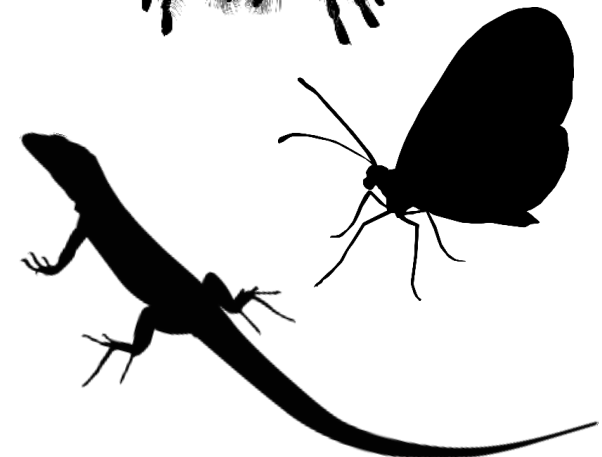
**PhD on cichlid fish  
Speciation in Bern,  
Switzerland**



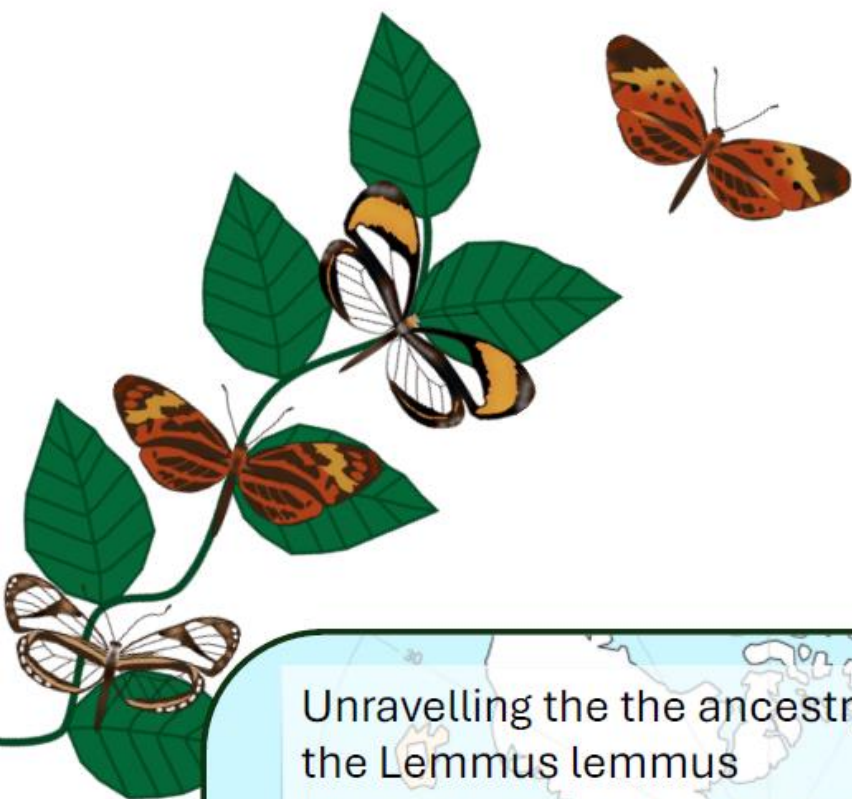
**Postdoc at the  
University of  
Cambridge, UK**



