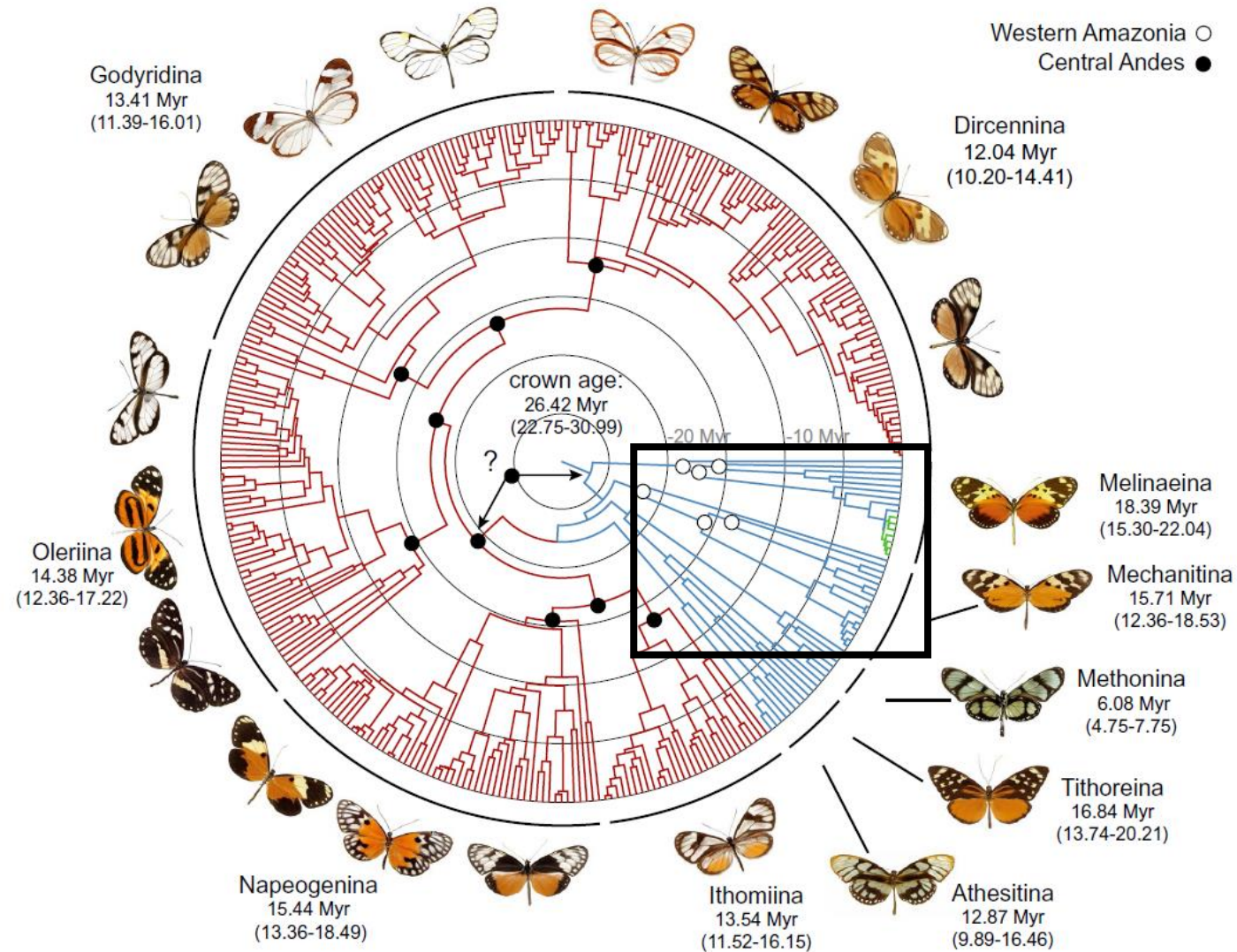
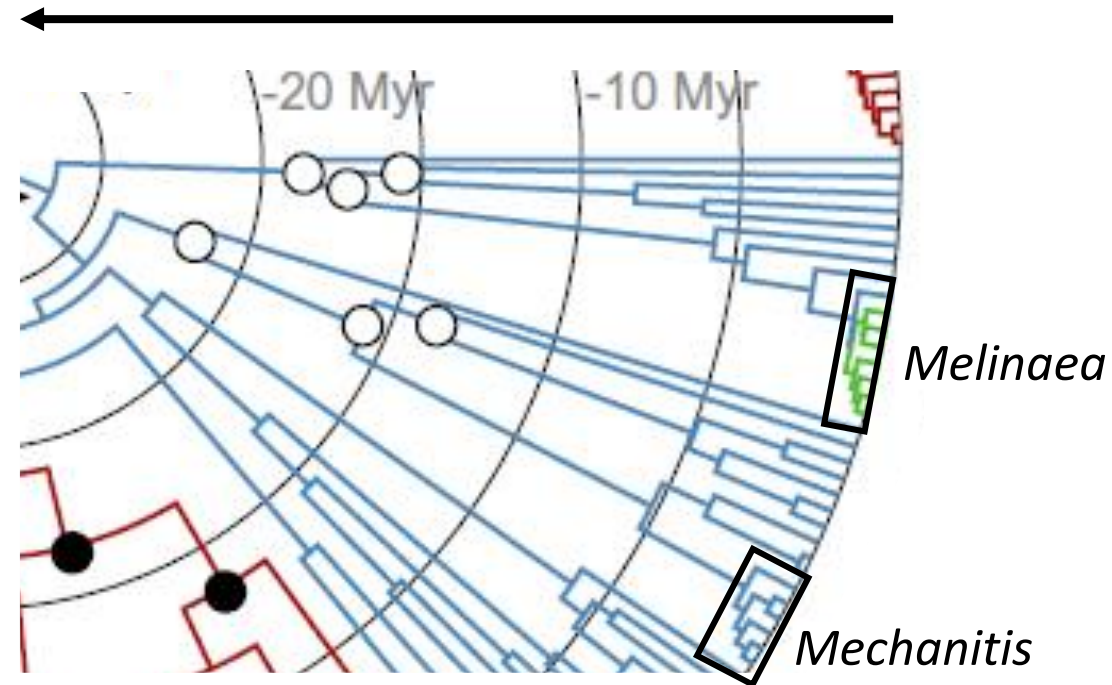


