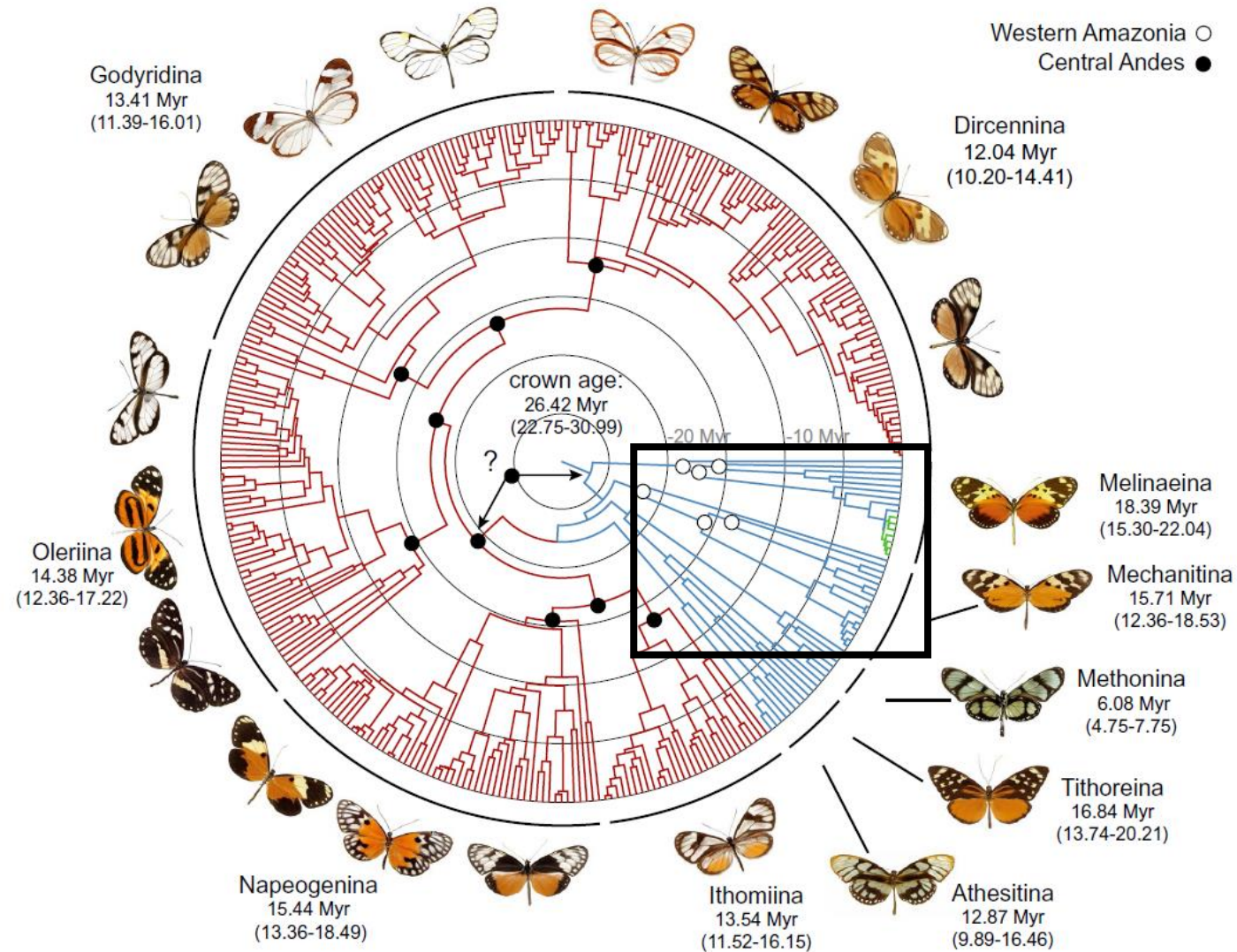
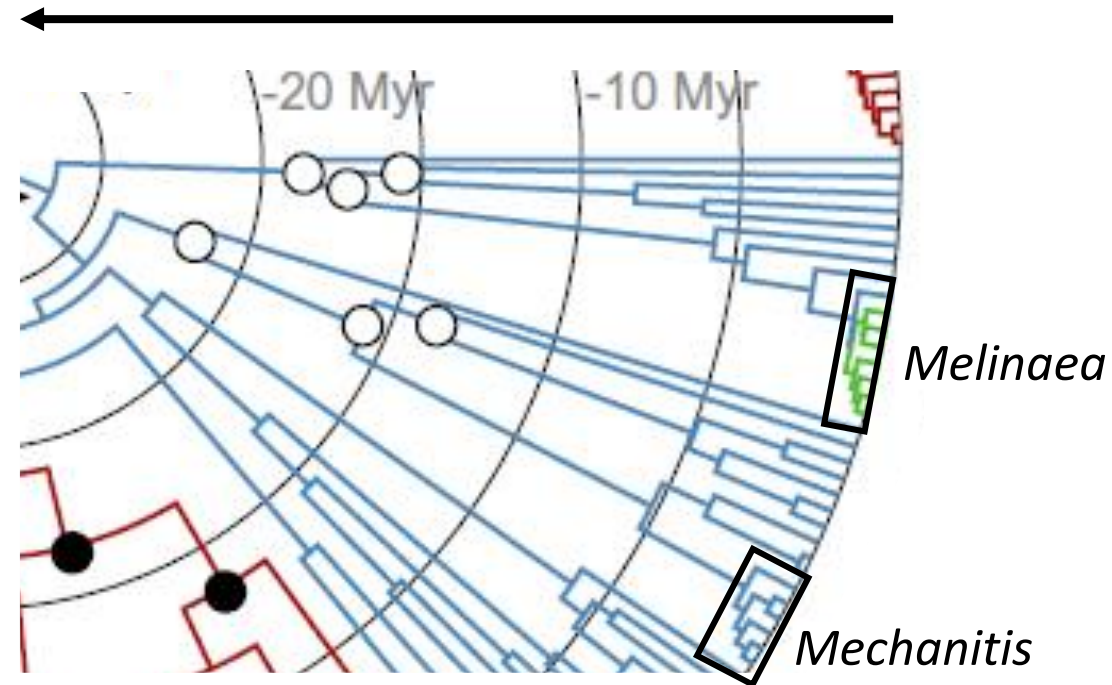