**Group leader at the  
Wellcome Sanger  
Institute**







## Karin Näsval, PhD

Postdoctoral fellow

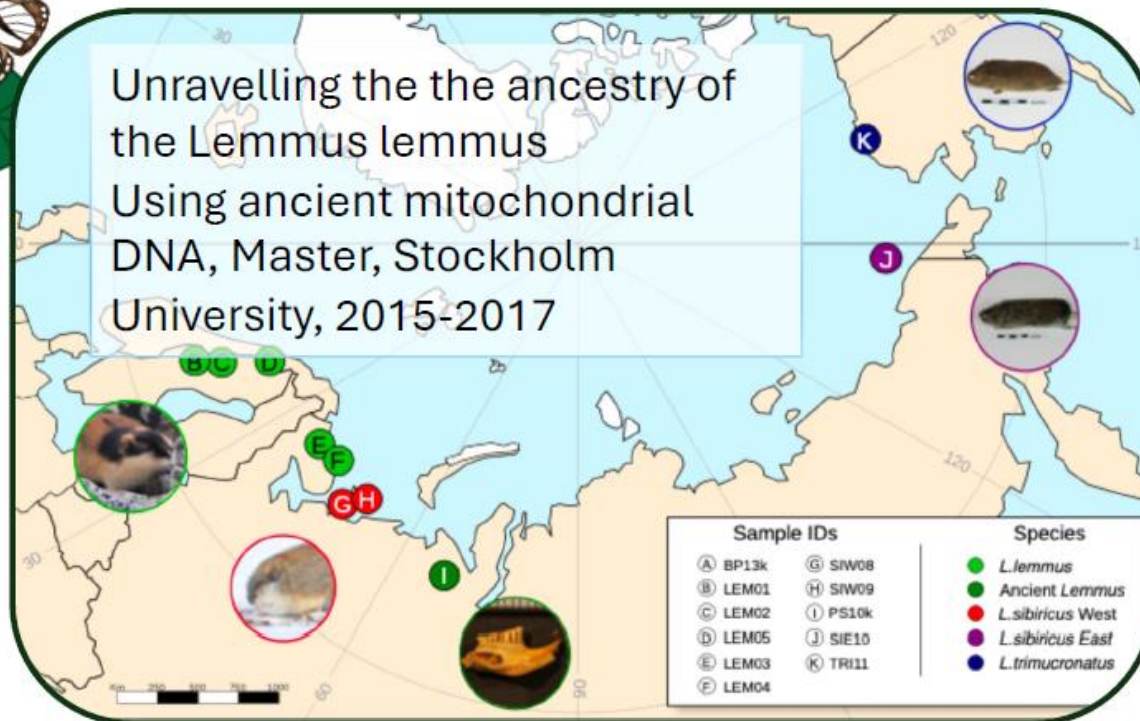
Rapid speciation group, Tree of Life

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

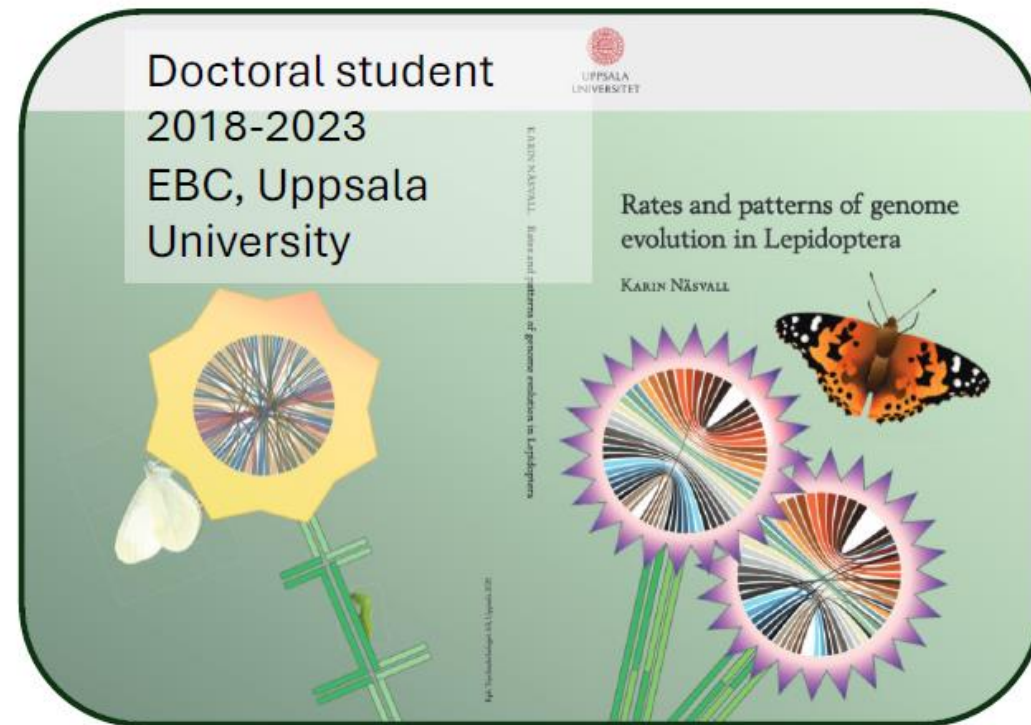
EBC, Uppsala

University

