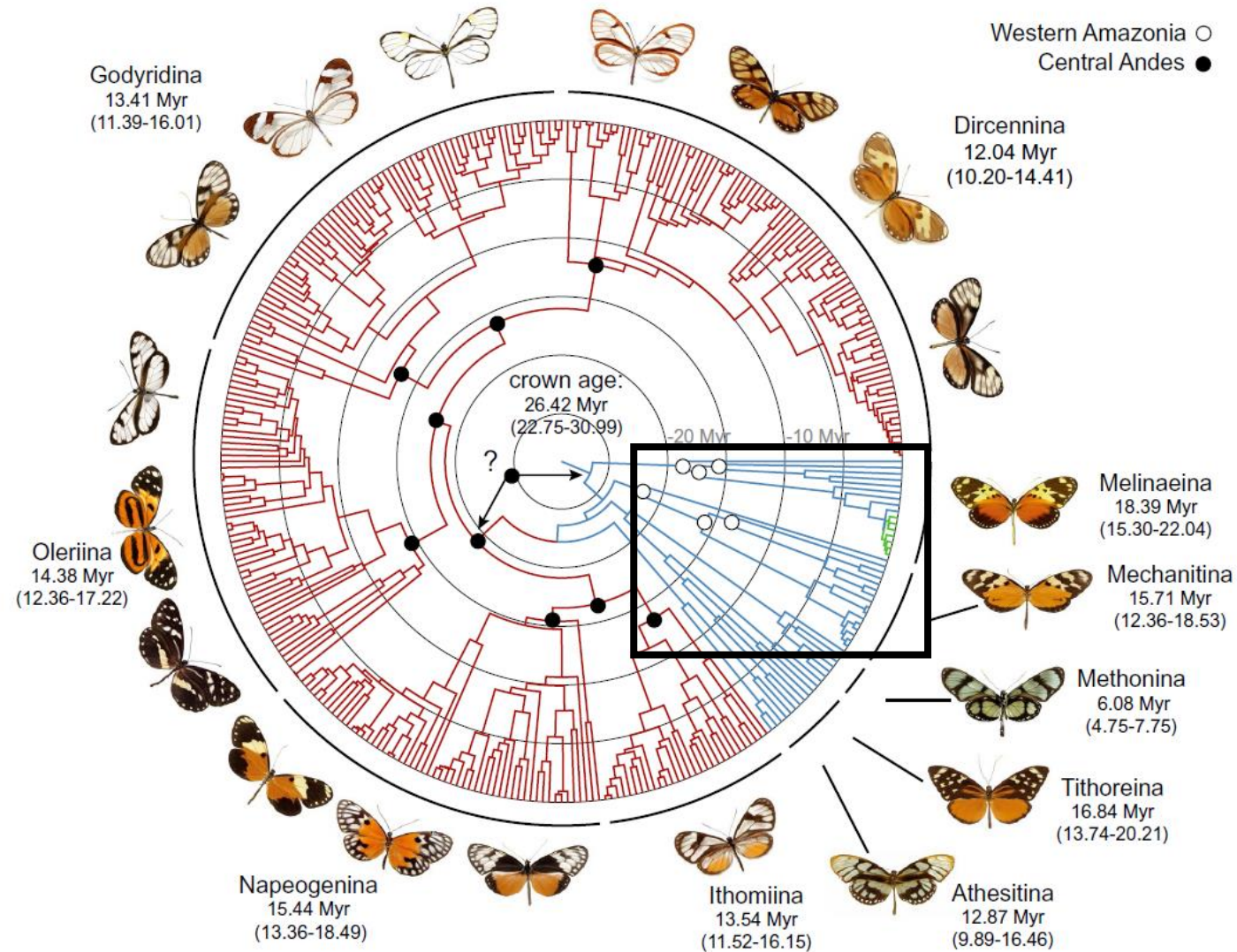
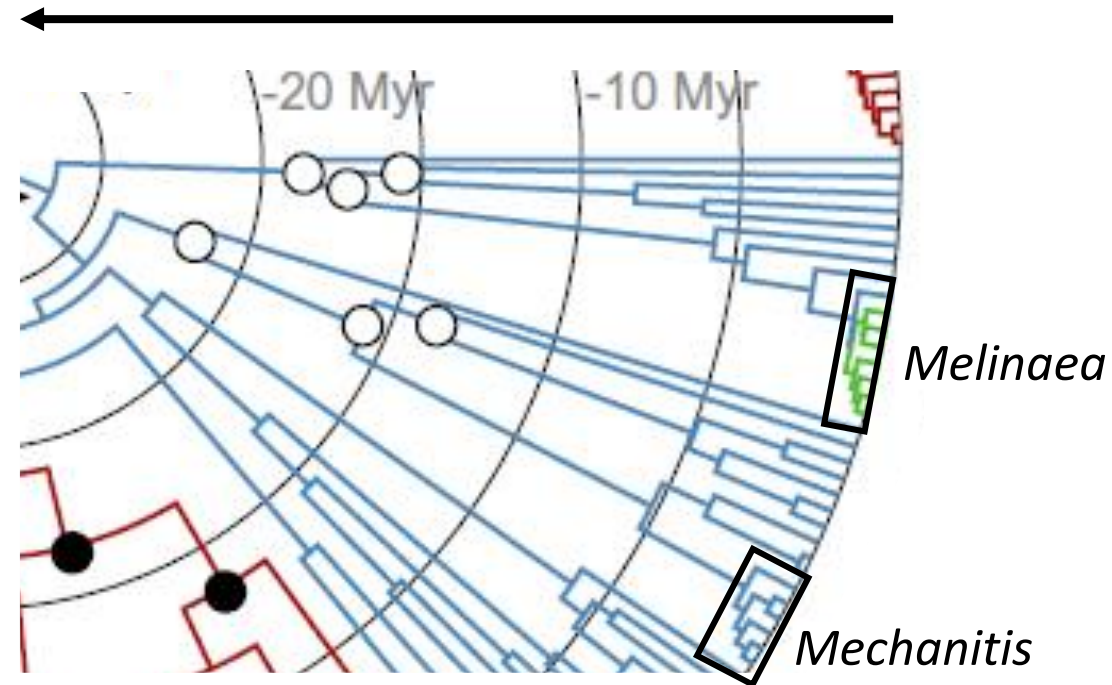


