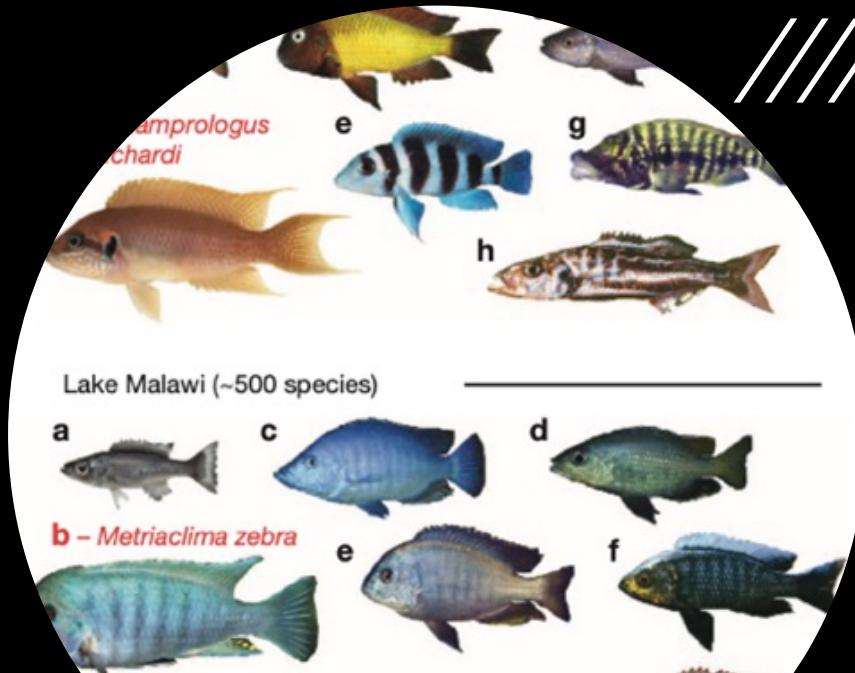
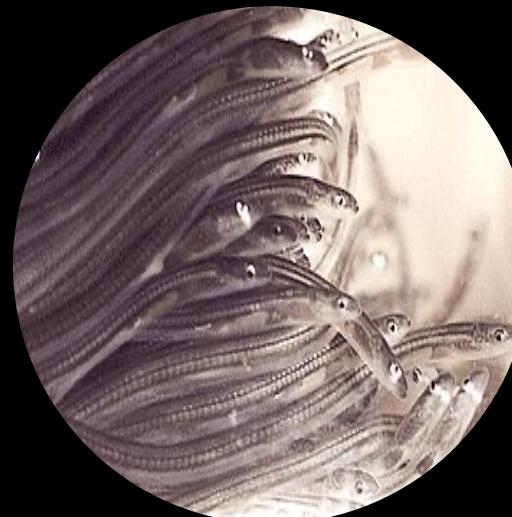


Molecular Methods in Ecology and Evolution

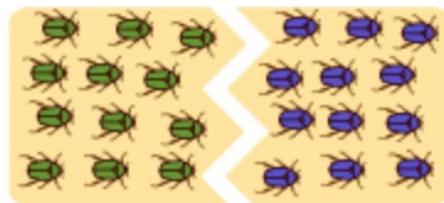
2025



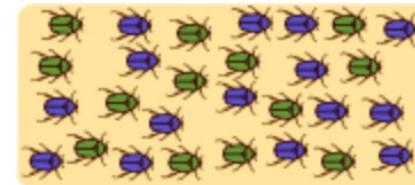
The theme:

Understand the evolutionary and ecological drivers of population divergence and speciation

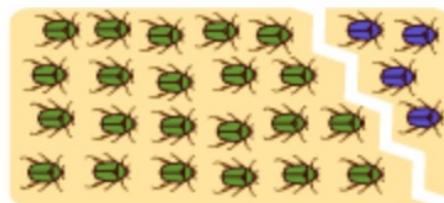
Geographic modes of speciation



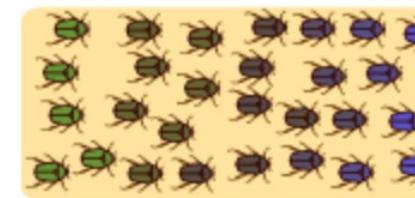
Allopatric: (allo = other) New species formed from geographically isolated populations



Sympatric: (sym = same) New species formed from within the range of the ancestral population



Peripatric: (peri = near) New species formed from a small isolated population at the edge of a larger population



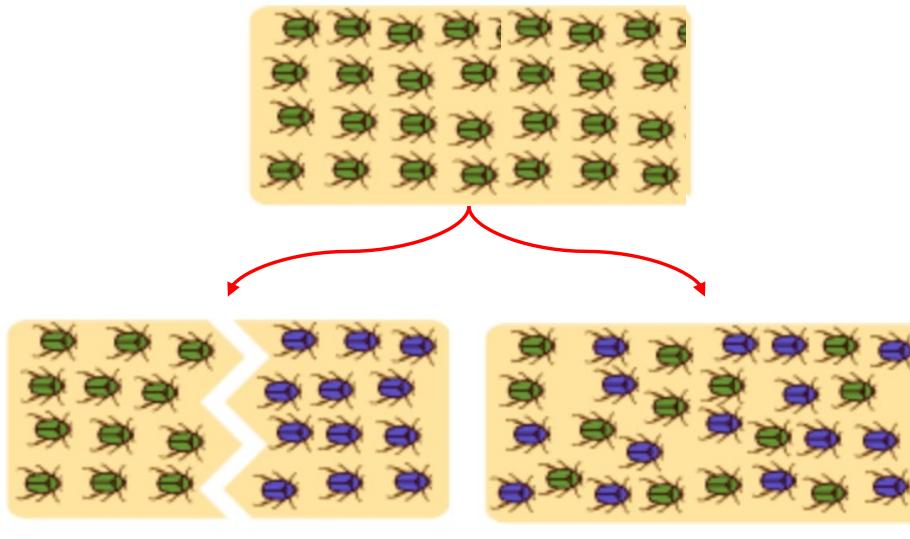
Parapatric: (para = beside) New species formed from a continuously distributed population

The theme:

Understand the evolutionary and ecological drivers of population divergence and speciation



Isthmus of Panama



Geographical / Allopatric
divergence

Ecological / sympatric
divergence



Scincid lizards

The theme:

Understand the evolutionary and ecological drivers of population divergence and speciation

A special case of parapatric speciation: Greenish warbler (*Phylloscopus trochilloides*)

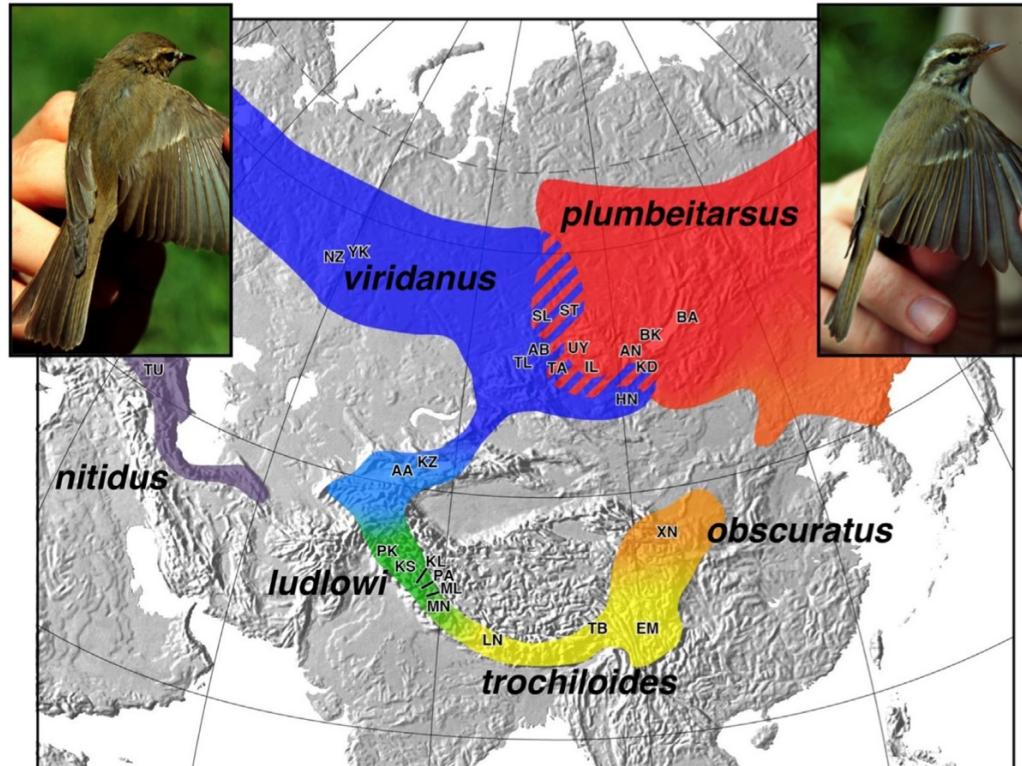
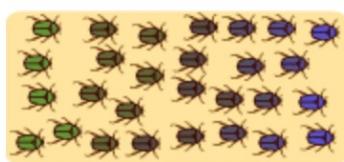
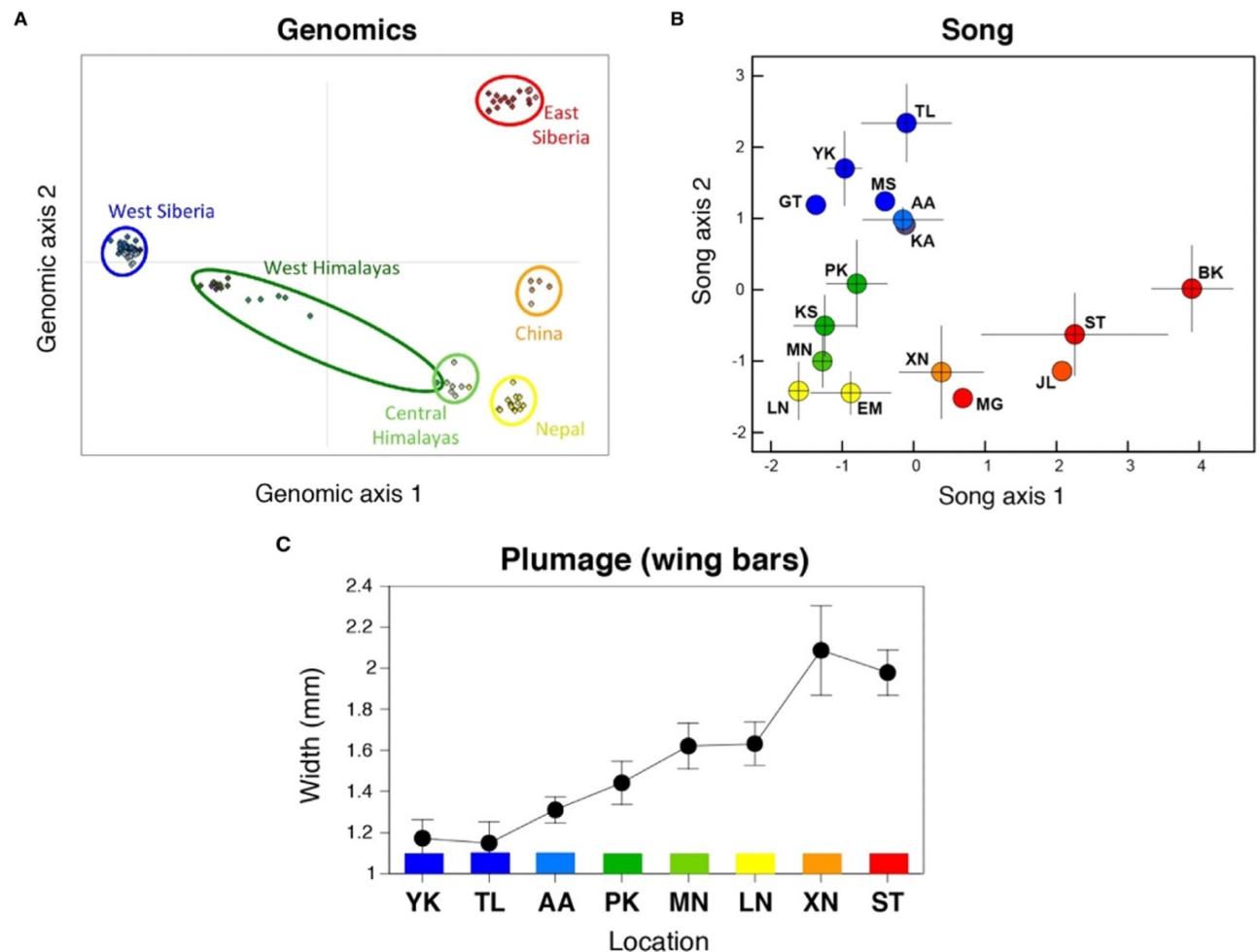
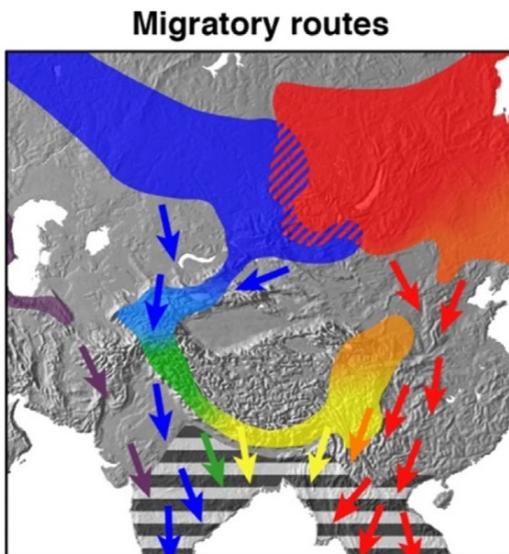


Fig. 4 The breeding range of greenish warblers (*Phylloscopus trochilloides*) in Asia. Subspecies designations according to Ticehurst (1938) are shown with different colors: *viridanus* in blue, *ludlowi* in green, *trochilooides* in yellow, *obscuratus* in orange, *plumbeitarsus* in red, and *nitidus* (outside of the main ring) in purple. Photos show the difference in wing bars between *viridanus* (upper left, with a single wing bar), and *plumbeitarsus* (upper right, with two wing bars).

The theme:

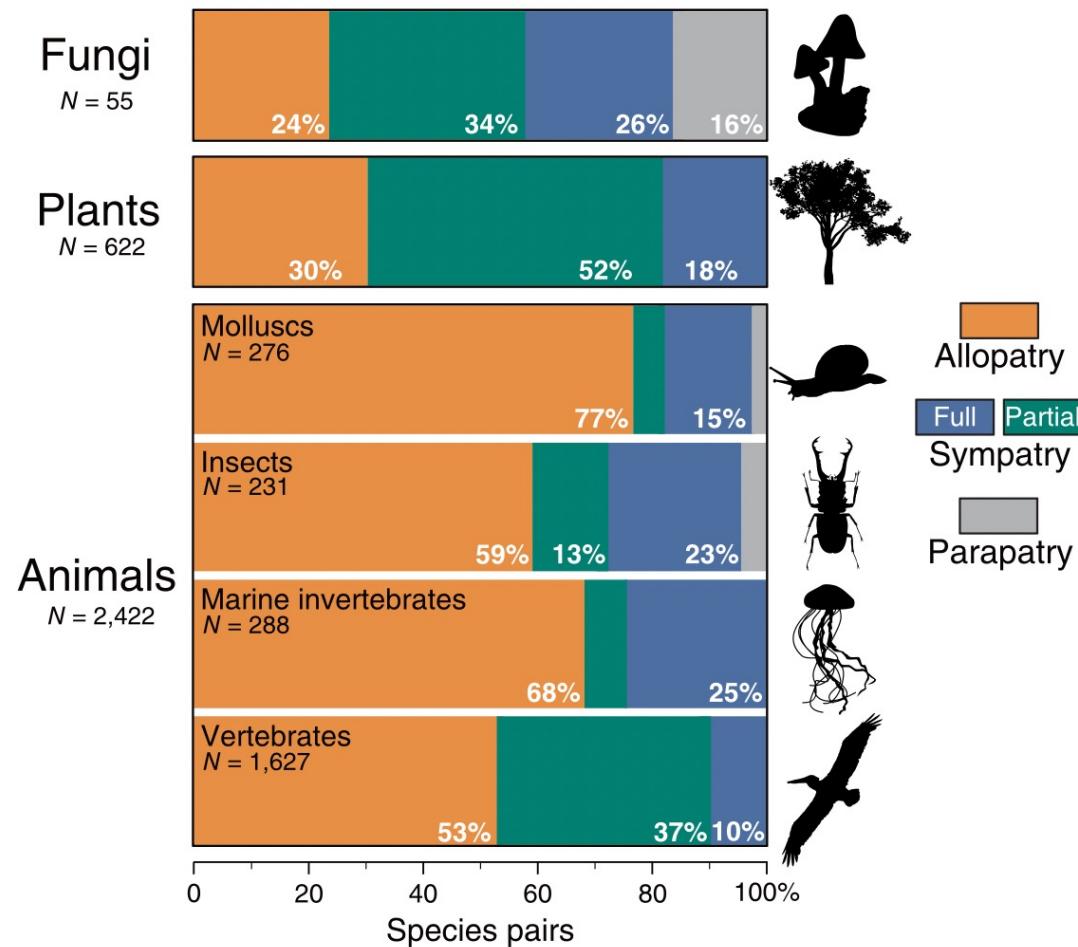
Understand the evolutionary and ecological drivers of population divergence and speciation

Patterns of genomic and phenotypic variation show strong differentiation between the major two forms, but gradual / stepwise variation through the chain of populations to the south.