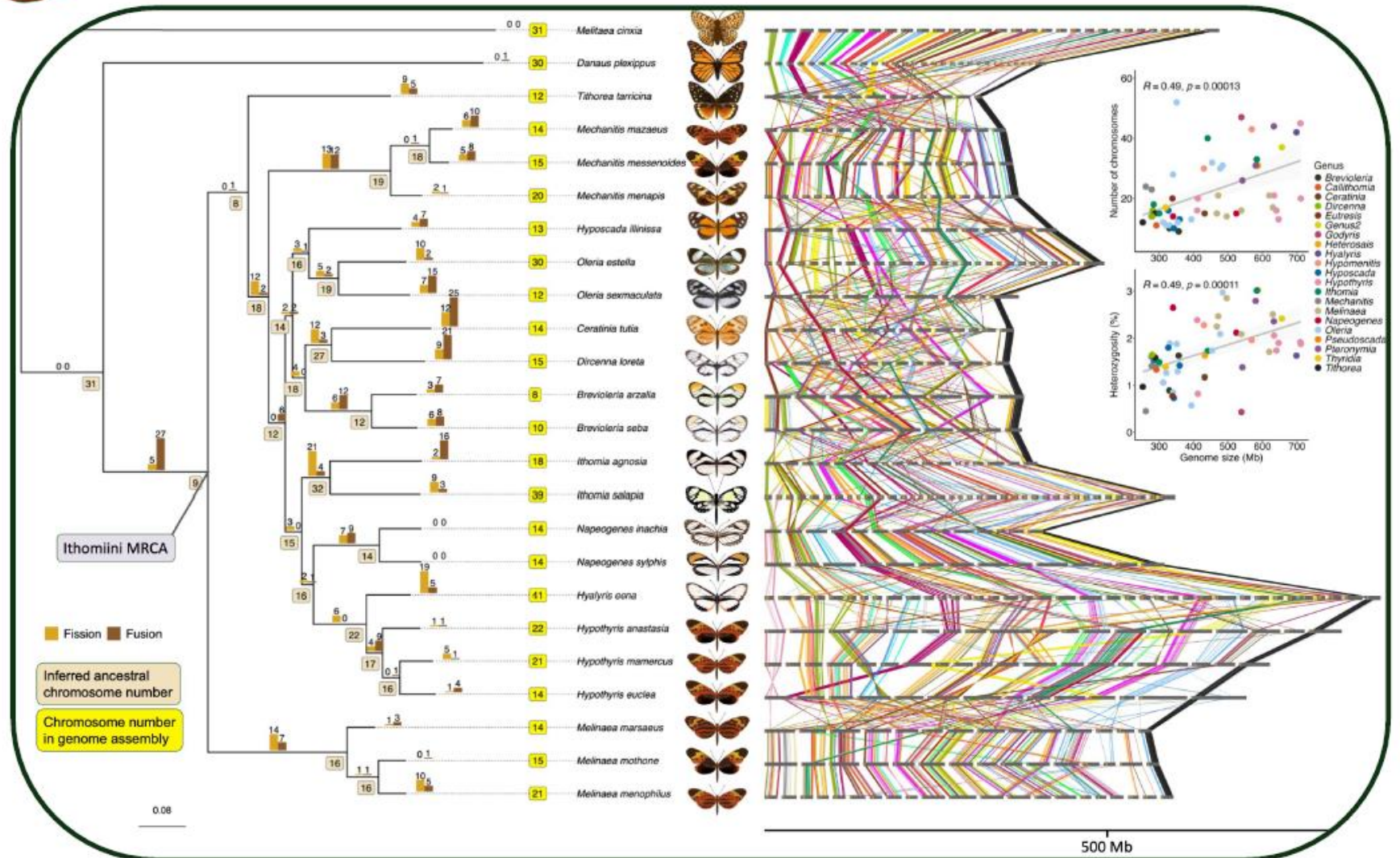
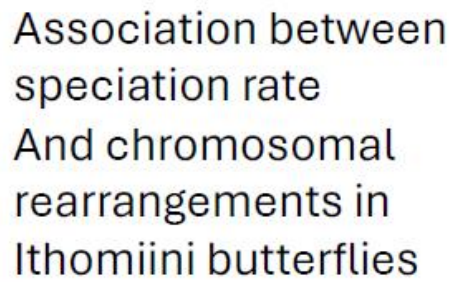


Rates and patterns of genome  
evolution in Lepidoptera

KARIN NÄSVALL







# 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. 40(157):653-663, noviembre-diciembre de 2016  
doi: <https://doi.org/10.15445/racyn.792>