Phylogenomics of fast-speciating Ithomiini genera



Time since last common ancestor

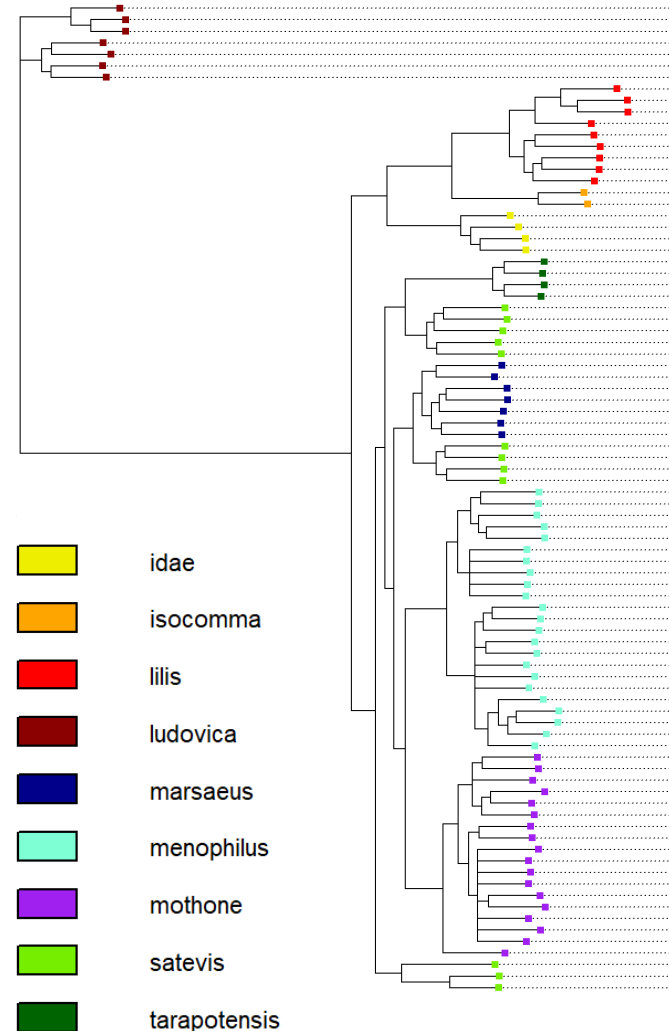


Melinaea butterflies are very closely related

Melinaea species



whole-genome phylogeny



ludovica

lilis

isocomma

idae

tarapotensis

satevis maeolus / cydon (Pe/Co)

marsaeus

satevis maeonis (Ec)

menophilus

mothone

mneme (Co/FG)