The theme:

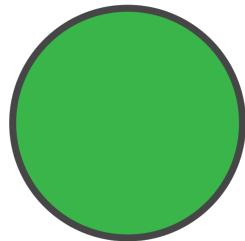
Understand the evolutionary and ecological drivers of population divergence and speciation



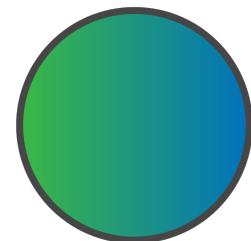
The Speciation Continuum

Panmictic population

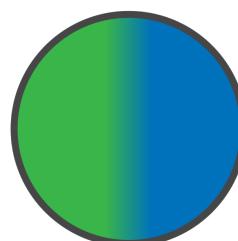
Two isolated species



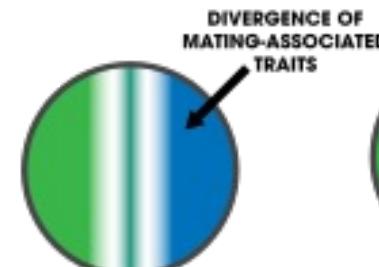
ORIGINAL POPULATION



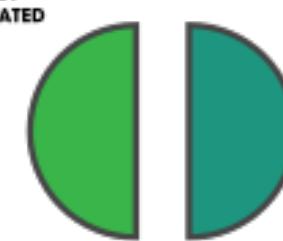
DIVERGENCE ACROSS A CLINE



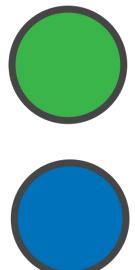
HYBRID ZONE



SELECTION AGAINST HYBRIDS



INCIPIENT SPECIES



SPECIATION

Strength of Reproductive Isolation (RI)

Time

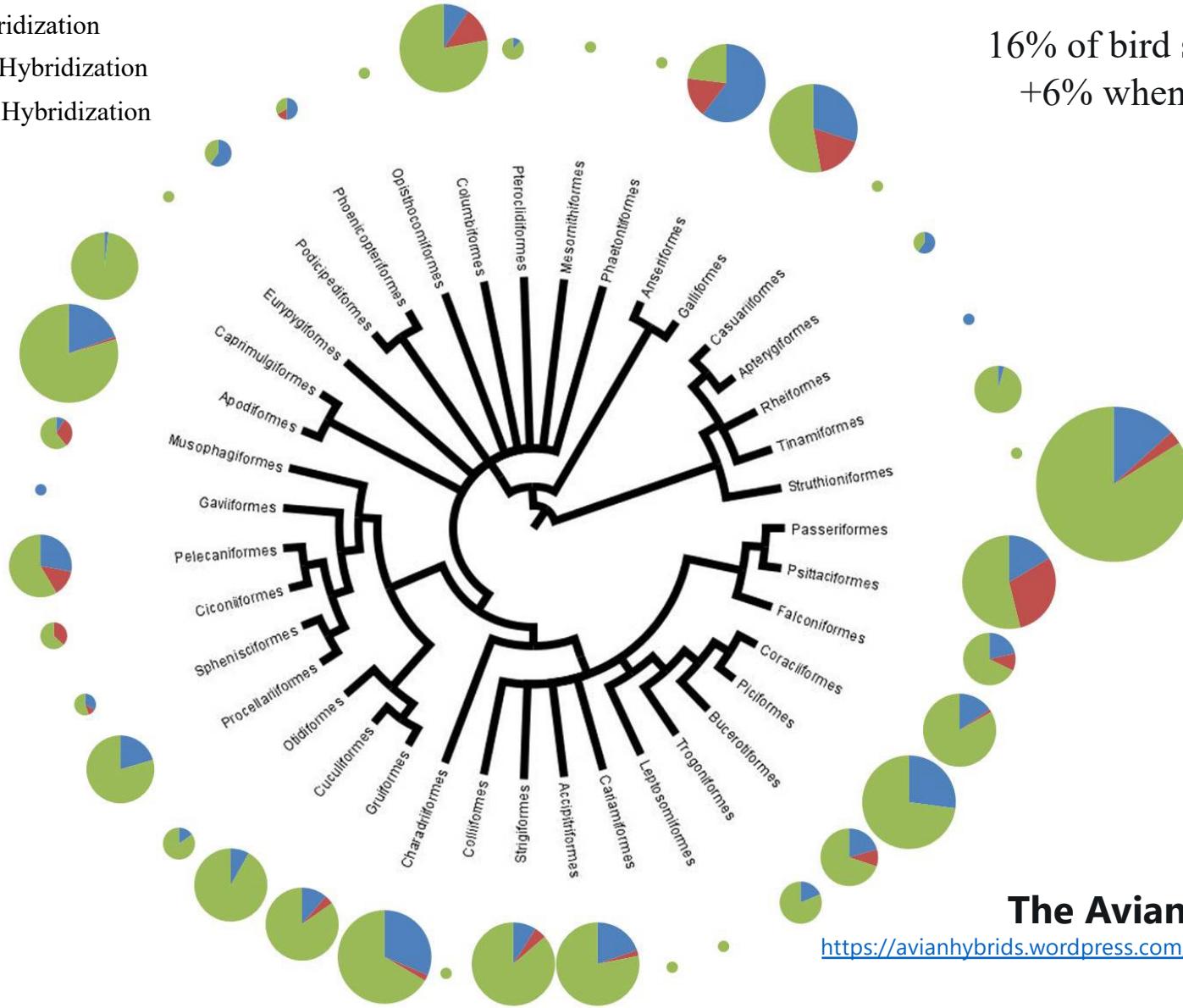
Speciation

collapse

completion

The speciation process is dynamic, bidirectional and continuous.


 No Hybridization
 Natural Hybridization
 Captive Hybridization



16% of bird species hybridize in the wild
 +6% when including captive hybrids

The Avian Hybrids Project

<https://avianhybrids.wordpress.com/2017/12/01/hybridization-in-birds-the-trilogy/>

Ottenburghs et al. (2015) *Ibis*

The goal:

To give you an insight to how biologists use specific techniques and tools to tackle ecological and evolutionary questions

To gain experience on some of these approaches, and the application of the scientific method to real-world systems.



- Marker gene amplification and sequencing
- Restriction site Associated DNA sequencing (RADseq)



- Phylogenetic reconstruction
- Population genetics
- Population structure analyses
- Genomic-scale analyses of natural selection
-

Project 1.

A mysterious frog



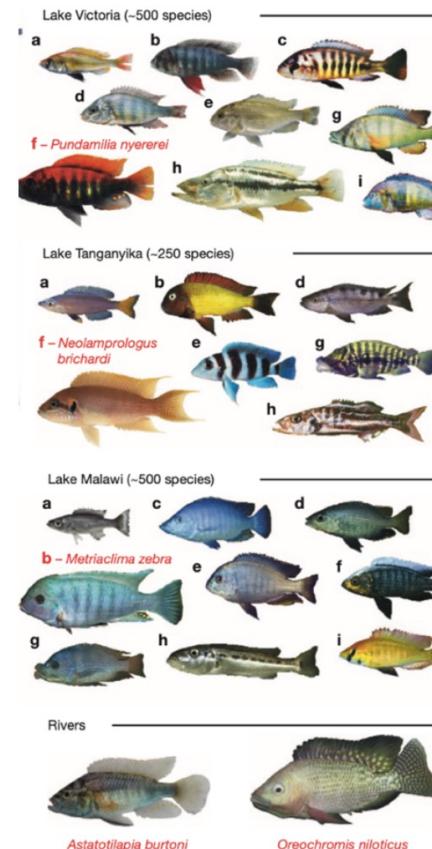
Project 2.

Hylid frogs



Project 3.

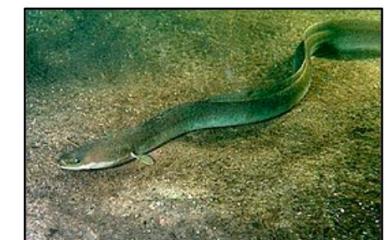
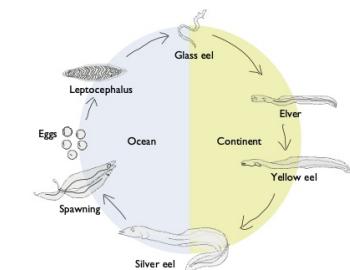
Cichlids



Brawand et al., 2014

Project 4.

European eel



Schedule

Time	Monday Sept 29	Tuesday Sept 30	Wednesday Oct 1st	Thursday Oct 2nd	Friday Oct 3rd
08:00 - 08:45	DNA extraction	PCR Gel preparation	Sequencing prep	Lecture IS	
09:00 - 09:45					
10:15 - 11:00	Lecture IS	Lecture IS	Lecture IS	Lecture NS	
11:15 - 12:00					
12:15 - 13:00				DEE Seminar	
13:15 - 14:00	TP Introduction	Electrophoresis		Lecture LF	
14:15 - 15:00	DNA extraction				Lecture NS
15:15 - 16:00	Quantification	Lecture			
16:15 - 17:00	Dilution	IS		Introduction & Installation	
17:15 - 18:00		PCR purification			

Project 1. →

Time	Monday Oct 6th	Tuesday Oct 7th	Wednesday Oct 8th	Thursday Oct 9th	Friday Oct 10th
08:00 - 08:45	Project 1				
09:00 - 09:45	Phylogeny- Sanger				
10:15 - 11:00	Lecture LF	last comments project 2 & start Project 3		Project 4. & Final questions	
11:15 - 12:00					
12:15 - 13:00				DEE Seminar	
13:15 - 14:00		Project 3.			
14:15 - 15:00	Project 2	Genomic analyses of	Project 4. The		
15:15 - 16:00	Cryptic speciation in hylid frogs.	divergence between Lake Malawi cichlids	curious case of the European Eel	Personal Research Work	
16:15 - 17:00					

Wet-Lab Experiment	POL 203 and 205
Lecture	POL 334
Computer Analyses	POL 204.2



Project 2.



Project 3.



Project 4.

The report

General introduction
Wet lab / Project 1 <ul style="list-style-type: none">- methods- results & Discuss
Computer lab: Project 1 & 2. <ul style="list-style-type: none">- Intro- methods- results- discussion- conclusion- references
Project 3. <ul style="list-style-type: none">- Intro- methods- results- discussion- conclusion- references
Project 4. <ul style="list-style-type: none">- Intro- methods- results- discussion- conclusion- references
General Discussion

max **5 pages** per project
(including text and figures)

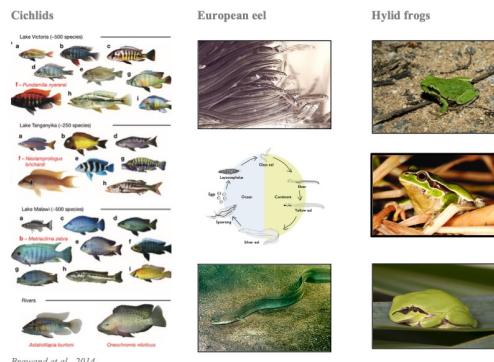
max **25 pages** in total
(including text, figures and references)

DEADLINE: 27 / 10 / 25

Report grading

Molecular Methods in Ecology and Evolution – 2025

Using molecular approaches to understand the drivers of population divergence and speciation.



See “**Advice on preparing your report**” section in your manual, these guidelines are there to help you write your report, but they will also be the basis of the marking scheme used to grade your reports.

Prof. Ian R. Sanders, Dr. Luca Fumagalli, Prof. Nicolas Salamin

Teaching assistants: Dr. Soon-jae Lee, Dr. Angélica Pujido, Dr. Anna Hewett, Dr. Jaime Gonzalez, Dr Ricardo Arraiano, Marion Nyamari, Kenneth Kim.

<https://github.com/Angelica-Pulido/MMEE-2025/>

S Angelica-Pulido / MMEE-2025

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MMEE-2025 Public

main 1 Branch 0 Tags Go to file Add file Code

Angelica-Pulido	Add files via upload	bbd7455 · last week	77 Commits
1.Frogs_Sanger	Add files via upload	27 days ago	
2.Frogs_RADseq	Add files via upload	27 days ago	
3.Cichlids	Add files via upload	27 days ago	
4.Eels	Add files via upload	27 days ago	
MMEE_2025_Manual.pdf	Add files via upload	last week	
README.md	Add files via upload	27 days ago	
Schedule.png	Add files via upload	27 days ago	

README

Molecular Methods in Ecology and Evolution - 2025 - University of Lausanne

This is the repository for the master course "Molecular Methods in Ecology and Evolution - 2025 - UNIL"
Here you will find all the information and data you will need for the computer analyses of the course.

About

This is the repository for the course "Molecular Methods in Ecology and Evolution - 2025 - UNIL Master"

Readme Activity 0 stars 2 watching 1 fork

Releases

No releases published [Create a new release](#)

Packages

No packages published [Publish your first package](#)

Contributors 2

Angelica-Pulido Angélica Pulido sciencesj AMF.S.J

<https://github.com/Angelica-Pulido/MMEE-2025/>

Files

- main
- +
- Go to file

- > 1.Frogs_Sanger
- > 2.Frogs_RADseq
- > 3.Cichlids
- > 4.Eels
- MMEE_2025_Manual.pdf
- README.md
- Schedule.png

MMEE-2025 / README.md

Preview Code Blame 50 lines (26 loc) · 2.01 KB

To be able to install and use all packages required you may need to use R version 3.6.x instead of R version 4.x.x. Consider switching versions if you have trouble installing the packages. If you already have an R version installed on your computer and want to change it, you can find instructions on how to do it [here](#).