Phylogenomics of fast-speciating Ithomiini genera



Time since last common ancestor

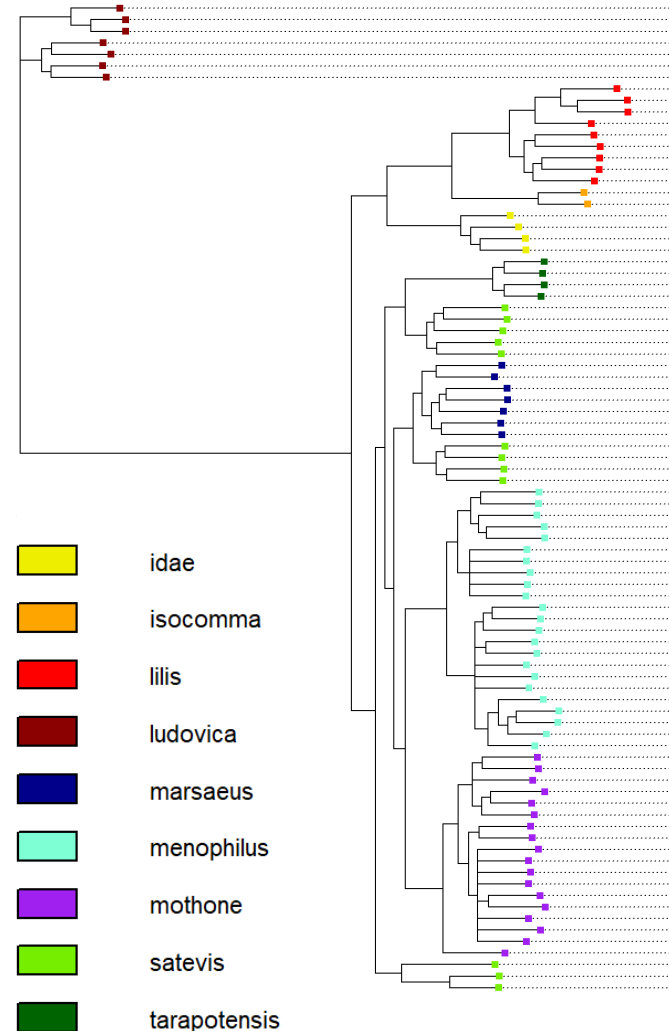


Melinaea butterflies are very closely related

Melinaea species



whole-genome phylogeny



ludovica

lilis

isocomma

idae

tarapotensis

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

marsaeus

***satevis maeonis* (Ec)**

menophilus

mothone

mneme (Co/FG)