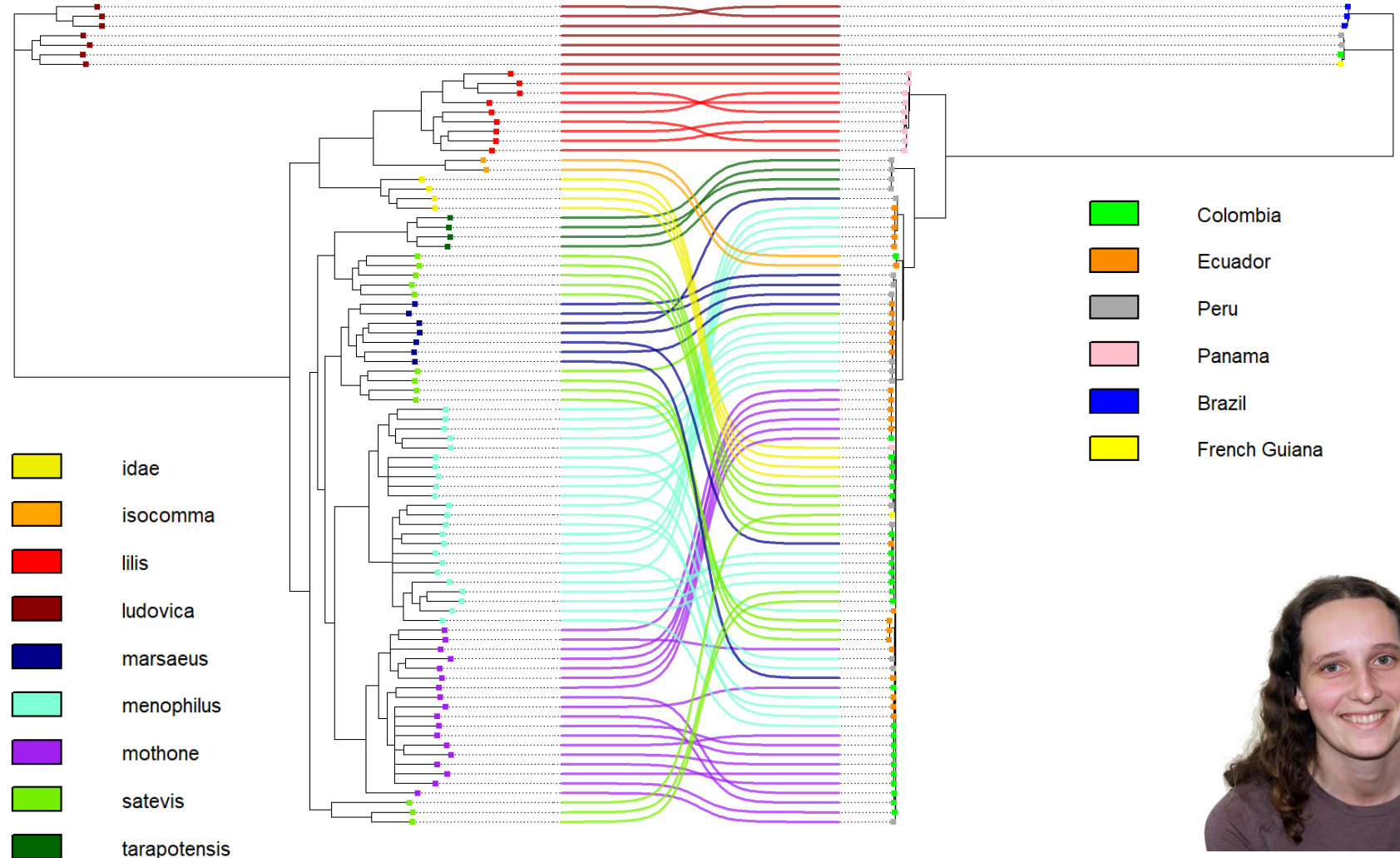
Eva van der Heijden

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Melinaea species



whole-genome phylogeny

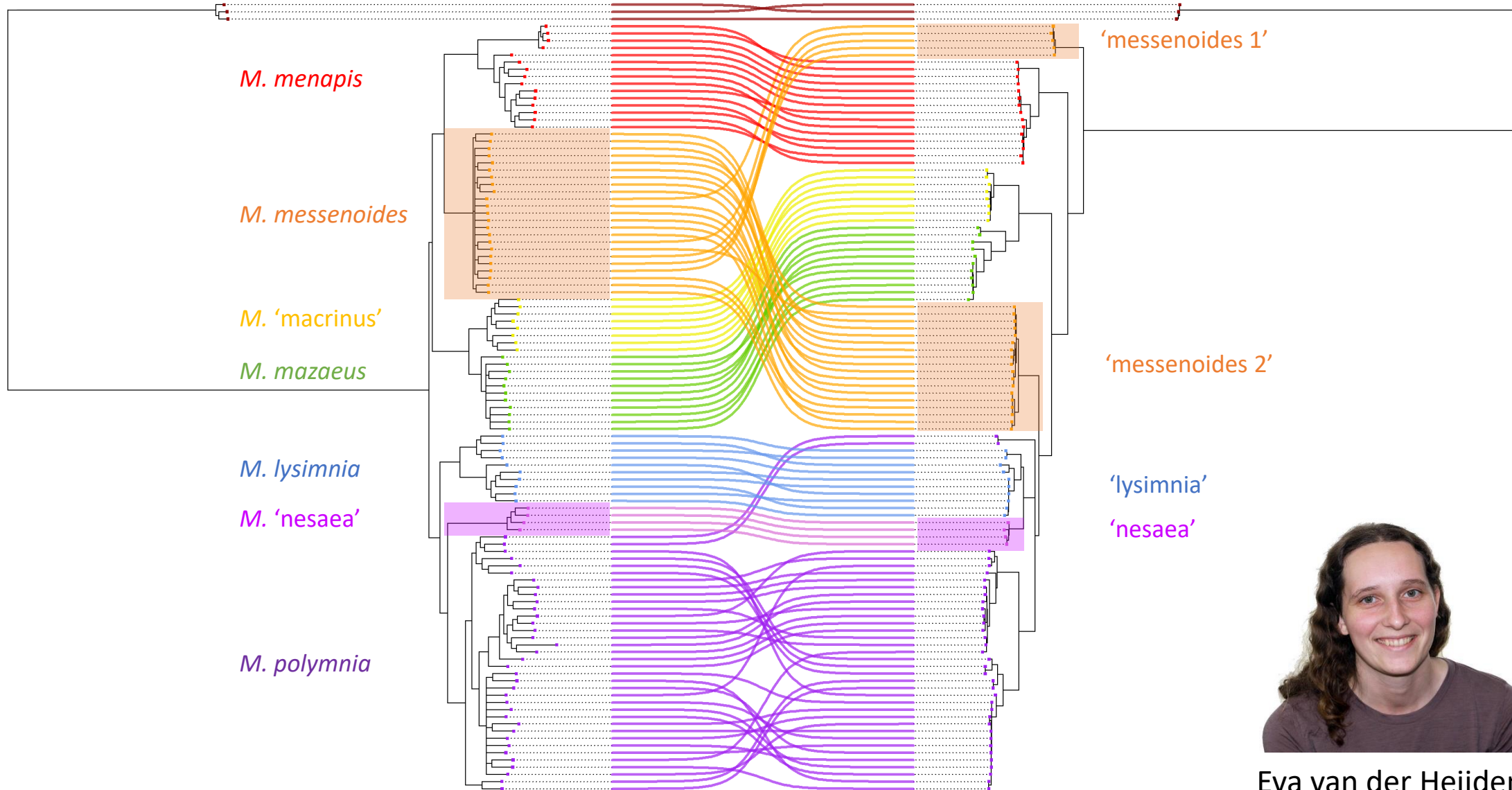


Eva van der Heijden

Mechanitis butterflies show vast cytonuclear discordance