Packages installation

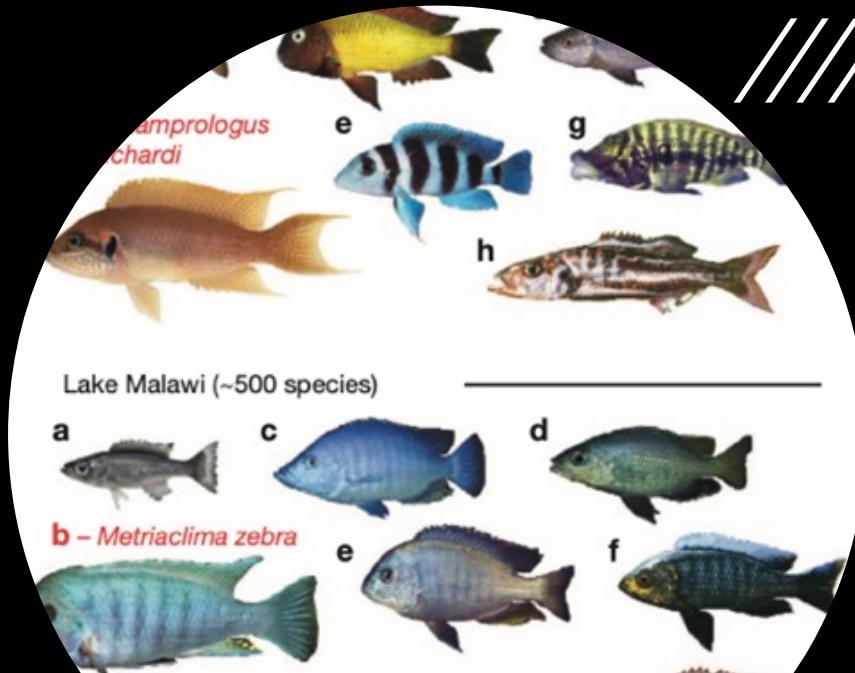
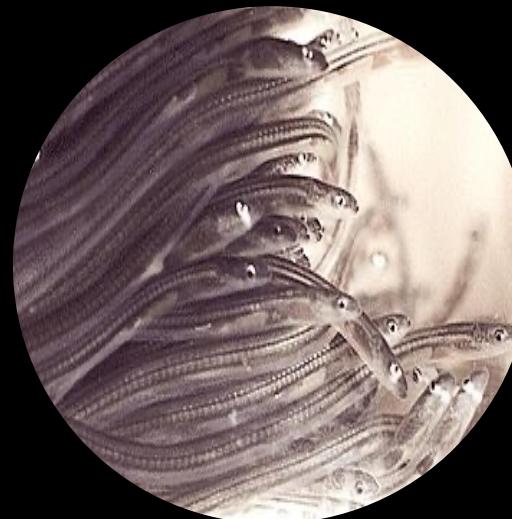
To install all packages required, please run the following commands:

In case you don't have administrator's access to your computer, you can specify where the packages should be installed with the `lib` option in `install.packages()`

```
install.packages("ape", dependencies = TRUE)  
install.packages("phangorn", dependencies = TRUE)  
install.packages("seqinr", dependencies = TRUE)  
install.packages("adegenet", dependencies = TRUE)  
install.packages("pegas", dependencies = TRUE)  
install.packages("hierfstat", dependencies = TRUE)  
install.packages("raster", dependencies = TRUE)  
if (!requireNamespace("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")  
BiocManager::install("LEA", dependencies = TRUE)  
install.packages("outliers", dependencies = TRUE)  
install.packages("EnvStats")
```

Molecular Methods in Ecology and Evolution

2025



Time	Monday Oct 6th	Tuesday Oct 7th	Wednesday Oct 8th	Thursday Oct 9th	Friday Oct 10th
08:00 - 08:45	Project 1				
09:00 - 09:45	Phylogeny- Sanger				
10:15 - 11:00	Lecture				
11:15 - 12:00	LF				
12:15 - 13:00					
13:15 - 14:00		Project 2.			
14:15 - 15:00	Cryptic speciation in hylid frogs.	Project 3.			
15:15 - 16:00		Genomic analyses of divergence between Lake Malawi cichlids			
16:15 - 17:00			Project 4. The curious case of the European Eel	Personal Research Work	

Project 2

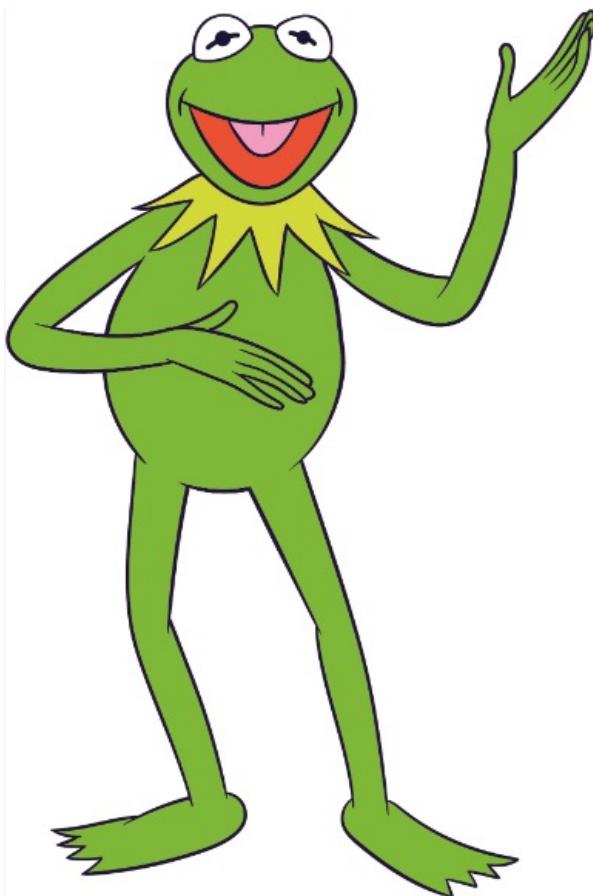
Project 3

Project 1

Project 4

Final questions & Writing

Wet-Lab Experiment	POL 203 and 205
Lecture	POL 334
Computer Analyses	POL 204.2



Project 1

Identifying a mysterious frog species

Using Sanger Sequencing

<https://github.com/Angelica-Pulido/MMEE-2025/>

Angelica-Pulido / MMEE-2025

Type to search

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Files

main Go to file

1.Frogs_Sanger Data/Phylo 1.0 README_Frogs_Sanger.md 2.Frogs_RADseq 3.Cichlids 4.Eels MMEE_2025_Manual.pdf README.md Schedule.png

MMEE-2025 / 1.Frogs_Sanger / 1.0.README_Frogs_Sanger.md

Angelica-Pulido Update 1.0.README_Frogs_Sanger.md 03289f8 · nc

Preview Code Blame 12 lines (10 loc) · 710 Bytes

Project: 1.Frogs_Sanger/

The folders and files for this project are as follow:

Data/Phylo/:

A directory with the forward and reverse reads from the sequencing marker for YOUR samples.

- rag1_Sanger_reference.fasta & rhod_Sanger_reference.fasta:
in case your file is empty, you can use these files.
- B2F_rag.ab1 , B2R_rag.ab1 , D2F_rho.ab1 , D2R_rho.ab1
forward and reverse reads from the markers used in the weblab, use this files on <https://www.gear-genomics.com/t>
- Rag1_Reference_sequences.fasta & Rhod_Reference_sequences.fasta
fasta formatted sequences for many frog species that you can use to built a phylogeny. Use the outgroup to root .

<https://github.com/Angelica-Pulido/MMEE-2025/>

Angelica-Pulido / MMEE-2025

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Files

main Go to file

1.Frogs_Sanger

Data/Phylo

- B2F_rag.ab1
- B2R_rag.ab1
- D2F_rho.ab1
- D2R_rho.ab1
- Rag1_Reference_sequences....
- Rhod_Reference_sequences...
- Rhod_Reference_sequences...
- rag1_Sanger_reference.fasta
- rhod_Sanger_reference.fasta
- 1.0 README_Frogs_Sanger.md

MMEE-2025 / 1.Frogs_Sanger / Data / Phylo /

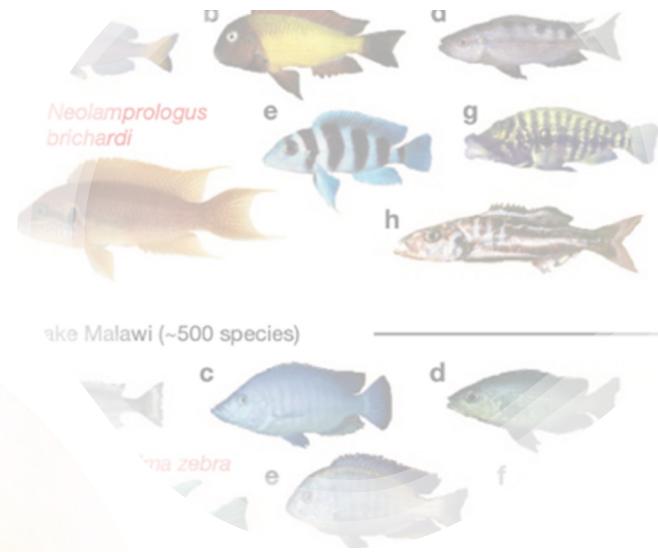
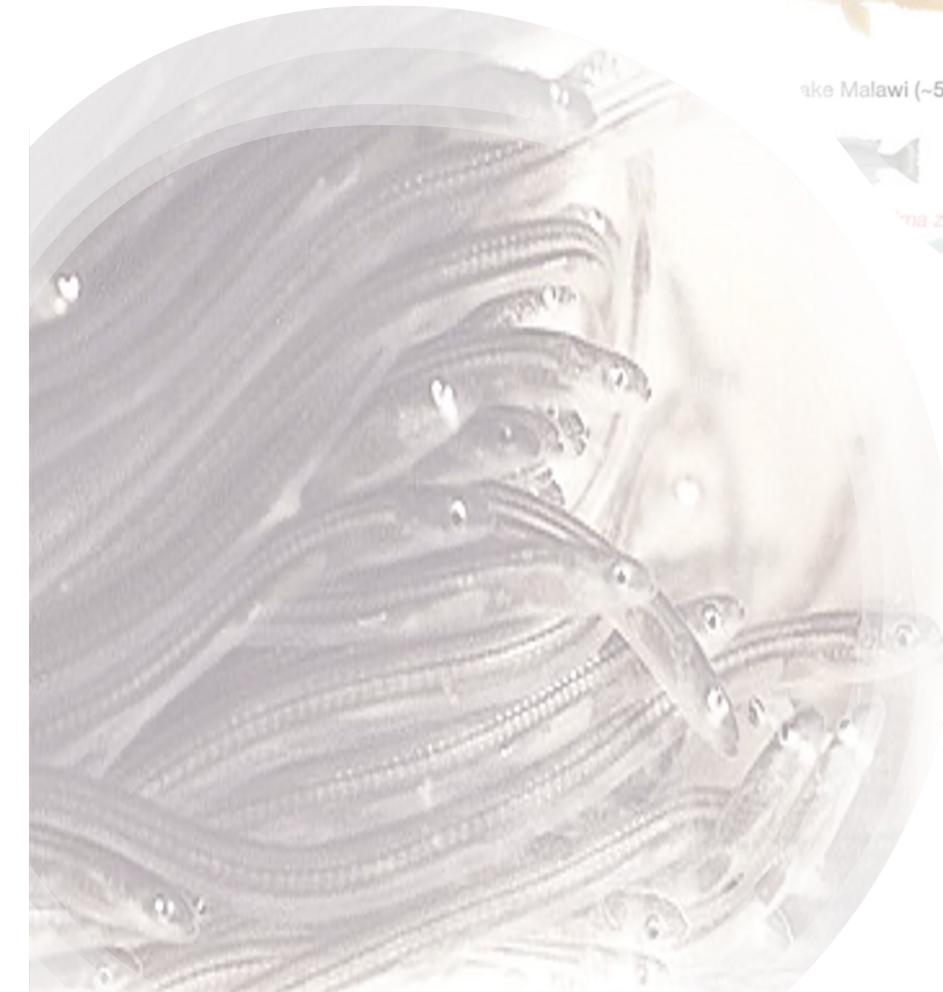
sciencesj Add files via upload

Name	Last commit message
..	Add files via upload
B2F_rag.ab1	Add files via upload
B2R_rag.ab1	Add files via upload
D2F_rho.ab1	Add files via upload
D2R_rho.ab1	Add files via upload
Rag1_Reference_sequences.fasta	Add files via upload
Rhod_Reference_sequences.fasta	Add files via upload
Rhod_Reference_sequences_all_position_aligned.fas	Add files via upload
rag1_Sanger_reference.fasta	Add files via upload

Q. 1. What can you say about your sample? Does your sample cluster with other species?

Q. 2. What does this result mean regarding your sample?

Q. 3. What complementary analysis can you think of to better characterize your sample?



Project 2

Cryptic speciation in tree frogs

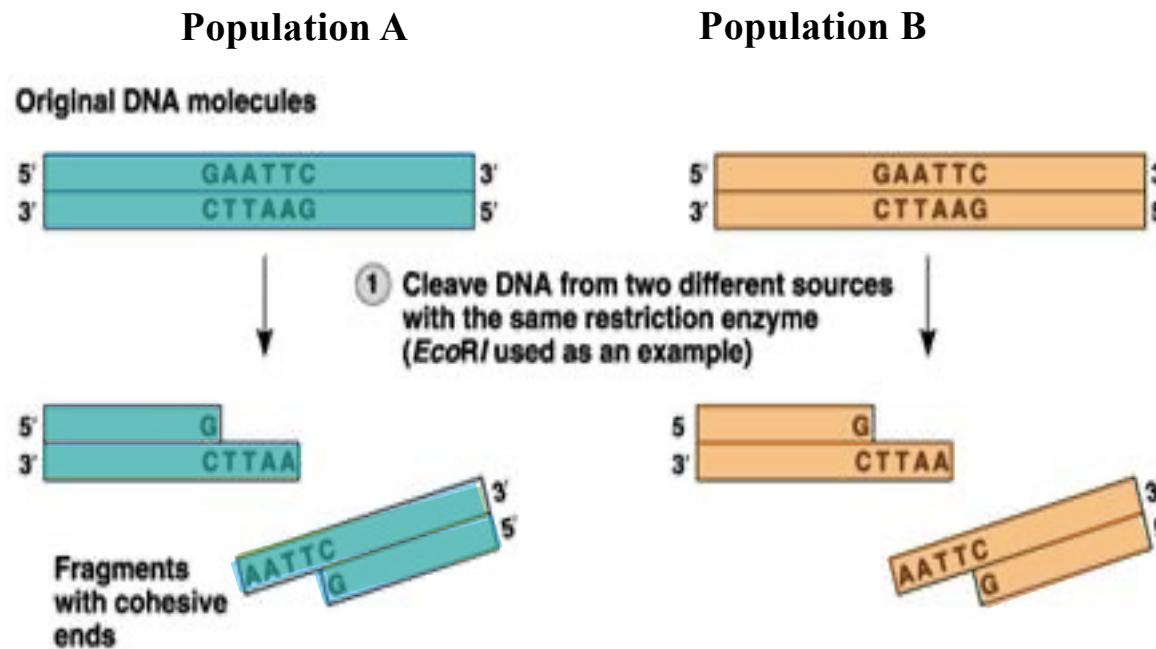
Allopatric divergence – are they different species?