Artículo original

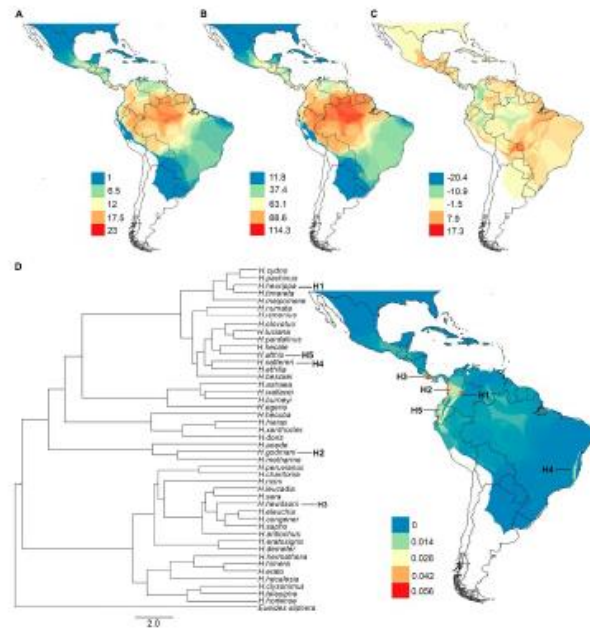
ciencias Naturales

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

Nicol Rueda-M<sup>1</sup>\*, M. Gonzalo Andrade-G<sup>2</sup>



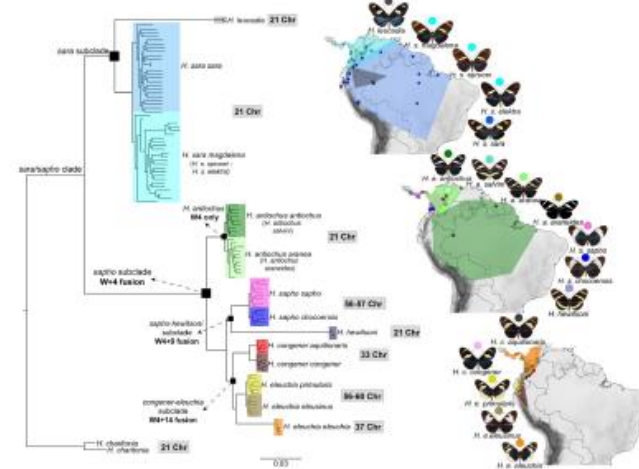
# Drivers of diversification in *Heliconius*, with special focus on the *sara/sapho* clade



2021

Environmental Drivers of Diversification and Hybridization in Neotropical Butterflies

Ricci Rueda M., Esham C., Salgado-Alvarez C., Carlos R., Santos O., Carolina Parla-Diaz, and Carlos Salazar

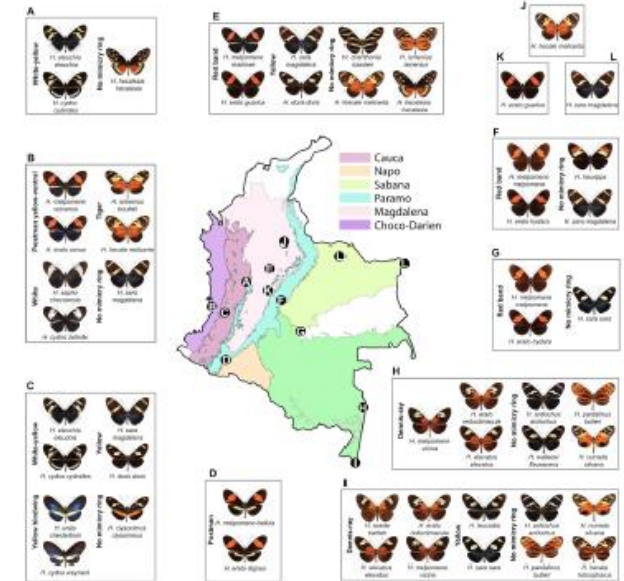


PLOS GENETICS

2024

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

Ricci Rueda M.<sup>1,2</sup>, Carolina Parla-Diaz<sup>1</sup>, Gabriela Montoya-Kovachovich<sup>1</sup>, W. Owen McMillan<sup>3</sup>, Koyatol M. Kuzak<sup>4,5</sup>, Carlos F. Arce<sup>1,6</sup>, Jonathan Ready<sup>1,7</sup>, Shane McCarthy<sup>8</sup>, Richard Durbin<sup>9</sup>, Chris D. Jiggins<sup>10</sup>, Joana I. Meier<sup>11,12</sup>, Camilo Salazar<sup>1,13</sup>



WORK IN PROGRESS