# Phylogenomics of fast-speciating Ithomiini genera



Time since last common ancestor

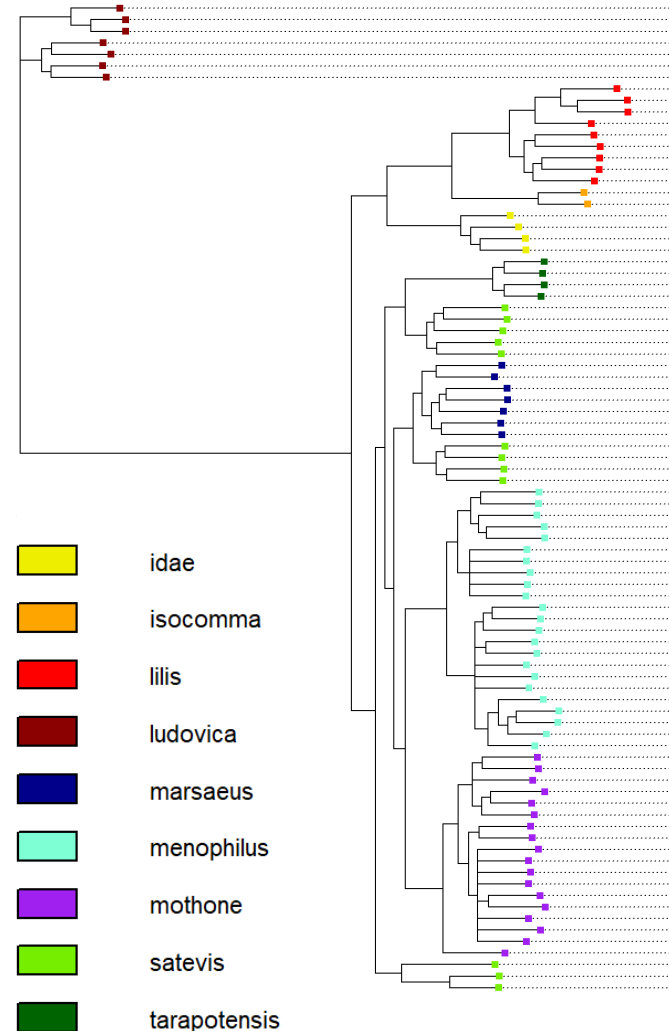


# *Melinaea* butterflies are very closely related

*Melinaea* species



whole-genome phylogeny



*ludovica*

*lilis*

*isocomma*

*idae*

*tarapotensis*

***satevis maeolus / cydon* (Pe/Co)**

*marsaeus*

***satevis maeonis* (Ec)**

*menophilus*

*mothone*

*mneme* (Co/FG)