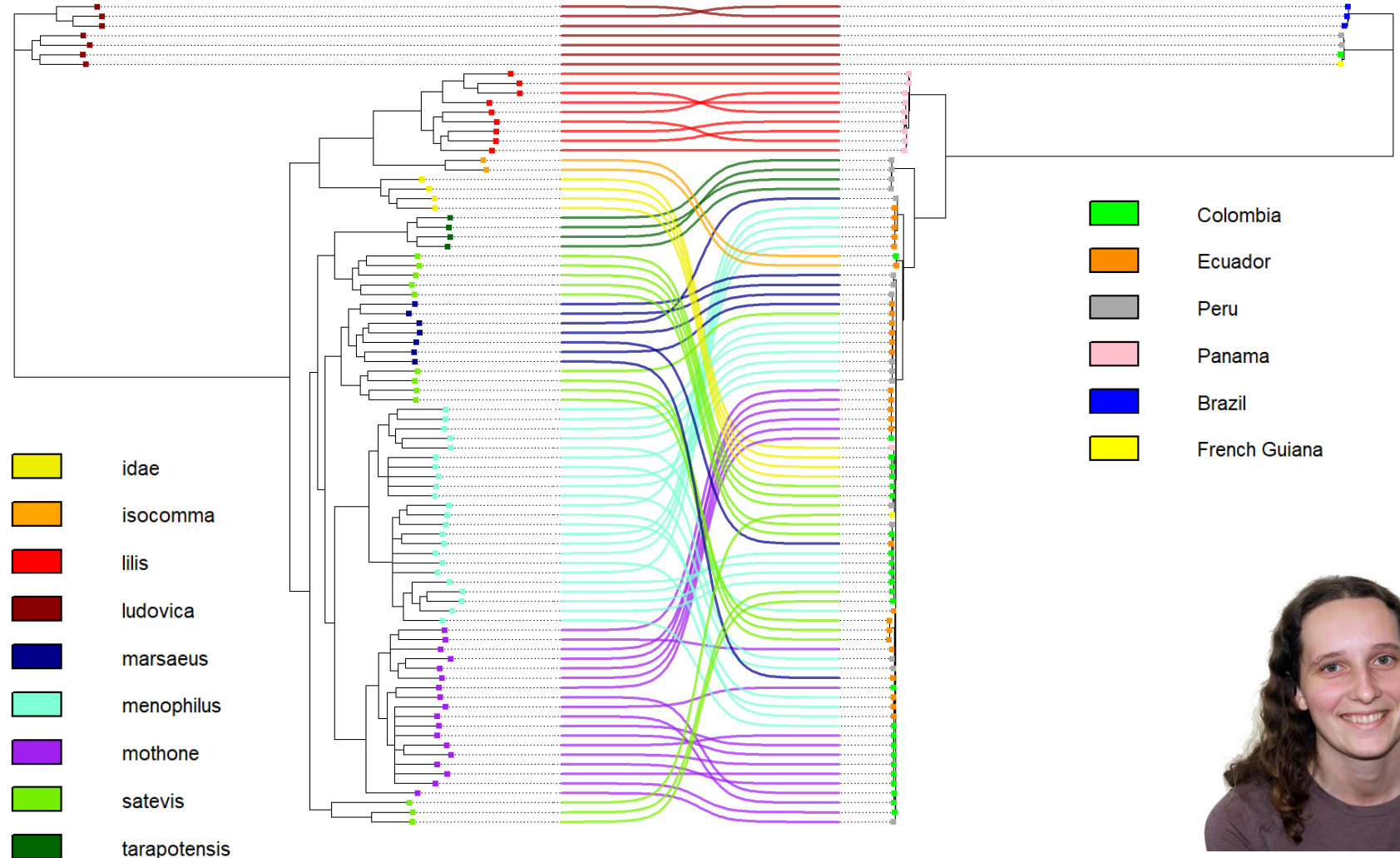
Eva van der Heijden

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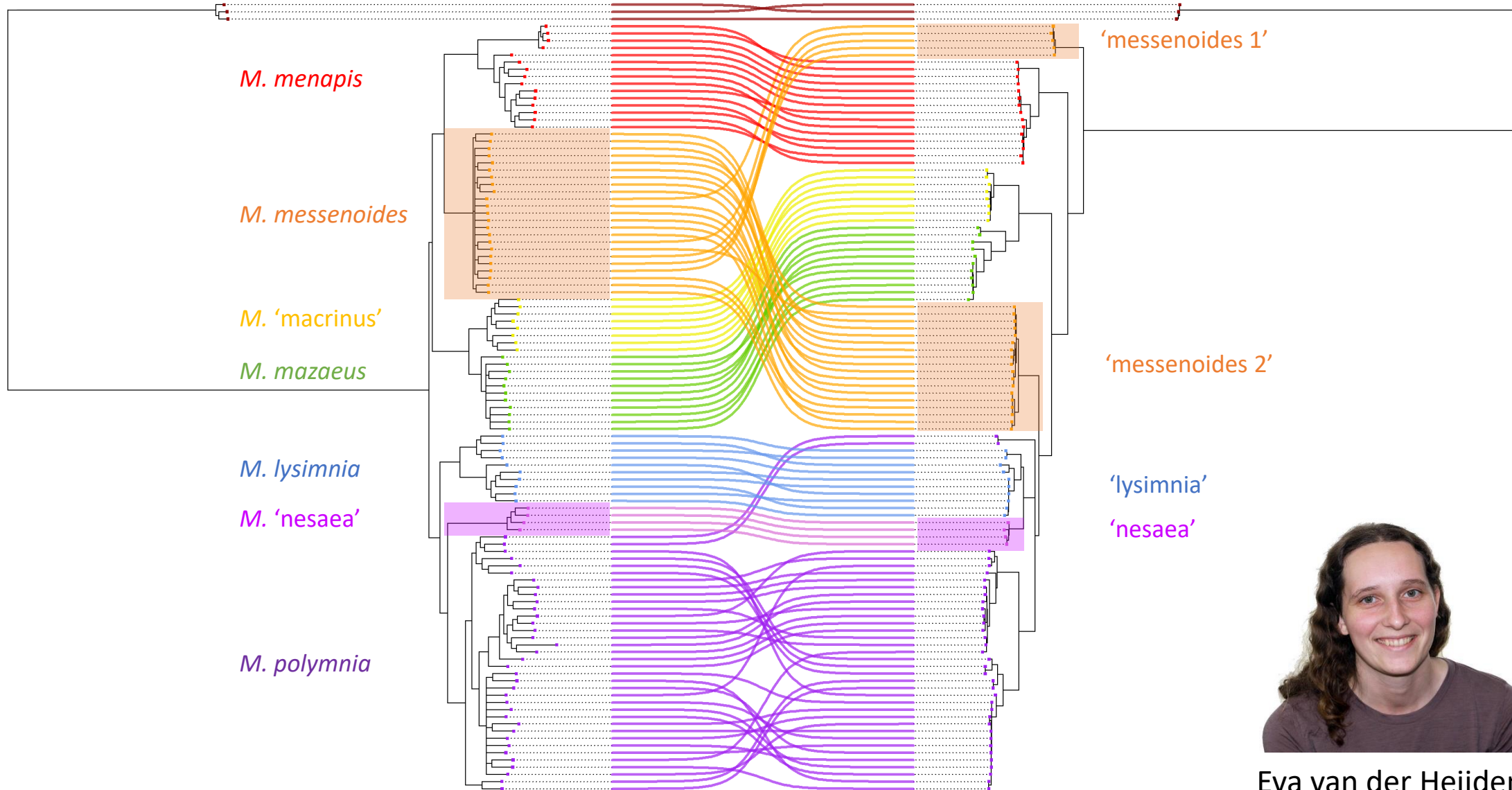


Eva van der Heijden

Mechanitis butterflies show vast cytonuclear discordance

Whole-genome phylogeny

Mitochondrial phylogeny



Eva van der Heijden

Hybrid species with new trait combinations?