RAD sequencing

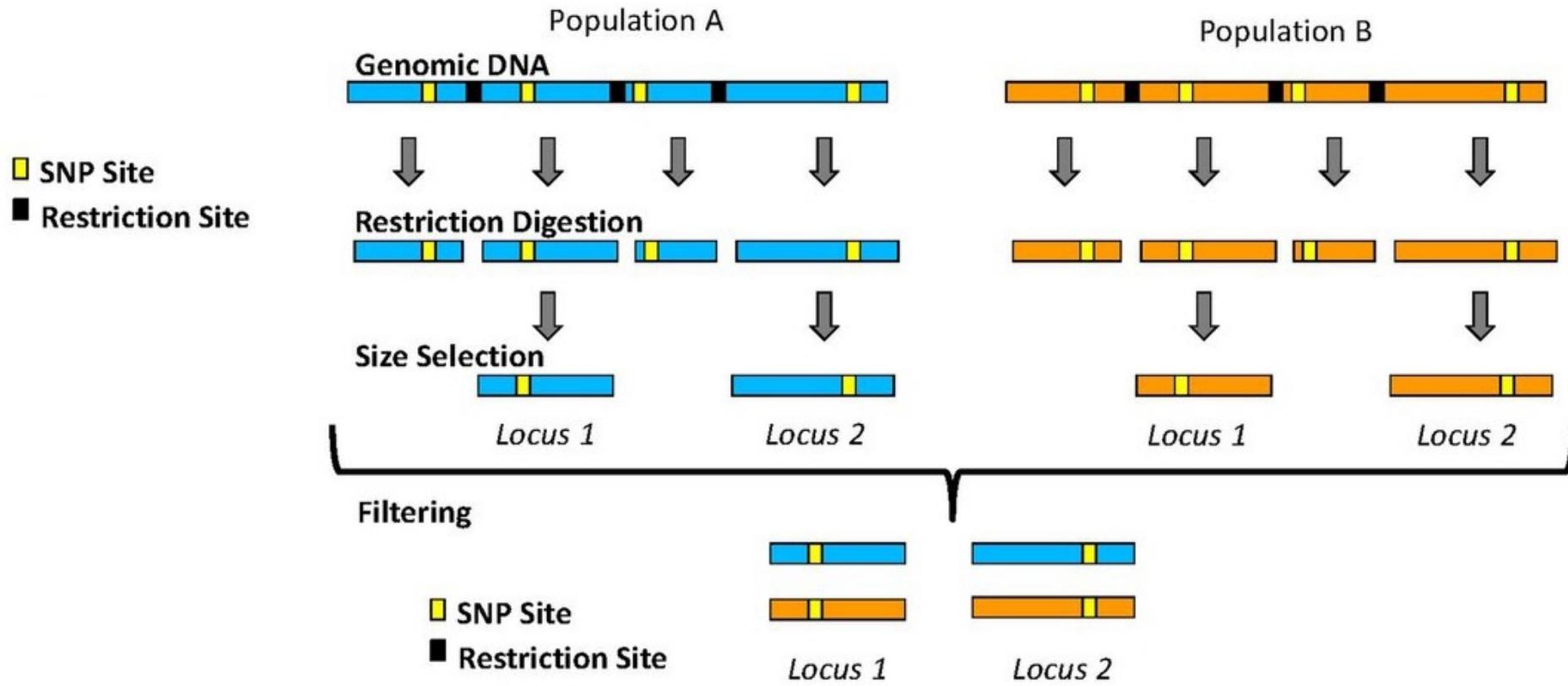
RAD-seq:

Restriction-site Associated DNA (RAD) sequencing

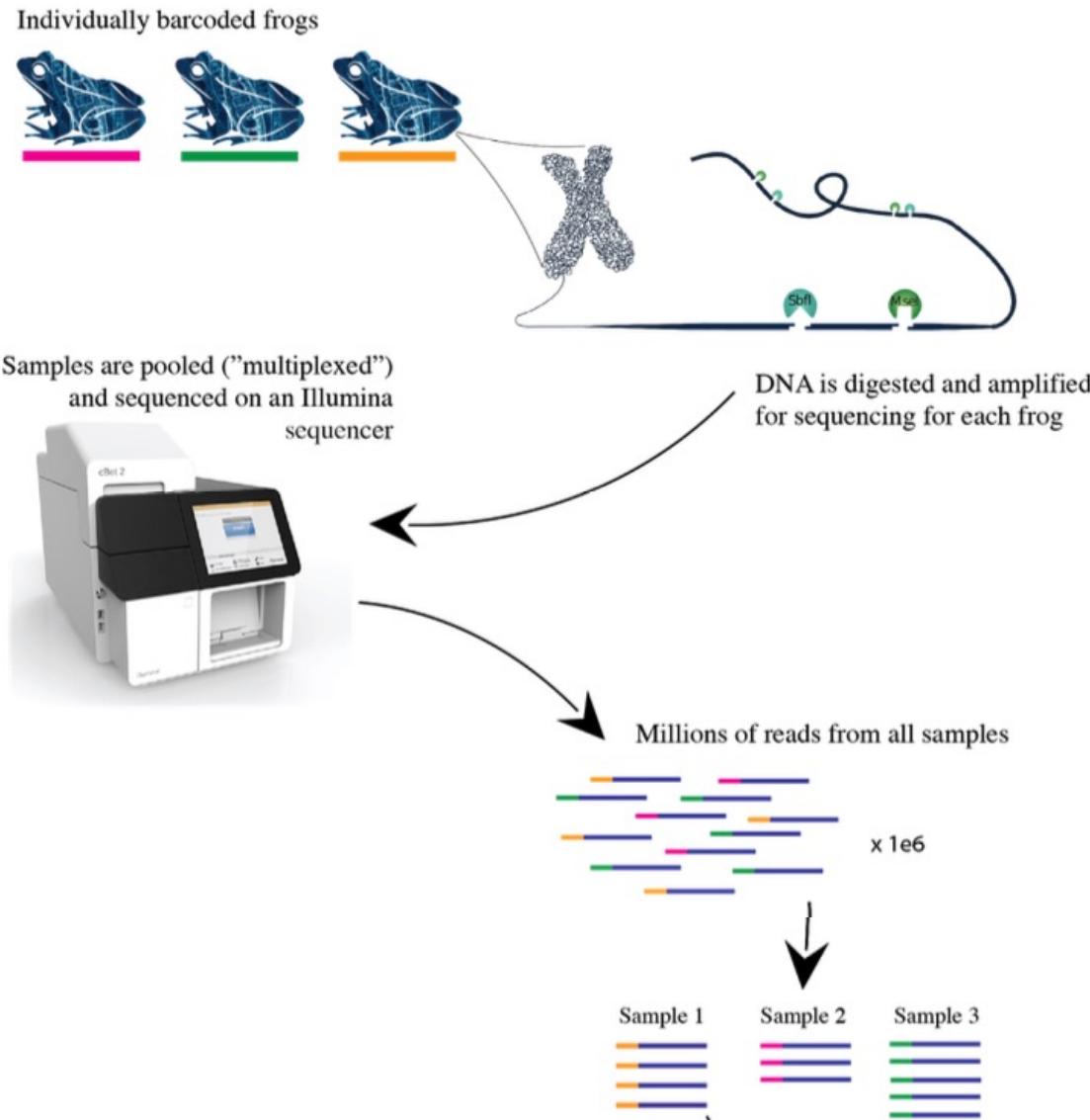
Reduced representation sequencing method



RAD-seq



RAD-seq



SNP: Single Nucleotide Polymorphism

- SNP Site
- Restriction Site

Population A 
Population B 

Locus 1



SNP: Single Nucleotide Polymorphism

Most common type of **genetic variation** and can originate by **mutations**.

They can accumulate over time and spread across individuals in a population.

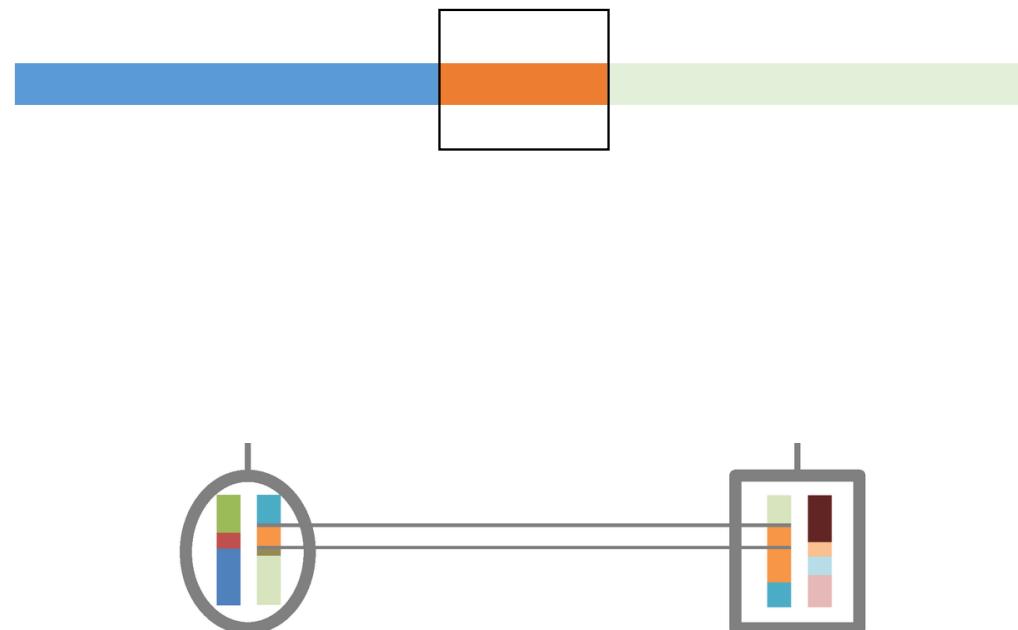
Individual 1
Maternal . . . CGATATTCC T ATCGAATGTC . . .
Paternal . . . CGATATTCC T ATCGAATGTC . . .
Individual 2
Maternal . . . CGATATTCC T ATCGAATGTC . . .
Paternal . . . CGATATTCC T ATCGAATGTC . . .
Individual 3
Maternal . . . CGATATTCC A ATCGAATGTC . . .
Paternal . . . CGATATTCC A ATCGAATGTC . . .
Individual 4
Maternal . . . CGATATTCC A ATCGAATGTC . . .
Paternal . . . CGATATTCC A ATCGAATGTC . . .

By comparing SNP patterns across different species or populations, we can:

- Build phylogenetic trees between populations and species
- Understanding Population Evolution: e.g hybridization, bottle necks, migration patterns
- Identifying Selection Pressure: Type of selection, Adaptive traits (SNPs associated with traits)

Why RAD-seq?

... Whole-genome data
... Recombination

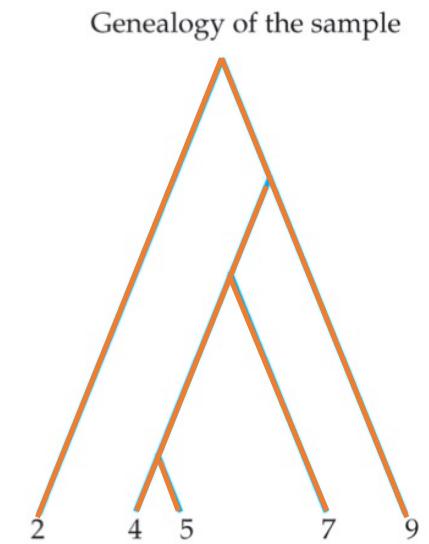
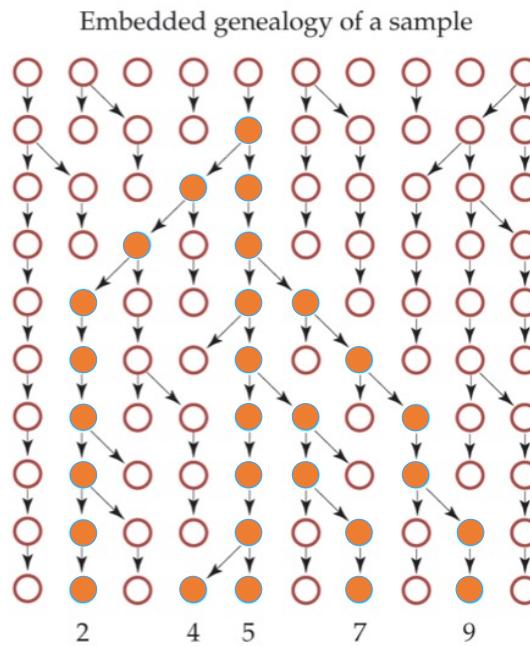
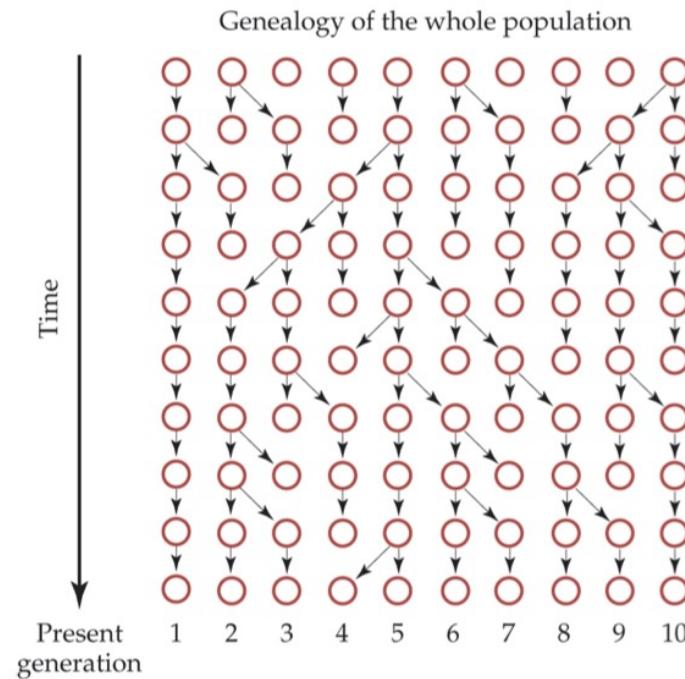


Why RAD-seq?

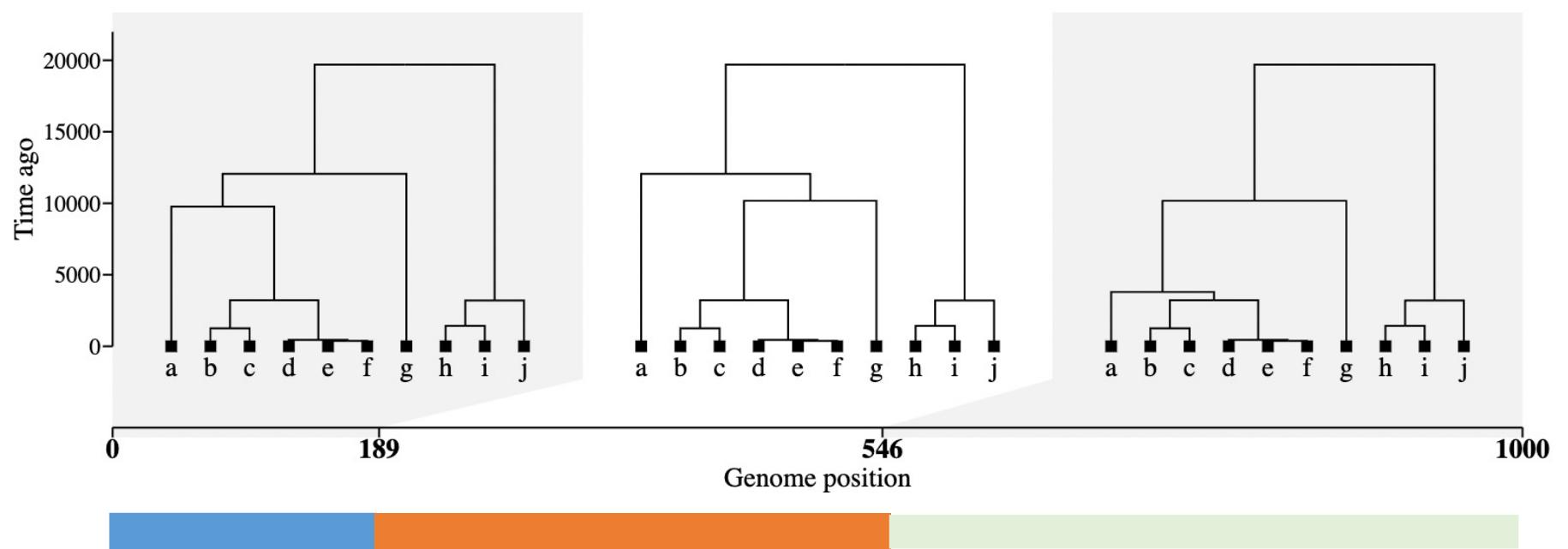
Recombination



The Species Coalescent



The Species Coalescent across the genome





Contents lists available at ScienceDirect

Molecular Phylogenetics and Evolution

journal homepage: www.elsevier.com/locate/ympev



Short Communication

Mitochondrial and nuclear phylogeny of circum-Mediterranean tree frogs from the *Hyla arborea* group