Eva van der Heijden

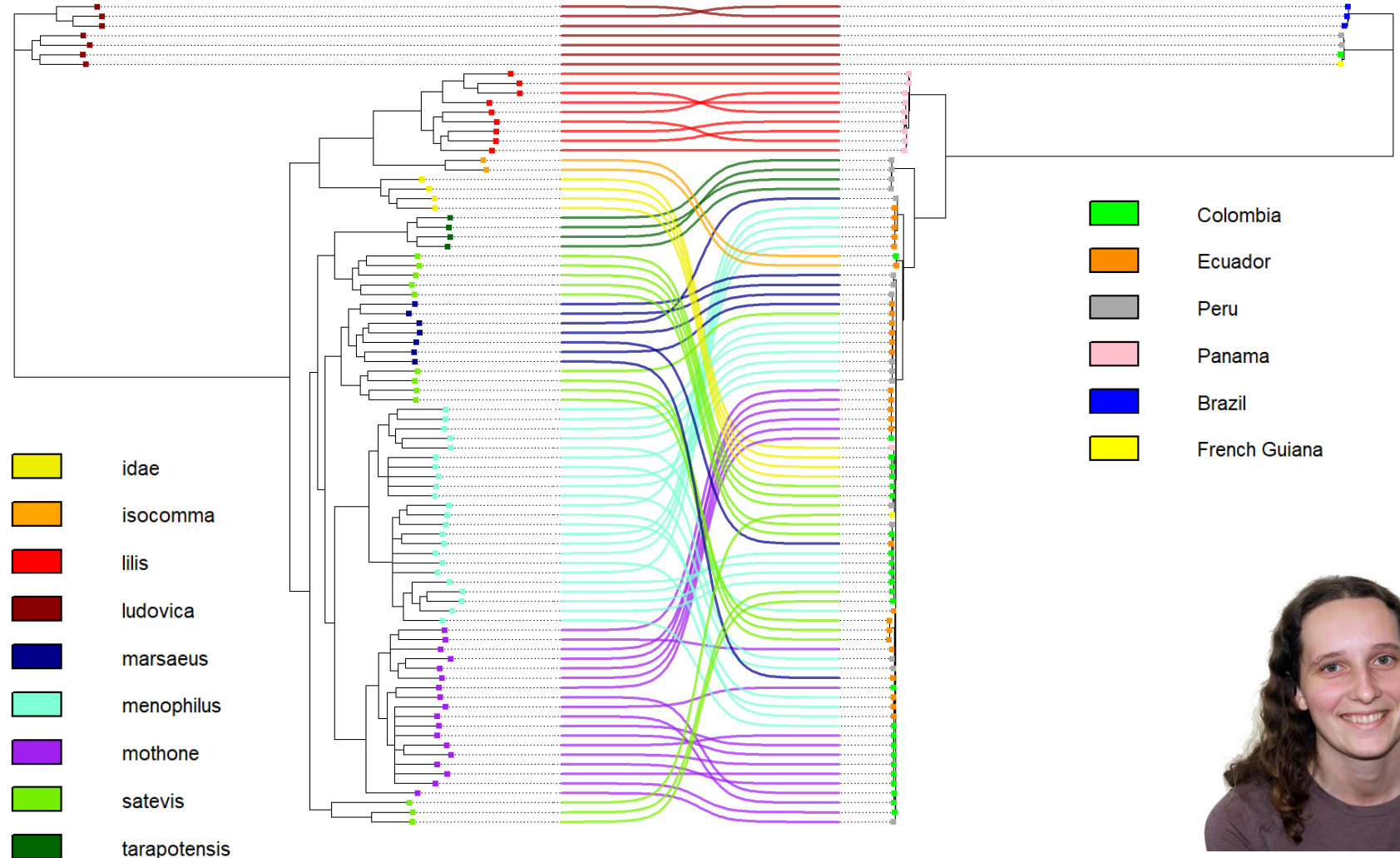


# *Melinaea* butterflies are very closely related

*Melinaea* species



whole-genome phylogeny

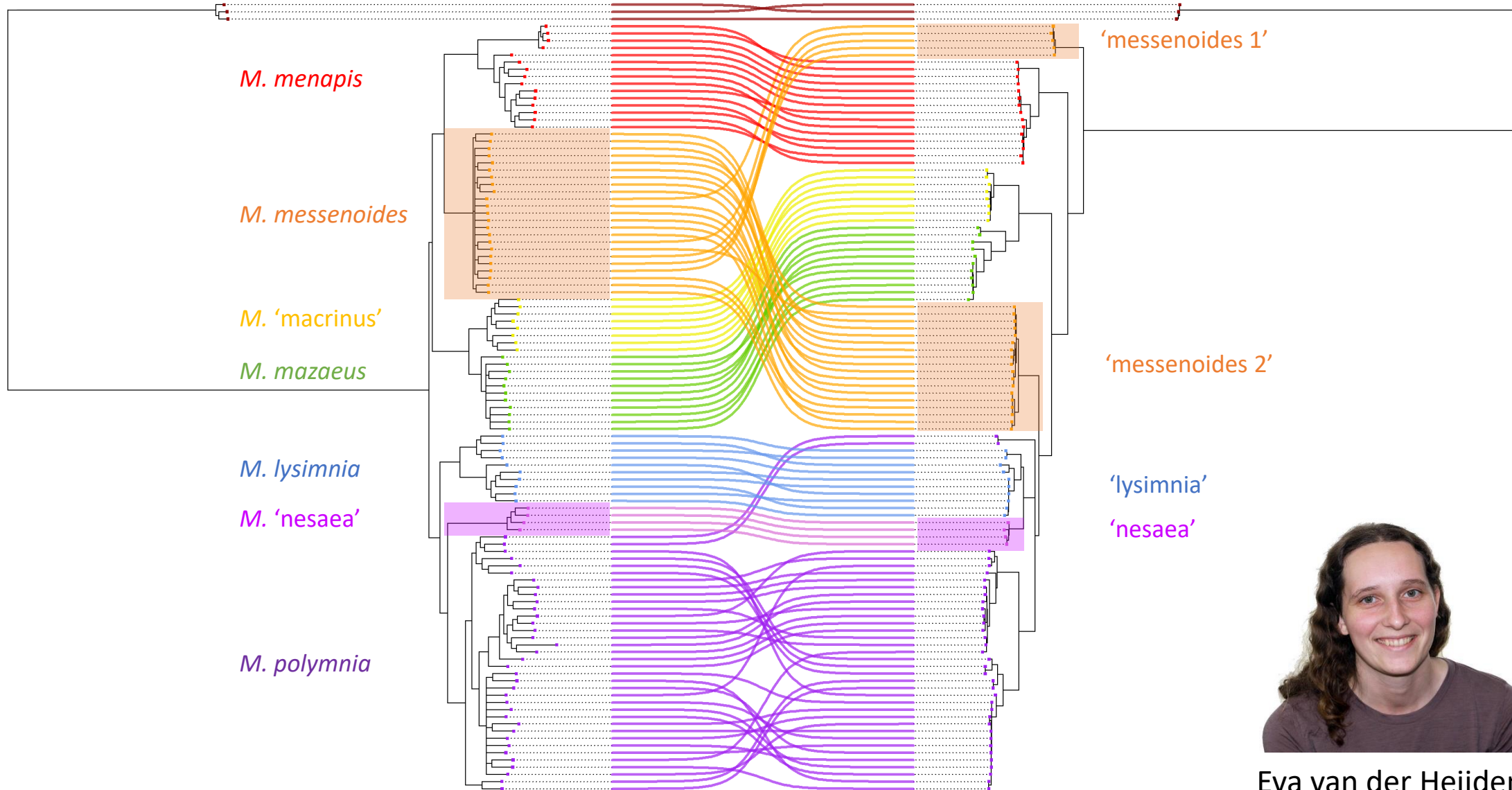


Eva van der Heijden

# *Mechanitis* butterflies show vast cytonuclear discordance

Whole-genome phylogeny

Mitochondrial phylogeny



Eva van der Heijden

# Hybrid species with new trait combinations?

Phenotype:

Immature  
form (5<sup>th</sup> instar)

Wing  
patterning

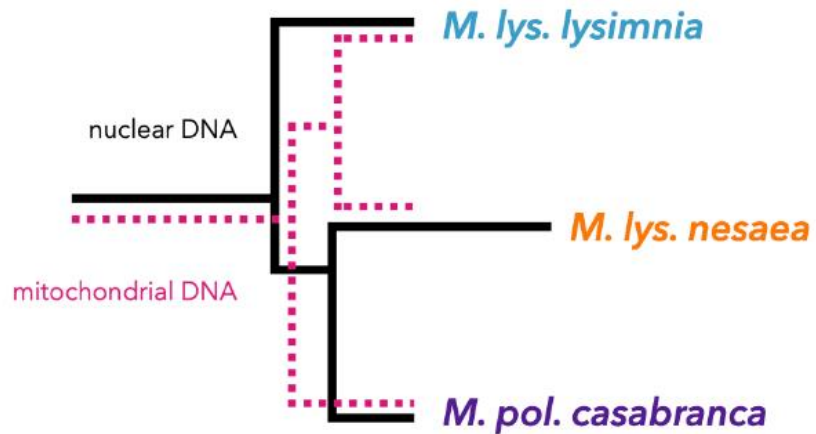
Chromosome  
count (n)

Pheromonal  
bouquet  
composition  
(PCA)

*M. lys. nesaea* is more similar to:

*M. lys. lysimnia*

*M. pol. casabranca*



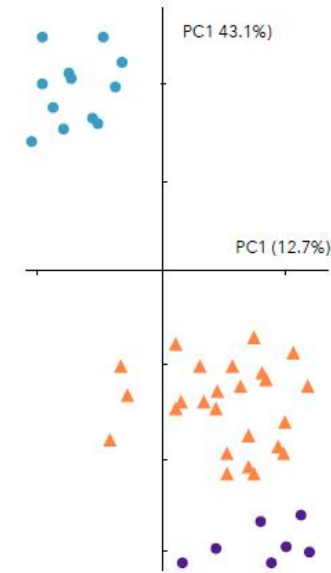
18-19



17



14-16

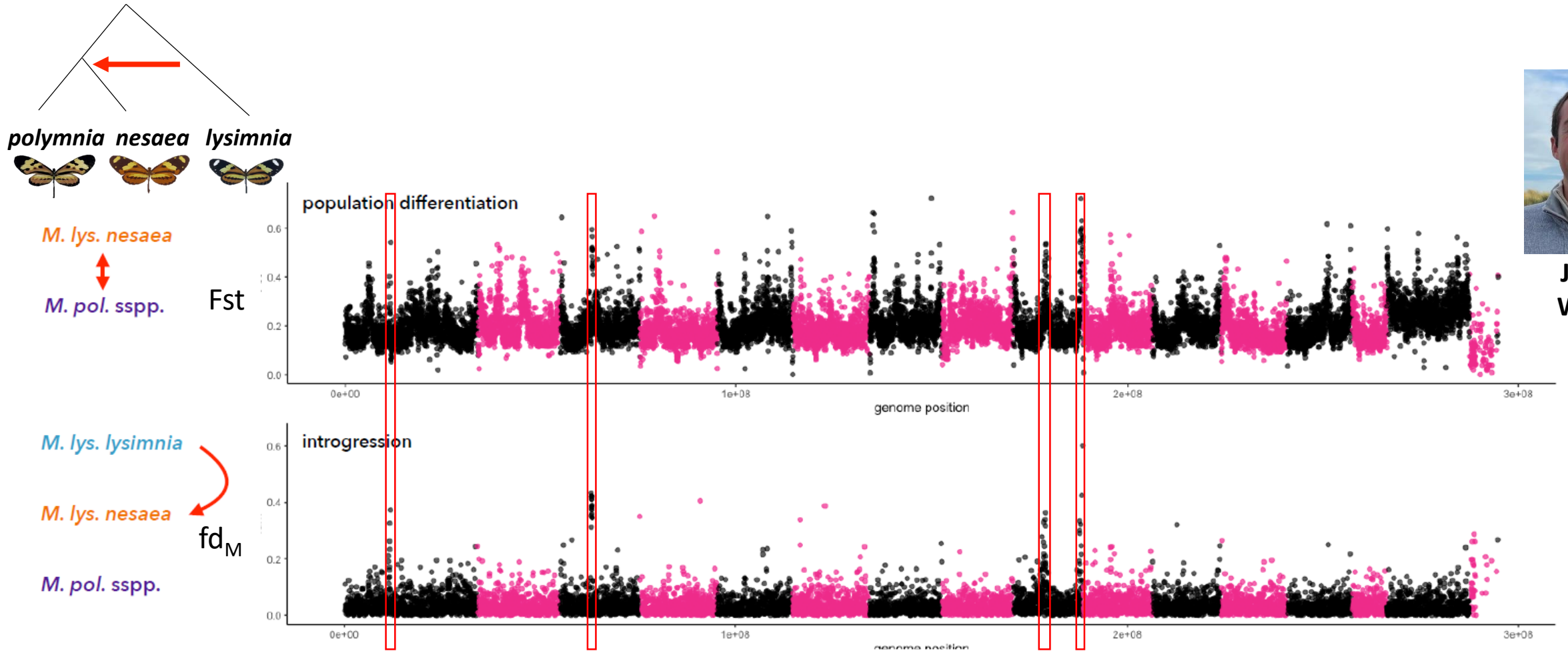


Jonah Walker



André Freitas  
U Campinas, Brazil

# Many regions that differentiate *M. nesaea* from *M. polymnia* show introgression from *M. lysimnia*



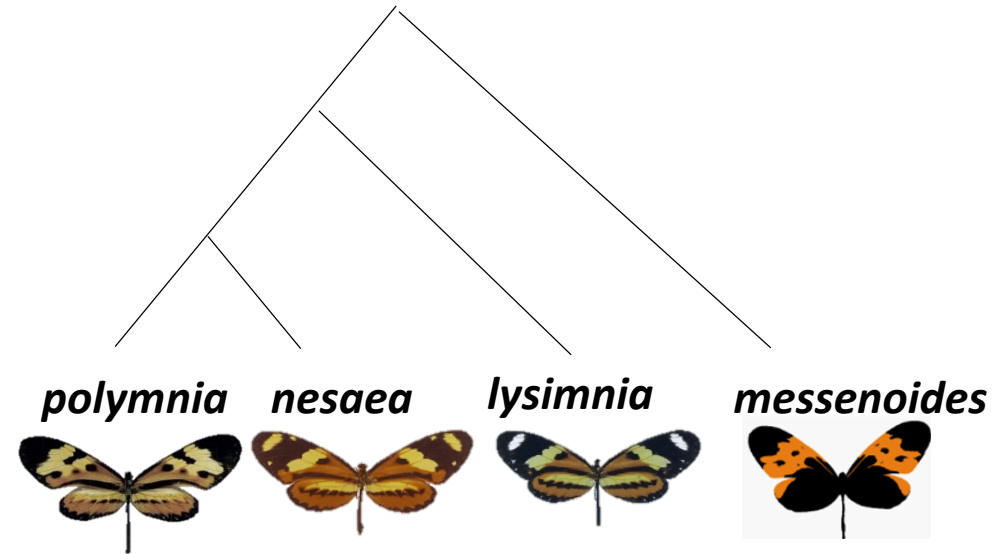
Jonah Walker



# Exercises with Mechanitis.vcf file

- In the vcf file we have:

- 5 *Mechanitis polymnia*
- 5 *Mechanitis lysimnia*
- 5 *Mechanitis nesaea*
- 5 *Mechanitis messenoides*