Phenotype:

Immature
form (5th instar)

Wing
patterning

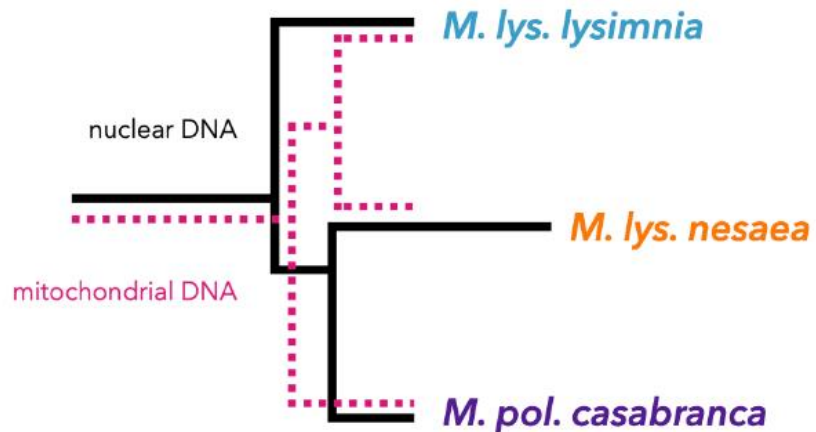
Chromosome
count (n)

Pheromonal
bouquet
composition
(PCA)