Matthias Stöck^{a,*}, Sylvain Dubey^{a,b}, Cornelya Klütsch^{c,d}, Spartak N. Litvinchuk^e, Ulrich Scheidt^f, Nicolas Perrin^a

frontiers
in Ecology and Evolution

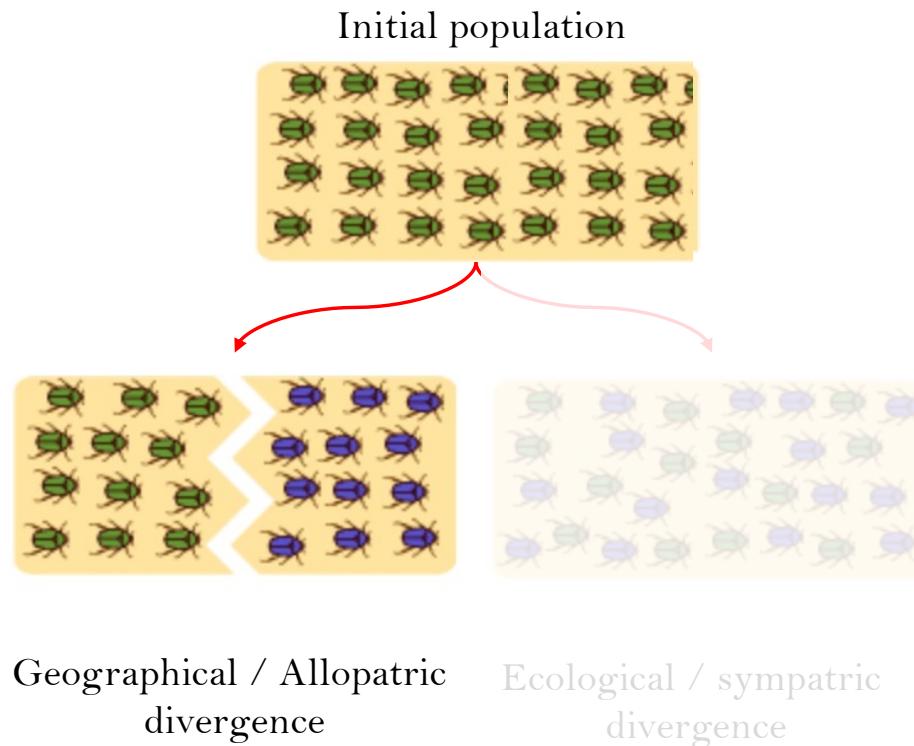
ORIGINAL RESEARCH
published: 02 October 2018
doi: 10.3389/fevo.2018.00144



Genomic Evidence for Cryptic Speciation in Tree Frogs From the Apennine Peninsula, With Description of *Hyla perrini* sp. nov

Christophe Dufresnes^{1,2,3*}, Glib Mazepa^{1,4}, Nicolas Rodrigues¹, Alan Brelsford^{1,5}, Spartak N. Litvinchuk⁶, Roberto Sermier¹, Guillaume Lavanchy¹, Caroline Betto-Colliard¹, Olivier Blaser¹, Amaël Borzée⁷, Elisa Cavoto¹, Guillaume Fabre¹, Karim Ghali¹, Christine Grossen¹, Agnes Horn¹, Julien Leuenberger¹, Barret C. Phillips¹, Paul A. Saunders¹, Romain Savary¹, Tiziano Maddalena⁸, Matthias Stöck⁹, Sylvain Dubey^{1,3}, Daniele Canestrelli¹⁰ and Daniel L. Jeffries¹

Cryptic speciation in tree frogs. Allopatric divergence



<https://github.com/Angelica-Pulido/MMEE-2025/>

Angelica-Pulido / MMEE-2025

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Files

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1.Frogs_Sanger
2.Frogs_RADseq
Data
2.0.README_Frogs_RADseq....
3.Cichlids
4.Eels
Introduction for MMEE.pdf
MMEE_2025_Manual.pdf
README.md
Schedule.png

MMEE-2025 / 2.Frogs_RADseq / 2.0.README_Frogs_RADseq.md

Angelica-Pulido Update and rename 1.0.README_Frogs_RADseq.md to 2.0.README_Frogs_RADseq.md · b7f58cf · 9 minutes ago

Preview Code Blame 19 lines (15 loc) · 796 Bytes

Raw

Project: 2.Frogs_RADSeq/

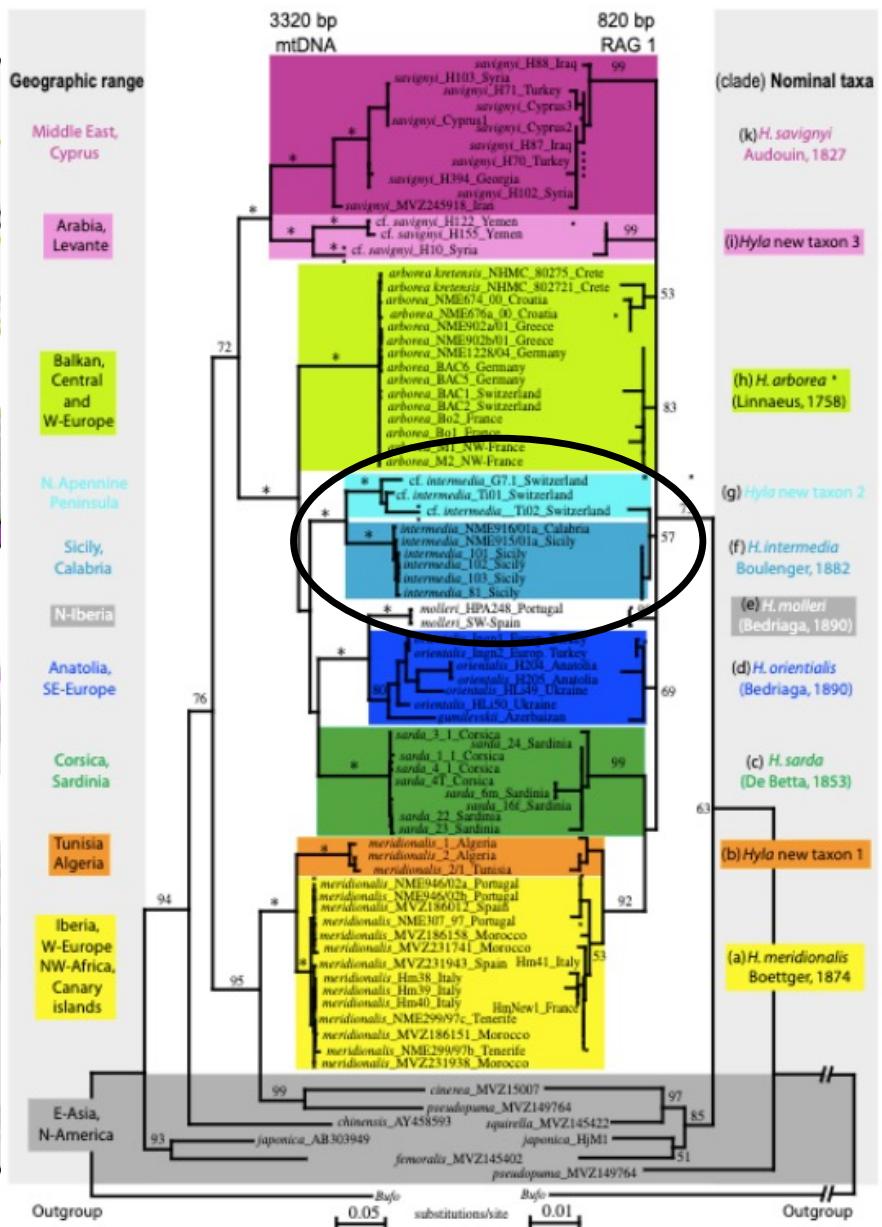
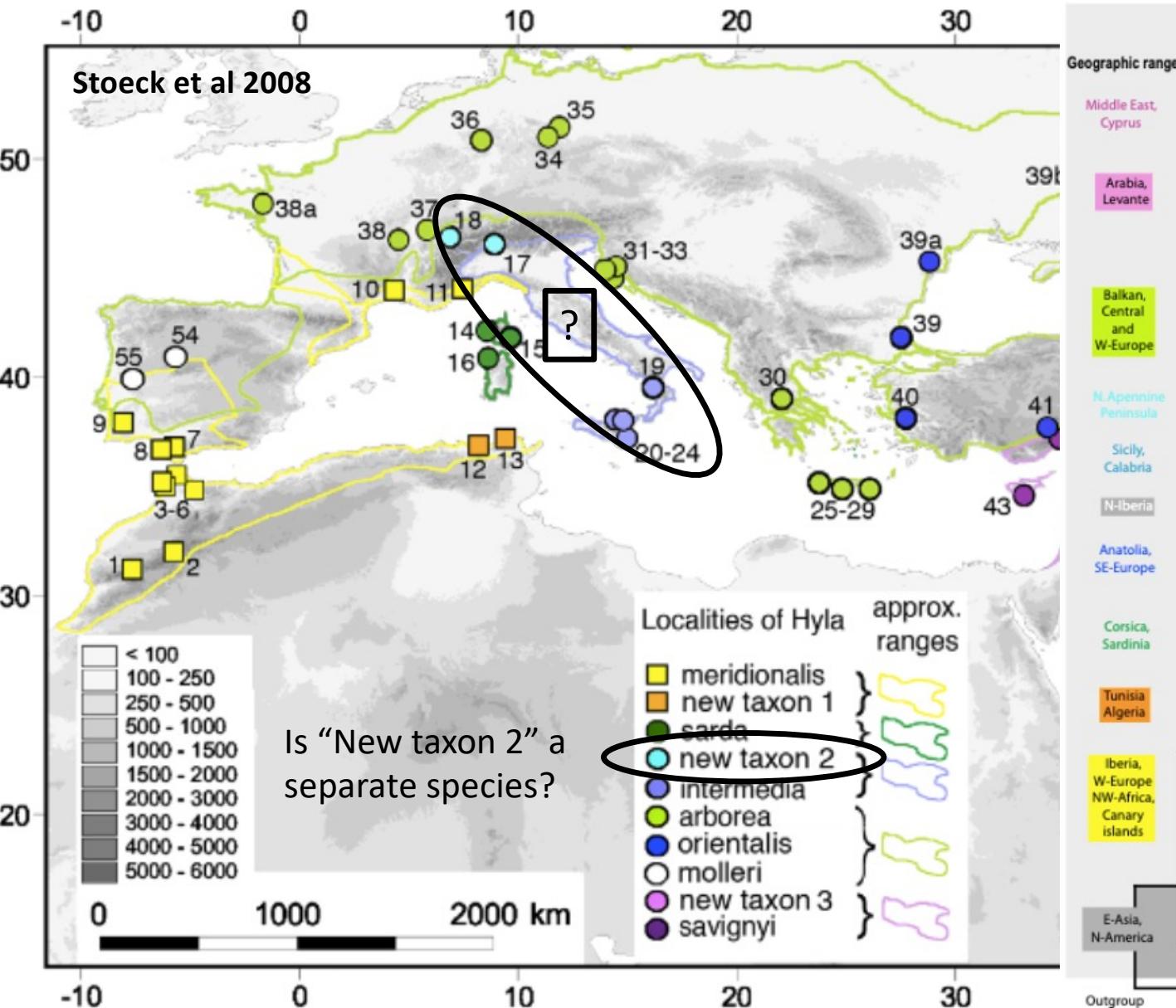
The folders and files for this project are as follow:

Data/RADphylo/

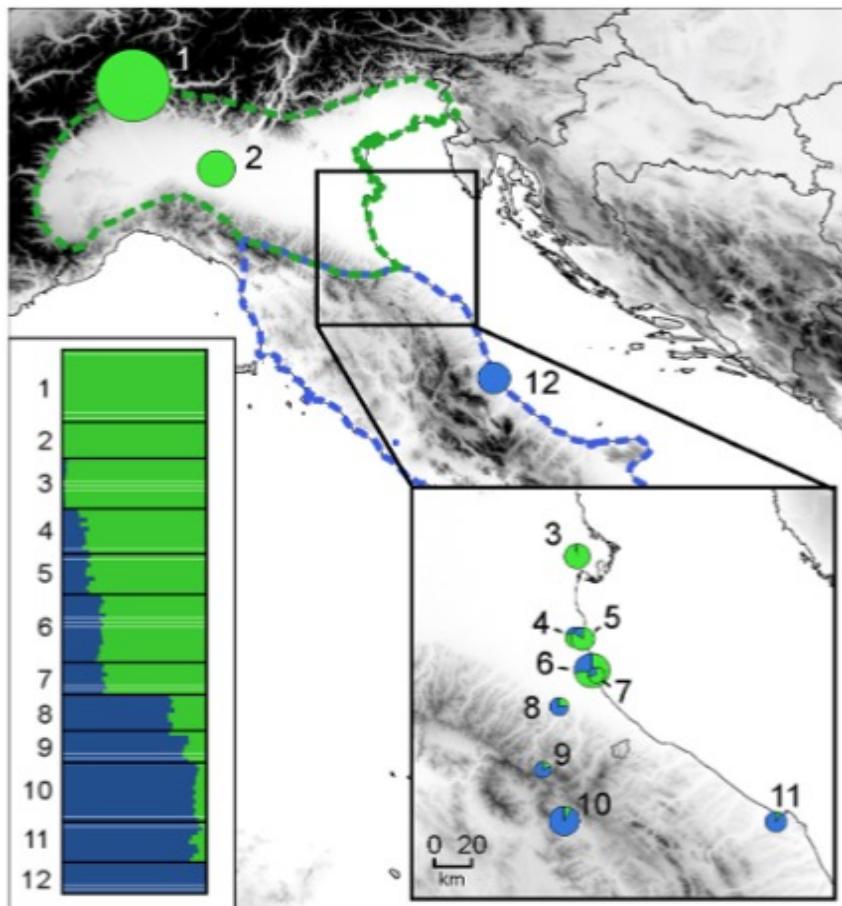
You can use this file to check plot a NJ tree of Hyla individuals. But this is optional, you don't need this file in

Data/RADpopgen/

- hyla_FSTAT.dat
Data for population analyses in fstat format
- populations_numeric_codes.txt
File with a numeric code for each population.
You have to use this file to change the population column in the R object created when you read the hyla_FSTAT.dat file.



Hyla mtDNA / RADseq populations



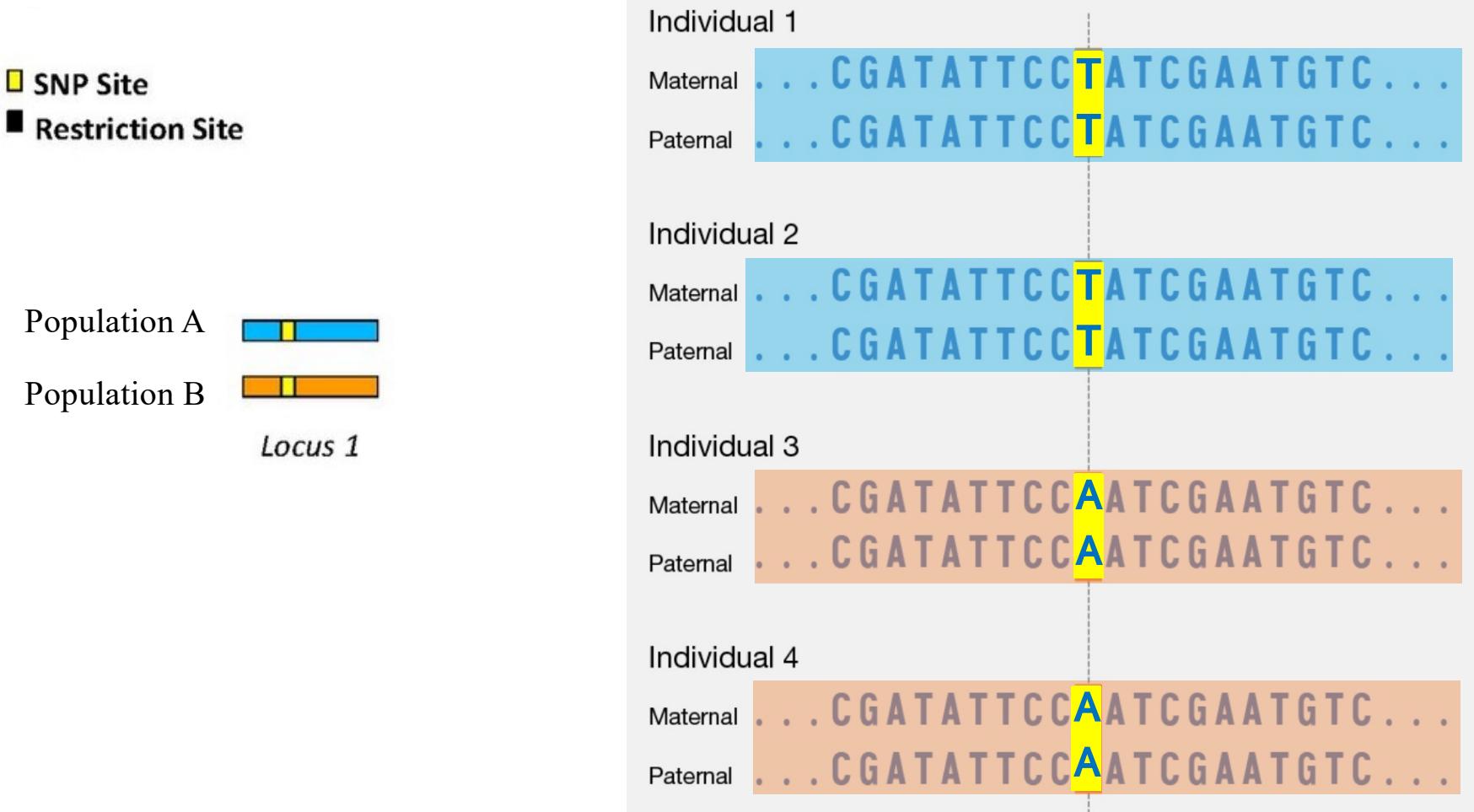
Site #	Site code	N
1	PIA	16
2	CRE	8
3	SGI	11
4	ALB	9
5	PUA	10
6	LDC	15
7	LDS	7
8	MAG	8
9	BAG	7
10	SSE	13
11	SLO	9
12	ROS	7
		120

Dufresnes et al 2018

Q.1. What caused the divergence between these lineages / species?