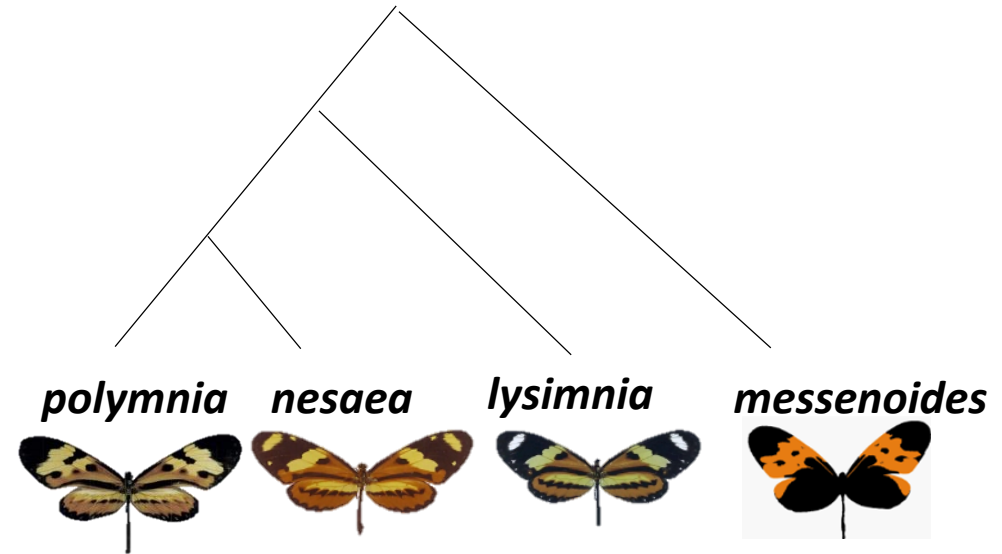


- We will run:

- PCA (Principal components analysis) with plink
- Phylogenetic tree with iqtree2
- Infer hybridisation with introgression
- Genome scans for Fst, Dxy, pi
- Genome scans for introgression

# Exercises with Mechanitis.vcf file

- In the vcf file we have:
  - 5 *Mechanitis polymnia*
  - 5 *Mechanitis lysimnia*
  - 5 *Mechanitis nesaea*
  - 5 *Mechanitis messenoides*



- We will run:
  - **PCA (Principal components analysis) with plink**
  - Phylogenetic tree with iqtree2
  - Infer hybridisation with introgression
  - Genome scans for Fst, Dxy, pi
  - Genome scans for introgression