Whole-genome phylogeny

Mitochondrial phylogeny



Eva van der Heijden

Hybrid species with new trait combinations?

Phenotype:

Immature
form (5th instar)

Wing
patterning

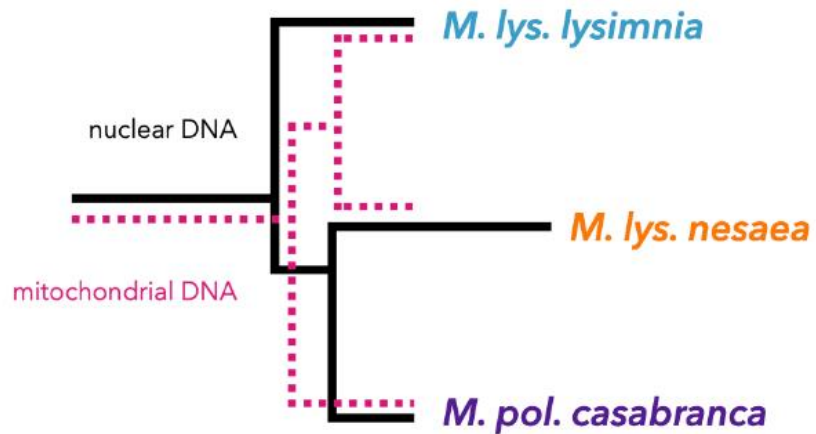
Chromosome
count (n)

Pheromonal
bouquet
composition
(PCA)