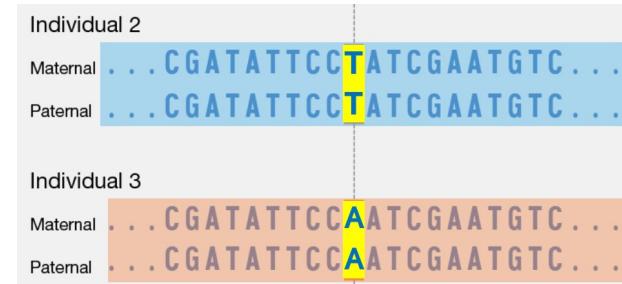
Q. 2. Are they one species, or two?

SNP: Single Nucleotide Polymorphism



The Variant Call Format (VCF)

tab-delimited text file that store genetic variations, such as single nucleotide polymorphisms (SNPs)



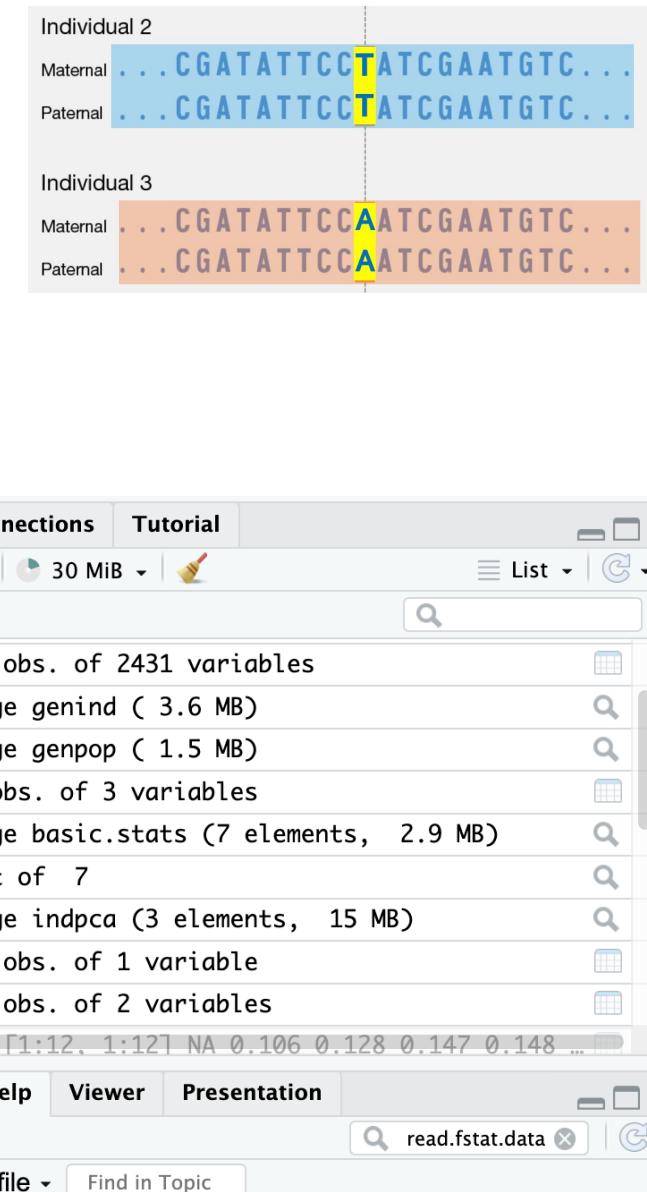
VCF

```
##fileformat=VCFv4.2
##contig=<ID=2,length=51304566>
##INFO=<ID=AC,Number=A,Type=Integer,Description="Allele count in genotypes">
##INFO=<ID=AN,Number=1,Type=Integer,Description="Total number of alleles in called genotypes">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT SAMPLE1 SAMPLE2 SAMPLE3 SAMPLE4
2 81170 . C T . . AC=9;AN=7424 GT:DP:GQ 0/0:4:12 0/0:3:9 0/1:1:3 0/1:9:24
2 81171 . G A . . AC=6;AN=7446 GT:DP:GQ 0/1:4:12 0/0:3:9 0/0:1:3 0/0:9:24
2 81182 . A G . . AC=5;AN=7506 GT:DP:GQ 0/0:5:15 0/0:4:12 0/0:5:15 0/0:9:24
2 81204 . T G . . AC=2;AN=7542 GT:DP:GQ 1/0:5:15 0/0:9:27 0/0:10:30 0/0:15:39
```

FSTAT

read.fstat.data {hierfstat}

	Pop	100057	100057.1	100057.2	100065	100216	100224	100224.1	100249	100397			
1	1	22		22	column 4: numeric with range 10 - 34								
2	1	22	22		31	22	31	31	42	11	22		
3	1	24	22		33	22	33	31	42	11	22		
4	1	22	22		33	22	31	11	22	11	22		
5	1	44		22	33	22	33	31					
6	1	22	22		33	22	33	31					
7	1	22	22		33	22	33	33					
8	1	22	22		31	22	33	31					
9	1	22	22		33	22	33	11					
10	1	22	22		11	21	11	33					
11	1	22	24		31	22	11	33					
12	1	22	22		31	22	11	33					
13	1	22	22		31	22	11	33					



```

### Create a map
library(maps)      # Provides functions that let us plot the maps
library(mapdata)   # Contains the hi-resolution points that mark out the countries.

map('worldHires', xlim = c(3,18), ylim = c(35,48))
points(Hyla_lat_long$Long, Hyla_lat_long$Lat,

```

HIERFSTAT:

HIERFSTAT is a package developed for R to study population structure with the help of genetic markers. Wright's F-statistics are commonly used to determine population structure and differentiation. HIERFSTAT allows you to estimate F-statistics and many other basic statistics important for the analyses of population-level genetic data.

Some commands and functions from HIERFSTAT that you might find useful are listed below but see here <https://www.rdocumentation.org/packages/hierfstat> and help pages of each function for more detailed information:

read.fstat.data(): import data formatted as a .dat file (the .dat file is the format used by the software FSTAT). The data will be read in as a dataframe.

basic.stats(): calculate basic statistics such as expected heterozygosity, observed heterozygosity, F_{IS} , etc for each population and each locus.

pairwise.neifst(): to calculate population pairwise Fst

indpca(): to carry out a PCA on the centred matrix of individual allele frequencies

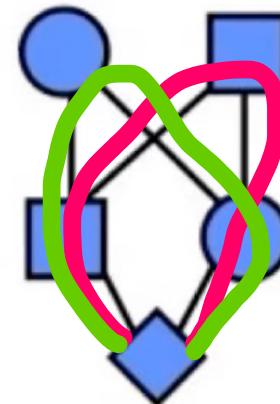
Inbreeding Coefficient (F)

- Measures the **probability** that two alleles at a locus in an individual are identical by descent (IBD).
- IBD: meaning they are copies of the same allele from a common ancestor.
- The level of inbreeding of an offspring is determined by the closeness of the pedigree relationship between the parents

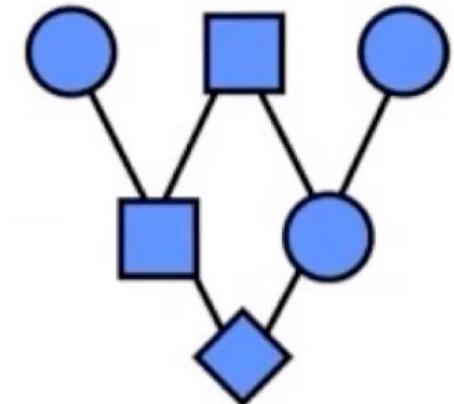
$$F = \sum \left(\frac{1}{2}\right)^N$$

FROH: The genomic inbreeding coefficient calculated by identifying **runs of homozygosity (ROH)**—segments of DNA where both copies of a chromosome are identical by descent from a common ancestor.

Full siblings



Half siblings



$$F = \left(\frac{1}{2}\right)^3 + \left(\frac{1}{2}\right)^3$$

$$\frac{1}{8} + \frac{1}{8} = \frac{1}{4} = 0.25$$

Inbreeding Coefficient within Subpopulations (F_{IS})

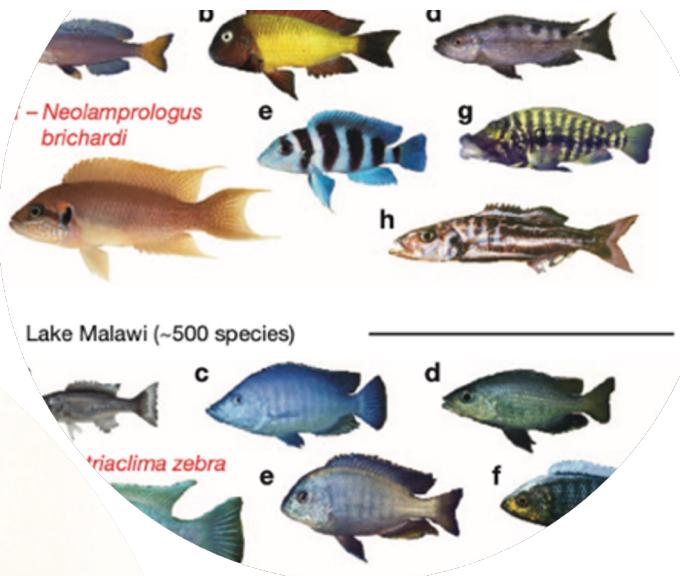
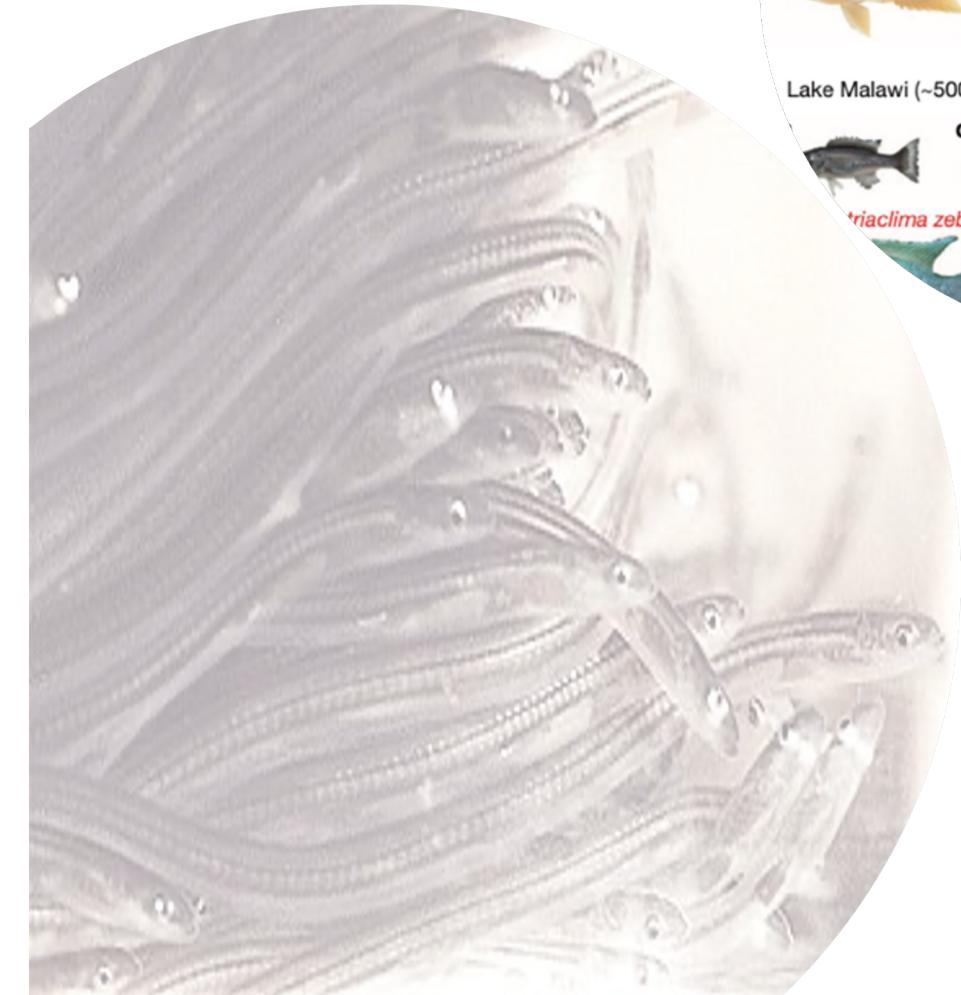
Wright's F-statistics and measures the reduction in heterozygosity of an individual relative to its subpopulation due to non-random mating.

$$F_{IS} = \frac{H_{\text{exp}} - H_{\text{obs}}}{H_{\text{exp}}}$$

$$F_{IS} > 0$$

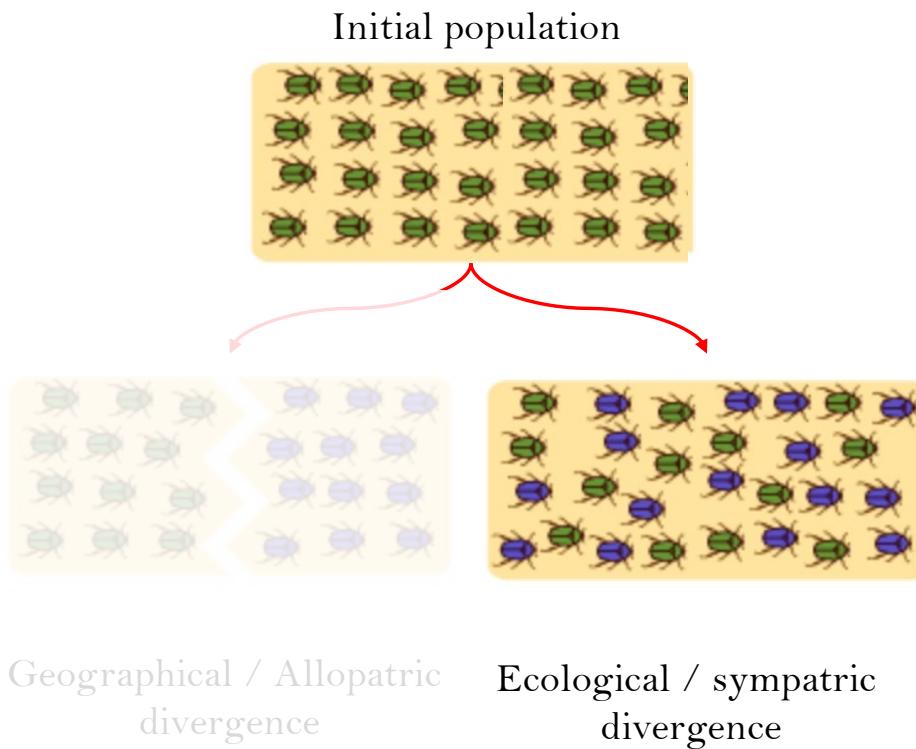
$$F_{IS} = 0$$

$$F_{IS} < 0$$



Project 3

Divergence between Lake Malawi cichlids. Ecological speciation in sympatry





Open Access

The genomic basis of cichlid fish adaptation within the deepwater “twilight zone” of Lake Malawi