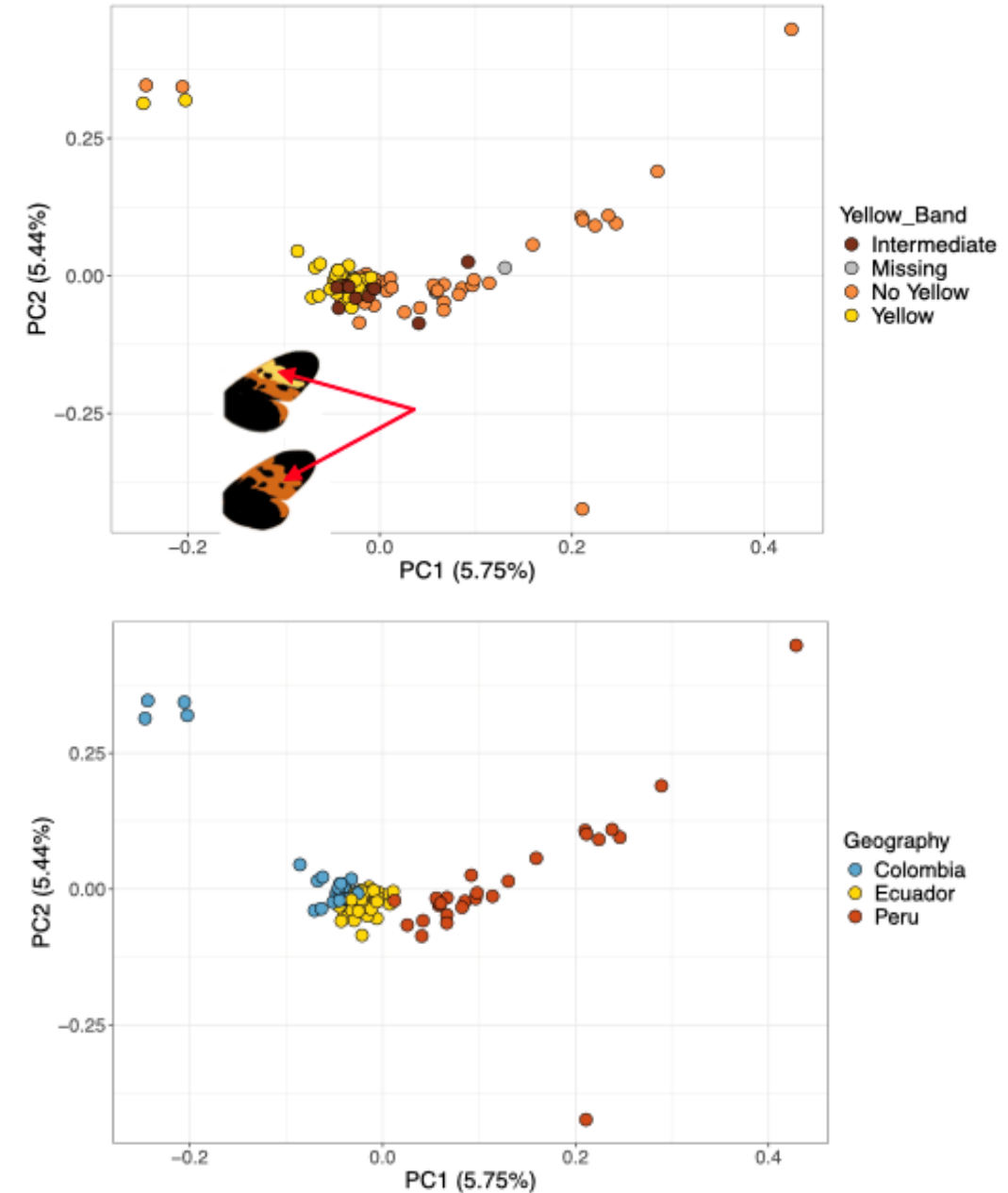
# PCA – Principal Components Analysis

- We want to convert the vcf file showing genotypes across all individuals and sites into something more visual that shows the differences and similarity between individuals
- PCA reduces the complexity / dimensionality of the data
- PCA aims identifies the main axes of variation in a dataset with each axis being independent of the next
- Eigenvalues: each axis has an eigenvalue, that can be transformed into the percentage of variance explained
- Eigenvectors: each individual has a position on each axis

# Why run a PCA?

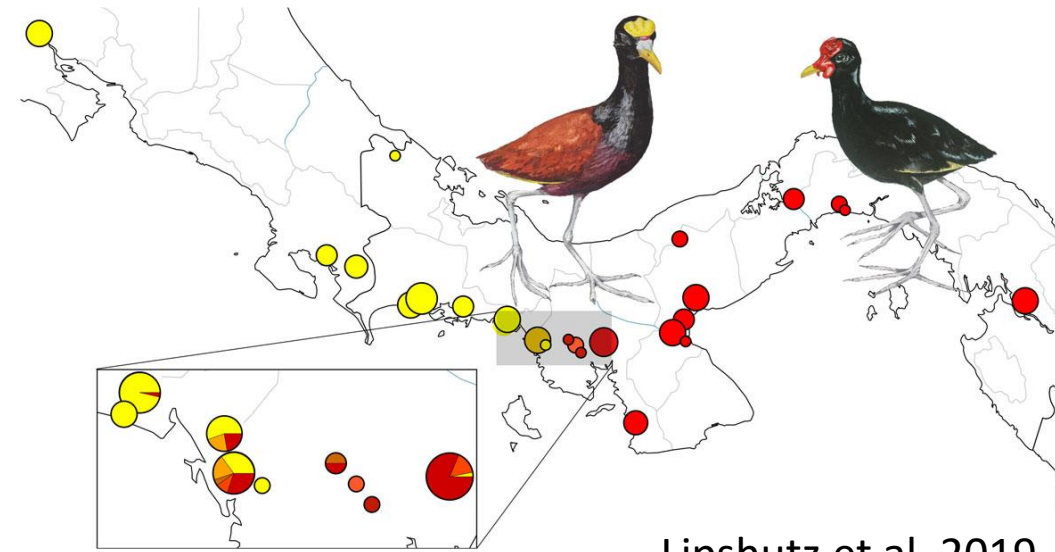
- Are all individuals clustering together as expected? (e.g. no outlier or misidentified individuals)
- Testing if individuals with different colour or morphology represent different species (cluster separately) or colour/ecomorphs (completely intermixed)?

Plots by Eva van der Heijden



# Why run a PCA?

- Are all individuals clustering together as expected? (e.g. no outlier or misidentified individuals)
- Testing if individuals with different colour or morphology represent different species (cluster separately) or colour/ecomorphs (completely intermixed)?
- **Are any individuals hybrids?**



Lipshutz et al. 2019