M. lys. nesaea is more similar to:

M. lys. lysimnia

M. pol. casabranca



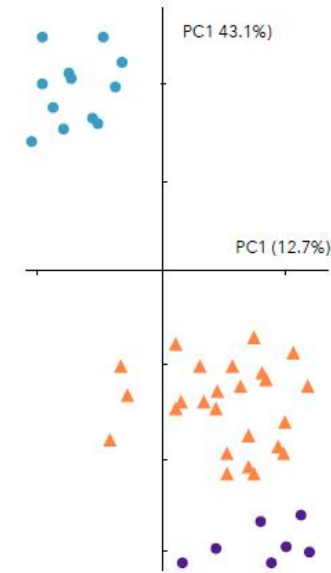
18-19



17



14-16

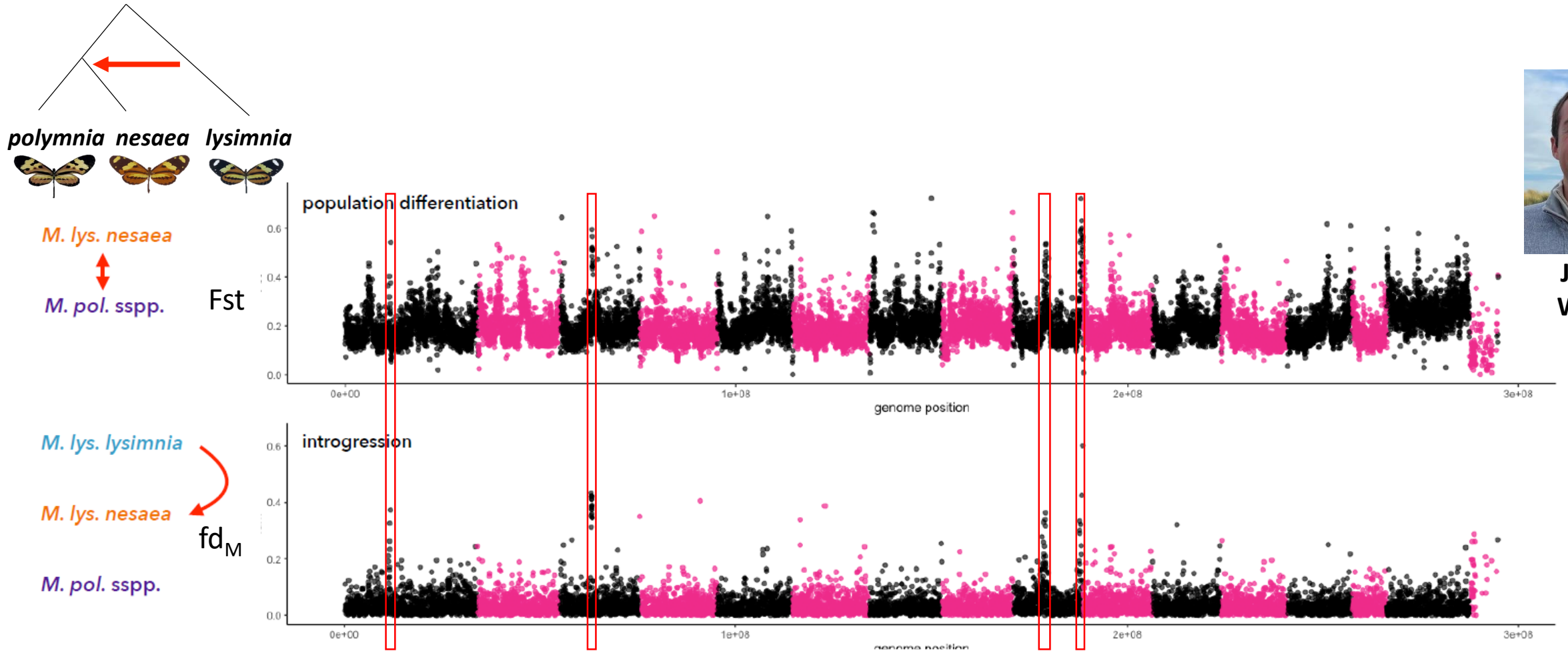


Jonah Walker



André Freitas
U Campinas, Brazil

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

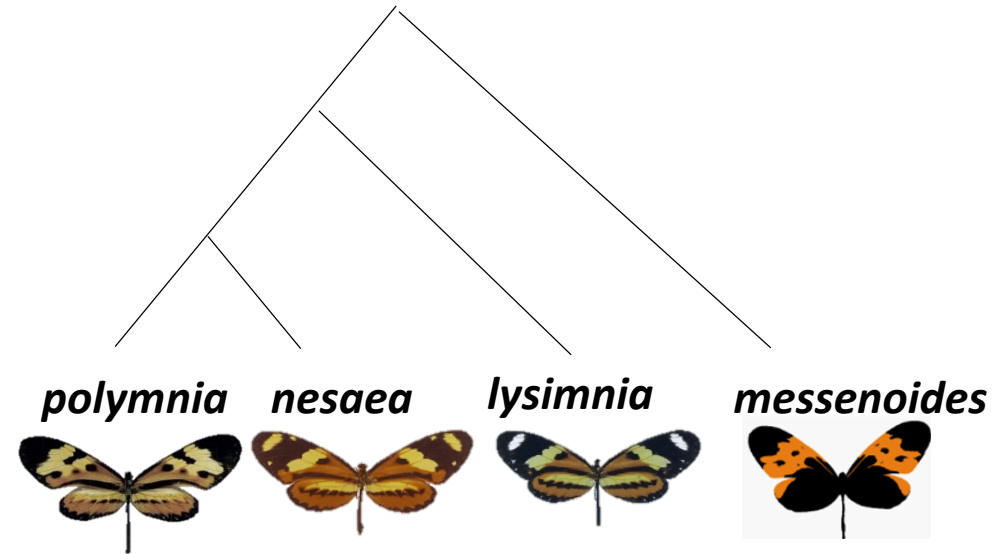


Jonah Walker

Exercises with Mechanitis.vcf file

- In the vcf file we have:

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

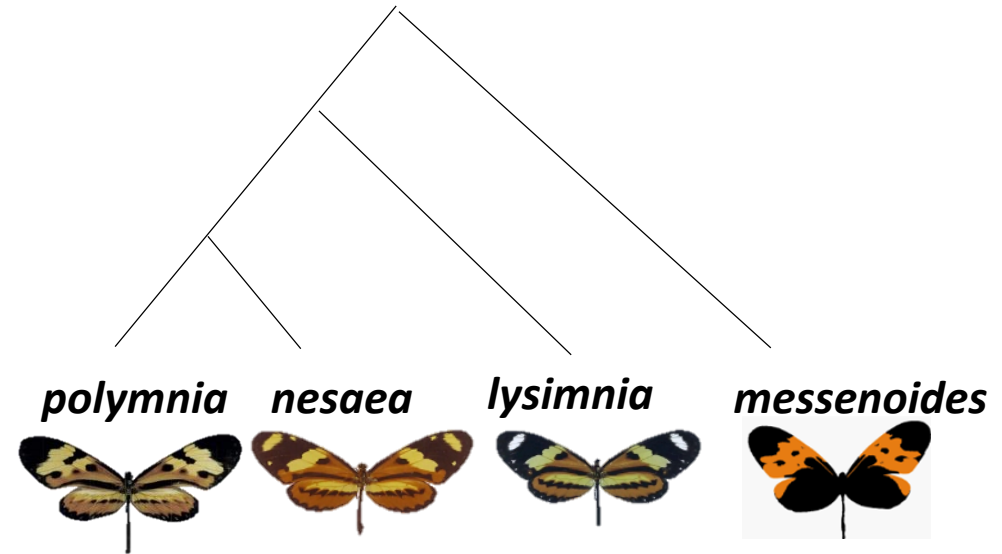


- We will run:

- 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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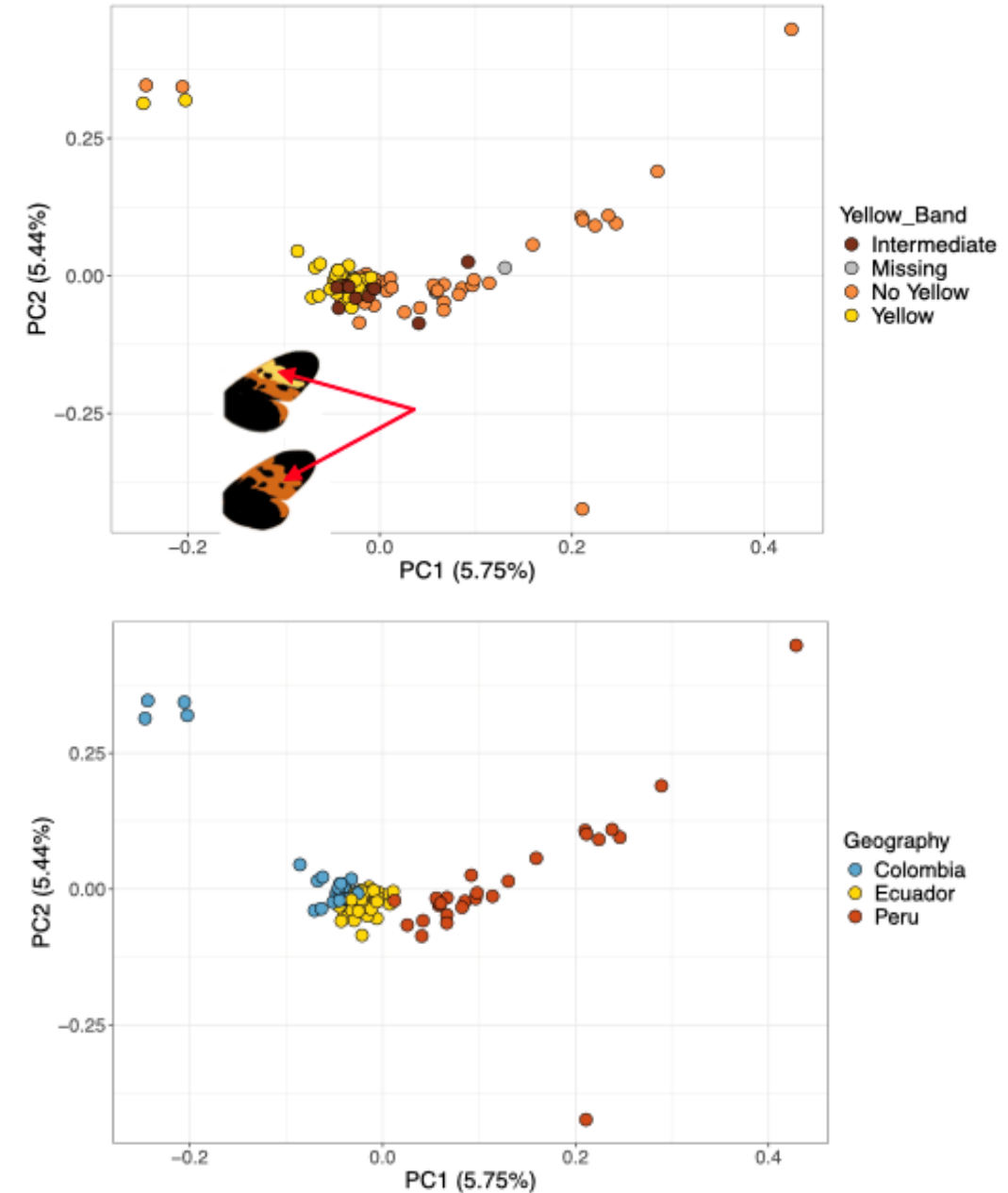
PCA – Principal Components Analysis

- 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?

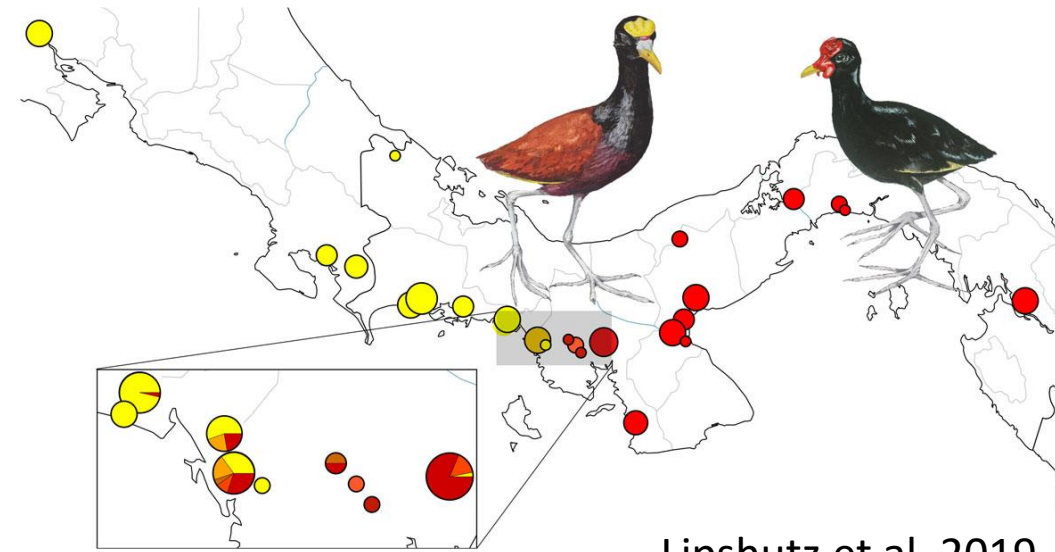
- Are all individuals clustering together as expected? (e.g. no outlier or misidentified individuals)
- Testing if individuals with different colour or morphology represent different species (cluster separately) or colour/ecomorphs (completely intermixed)?