M. lys. nesaea is more similar to:

M. lys. lysimnia

M. pol. casabranca



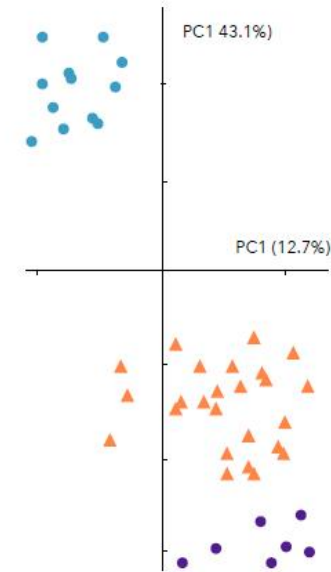
18-19



17



14-16

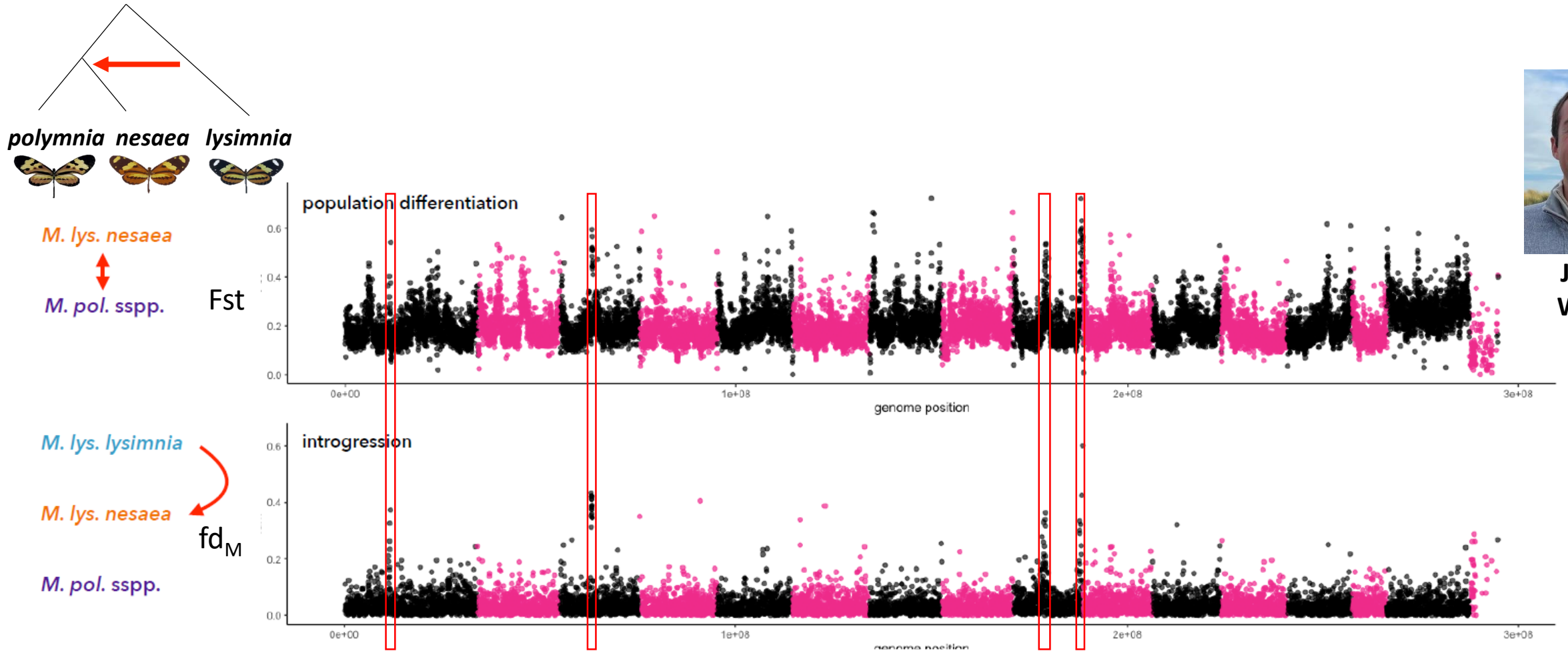


Jonah Walker



André Freitas
U Campinas, Brazil

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

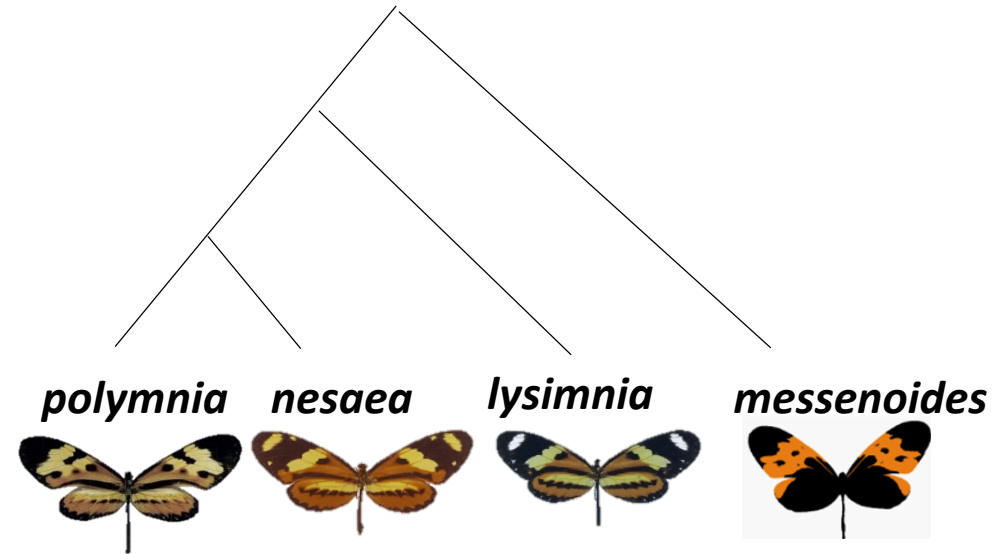


Jonah Walker

Exercises with Mechanitis.vcf file

- In the vcf file we have:

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



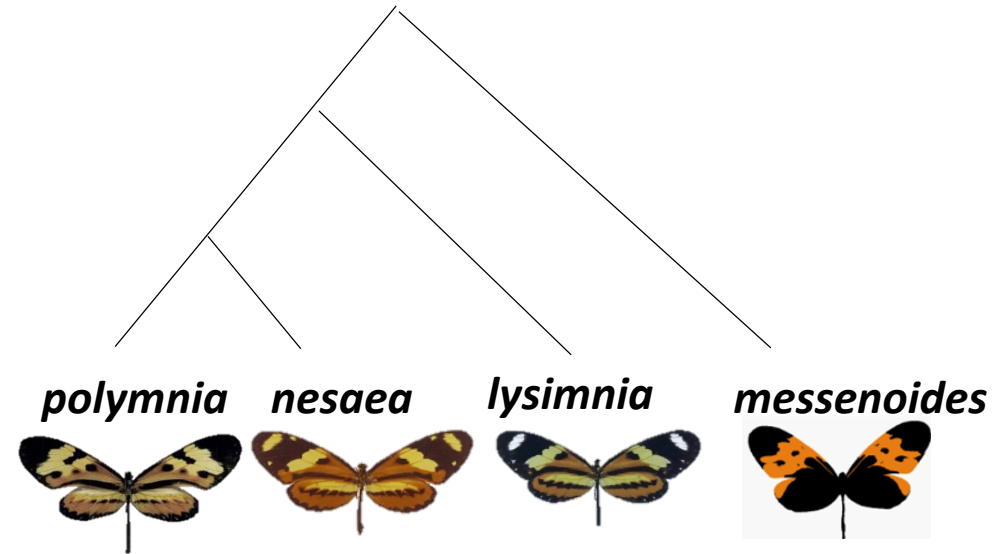
- We will run:

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

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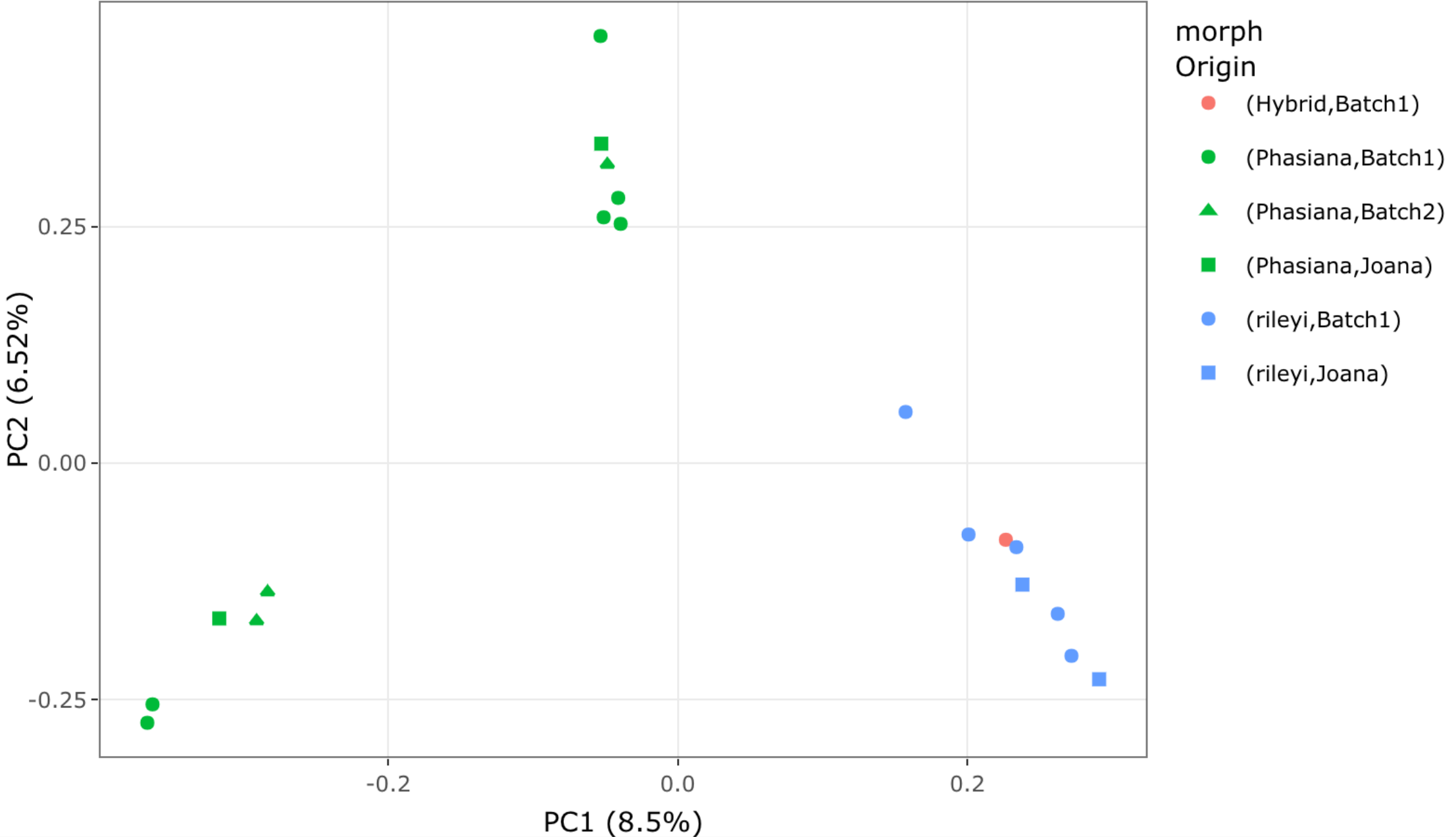
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- Genome scans for introgression

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

Example PCA

Melinaea_marsaeus



Why run a PCA?

- Are all individuals clustering together as expected? (e.g. no outlier or misidentified individuals)
- Are any individuals hybrids?