Christoph Hahn,^{1,2,3} Martin J Genner,⁴ George F Turner,⁵ and Domino A Joyce¹ 

¹*Evolutionary and Environmental Genomics Group (@EvoHull), School of Environmental Sciences, University of Hull, Hull HU5 7RX, United Kingdom*

²*Institute of Zoology, University of Graz, A-8010 Graz, Austria*

³*E-mail: christoph.hahn@uni-graz.at*

⁴*School of Biological Sciences, University of Bristol, Bristol Life Sciences Building, 24 Tyndall Avenue, Bristol BS8 1TQ, United Kingdom*

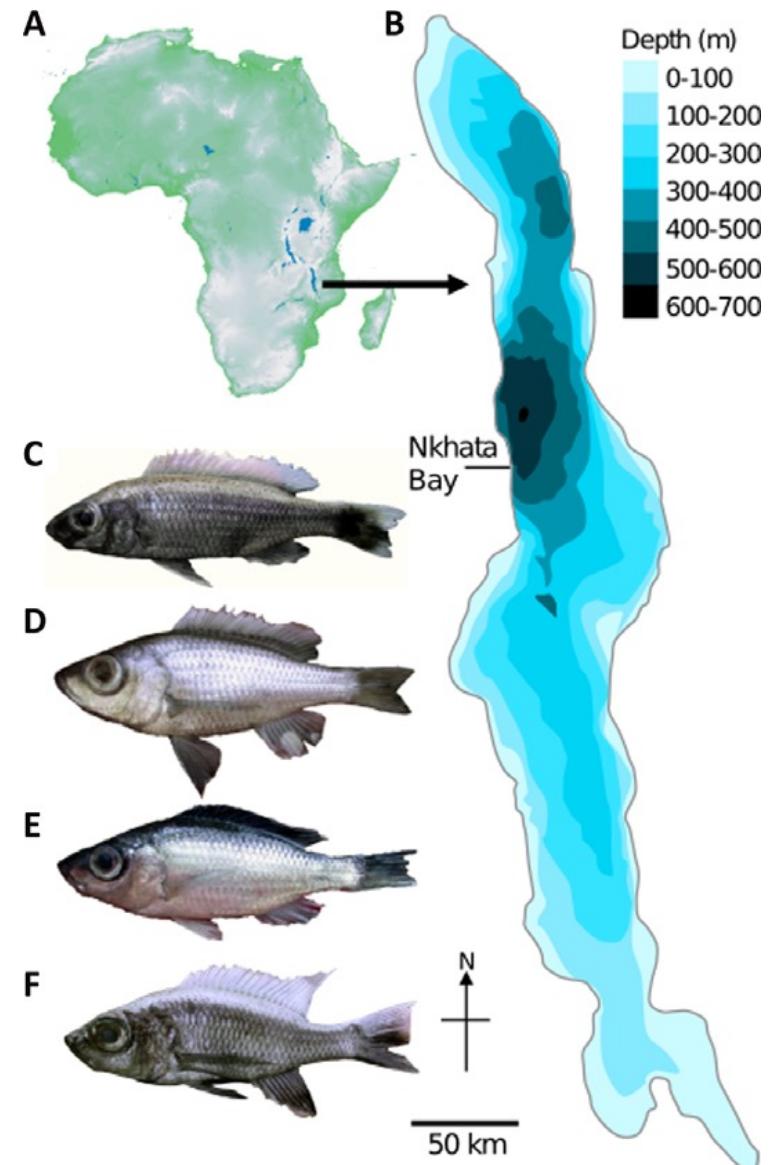
⁵*School of Biological Sciences, Bangor University, Bangor, Gwynedd LL57 2UW, Wales, United Kingdom*

Cichlids sympatric speciation:

Maps of Africa (topographic) and Lake Malawi indicating the sampling location Nkhata Bay.

Diplotaxodon spp

- (C) D. "limnothrissa black pelvic";
- (D) D. "macrops offshore";
- (E) D. "macrops black dorsal";
- (F) D. "macrops ngulube."



Cichlids sympatric speciation:

Deep water environment characteristics:

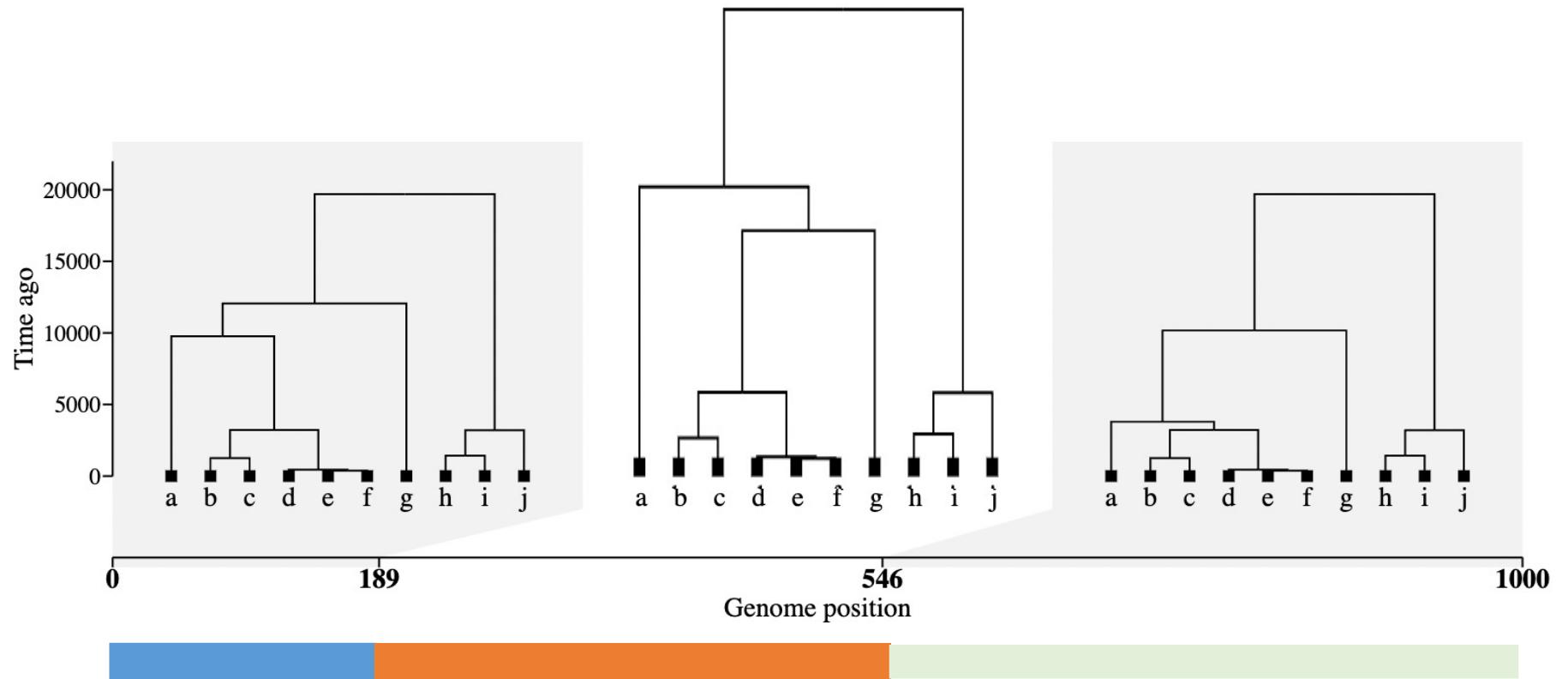
- High hydrostatic pressure
- Low light
- Low dissolved oxygen

Q.1. What can be driving this sympatric divergence?

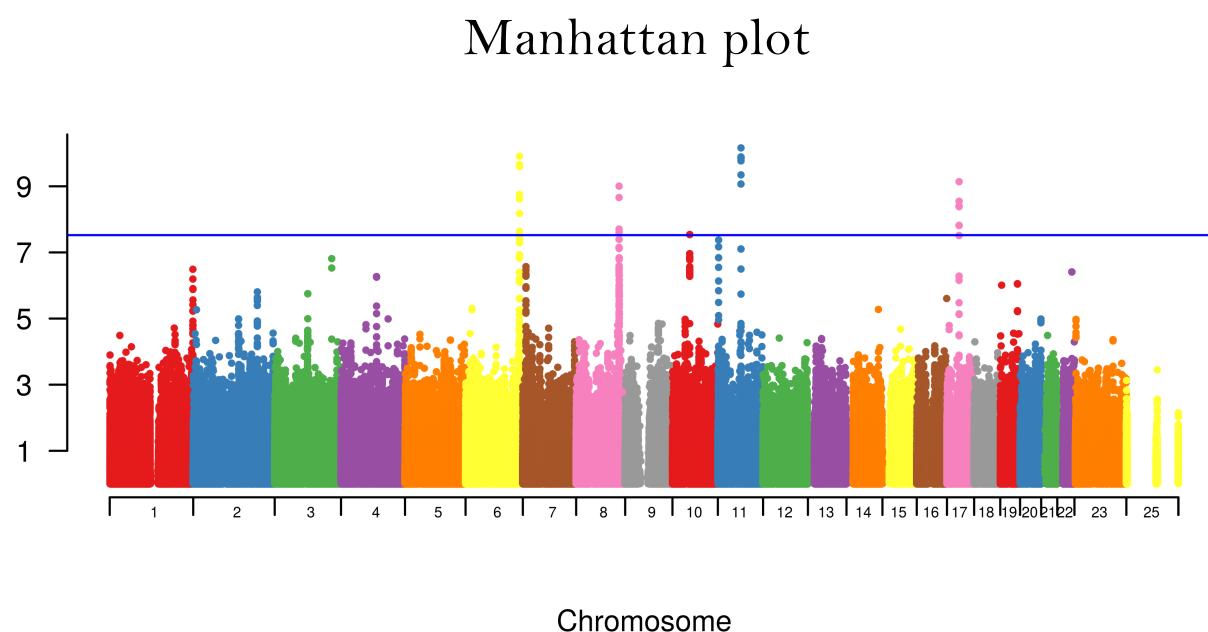
Q. 2. Are there some populations which are more diverged than others?
If so, why?

Q.3. Can you identify candidate loci under selection?

The Species Coalescent across the genome



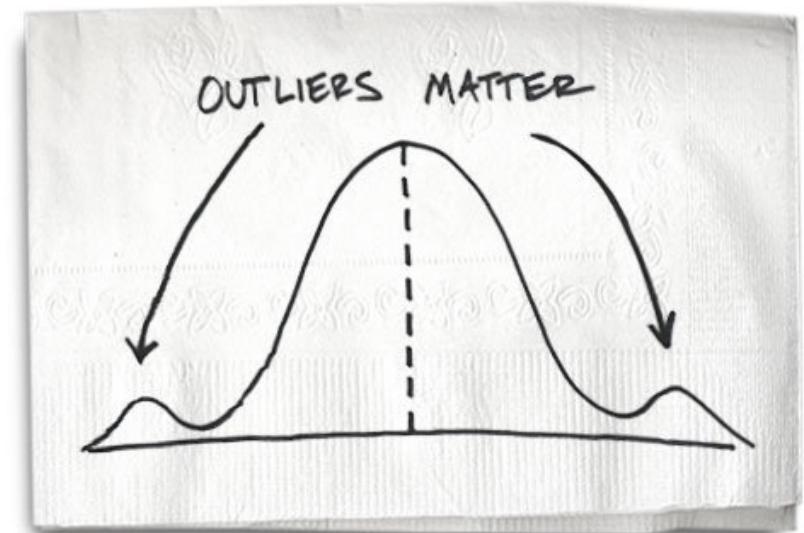
Plot genomic data:



Outlier detection:

Causes of outliers:

- Data entry and measurements errors
- Experimental
- Data processing errors
- Natural (not an error!!!! novelties in data)



<https://github.com/Angelica-Pulido/MMEE-2025/>

Angelica-Pulido / MMEE-2025

Code Issues Pull requests Actions Projects Wiki Security Insights Settings

Files

main + 🔎 Go to file

> 1.Frogs_Sanger
> 2.Frogs_RADseq
3.Cichlids
> Data
3.0 README_Cichlids.md
> 4.Eels
Introduction for MMEE.pdf
MMEE_2025_Manual.pdf
README.md
Schedule.png

MMEE-2025 / 3.Cichlids / 3.0.README_Cichlids.md

Angelica-Pulido Update and rename 2.0.README_Cichlids.md to 3.0.README_Cichlids.md 8ceed26 · 8 minutes ago

Preview Code Blame 24 lines (15 loc) · 684 Bytes

Project: 3.Cichlids/

The files and folders for this project are as follow:

Data/:

- cichlid_hierfstat.dat
Data for population analyses in fstat format.
- pop.txt
File with information about samples and populations.
You have to use this file to change the population column in the R object created when you read the cichlid_hier
- Di_1-Di_2_global_mod.tsv
Pairwise FST from two species: limnothrissa black pelvic (peak abundance:60m) and macrops offshore (peak abundance:100m)

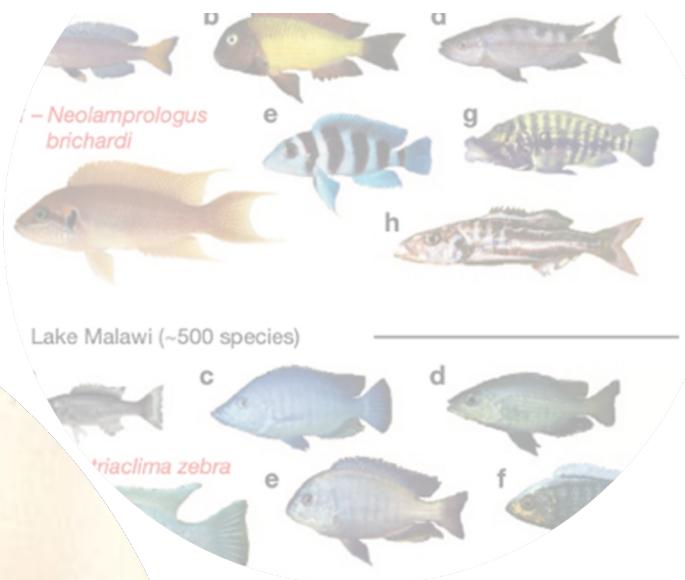
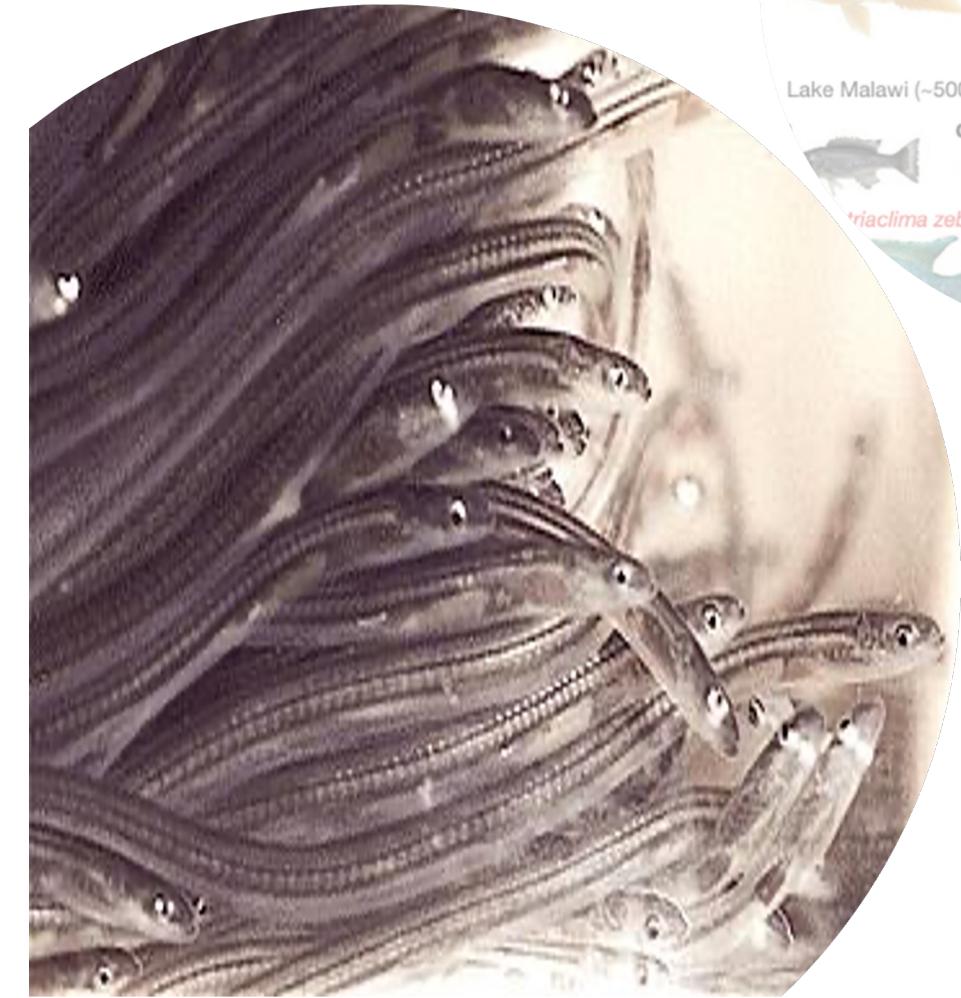
Correspondence between population number and Species names:

- 1 - macrops ngulube
- 2 - macrops black dorsal
- 3 - macrops offshore

Q.1. What can be driving this sympatric divergence?

Q. 2. Are there some populations which are more diverged than others?
If so, why?

Q.3. Can you identify candidate loci under selection?



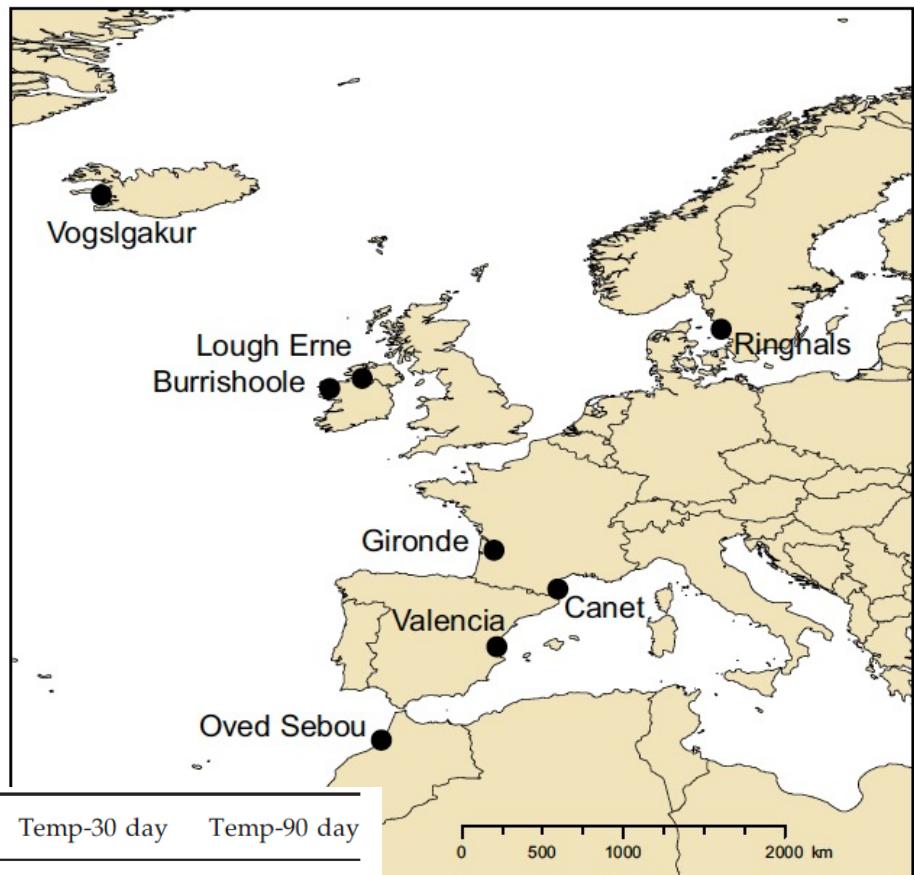
Project 4

The curious case of the European Eel.

Genome-wide single-generation signatures of local selection in the panmictic European eel

J. M. PUJOLAR,* M. W. JACOBSEN,* T. D. ALS,†‡ J. FRYDENBERG,* K. MUNCH,§ B. JÓNSSON,¶
J. B. JIAN,** L. CHENG,†† G. E. MAES,†‡§§ L. BERNATCHEZ¶¶ and M. M. HANSEN*

**8 populations
240 individuals**



Location	Code	N	Coordinates	Sampling date	Temp-10 day	Temp-30 day	Temp-90 day
Vogslækur, Iceland	ICE	34	64°69'N/22°33'W	2/7/2001	9.53	9.38	8.45
Ringhals, Sweden	RHG	30	57°21'N/12°27'E	15/3/2008	4.76	4.77	4.19
Lough Erne, Northern Ireland	LG	33	54°46'N/7°77'W	1/7/2008	13.93	13.81	13.85
Burrishoole, Ireland	BG	29	53°90'N/9°58'W	14/3/2005	9.36	9.79	9.57
Gironde, France	GG	37	44°86'N/0°42'W	16/4/2008	11.55	11.78	11.26
Canet, France	CAG	32	42°70'N/3°15'E	23/1/2008	12.73	12.61	13.24
Valencia, Spain	VG	31	39°46'N/0°24'W	15/1/2010	14.06	14.16	15.05
Oved Sebou, Morocco	MOR	33	34°26'N/6°70'W	28/4/2001	17.53	17.82	17.57

<https://github.com/Angelica-Pulido/MMEE-2025/>

Angelica-Pulido / MMEE-2025

Code Issues Pull requests Actions Projects Wiki Security Insights Settings

Files

main Go to file

- 1.Frogs_Sanger
- 2.Frogs_RADseq
- 3.Cichlids
- 4.Eels
- Data

4.0 README_Eels.md

Introduction for MMEE.pdf

MMEE_2025_Manual.pdf

README.md

Schedule.png

MMEE-2025 / 4.Eels / 4.0.README_Eels.md

Angelica-Pulido Update and rename 3.0.README_Eels.md to 4.0.README_Eels.md

Preview Code Blame 11 lines (7 loc) · 283 Bytes

Project: 4.Eels/

The files and folders for this project are as follow:

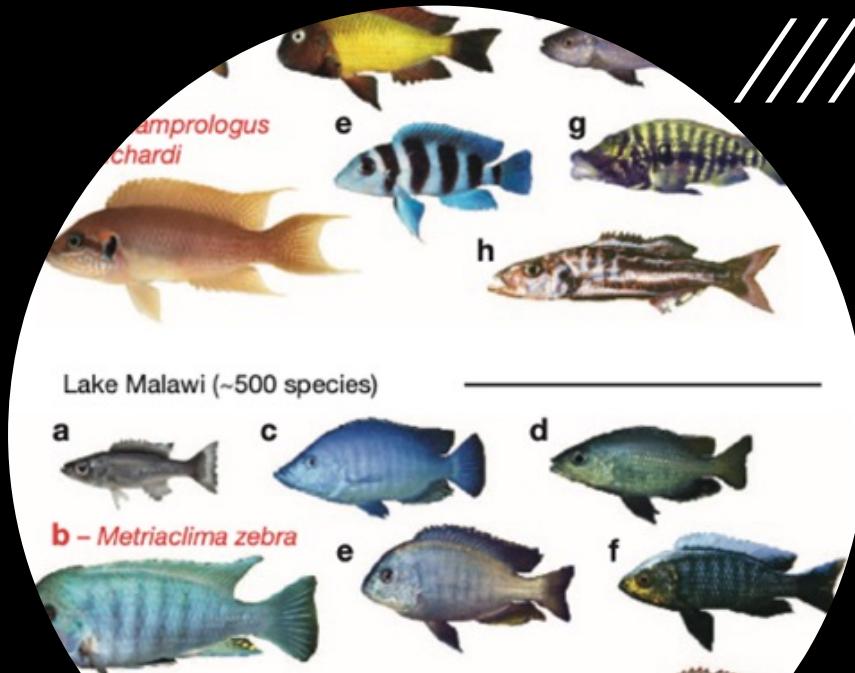
Data/

- eel_pops_lat_lon.tsv
Coordinates of populations used in this project. You can use it to plot Eels populations on a map.
- eel_snps_subset.gen
genetic data for the eels in Genpop format.

Q.1. Can you explain the mysterious patterns of divergence?

Molecular Methods in Ecology and Evolution

2025





Project 1.

Use sanger sequencing on genetic markers to identify a mysterious frog species.

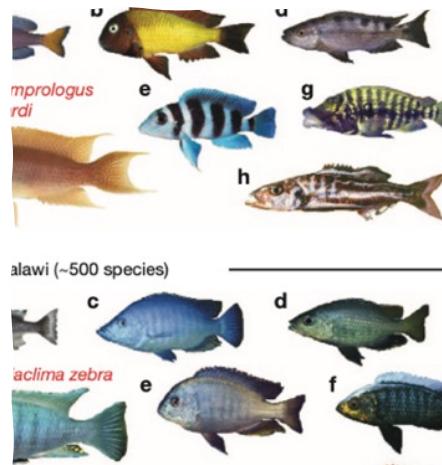


Project 2.

Cryptic speciation in tree frogs.

Allopatric divergence

Are they different species?



Project 3.

Divergence in Lake Malawi cichlids.

Ecological speciation in sympatry

What can be driving it?



Project 4.

The curious case of the European Eel.

Different types of **genetic markers**

- singleDNA,
- RAD sequencing data

Different **methods**

- phylogeny
- Within- AND between-populations statistics
- clustering
- genome scans
- PCA
- Outlier Analyses ...

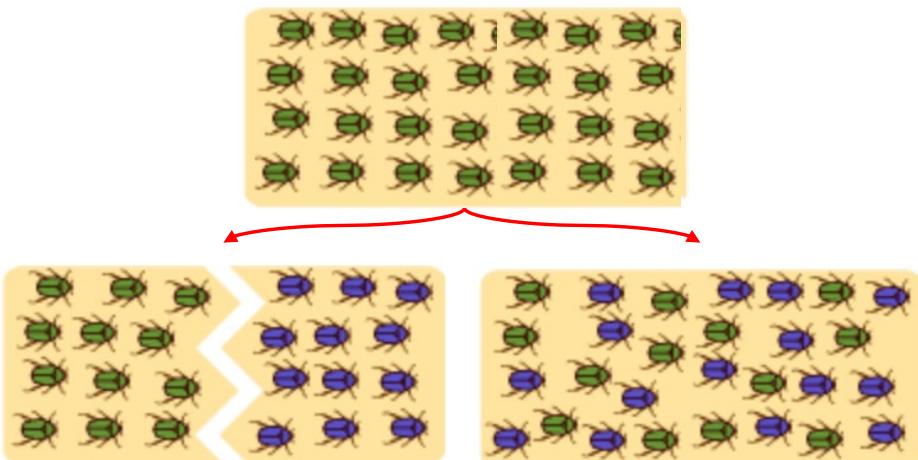
Different **geographic scales**

- Local (Fish)
- Regional (frogs)
- Continental (Eels)

The theme:

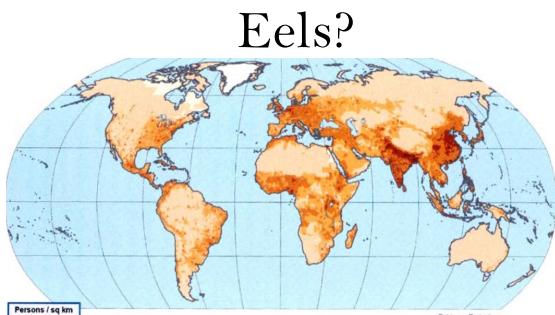
Understand the evolutionary and ecological drivers of population divergence and speciation

Initial population



Geographical / Allopatric divergence

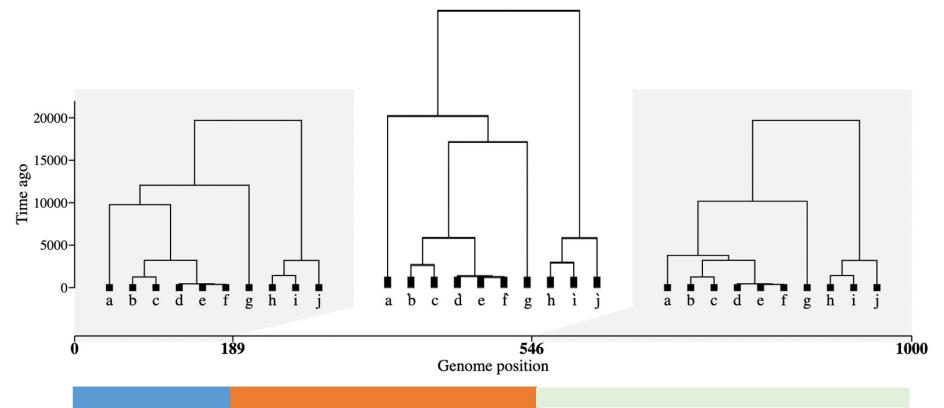
Ecological / sympatric divergence



The Speciation Continuum



Recombination



The report

General introduction
Wet lab / Project 1 <ul style="list-style-type: none">- methods- results & Discuss
Computer lab: Project 1 & 2. <ul style="list-style-type: none">- Intro- methods- results- discussion- conclusion- references
Project 3. <ul style="list-style-type: none">- Intro- methods- results- discussion- conclusion- references
Project 4. <ul style="list-style-type: none">- Intro- methods- results- discussion- conclusion- references
General Discussion

max **5 pages** per project
(including text and figures)

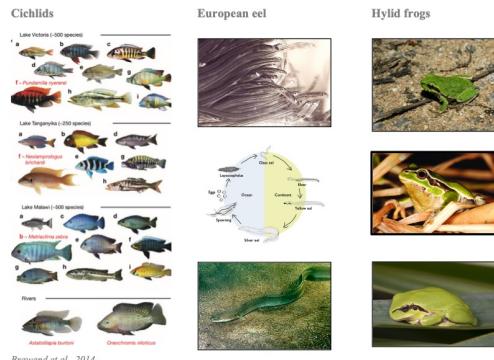
max **25 pages** in total
(including text, figures and references)

DEADLINE: 27 / 10 / 25

Report grading

Molecular Methods in Ecology and Evolution – 2025

Using molecular approaches to understand the drivers of population divergence and speciation.



Brawand et al., 2014

See “**Advice on preparing your report**” section in your manual, these guidelines are there to help you write your report, but they will also be the basis of the marking scheme used to grade your reports.

Prof. Ian R. Sanders, Dr. Luca Fumagalli, Prof. Nicolas Salamin

Teaching assistants: Dr. Soon-jae Lee, Dr. Angélica Pujido, Dr. Anna Hewett, Dr. Jaime Gonzalez, Dr Ricardo Arraiano, Marion Nyamari, Kenneth Kim.