Plots by Eva van der Heijden

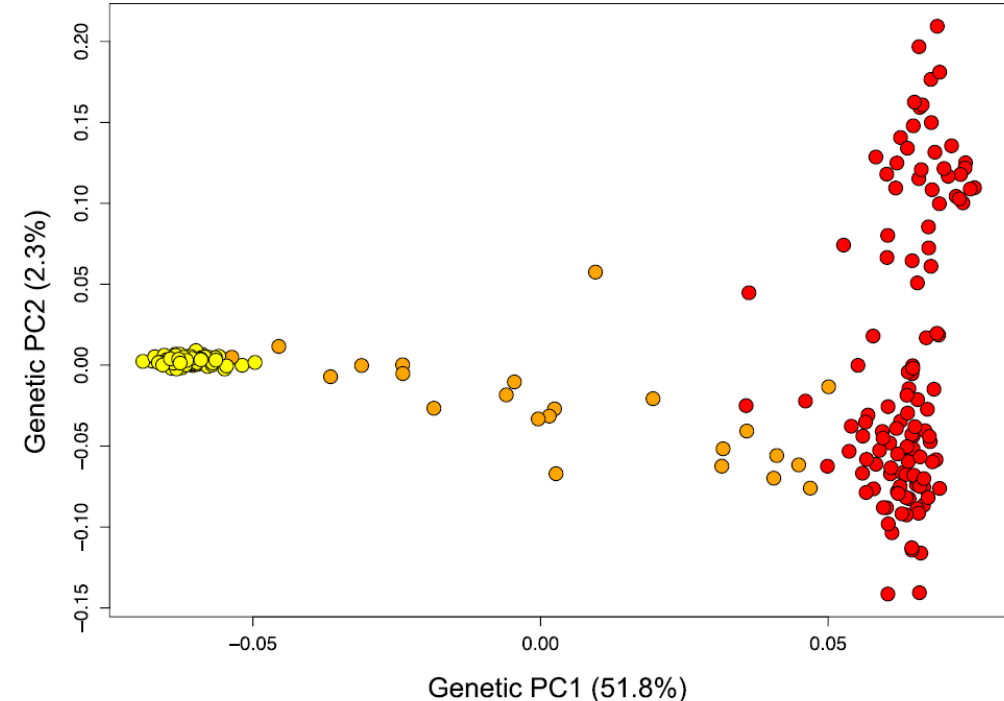


Why run a PCA?

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- Testing if individuals with different colour or morphology represent different species (cluster separately) or colour/ecomorphs (completely intermixed)?
- **Are any individuals hybrids?**

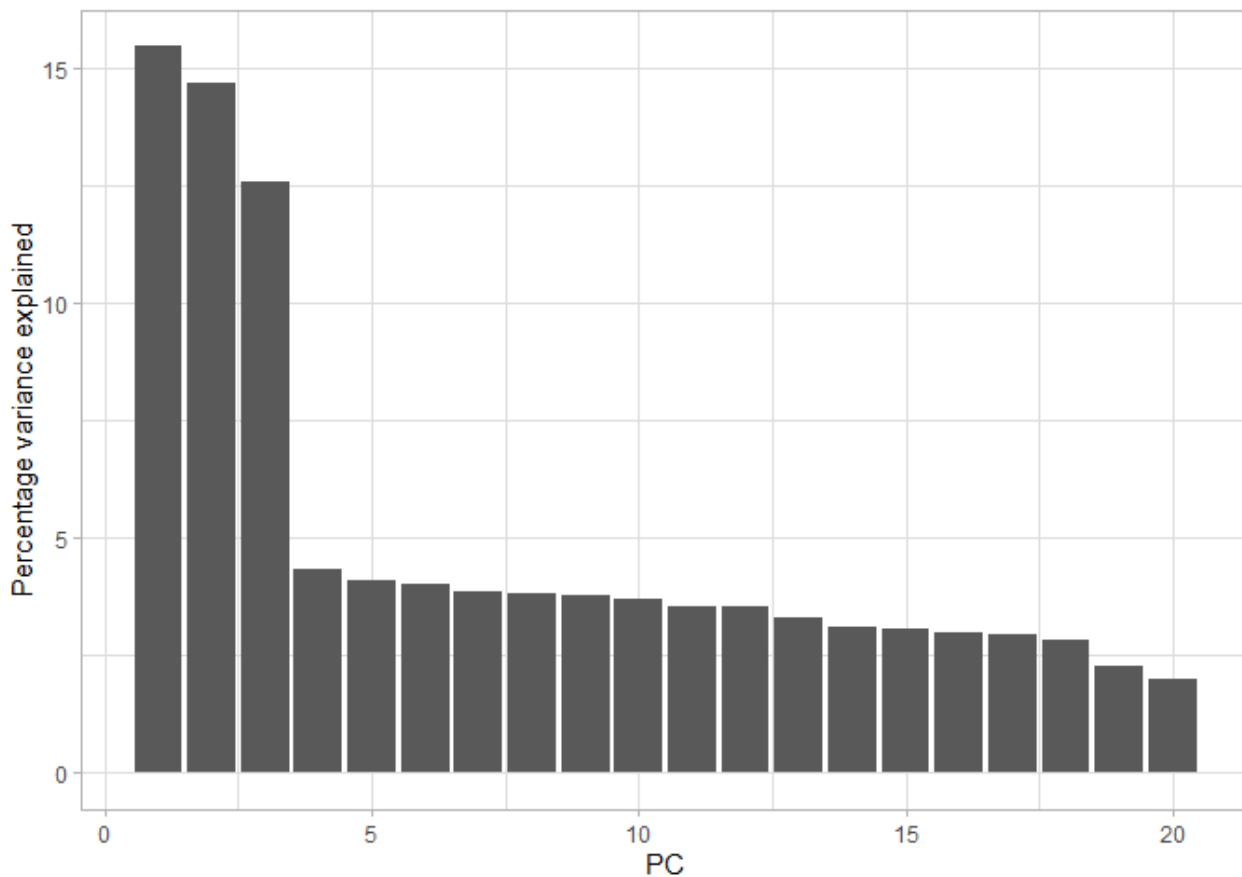


Lipshutz et al. 2019

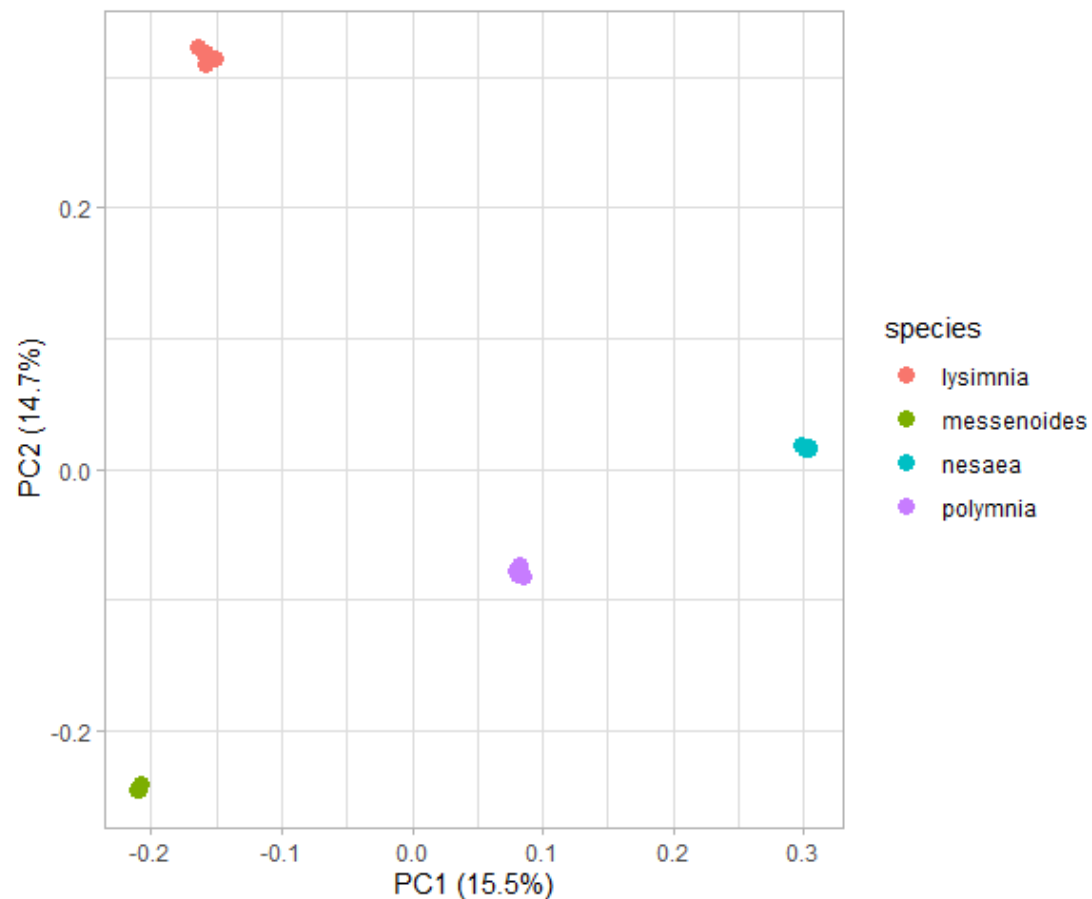


Plots generated during this exercise

Percentage of variance explained by each PC axis



PCA



Datasets with more than two different species

- With a dataset like this (different species where some are closely related, others more distant), running a PCA is great to find outliers and check if the individuals cluster by species, but the distance between the species is a bit unreliable. So running a phylogeny is better.
- iqtree gives us this phylogeny:

