Hybridisation

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Tree of Life Programme, Wellcome Sanger Institute

Outline

- What is hybridisation and introgression?
    - Defining terms
    - How common is it?

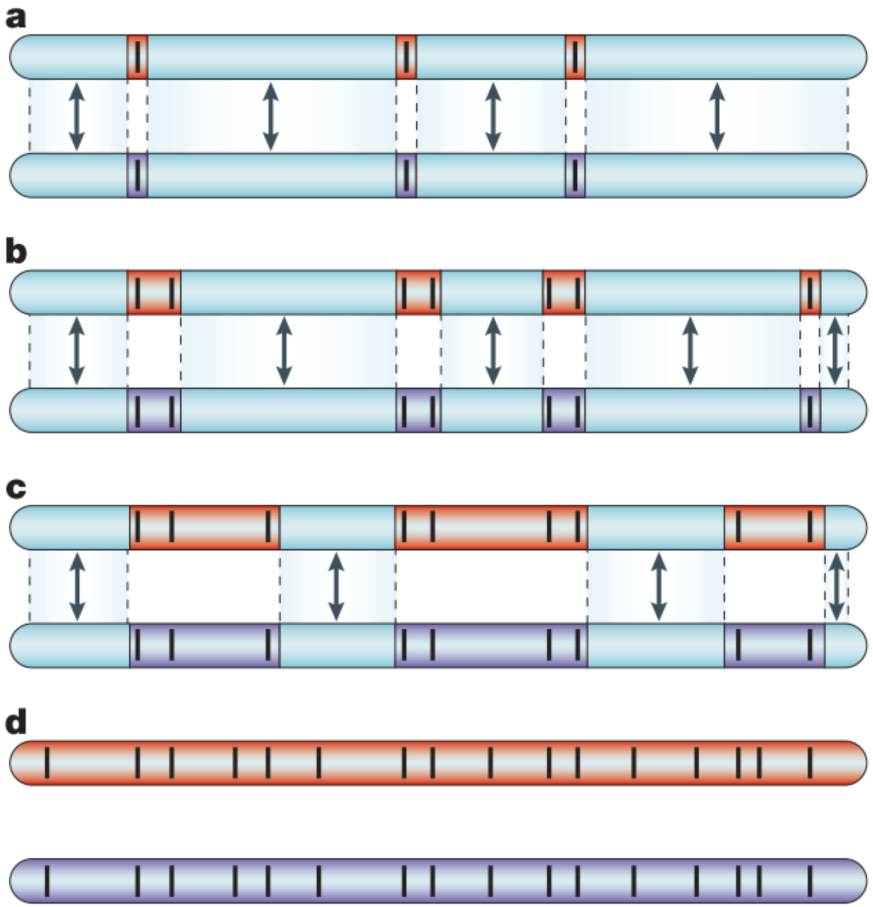
- Evolutionary consequences of hybridisation
    - From genome swamping to hybrid speciation

- Detecting hybridisation
    - Time scale matters (ongoing versus ancestral)

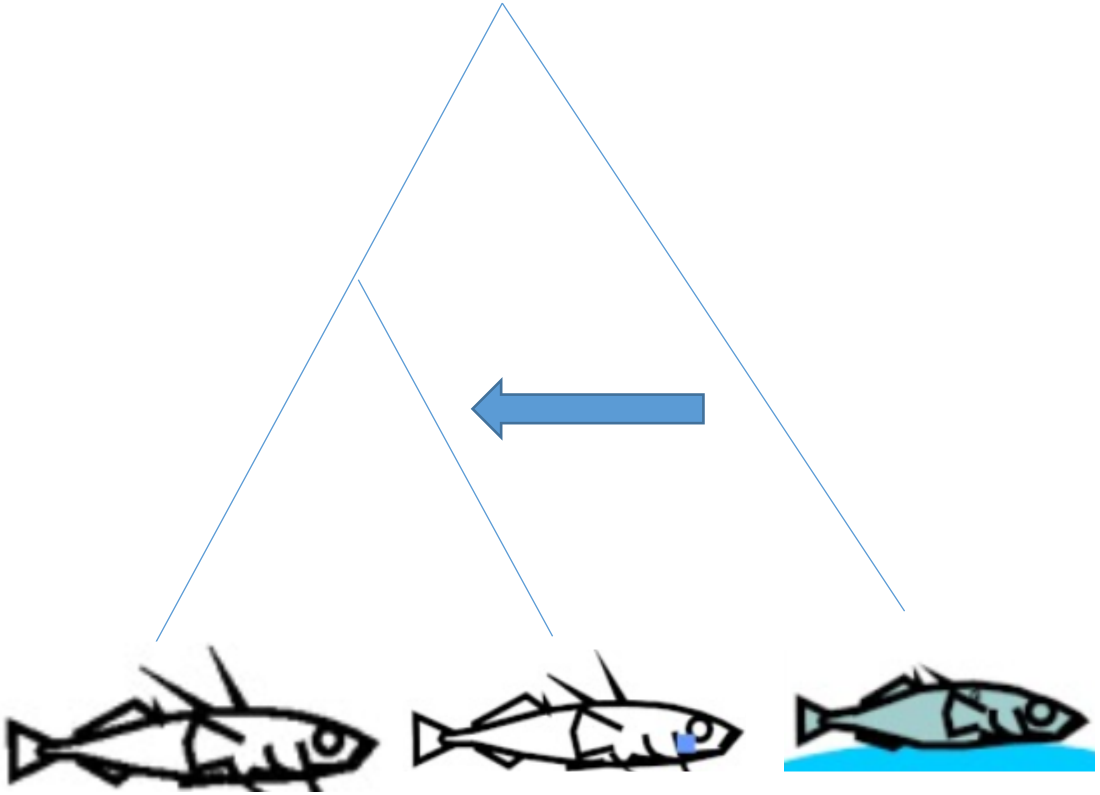
- An example of my work on hybridisation

The dual role of hybridisation in speciation and adaptation

Gene flow between sister taxa counteracts speciation

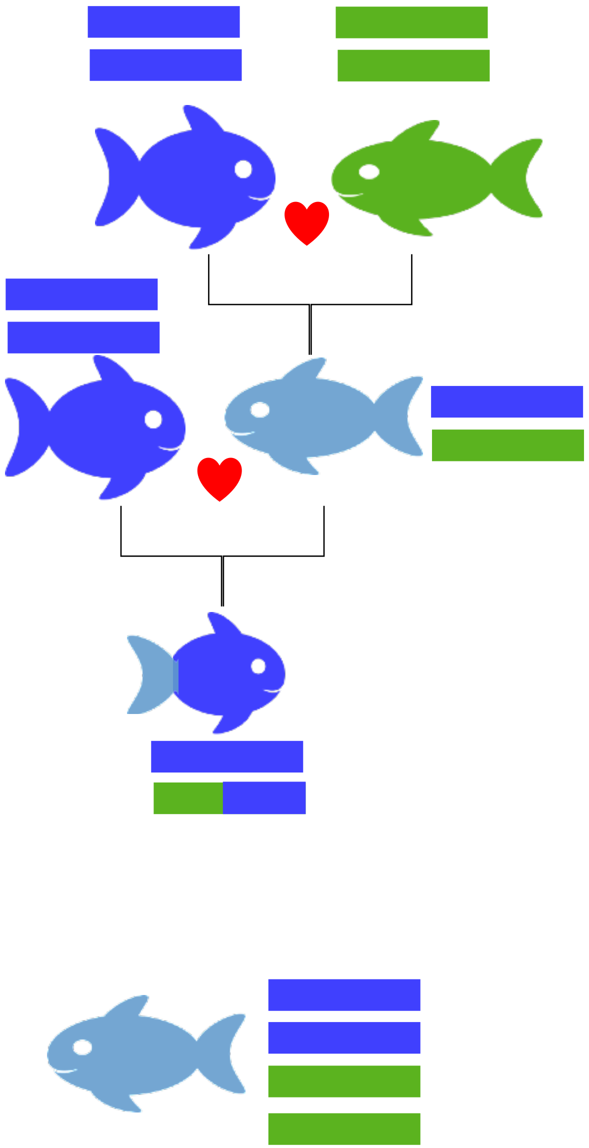


Hybridisation can introduce new genetic variation



Key terminology

- **Hybridisation**: sexual reproduction between individuals from different species or genetically divergent populations
- **Back-crossing**: hybrid individuals mating with «pure» individuals and thus leading to gene transfer between species
- **Admixture**: the genetic pattern of mixed ancestry in hybrid individuals
- **Introgression**: movement of gene variants across lineage boundaries through hybridisation and backcrossing
- **Gene flow**: gene exchange between closely related populations
- **Allopolyploid** : organism with multiple sets of chromosomes from different parental lineages due to hybridisation



History

Historically, zoologists considered hybridisation between species as a rare process or as a sign of incomplete speciation (Dobzhansky 1937; Mayr 1942). Botanists recognized that hybridisation may sometimes generate novel traits and even species (Lotsy, 1916) (Anderson 1949; Anderson and Stebbins 1954).

“The rarity of allopolyploids constitutes the greatest known difference between the evolutionary patterns in the two kingdoms" (Dobzansky, 1937, p. 219)

„the majority (if not all) of organisms have an evolutionary history (...) that includes genetic exchange events“ (Arnold, 2009, p. 183).

The majority of arctic plants are allopolyploid hybrids

Hybridisation is widespread but not common

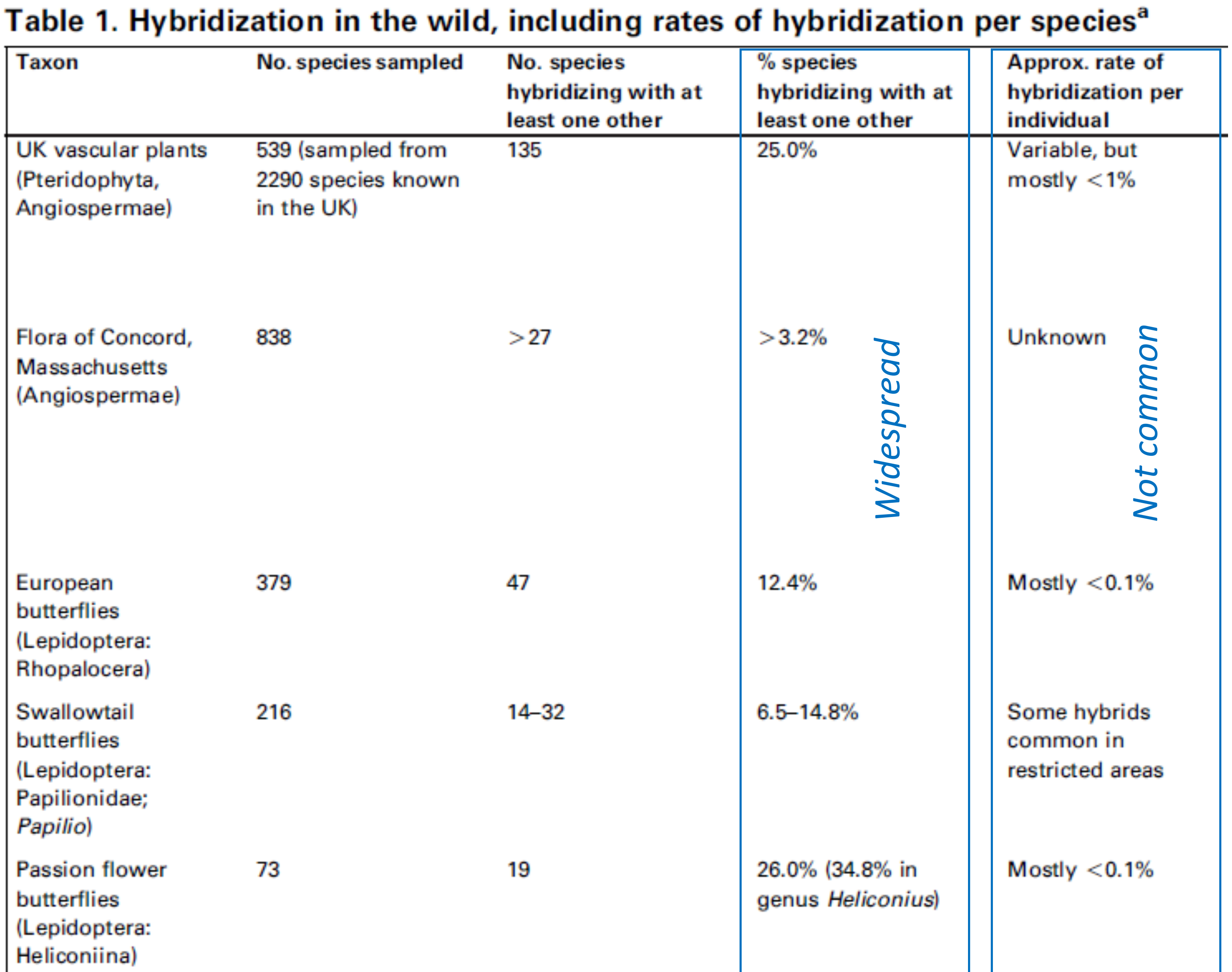


Table 1. Hybridization in the wild, including rates of hybridization per species[a]

Taxon	No. species sampled	No. species hybridizing with at least one other	% species hybridizing with at least one other	Approx. rate of hybridization per individual
UK vascular plants (Pteridophyta, Angiospermae)	539 (sampled from 2290 species known in the UK)	135	25.0%	Variable, but mostly <1%
Flora of Concord, Massachusetts (Angiospermae)	838	>27	>3.2%	Unknown
European butterflies (Lepidoptera: Rhopalocera)	379	47	12.4%	Mostly <0.1%
Swallowtail butterflies (Lepidoptera: Papilionidae; *Papilio*)	216	14–32	6.5–14.8%	Some hybrids common in restricted areas
Passion flower butterflies (Lepidoptera: Heliconiina)	73	19	26.0% (34.8% in genus *Heliconius*)	Mostly <0.1%

Widespread

Not common

Mallet 2005
Trends in Ecology & Evolution

Hybridisation is widespread but not common

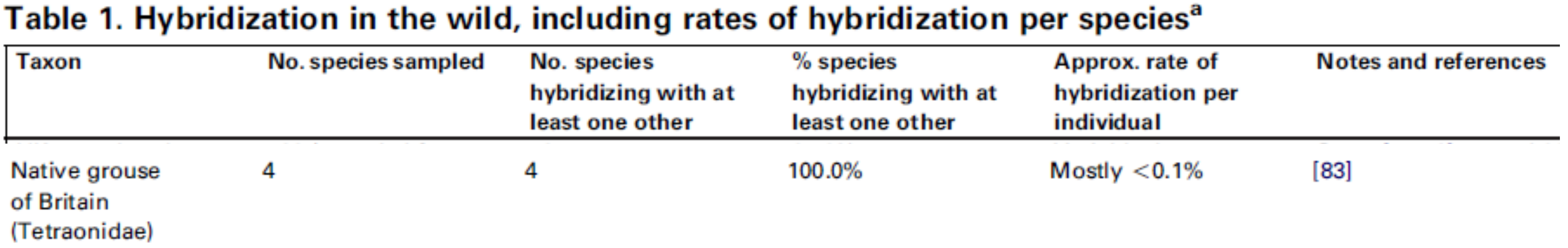


Table 1. Hybridization in the wild, including rates of hybridization per species[a]

Taxon	No. species sampled	No. species hybridizing with at least one other	% species hybridizing with at least one other	Approx. rate of hybridization per individual	Notes and references
Native grouse of Britain (Tetraonidae)	4	4	100.0%	Mostly <0.1%	[83]

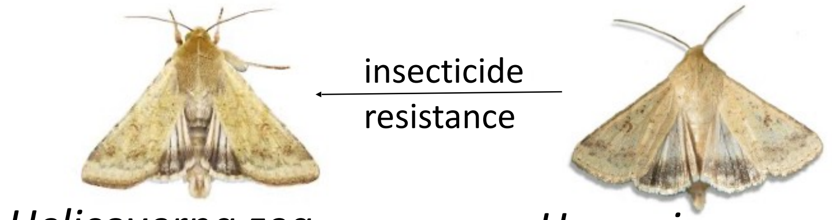
All grouse species of Britain hybridise with other species, but only <0.1% individuals are visible hybrids

Mallet 2005
Trends in Ecology & Evolution

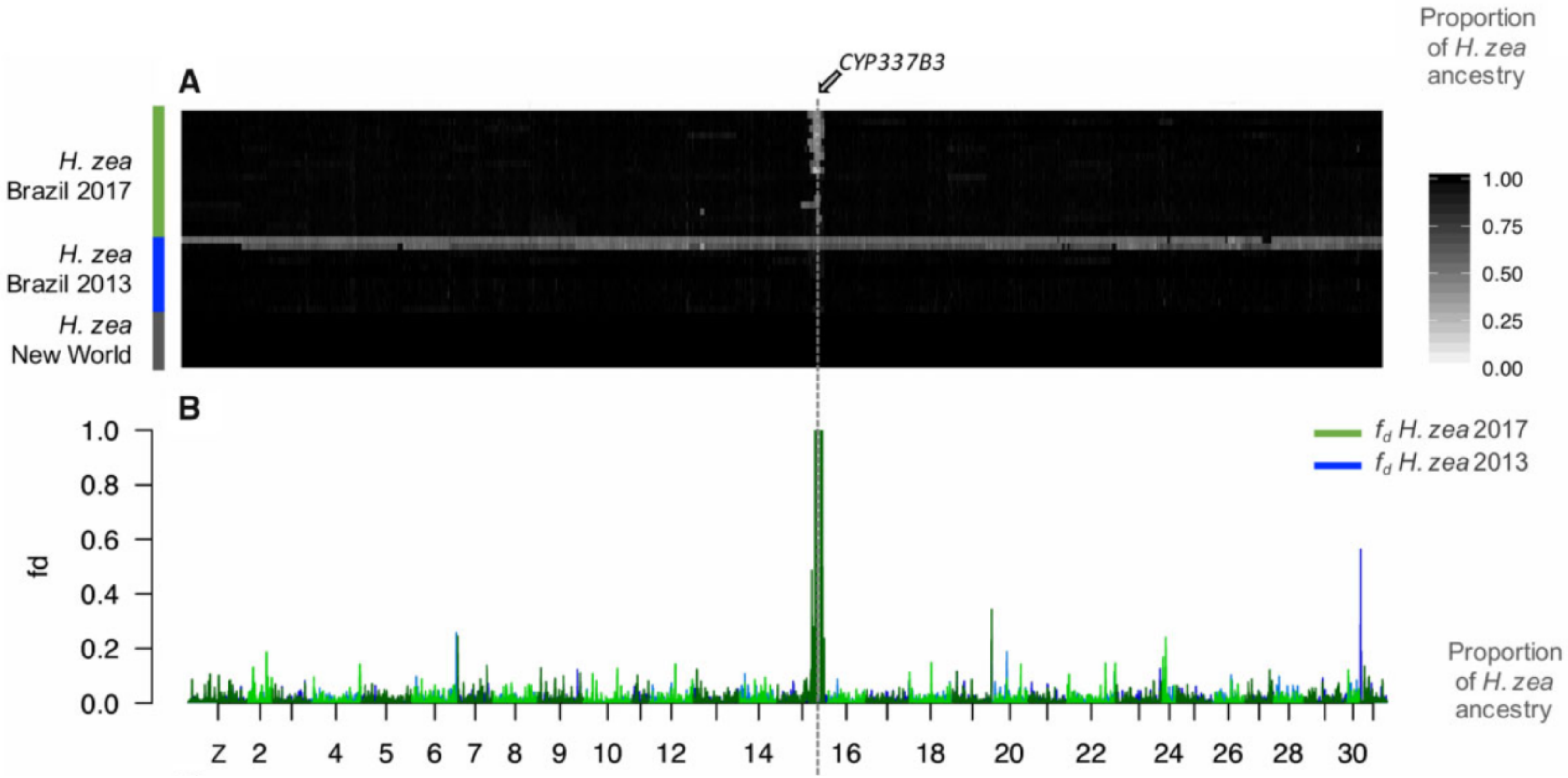
Hybridisation does not necessarily lead to introgression

Even if hybrids are very rare, introgression can be highly relevant, e.g. if beneficial allele introgresses

Insecticide resistance



Helicoverpa zea　　*H. armigera*



Valencia-Montoya et al. 2020, MBE

High altitude adaptation in Tibetans

Admixture between Denisovans and humans in Asia 50k-30k years ago led to 1-6% Denisovan ancestry in southeast Asians.

EPAS1 introgression from Denisovans increases the efficiency in oxygen transport in Tibetans, without straining the heart

Getty Images

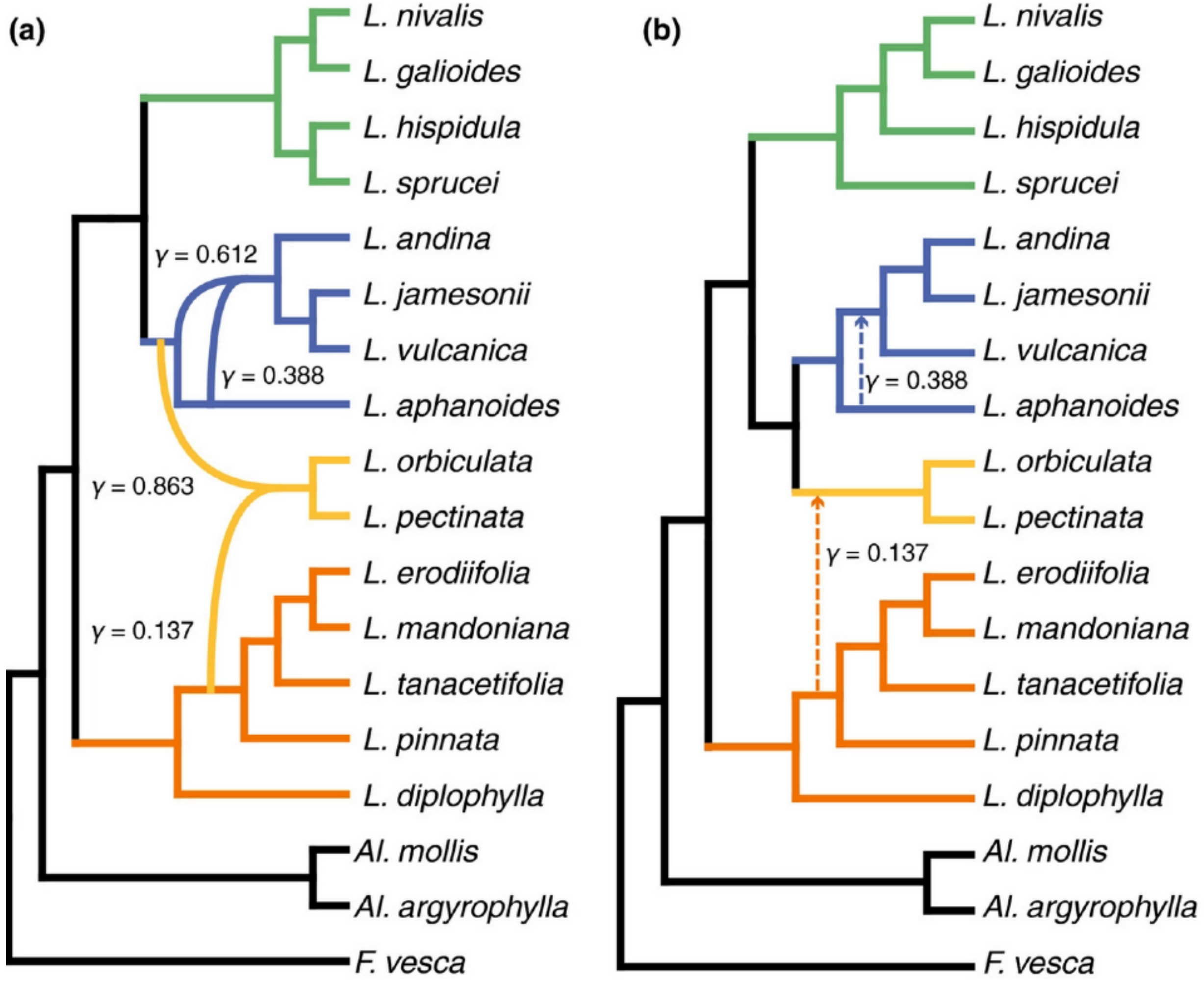
Because of introgression, the tree of life is actually a network of life

«With whole-genome sequencing we can study gene flow in the past and assess levels of reticulation but the quest for the ‘correct tree’ is flawed»

Walker et al. 2024 Common misconceptions of speciation

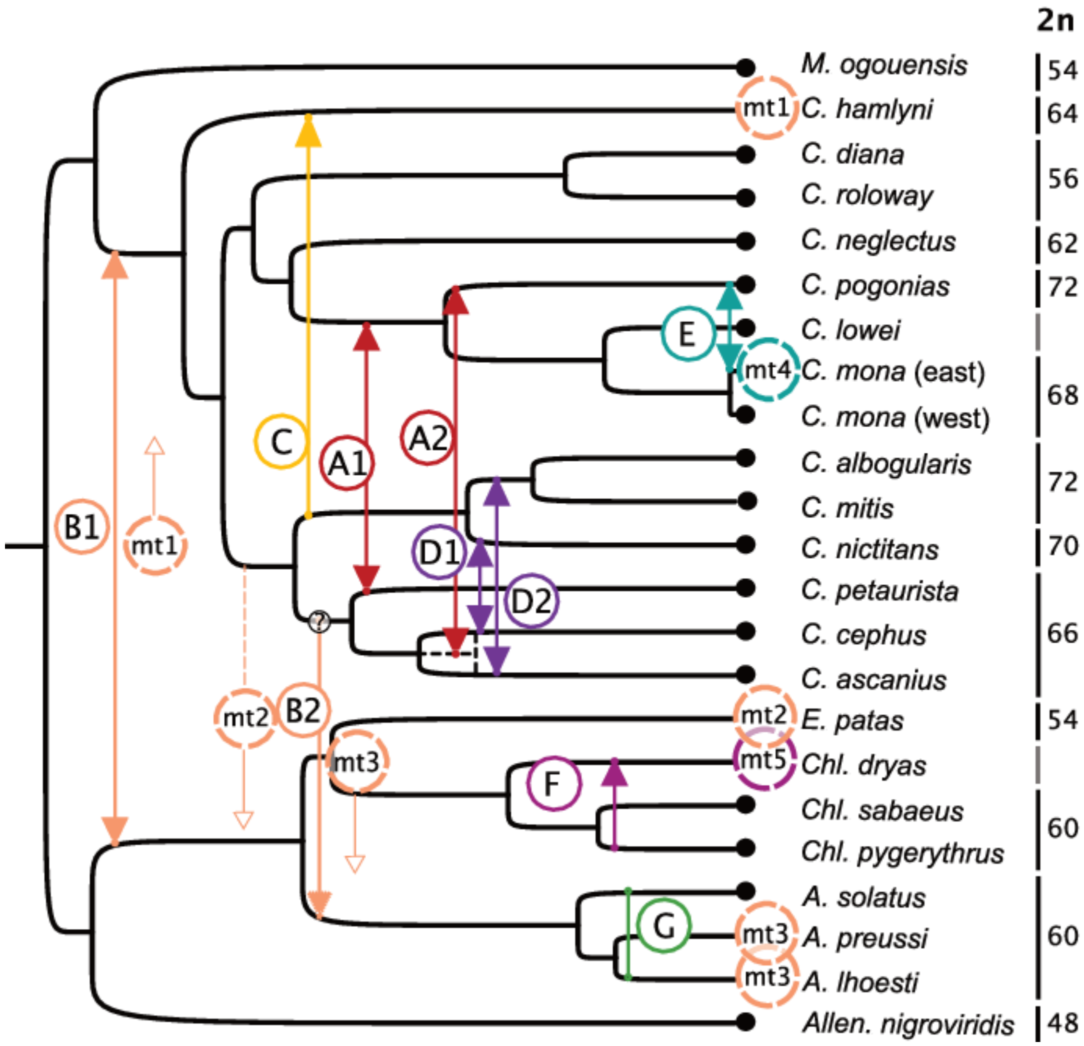
Phylogenies are inaccurate

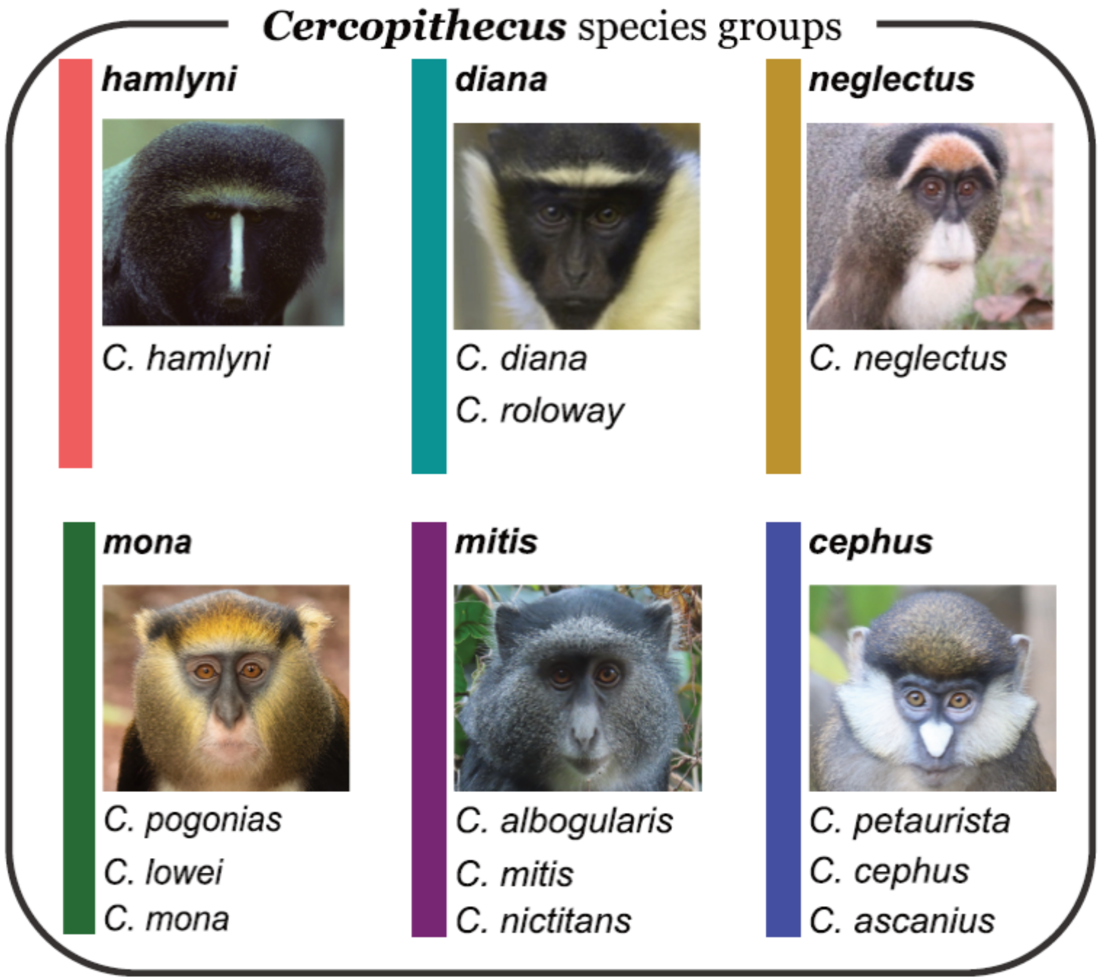
Lachemilla **(Rosaceae)**



Morales-Briones et al., 2018, New Phytologist

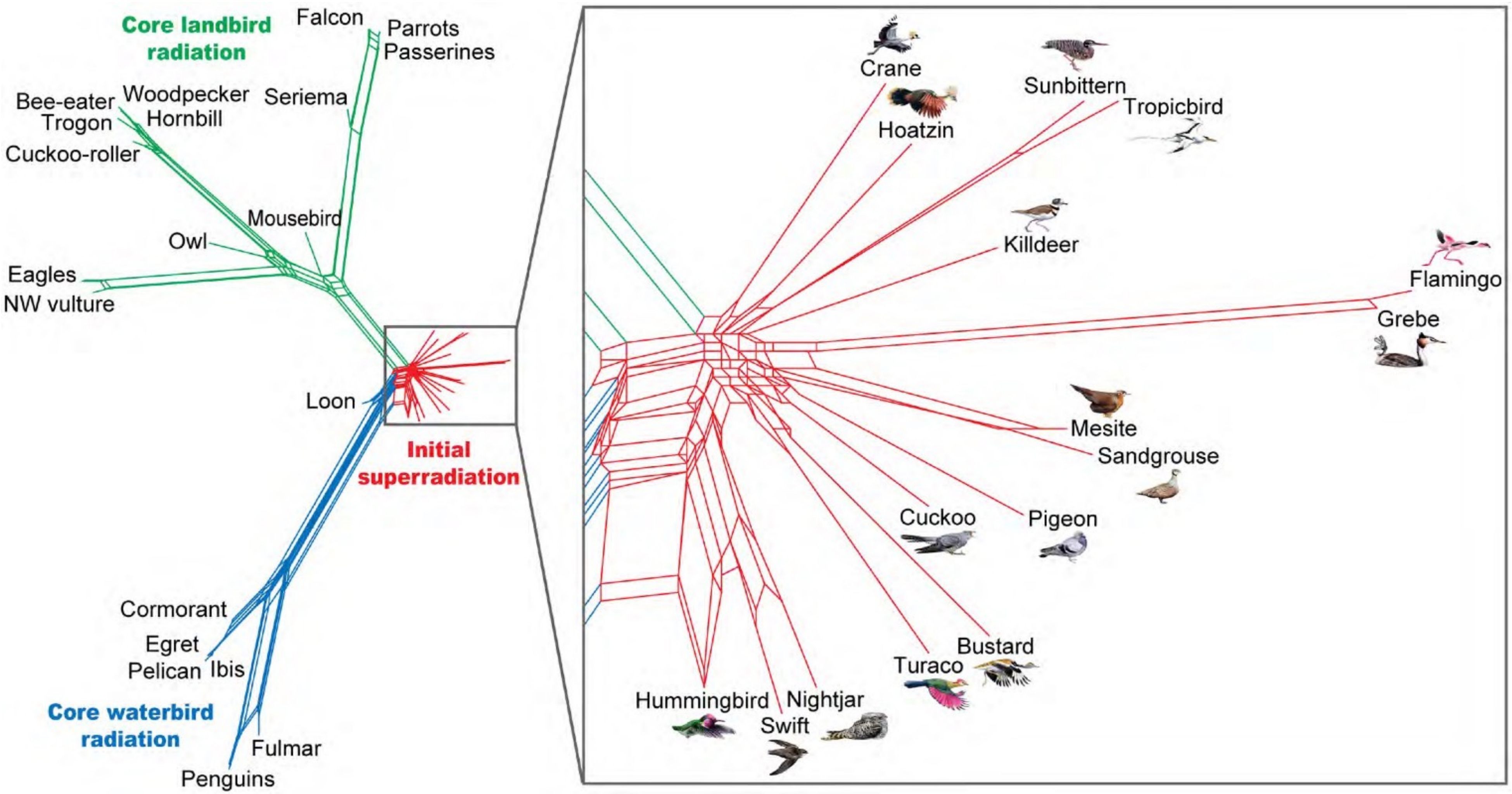
The same is true for animals (e.g. guenons)





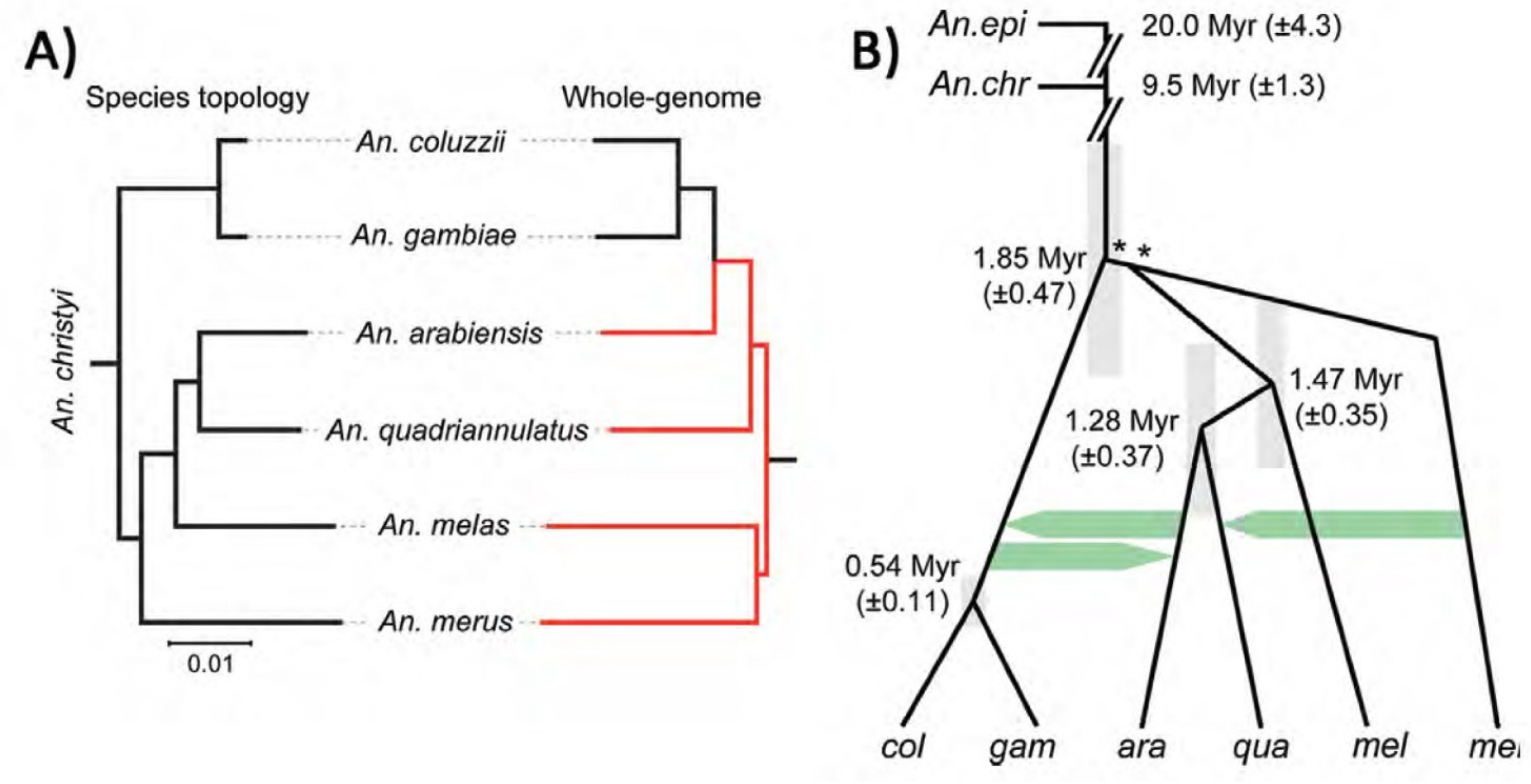
Jensen et al. 2023, MBE

Phylogenies as networks



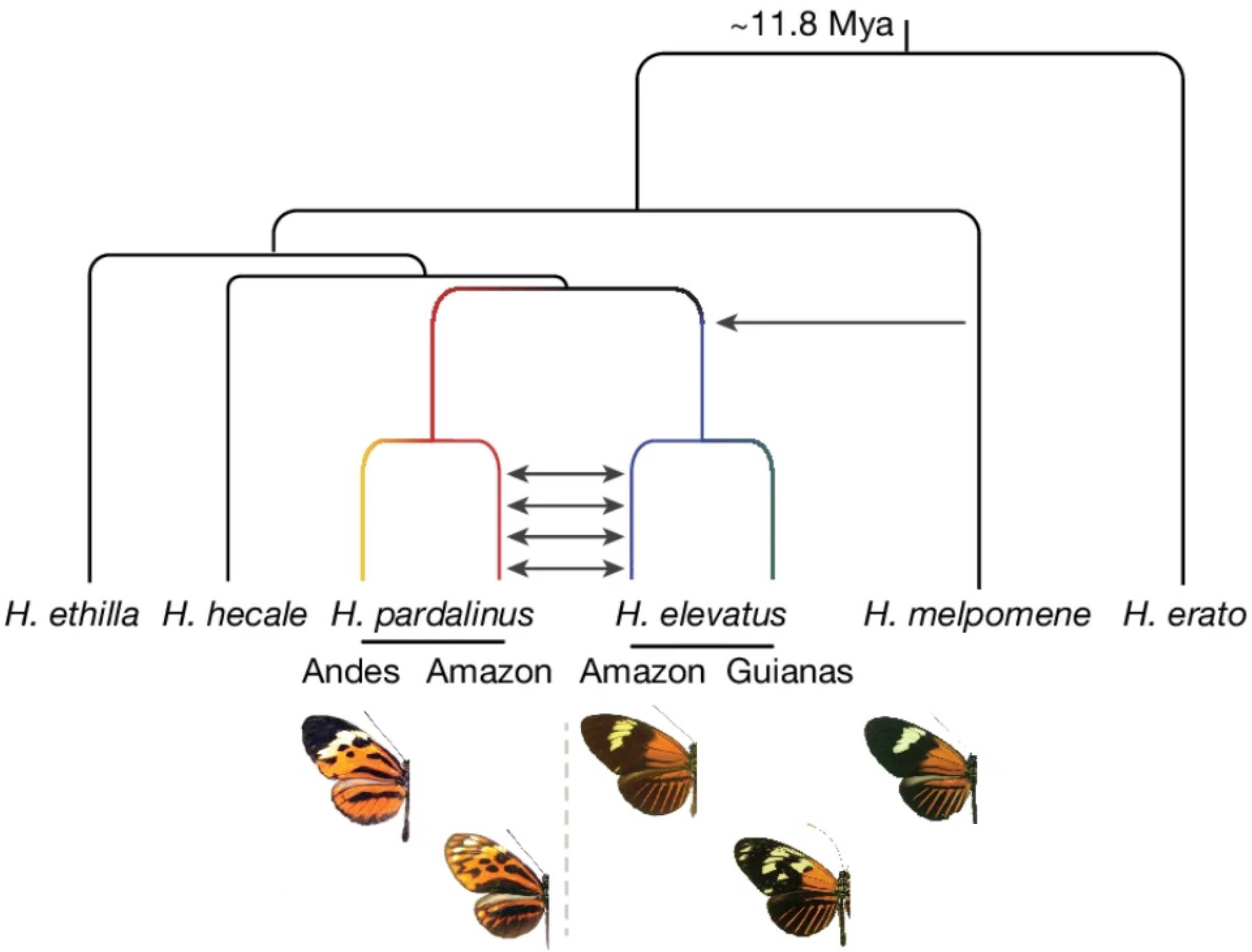
The bird radiation

Introgression can affect large amounts of the genome:
In *Anopheles* most parts of the genome do not represent the species tree

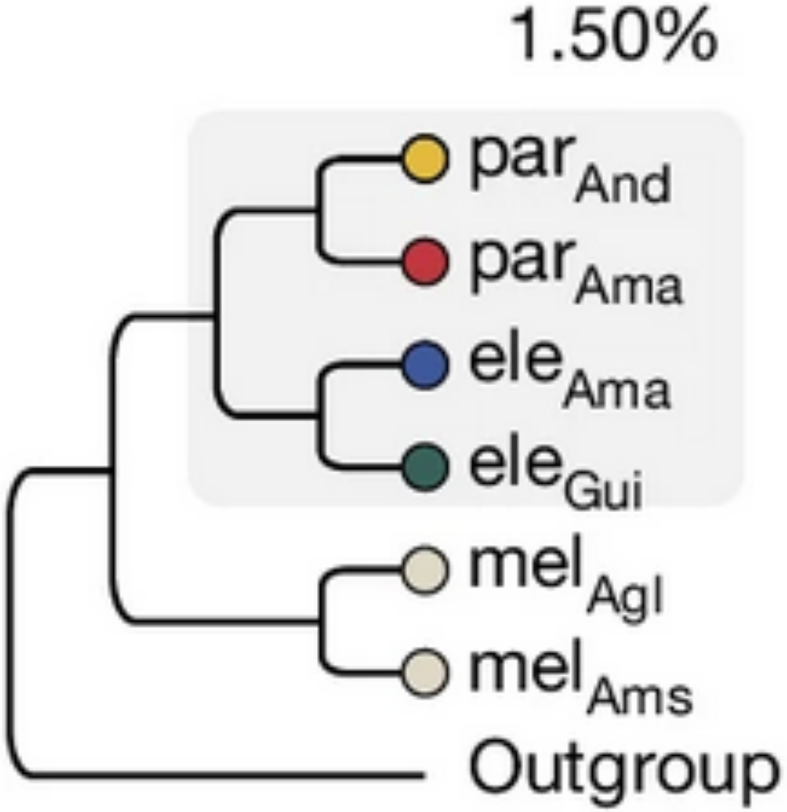


Fontaine et al., 2015, Science

Heliconius elevatus and *H. pardalinus*

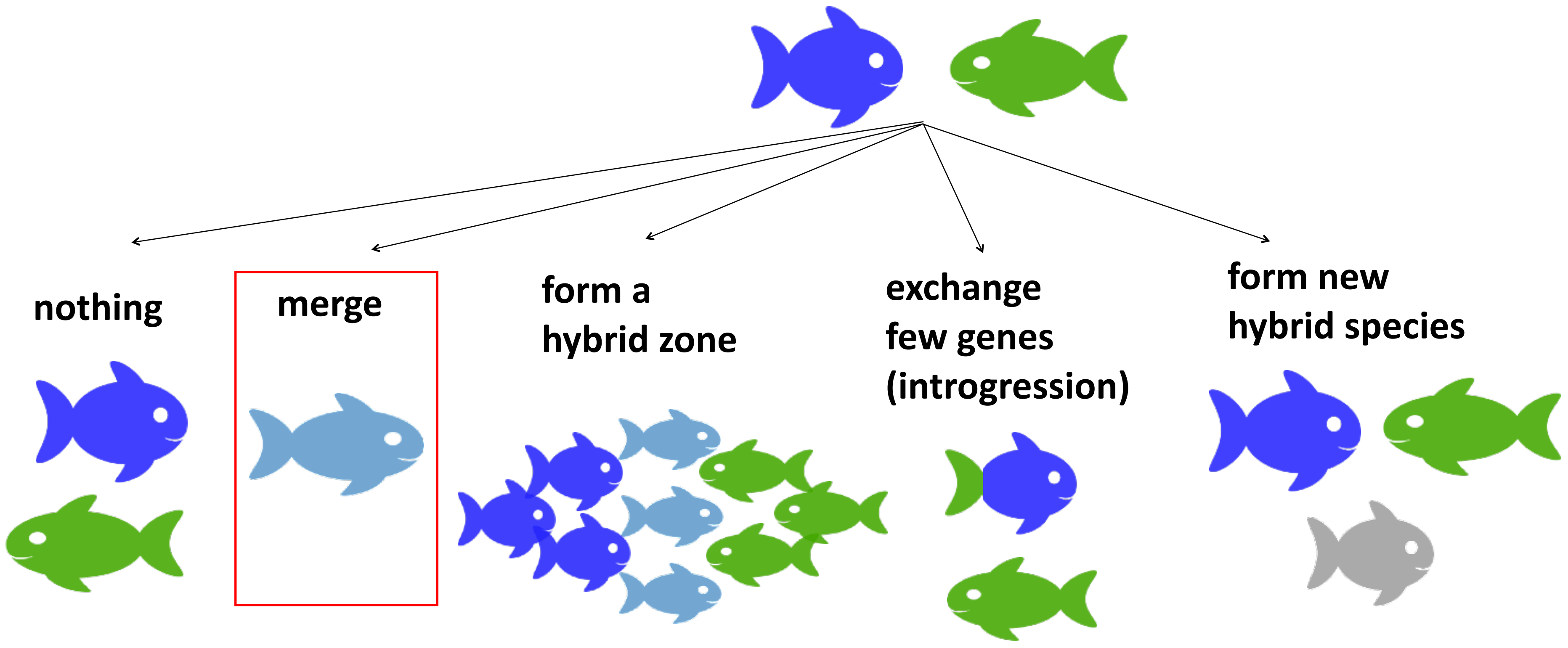


Only 1.5% of the phylogenies of different genomic windows show the species topology



Rosser & Seixas et al. 2024

Evolutionary consequences of hybridisation



nothing

merge

form a
hybrid zone

exchange
few genes
(introgression)

form new
hybrid species

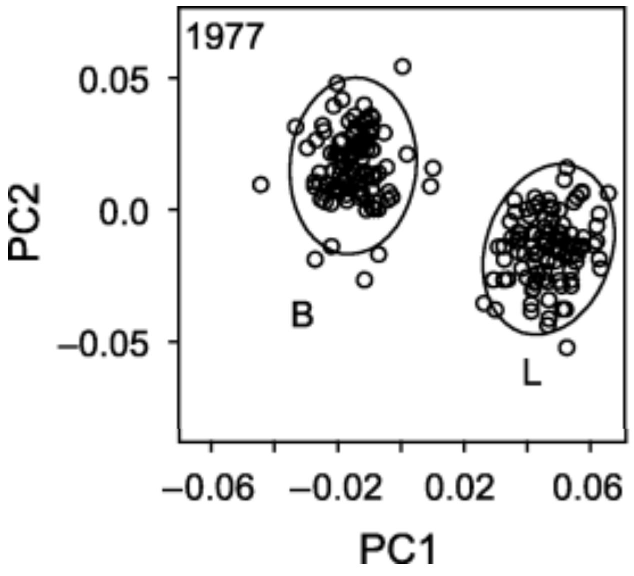
Local adaptation can be lost and species can fuse

Introduced mallards threaten local duck species through hybridisation

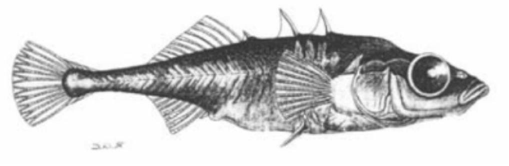
THE GLOBAL FERAL MALLARD THREAT

Worldwide, native ducks are vulnerable to invasion and hybridization with feral Mallards, particularly when already in jeopardy from habitat loss and introduced mammalian predators. The Mallard occurs naturally in the Northern Hemisphere, but because of its popularity, people have transported it to areas where it was not previously found. Mallard introductions have caused conflicts with native duck populations throughout the world. In New Zealand, descendants of game-farm Mallards, estimated to number 4 to 5 million, are responsible for the near extinction of the New Zealand Grey Duck. In South Africa, Mallards introduced by farmers and waterfowl collectors now threaten both the African Black Duck and Yellow-billed Duck.

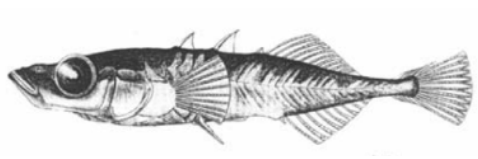
Stickleback despeciation / speciation reversal



benthic



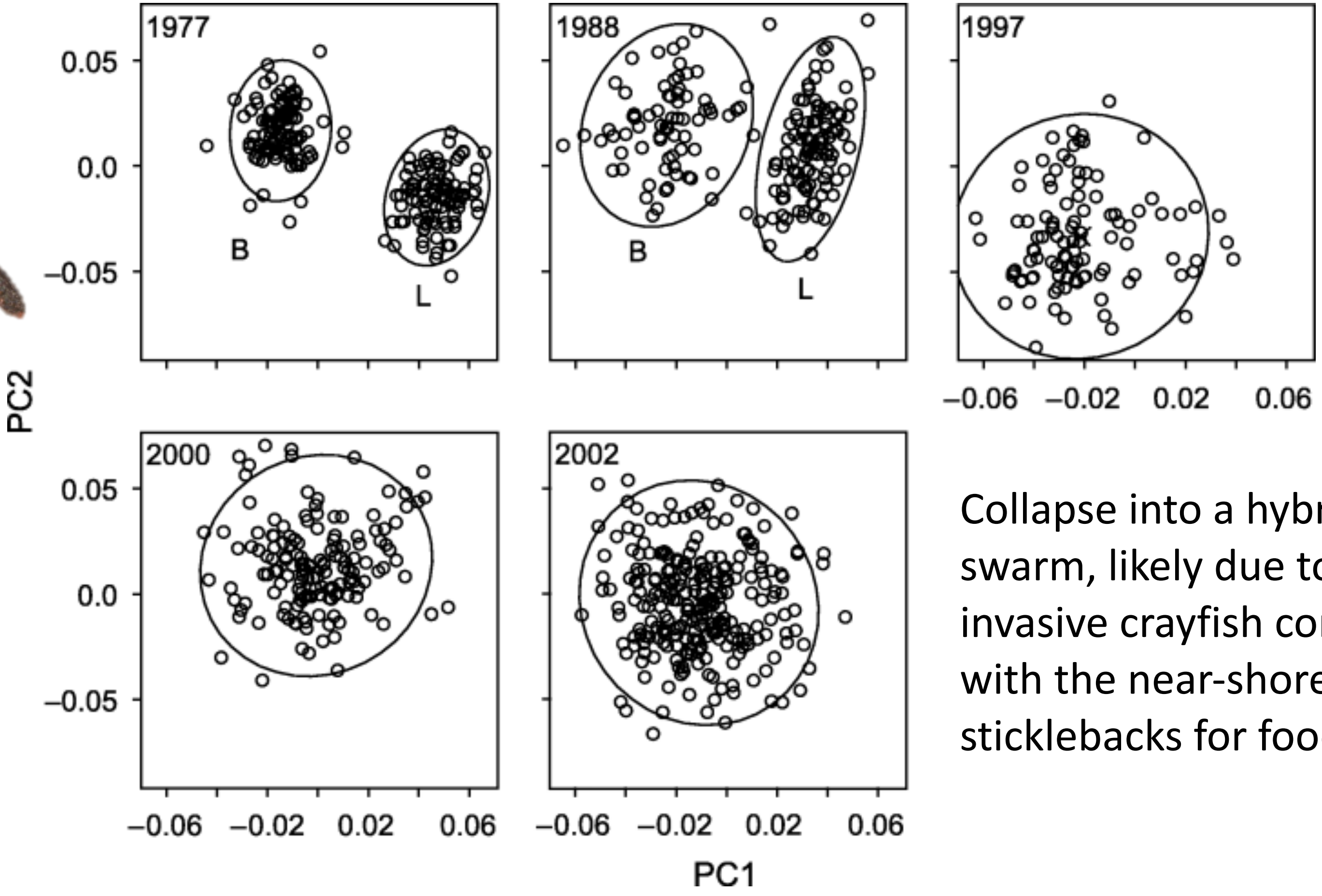
limnetic



Taylor et al. 2005

Stickleback despeciation / speciation reversal

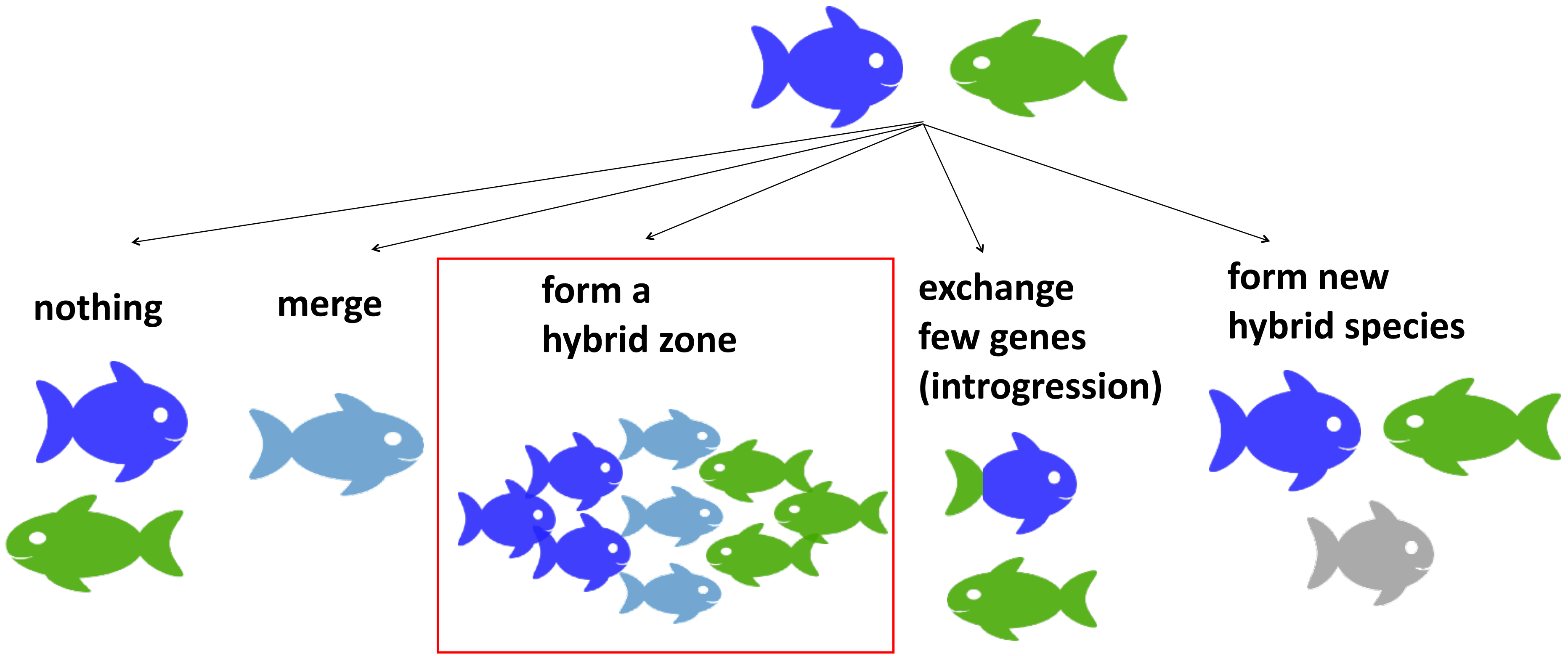
Morphological variation got more and more lost



Collapse into a hybrid swarm, likely due to the invasive crayfish competing with the near-shore sticklebacks for food.

Taylor et al. 2005

Evolutionary consequences of hybridisation



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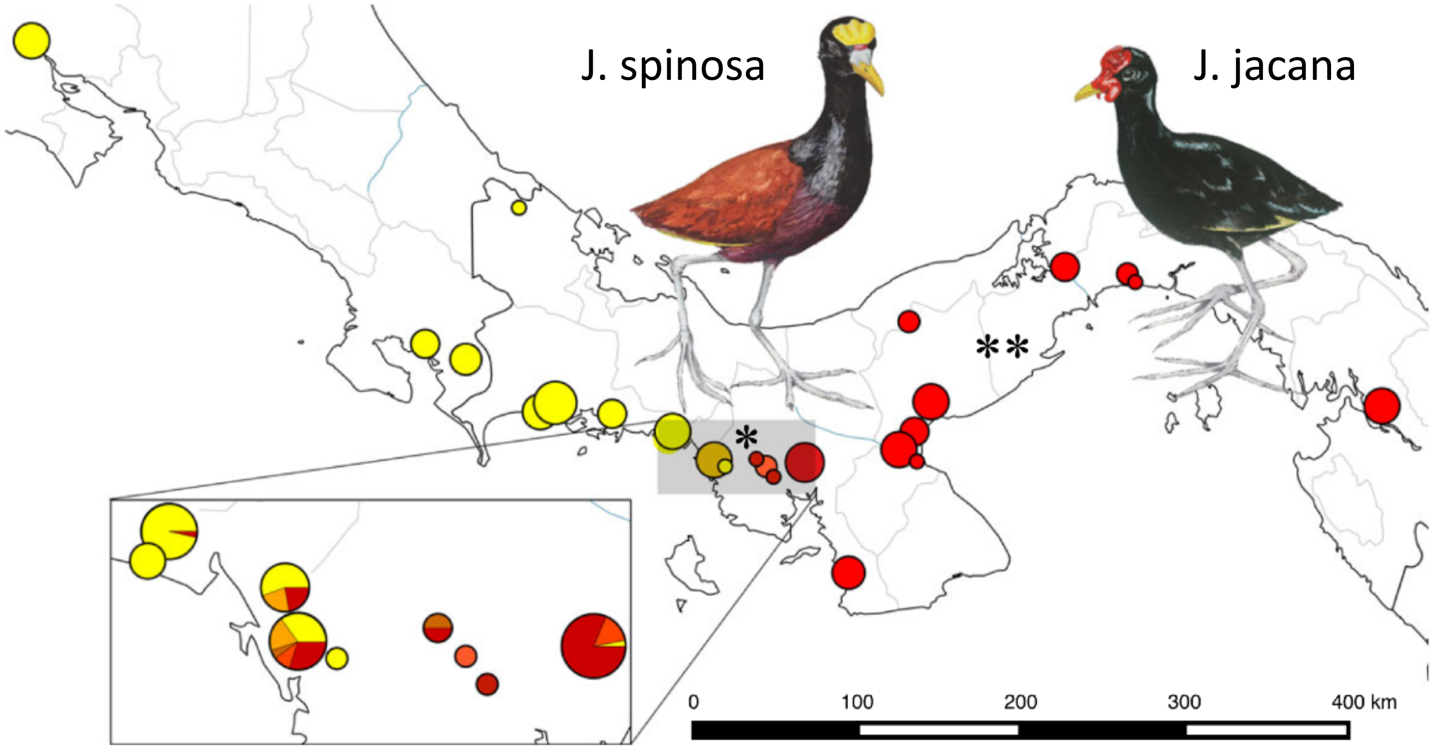
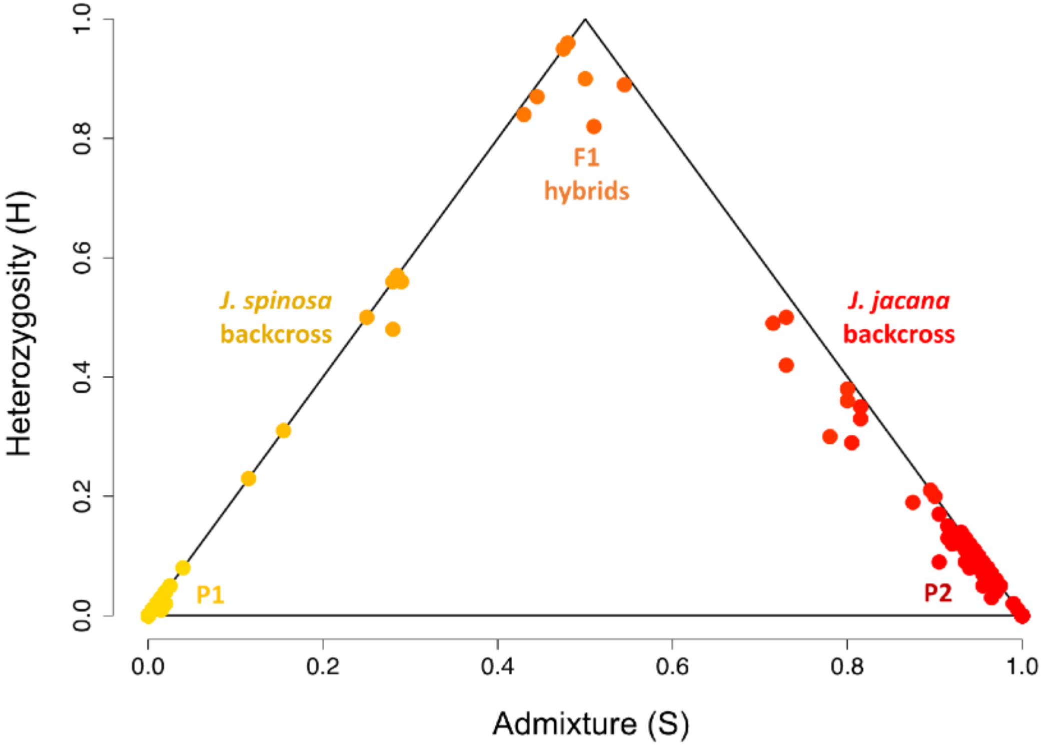
Jacana hybrid zone in Panama

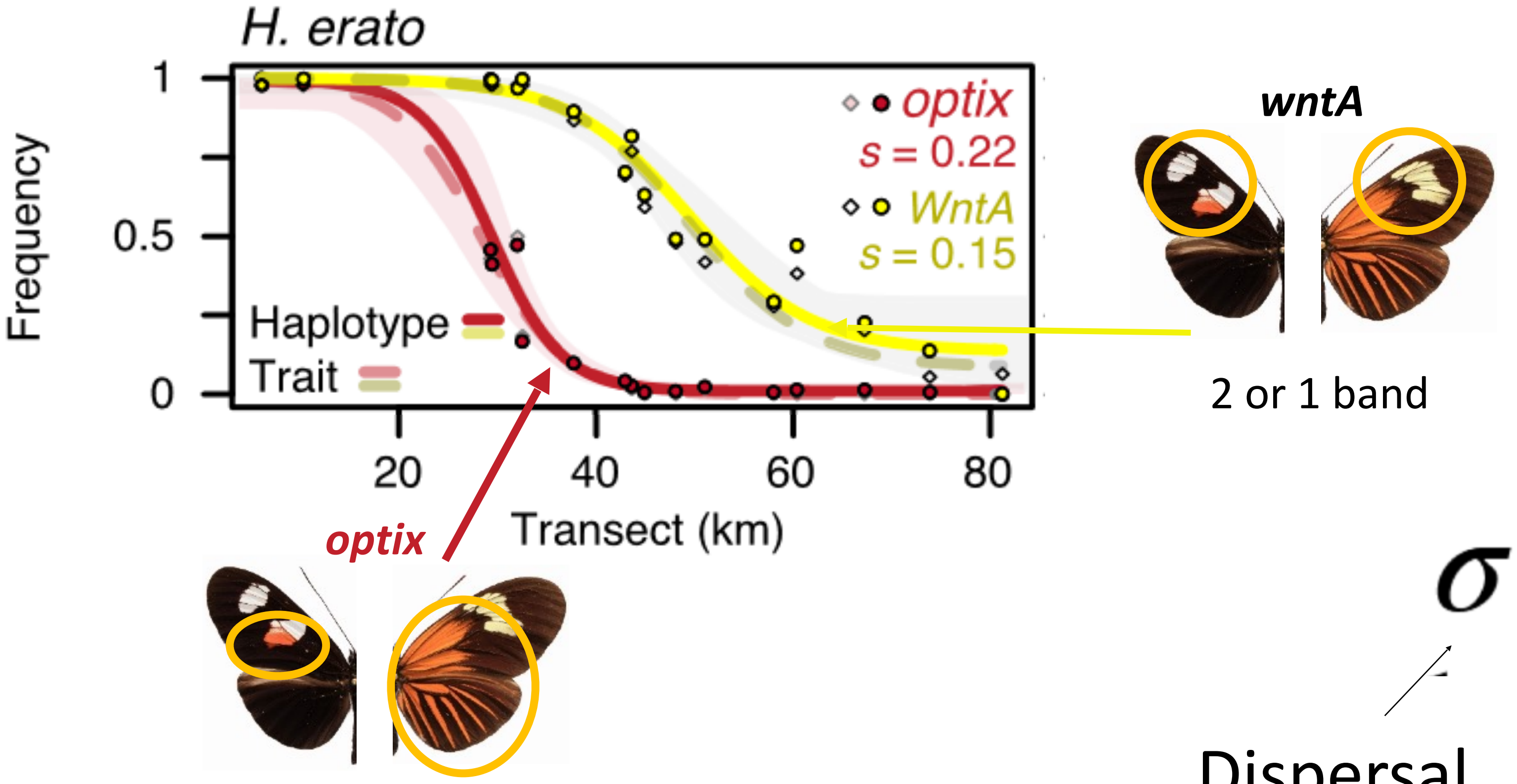


Triangle plot shows
assymmetric introgression



Lipshutz et al. 2019

Hybrid zones allow us to test for barriers to reproductive isolation and estimate selection



2 or 1 band

red patterns

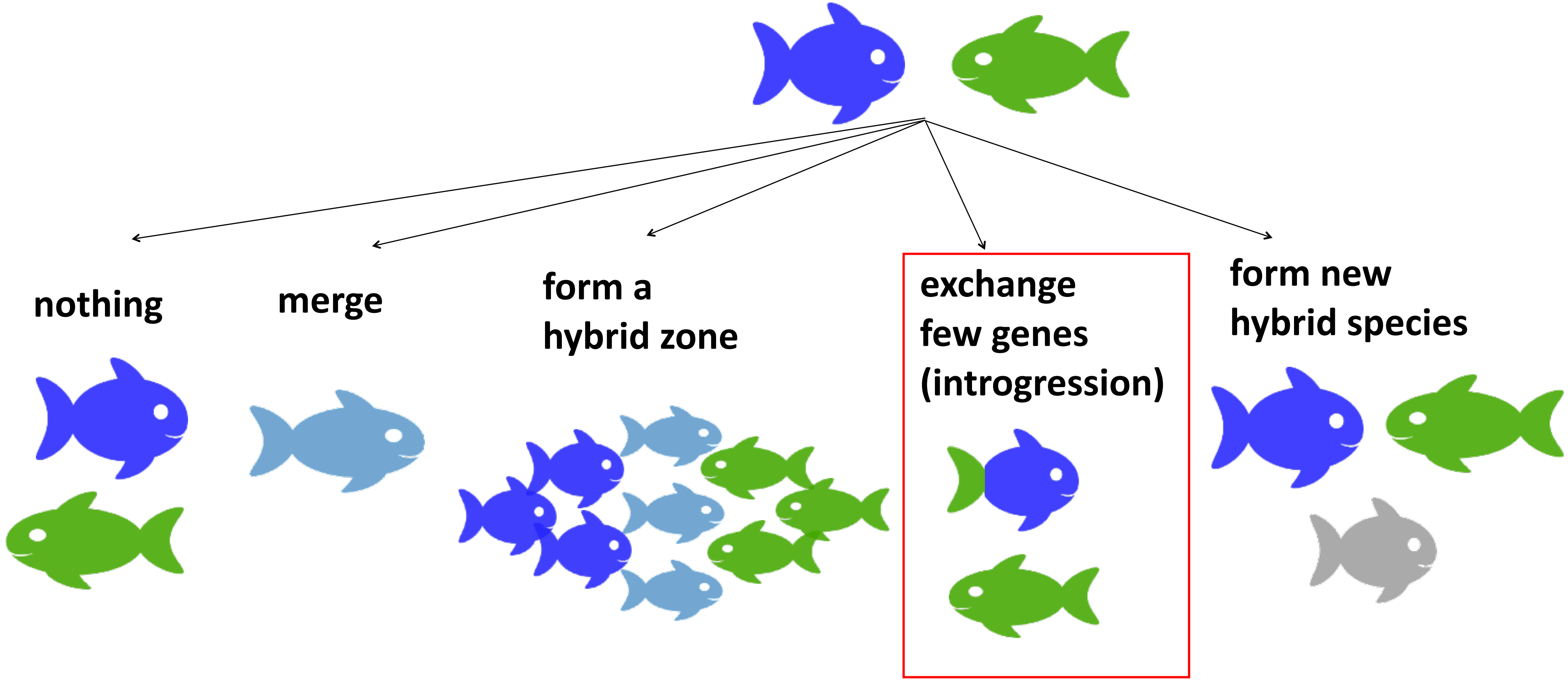
$$\sigma \sim w\sqrt{s/12}$$

Dispersal rate

Cline width

Selection coefficient

Evolutionary consequences of hybridisation



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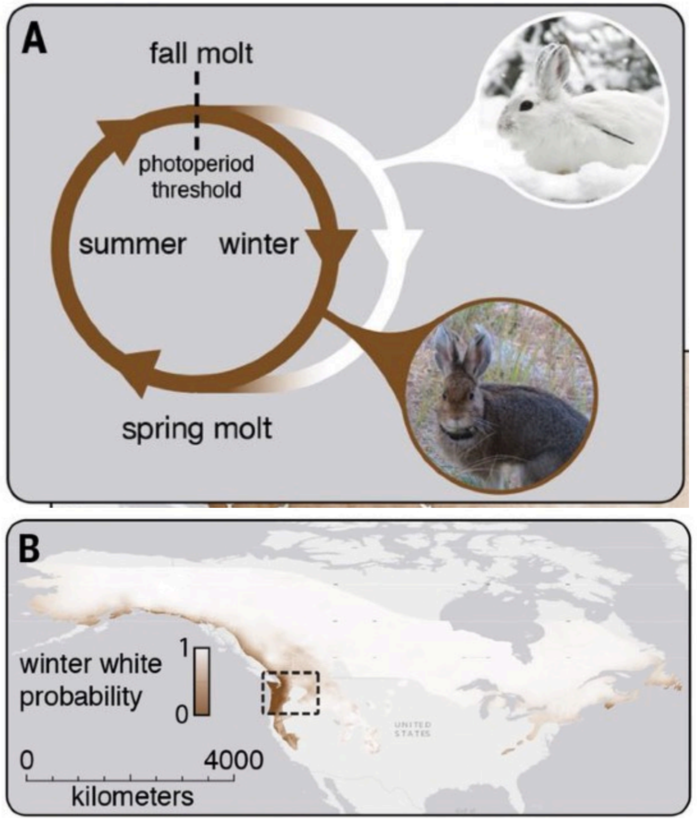
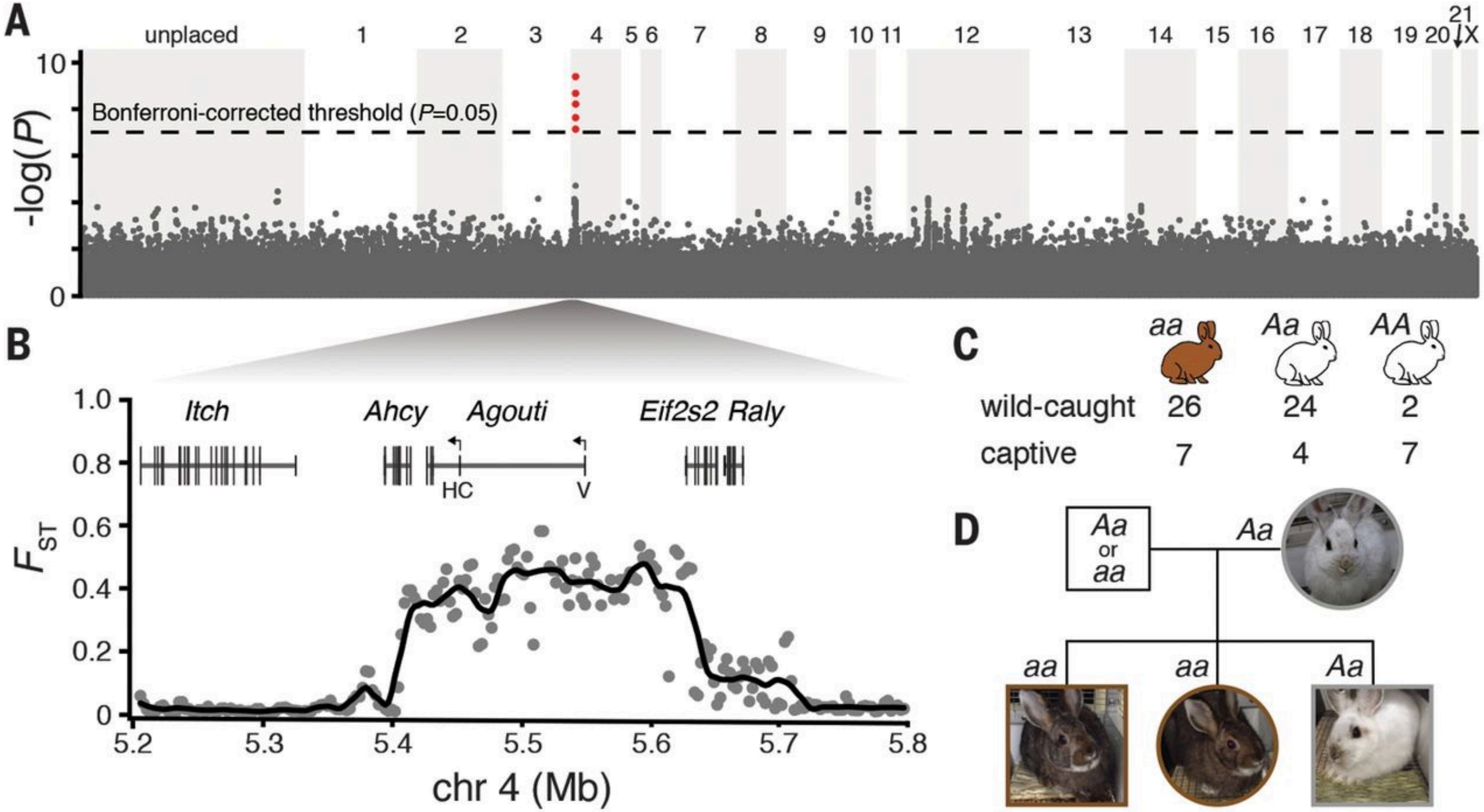
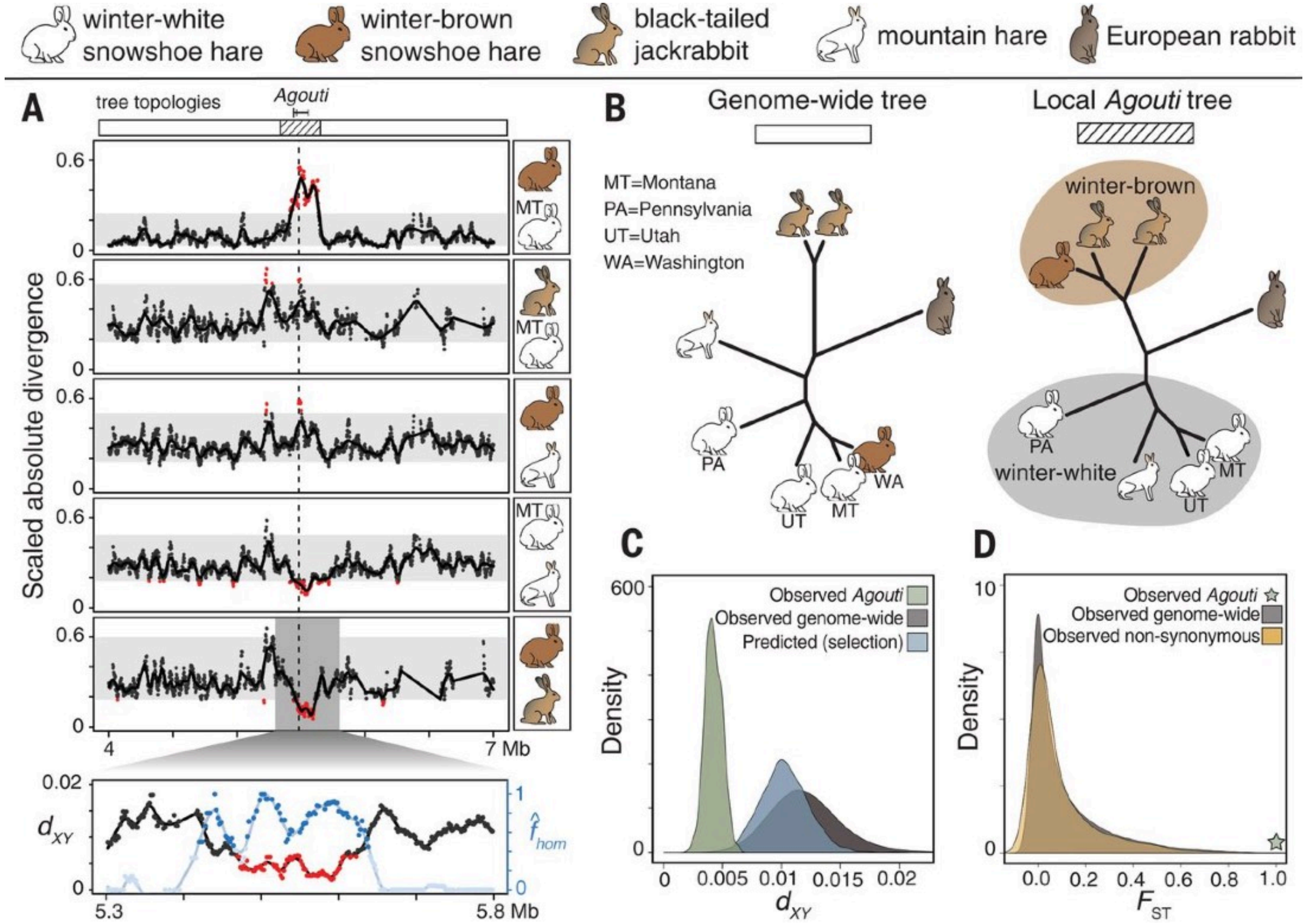
Example of adaptation to climate change: Adaptive introgression in snowshoe hares





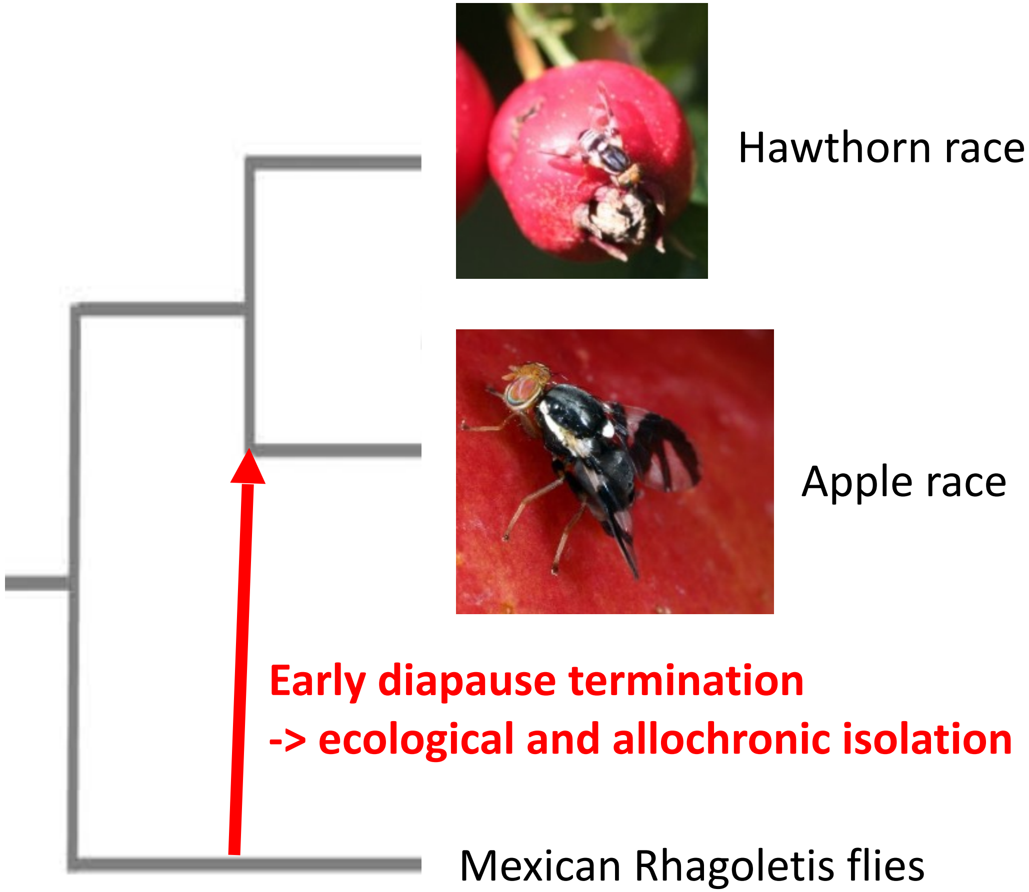
Jones et al. 2018

Example of adaptation to climate change: Adaptive introgression in snowshoe hares



Jones et al. 2018

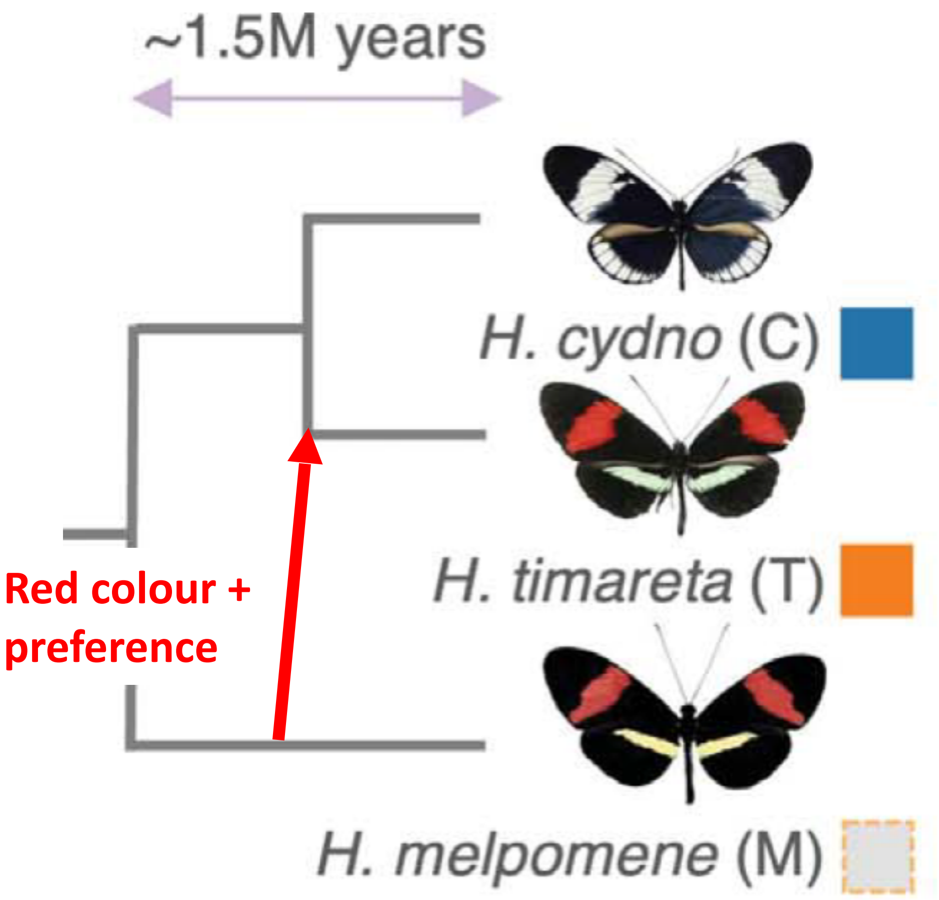
Introgression of key traits contributes to speciation


Hawthorn race

Apple race

Mexican Rhagoletis flies

Early diapause termination
-> ecological and allochronic isolation

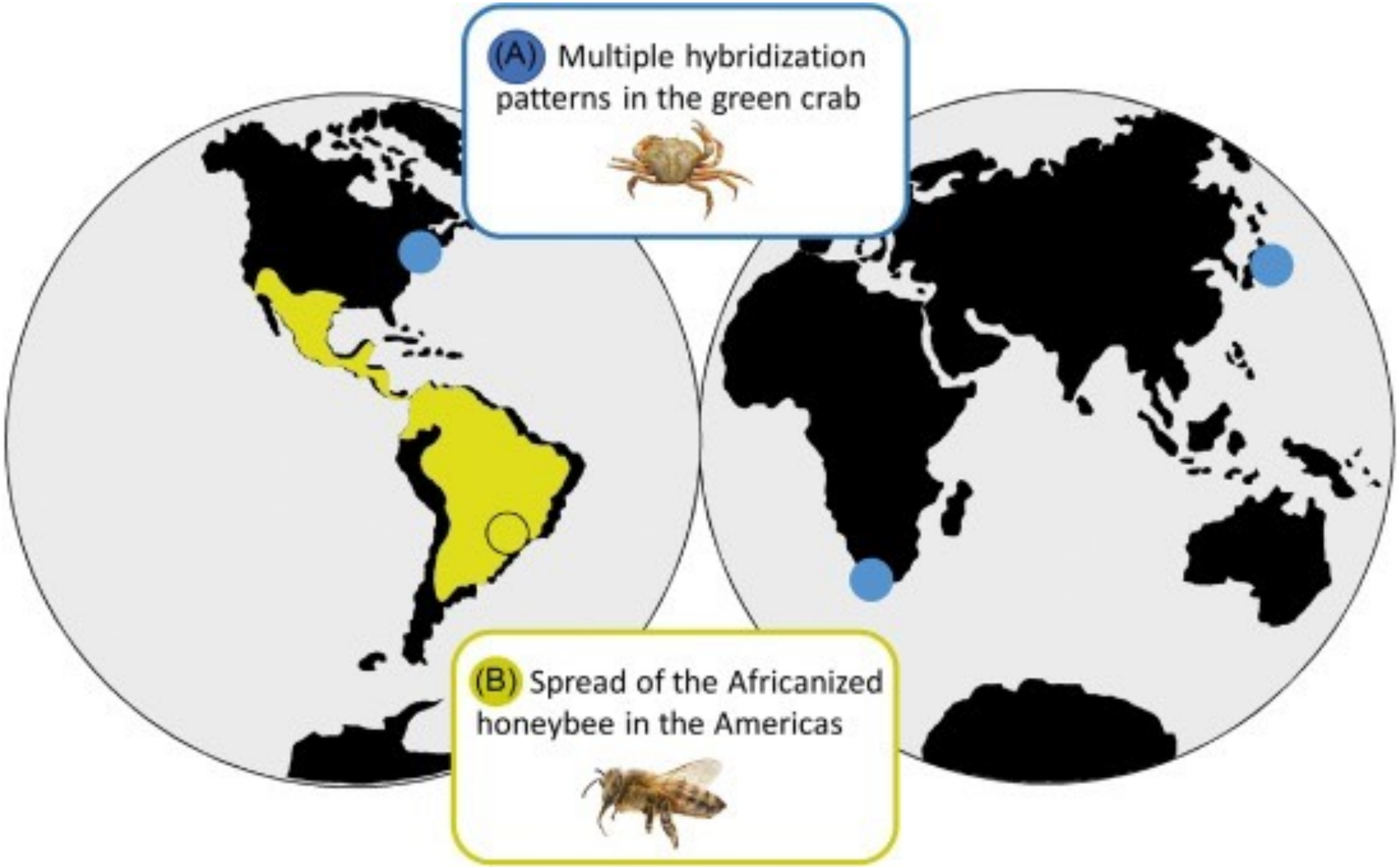


Red colour +
preference

Feder et a. 2003 PNAS; Xie et al 2008 JEB

Rossi et al. 2024 Science

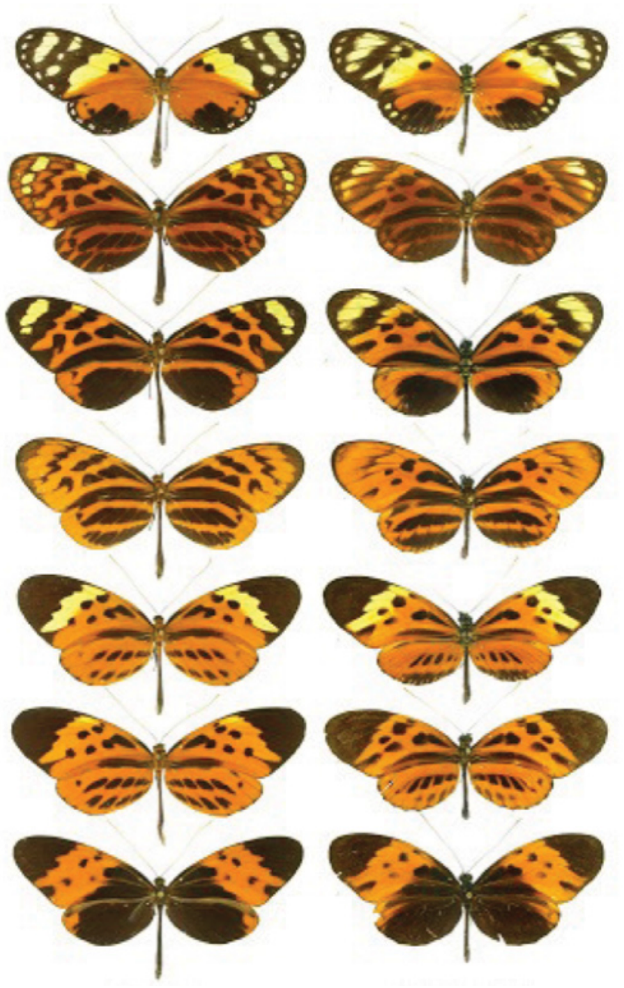
Hybridisation can facilitate invasiveness



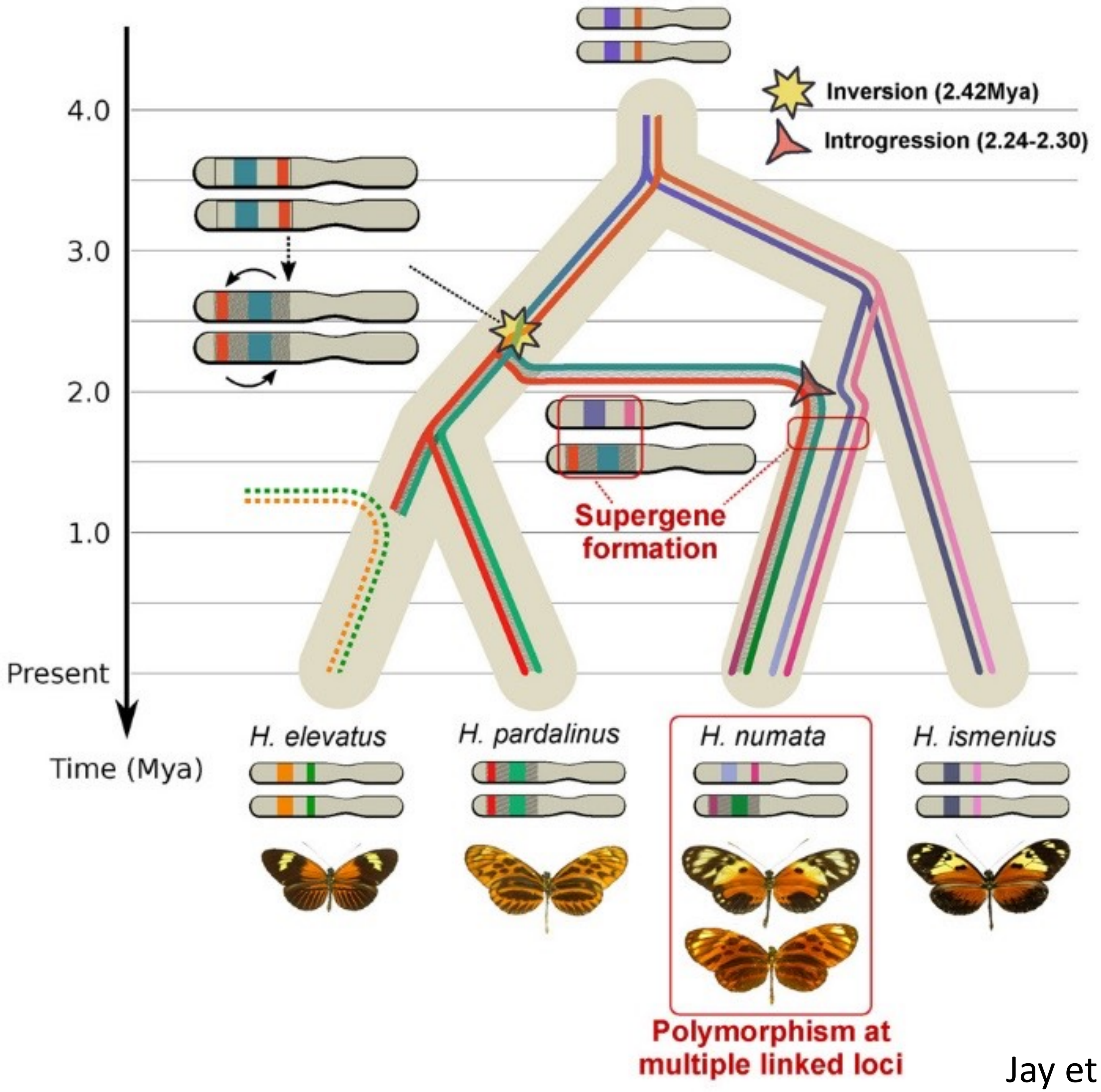
Trends in Ecology & Evolution

Porretta & Canestrelli, 2023

Supergene formation through introgression

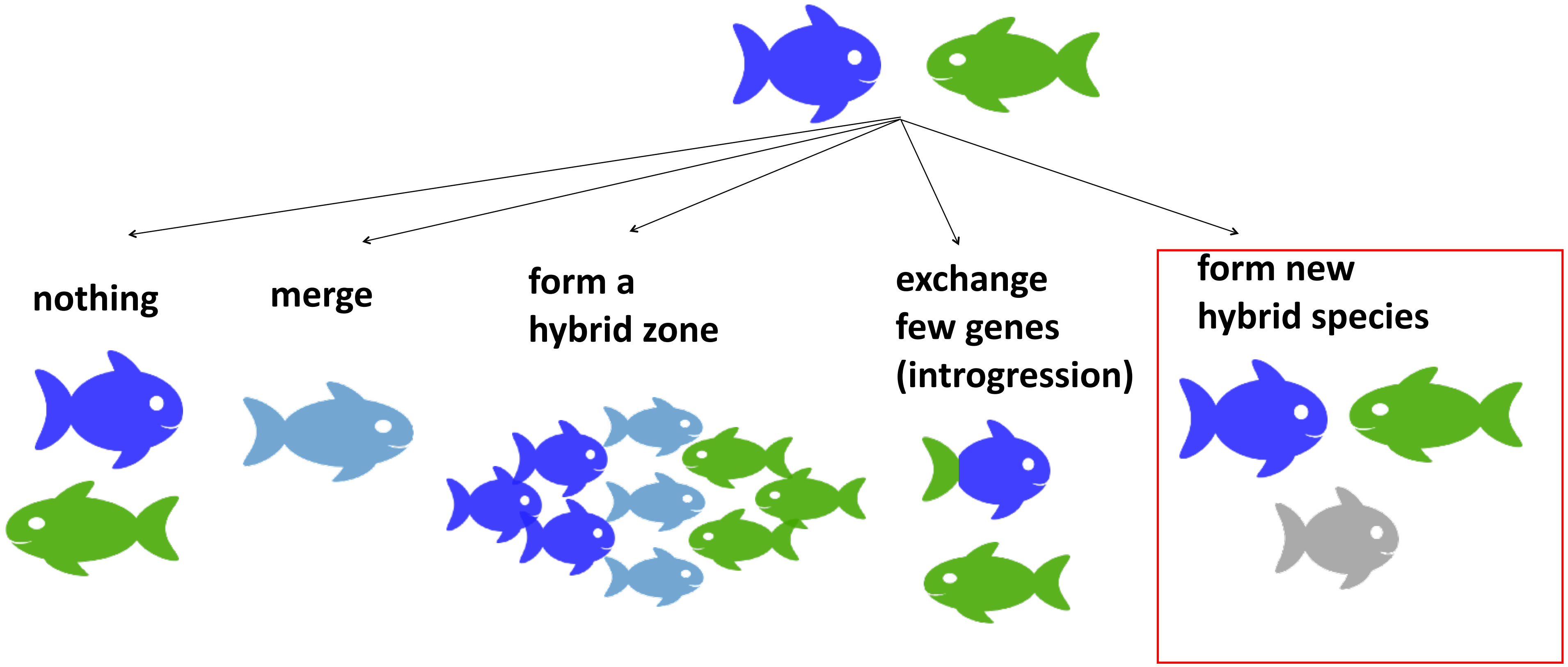


Melinaea species *Heliconius numata*



Jay et al. 2018

Evolutionary consequences of hybridisation



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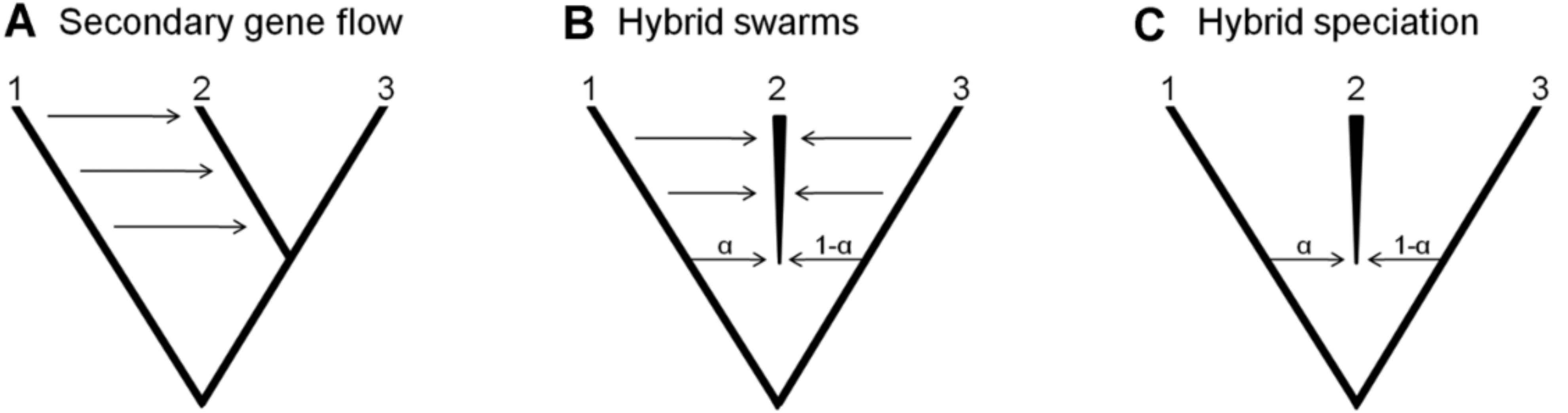
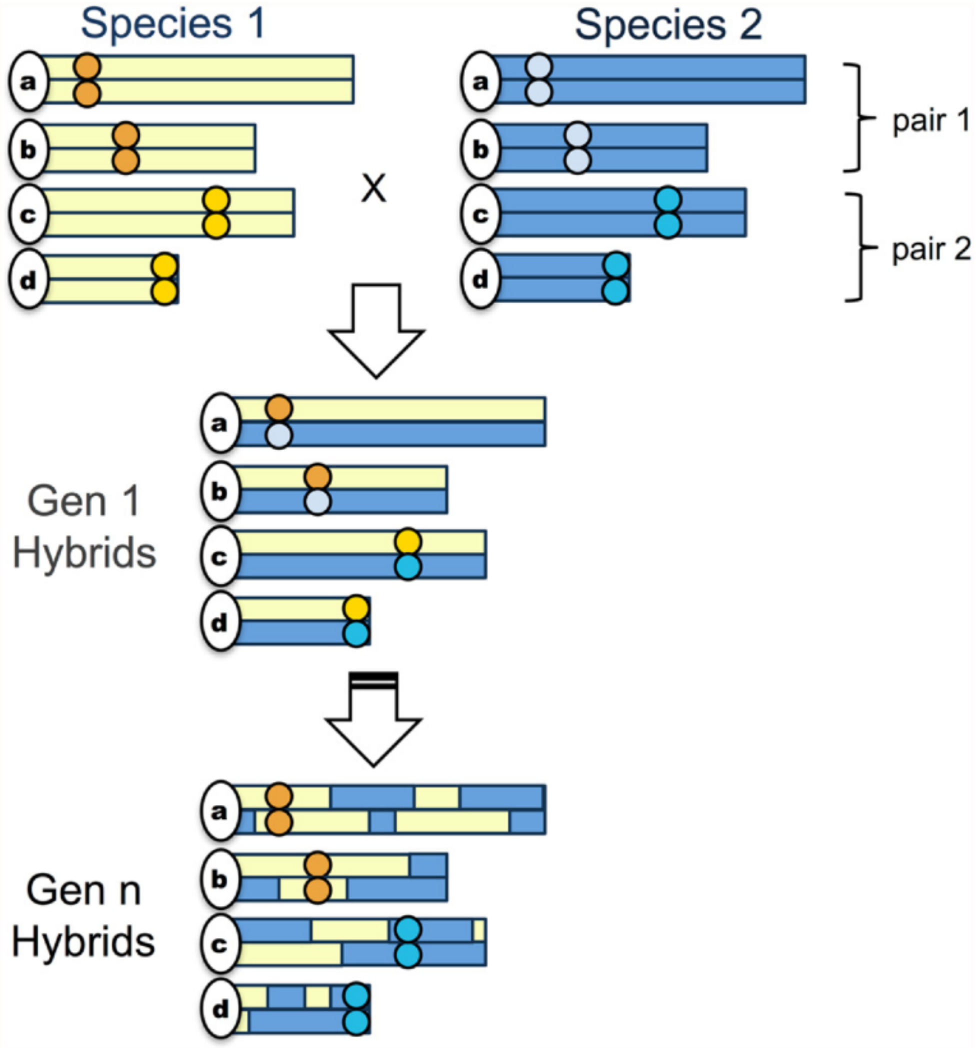
Homoploid hybrid speciation

- Hybridisation must precede speciation
- Hybrid species must be reproductively isolated from both parental lineages
- Hybridisation must be causal for reproductive isolation



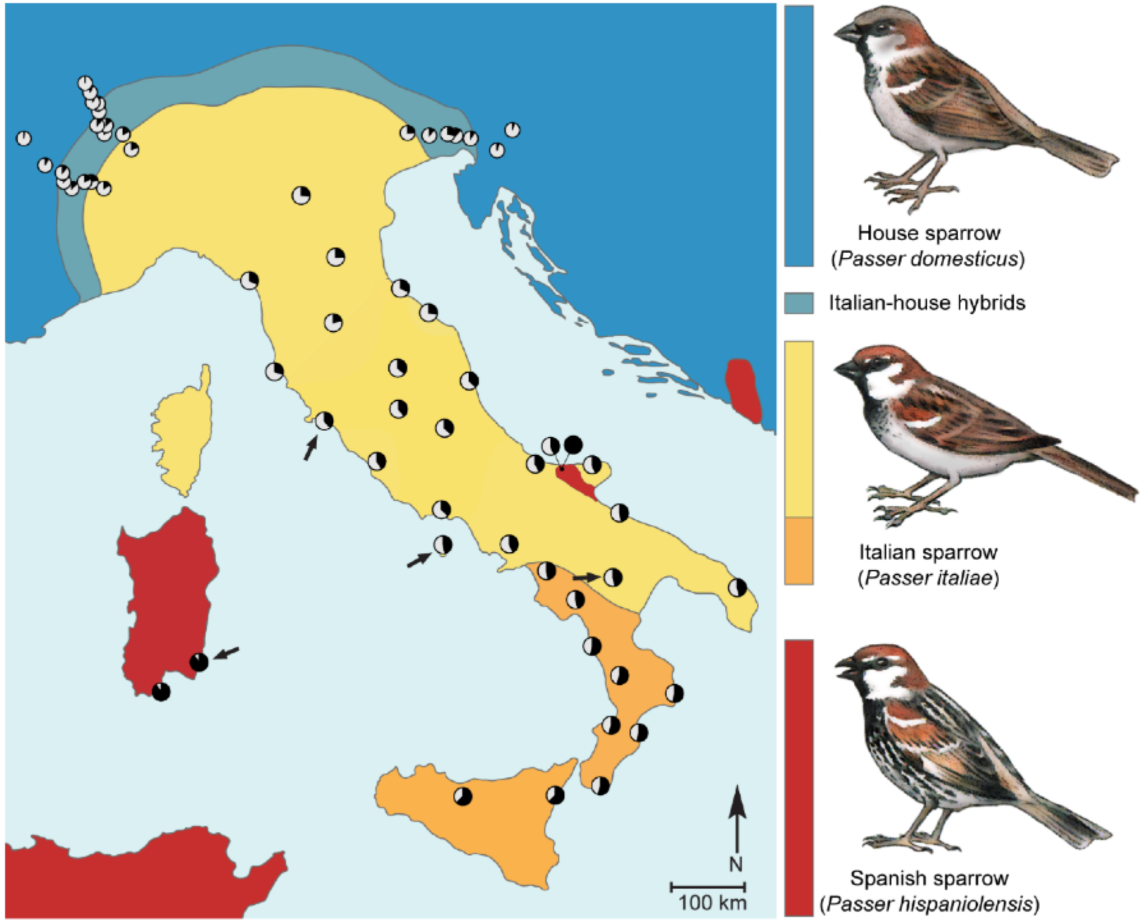
Schumer et al. 2014

Sorting of incompatibilites



Schumer et al. 2015

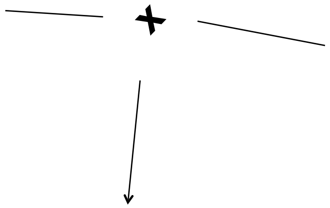
Italian sparrow: Putative hybrid species



Hermansen et al. 2014

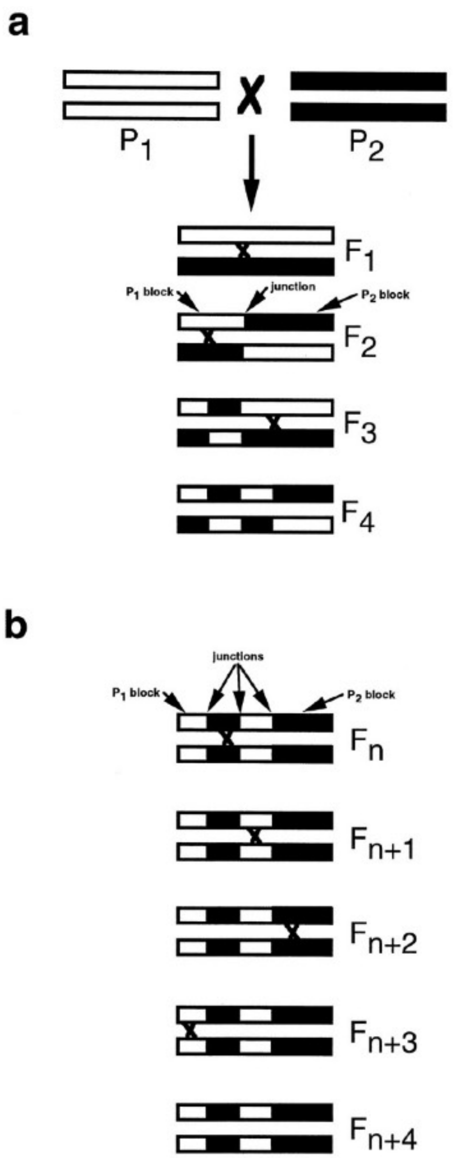
Hybrid sunflower species: homoploid hybrids

H. annuus



H. petiolaris

H. anomalus



Ungerer et al. 1998 PNAS

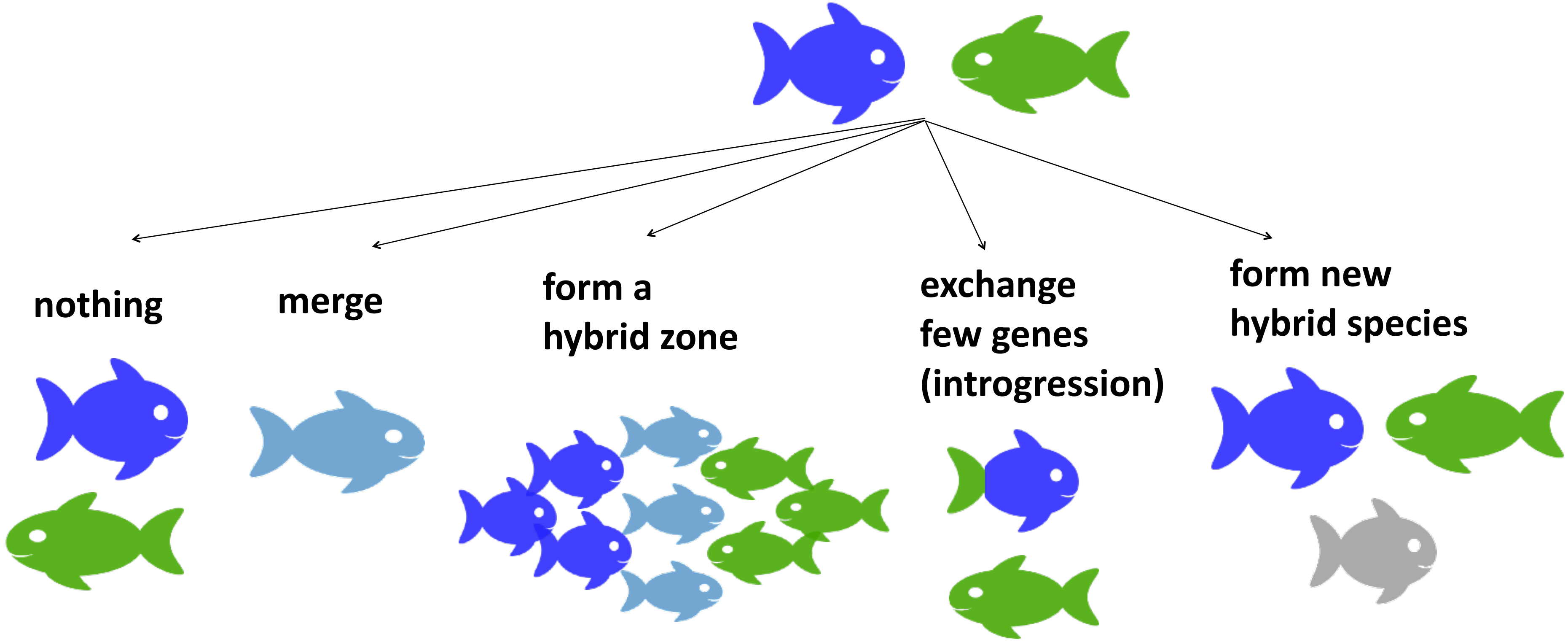
Allopolyploid hybrid species

Selection by Zohaid ul Hassan

Old genetic variants, often derived from hybridisation, contributed to fast speciation and adaptation

Marques*, Meier*, Seehausen, 2019, TREE

What determines the evolutionary consequences?



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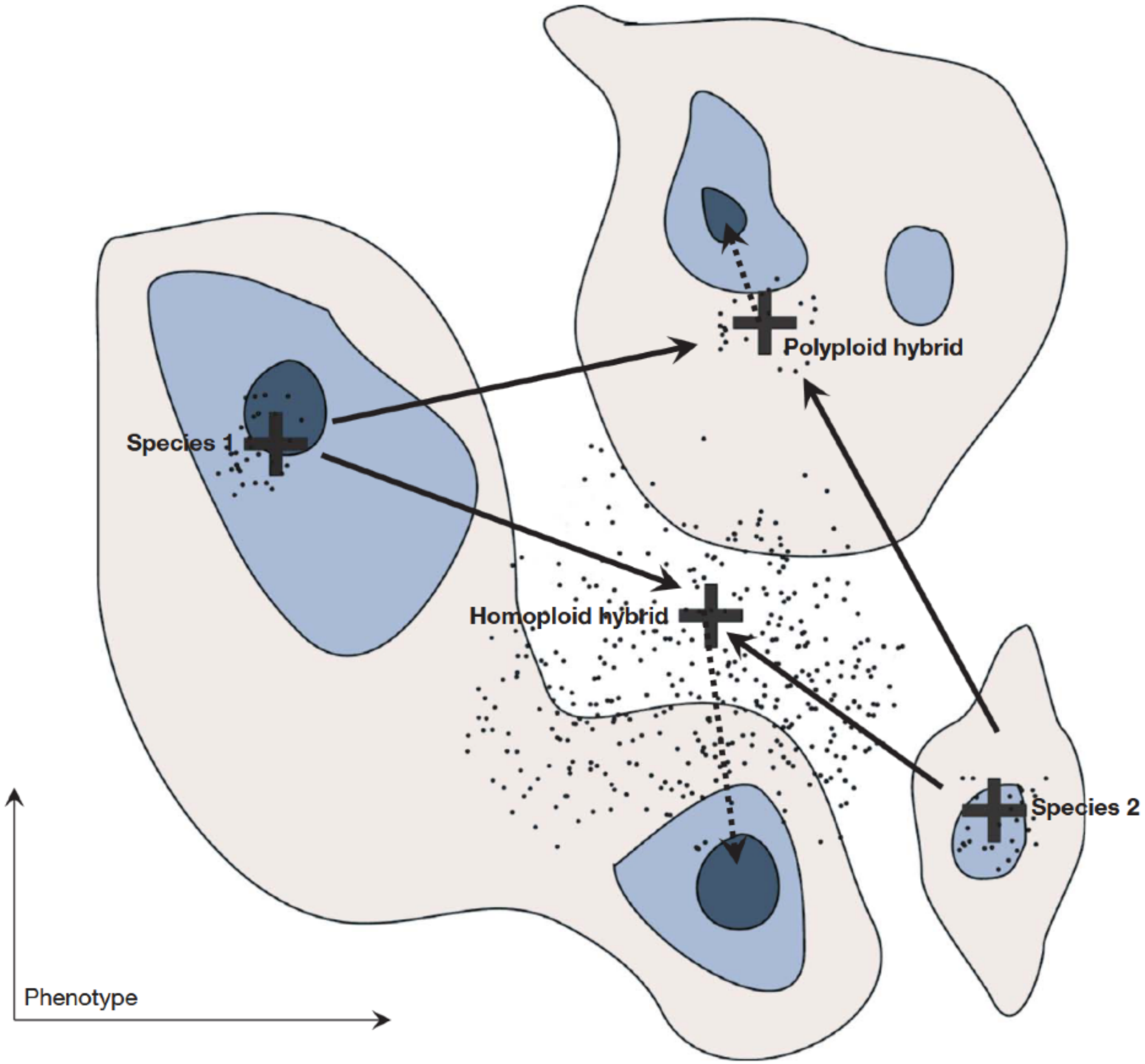
Fitness of hybrids is key



Hybrid speciation Fitness optima (‘adaptive peaks’) are coloured blue. Adaptive landscapes are not rigid, but are readily distorted by environmental or biotic changes, including evolutionary change. Mean phenotypes of species and their hybrids are shown as crosses, and offspring distributions as dots.

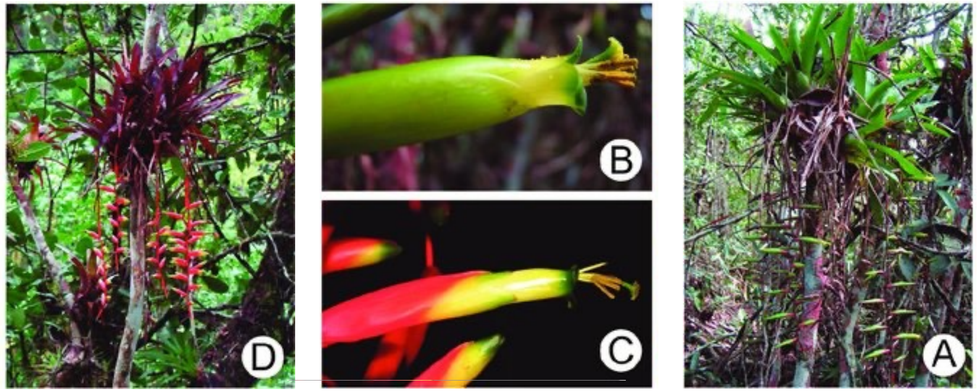
Mallet, 2007

The time scale matters

- Methods that only work with recent/ongoing hybridisation:
  - Hybrid zone study: cline analyses
  - Triangle plot
  - Clustering methods such as ADMIXTURE or STRUCTURE
  - FST and DXY to infer regions with low gene flow as barriers to reproduction
  - Haplotype assignment

- Methods that also work with ancient hybridisation:
  - Demographic modeling (e.g. Fastsimcoal, gIMble)
  - Phylogeny-based methods such as D statistics
  - TWISST (Martin et al. 2019)
  - MSCi (multispecies coalescent-with-introgression, in BPP: Flouri et al. 2020)
  - QuIBL (Edelman et al. 2019)
  - Network methods such as Phylonet, AIM, GPhoCS

Hybrid zones: Clustering methods to identify hybrids and infer ancestry proportions: Bromeliads

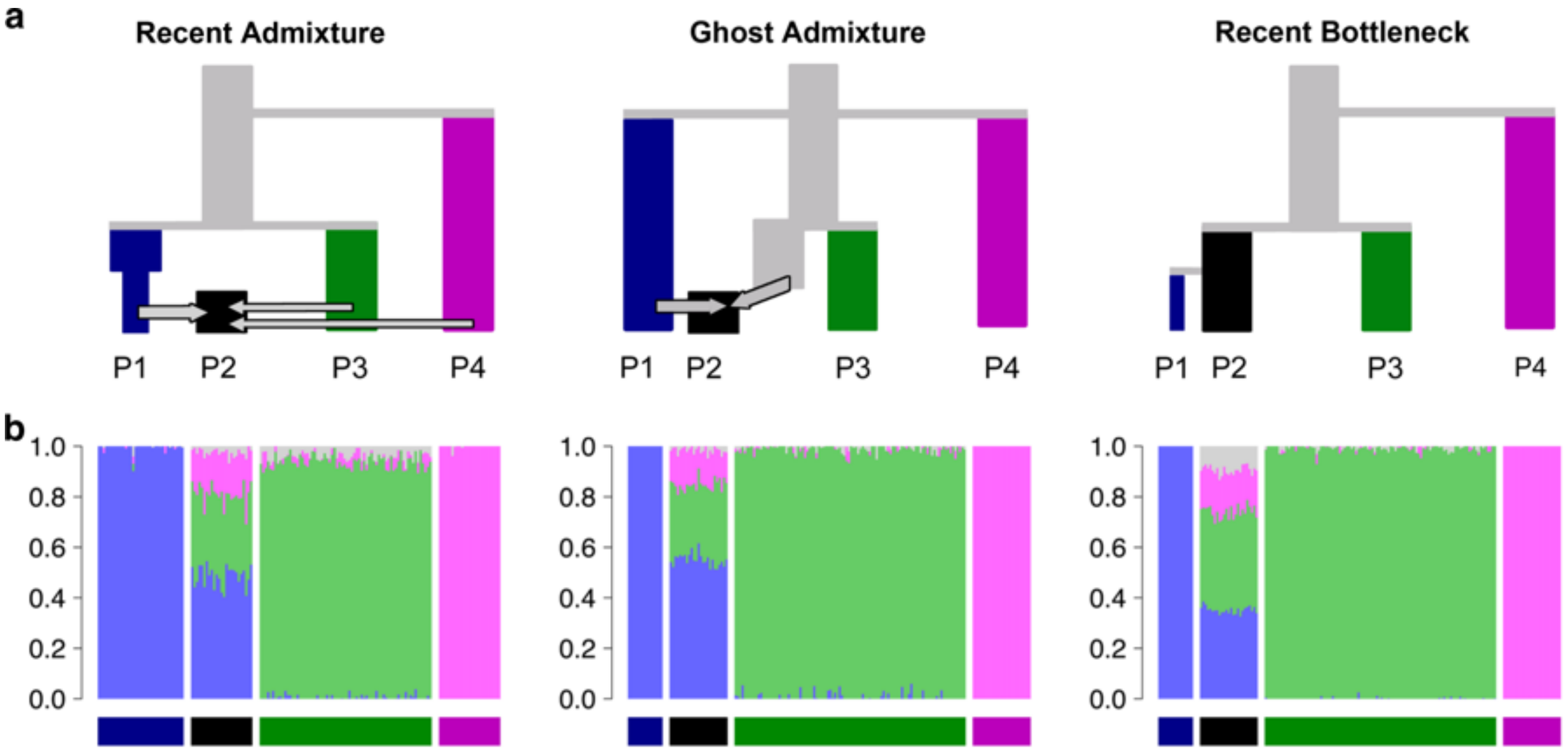


Vriesia simplex

Vriesia scalaris

Neri, et al., AoB Plants

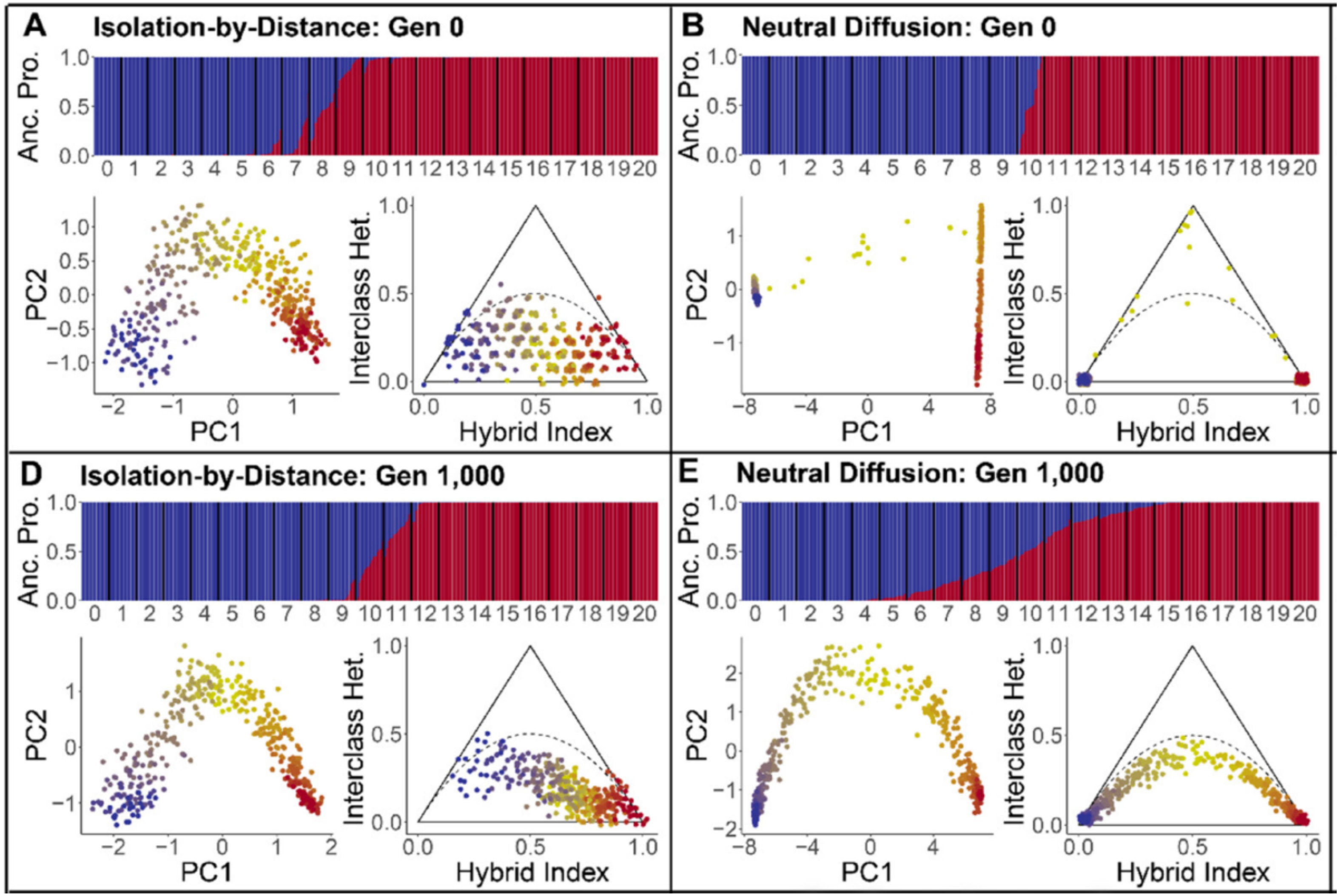
Very different evolutionary histories can give the same ADMIXTURE plot -> badMixture



Very important: Use STRUCTURE/ADMIXTURE plots only to get a first overview of genetic structure. Putative cases of hybridization need to be followed up with other analyses such as D statistics and/or demographic modeling.

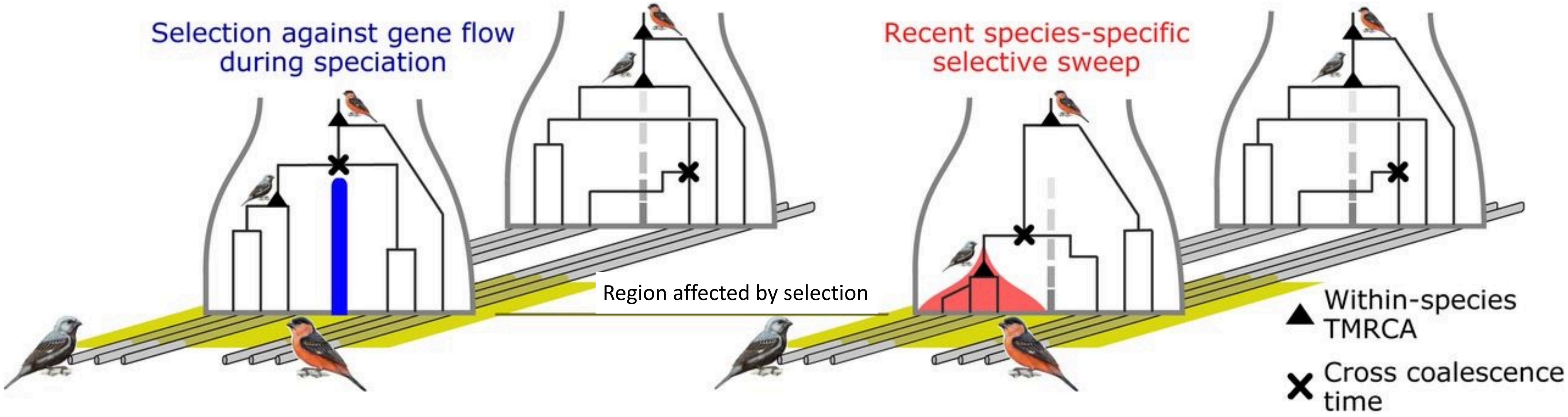
Lawson et al., 2018, NatComm

Isolation by distance can mimic hybridisation in STUCTURE plots -> use triangle plots



Wiens & Colella, 2024

Gene flow creates gene tree – species tree discordance

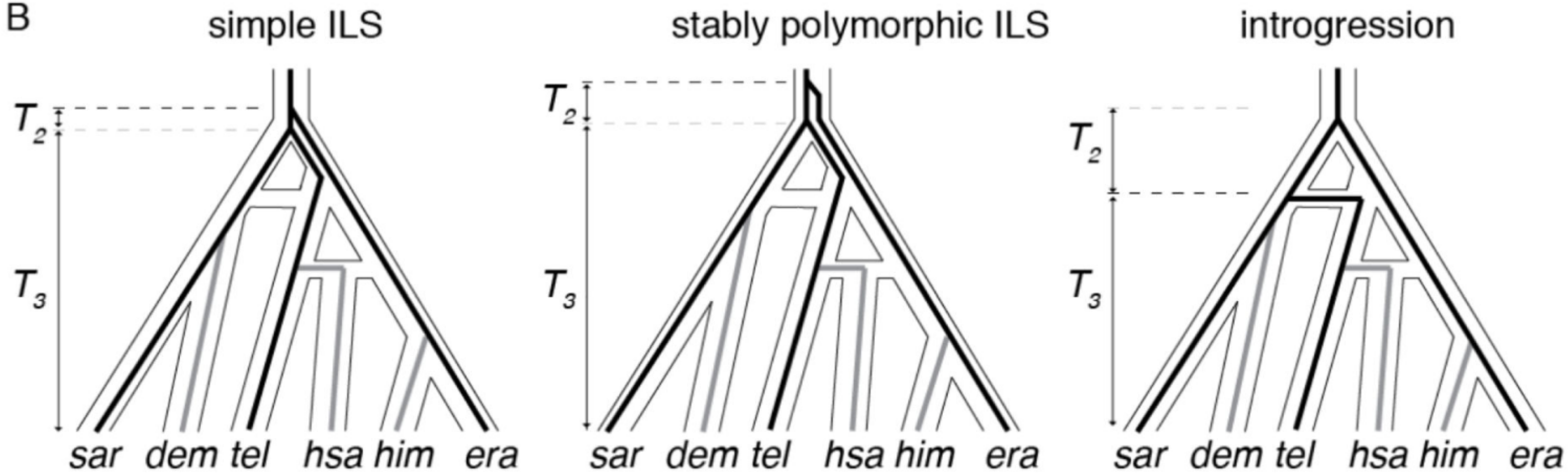


Genomic regions with selection against gene flow or recent selective sweeps show less ILS
-> Selection can affects levels of ILS

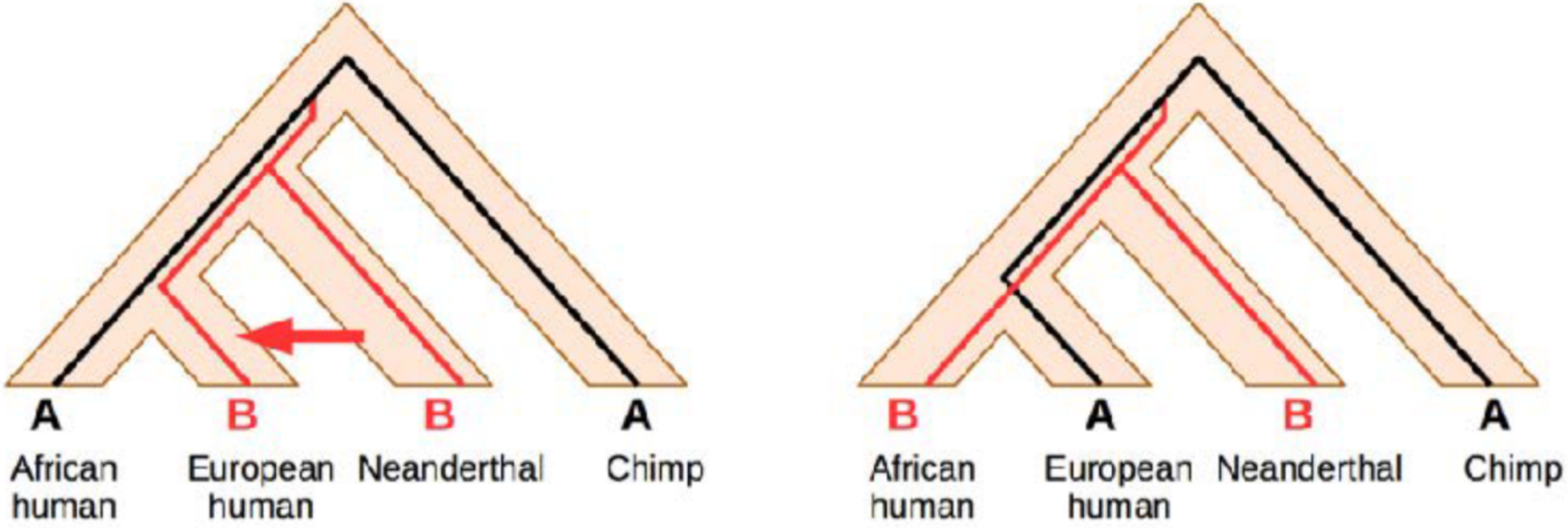
Hejase et al., 2020, PNAS

Methods that use branch lengths

e.g. QuIBL (Edelman et al. 2019)



Patterson’s D statistics to identify hybridisation

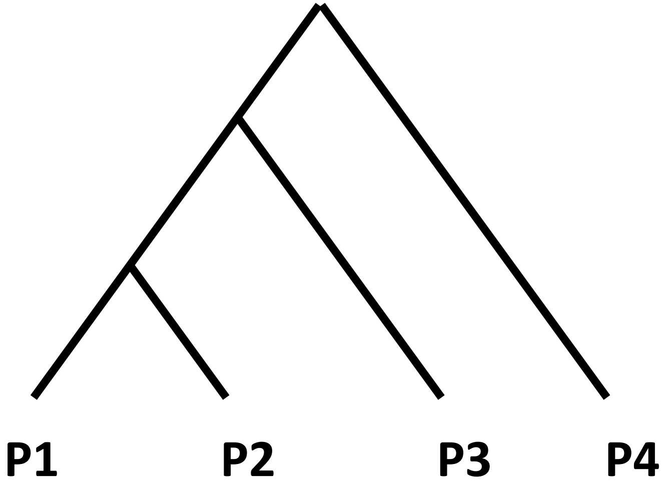


$$D(P_1, P_2, P_3, O) = \frac{\sum C_{ABBA}(i) - C_{BABA}(i)}{\sum C_{ABBA}(i) + C_{BABA}(i)} \qquad (1)$$

Green et al. 2010

Patterson’s D statistics to identify hybridisation

- Also called ABBA-BABA test: D=(ABBA-BABA)/(BABA+ABBA)

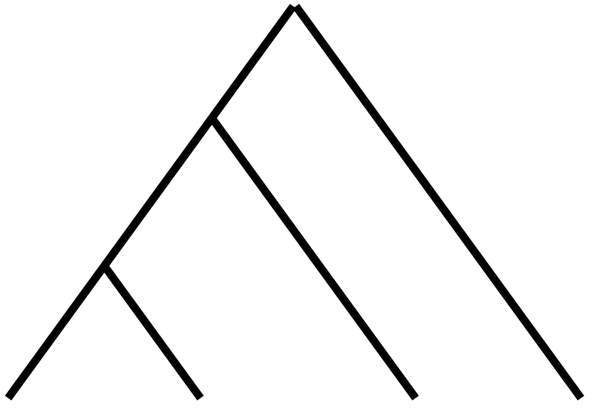


$$D = \frac{ABBA - BABA}{ABBA + BABA}$$

Pos 1	**T**	**T**	A	A	Concordant SNPs
Pos 20	**G**	**G**	**G**	T	
Pos 23	**C**	T	T	T	
Pos 35	**C**	A	**C**	A	Discordant SNPs
Pos 41	A	**T**	**T**	A	

Patterson’s D statistics to identify hybridisation

- Also called ABBA-BABA test: D=(ABBA-BABA)/(BABA+ABBA)



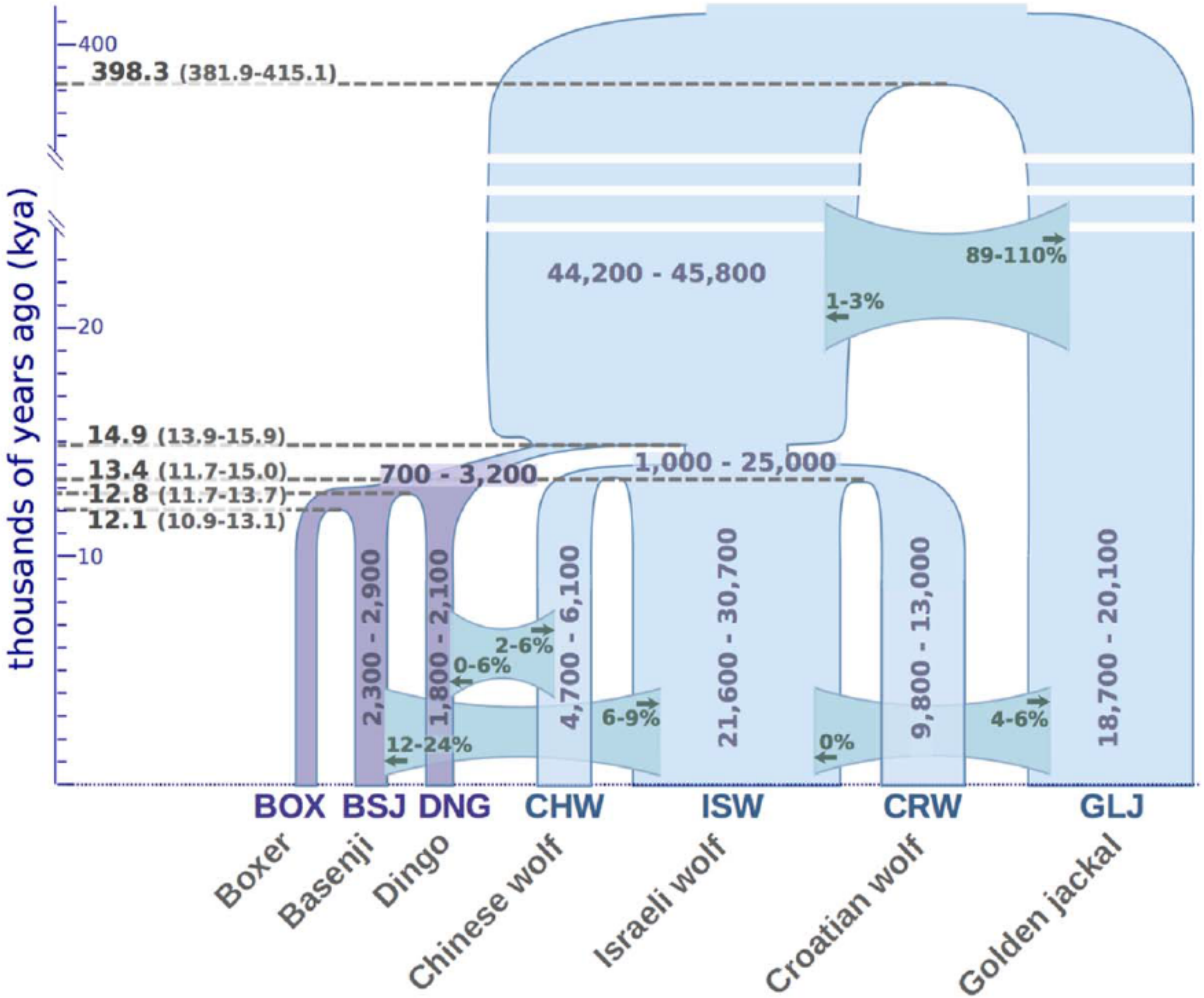
$$D = \frac{ABBA - BABA}{ABBA + BABA}$$

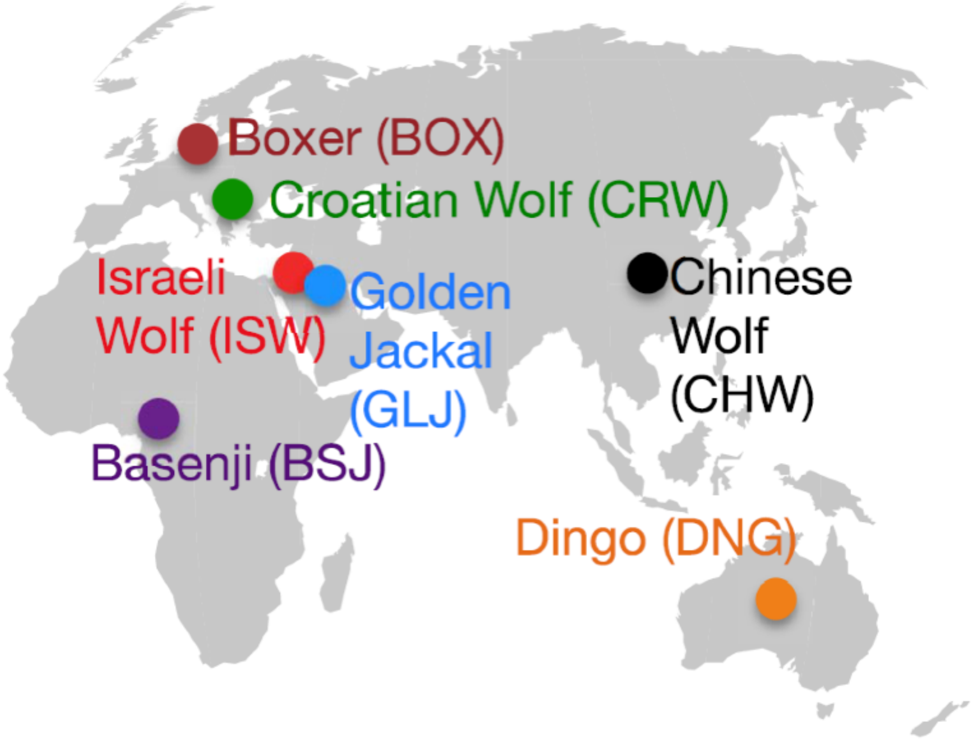
	P1	**P2**	**P3**	**P4**	
Pos 1	**T**	**T**	A	A	Concordant SNPs
Pos 20	**G**	**G**	**G**	T	
Pos 23	**C**	T	T	T	
Pos 35	**C**	A	**C**	A	← BABA
Pos 41	A	**T**	**T**	A	← ABBA
Pos 44	C	**G**	**G**	C	← ABBA

$$D = \frac{2-1}{2+1} =$$

1/3

Network methods, e.g. GPhoCS





Freedman et al., 2014, PLoS Genetics

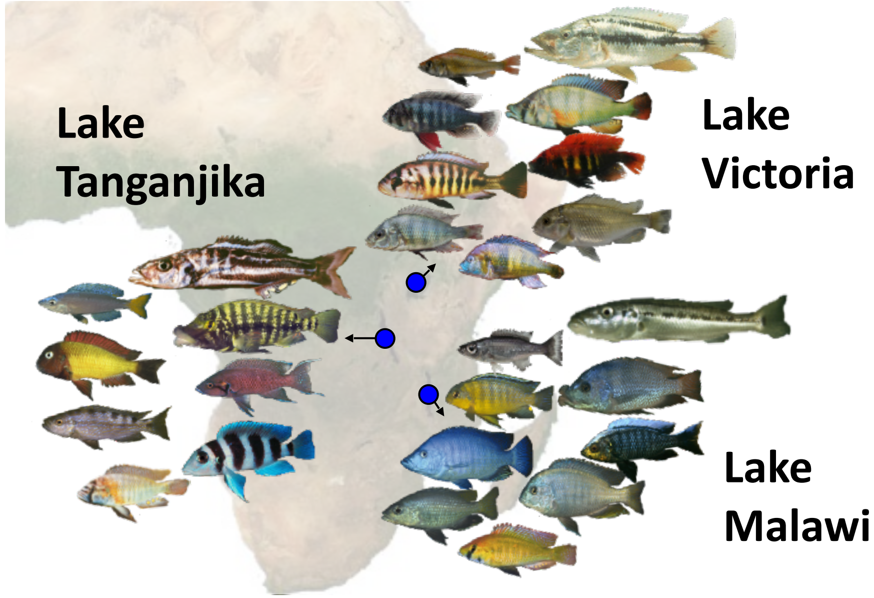
Examples from my work

Some lineages diversify again and again

***Anolis* lizards on the Caribbean islands and the mainland**

Huie et al., 2021

Cichlid fishes in East Africa

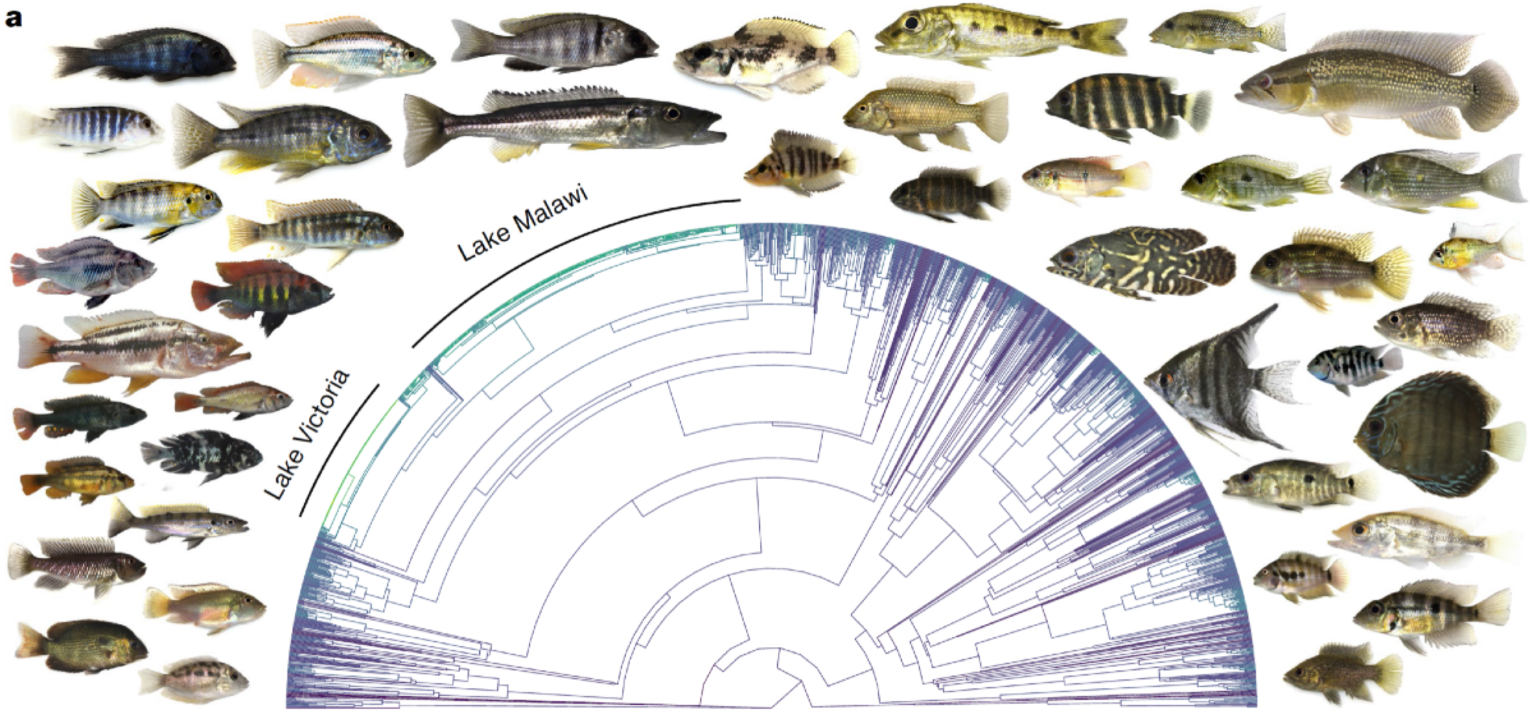


Brawand et al., 2014

Hawaiian lobeliads

Givnish et al. 2008

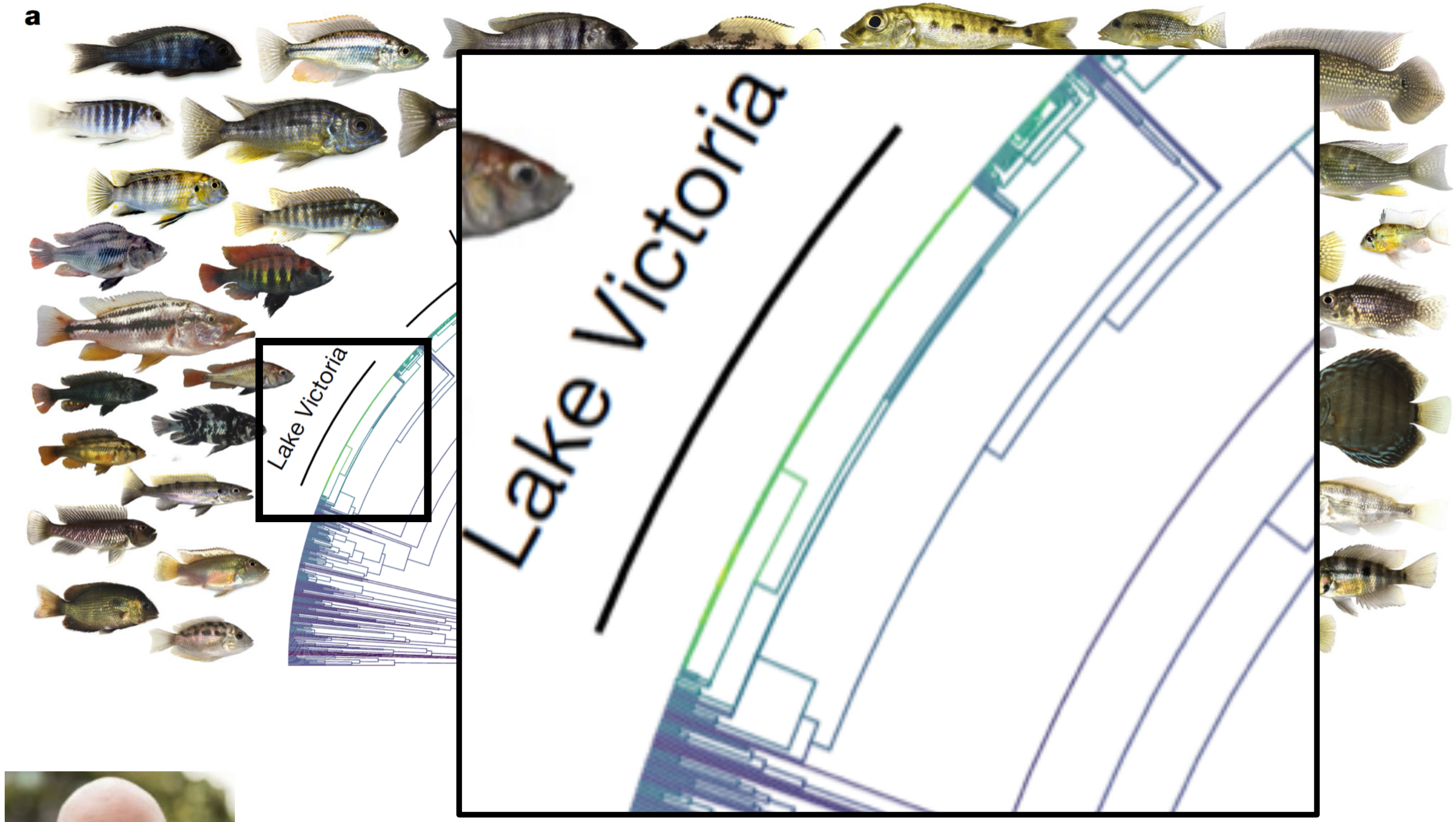
Extrinsic and intrinsic factors together best predict adaptive radiation



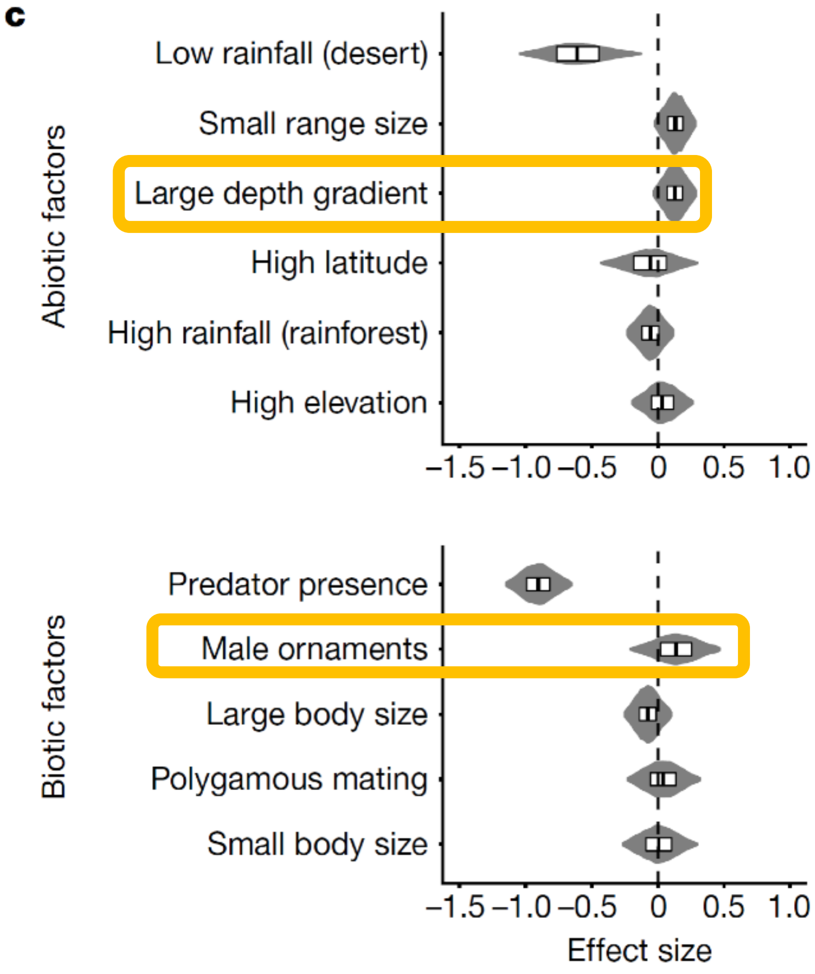
Matt McGee
(Monash U)

All described 1,712 species
McGee et al., 2020, Nature

Extrinsic and intrinsic factors together best predict adaptive radiation



Factors affecting speciation rates

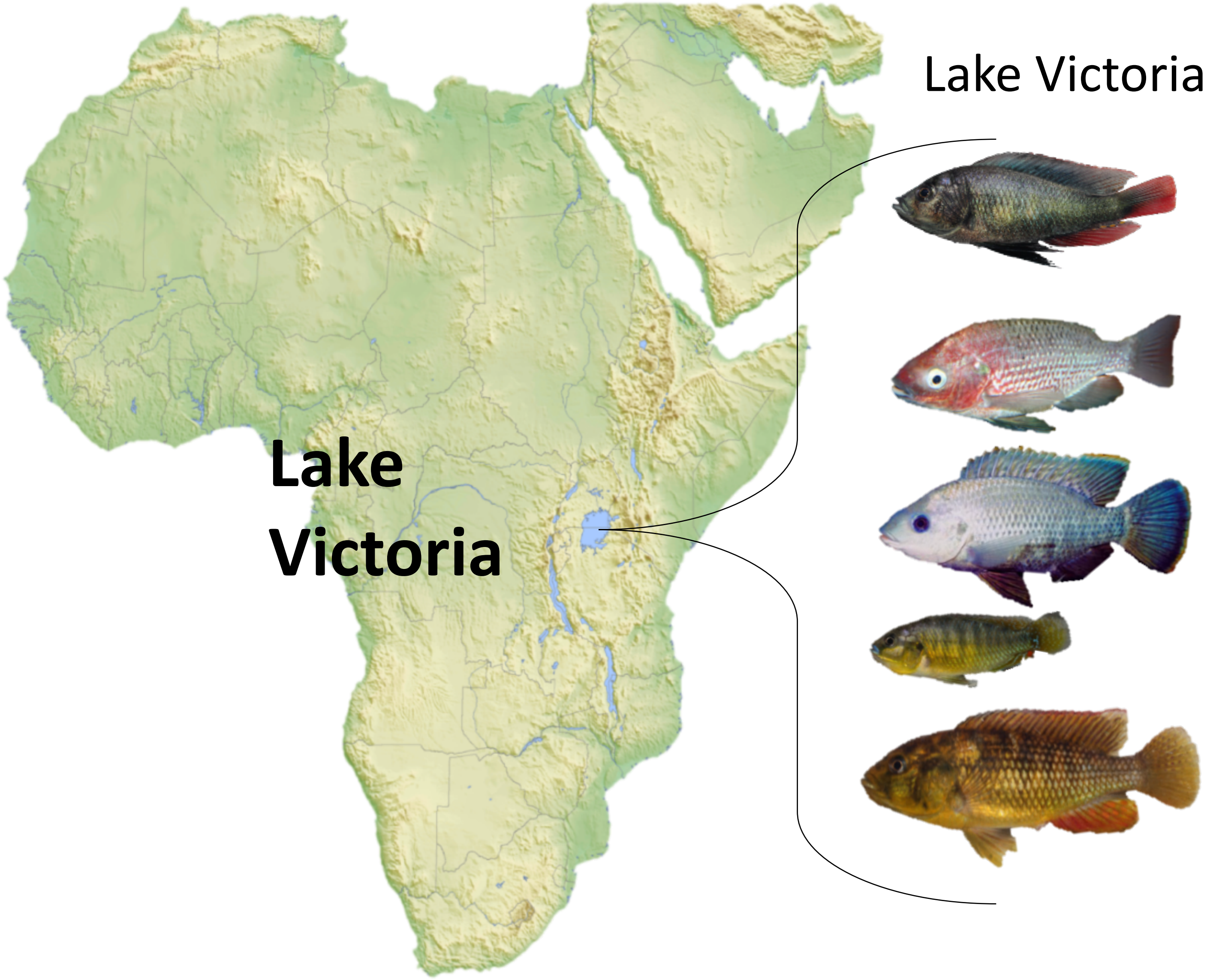


← constrains promotes →
speciation

Matt McGee
(Monash U)

All described 1,712 species
McGee et al., 2020, Nature

Cichlid lineages vary massively in species richness



Lake Victoria

Lake Victoria cichlid fishes

500 species

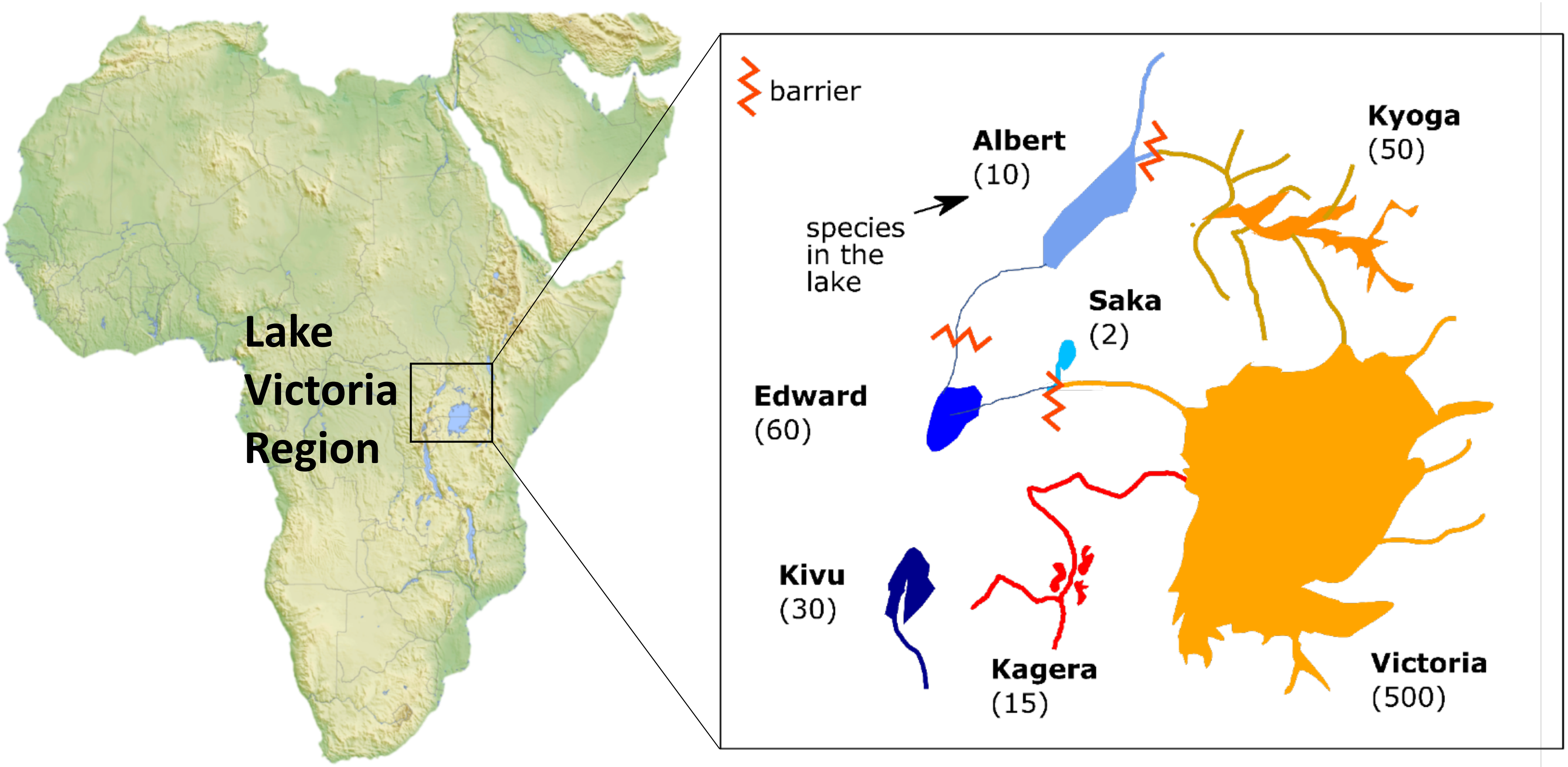
1 species

1 species

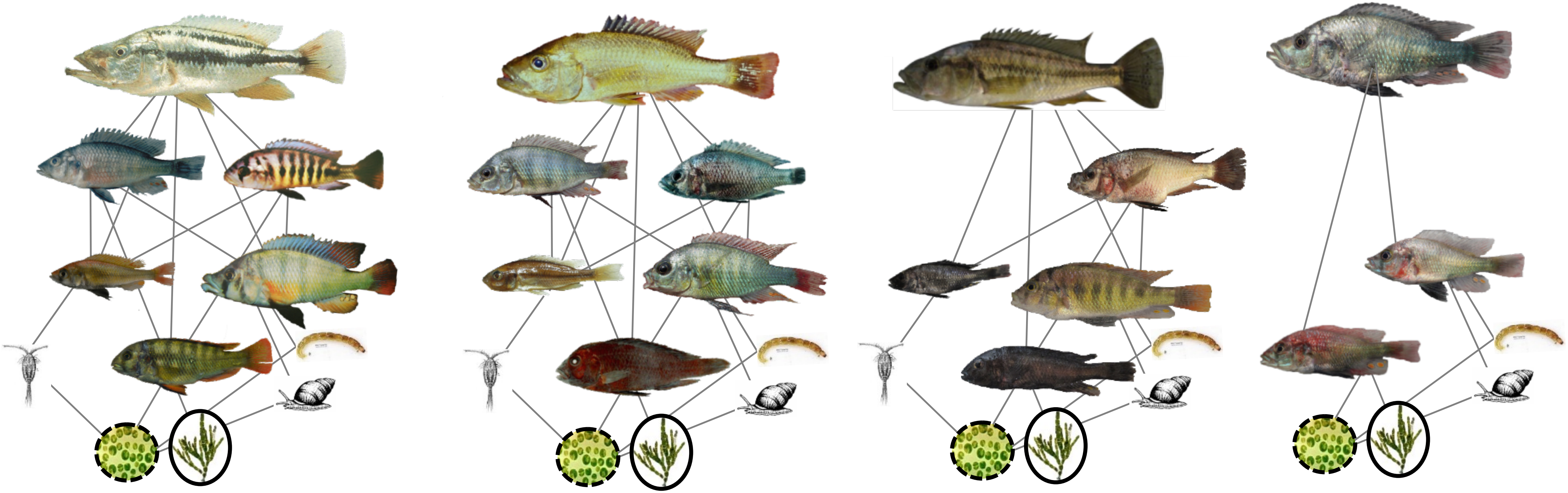
1 species

1 species

The same lineage diversified in all major lakes in the Lake Victoria Region in only 150,000 years into 700 species



In each lake, the cichlids form species assemblages with similar ecomorphs



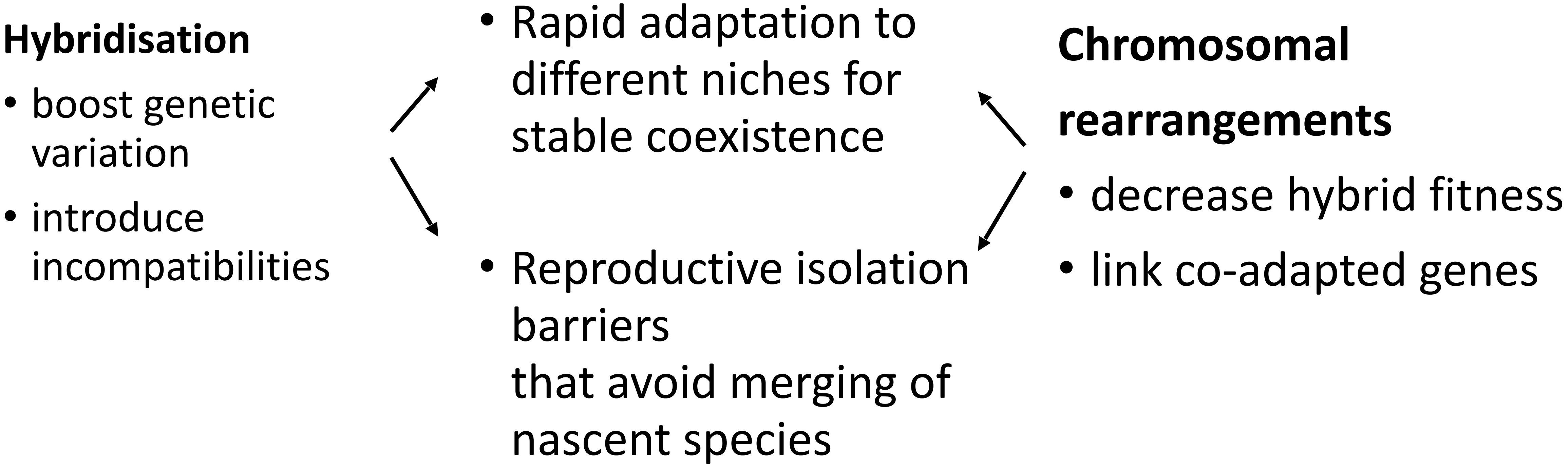
Lake Victoria

Lake Edward

Lake Kivu

Kagera Lakes

Requirements for rapid adaptive radiation



Hybridisation

- boost genetic variation
- introduce incompatibilities

- Rapid adaptation to different niches for stable coexistence
- Reproductive isolation barriers
  that avoid merging of nascent species

Chromosomal rearrangements

- decrease hybrid fitness
- link co-adapted genes

Ole Seehausen
(EAWAG,
U Bern,
Switzerland)

David Marques
(Natural History
Museum Basel,
Switzerland)

Laurent Excoffier
(U Bern,
Switzerland)

Salome Mwaiko
(EAWAG,
Switzerland)

Mary Kishe
(TAFIRI,
Tansania)

Katie Wagner
(U Wyoming,
USA)

Matt McGee
(Monash U,
Australia)

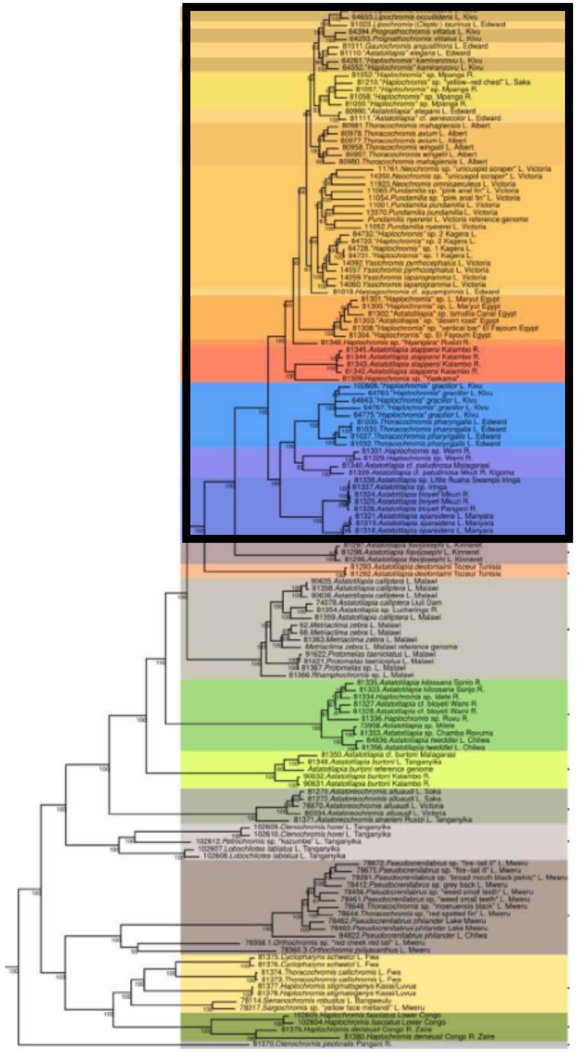
UNIVERSITÄT
BERN

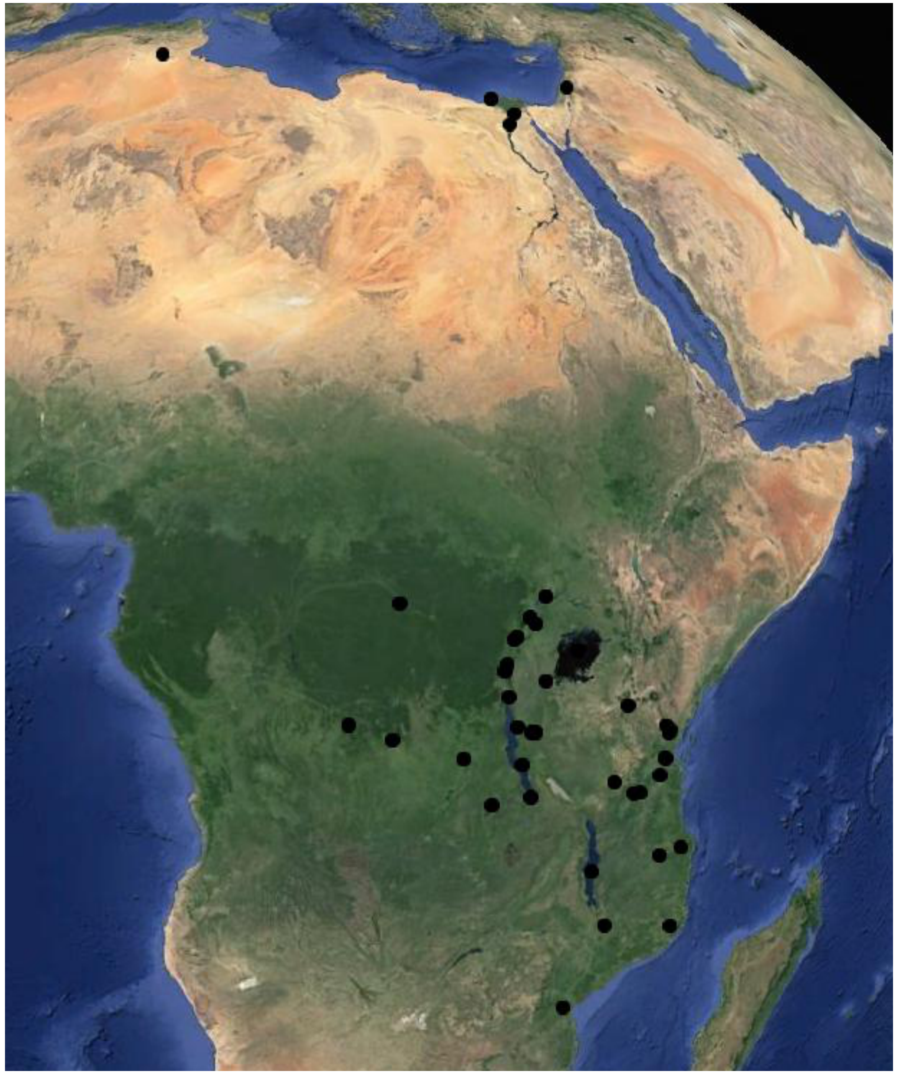
eawag
aquatic research

FNSNF

Identifying the closest relatives of the radiations

(RAD-sequencing of >100 cichlid species)





Meier *et al*. (2017) *Nat Commun*

Identifying the closest relatives of the radiations

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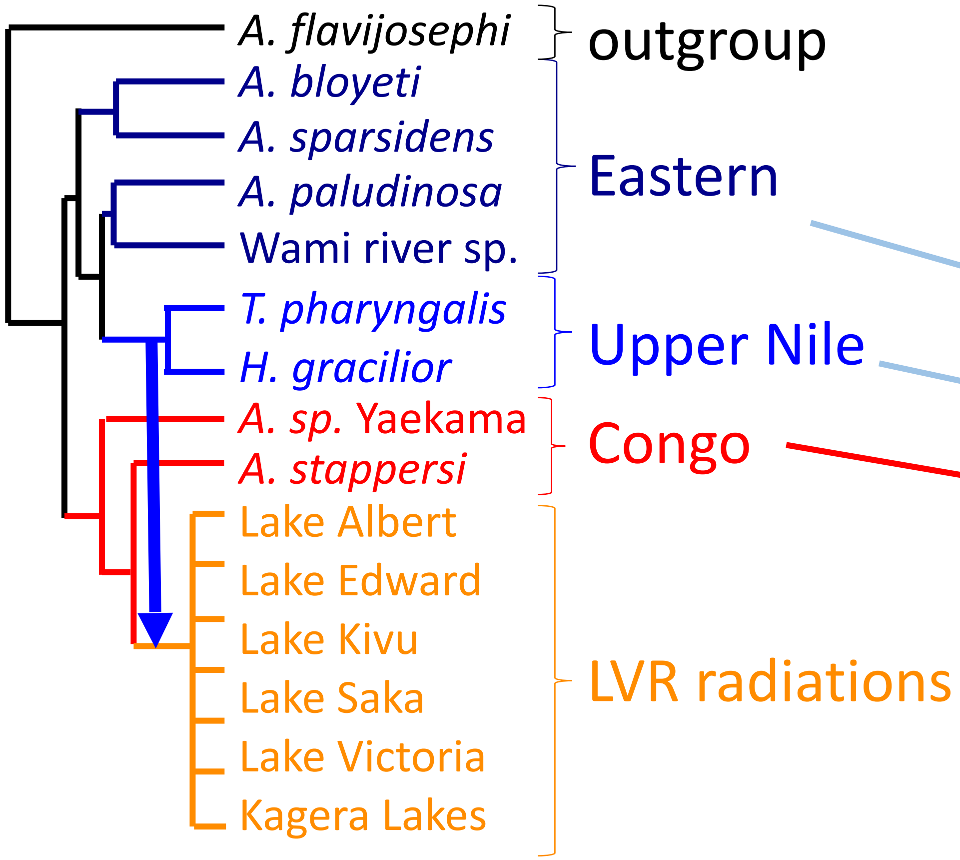


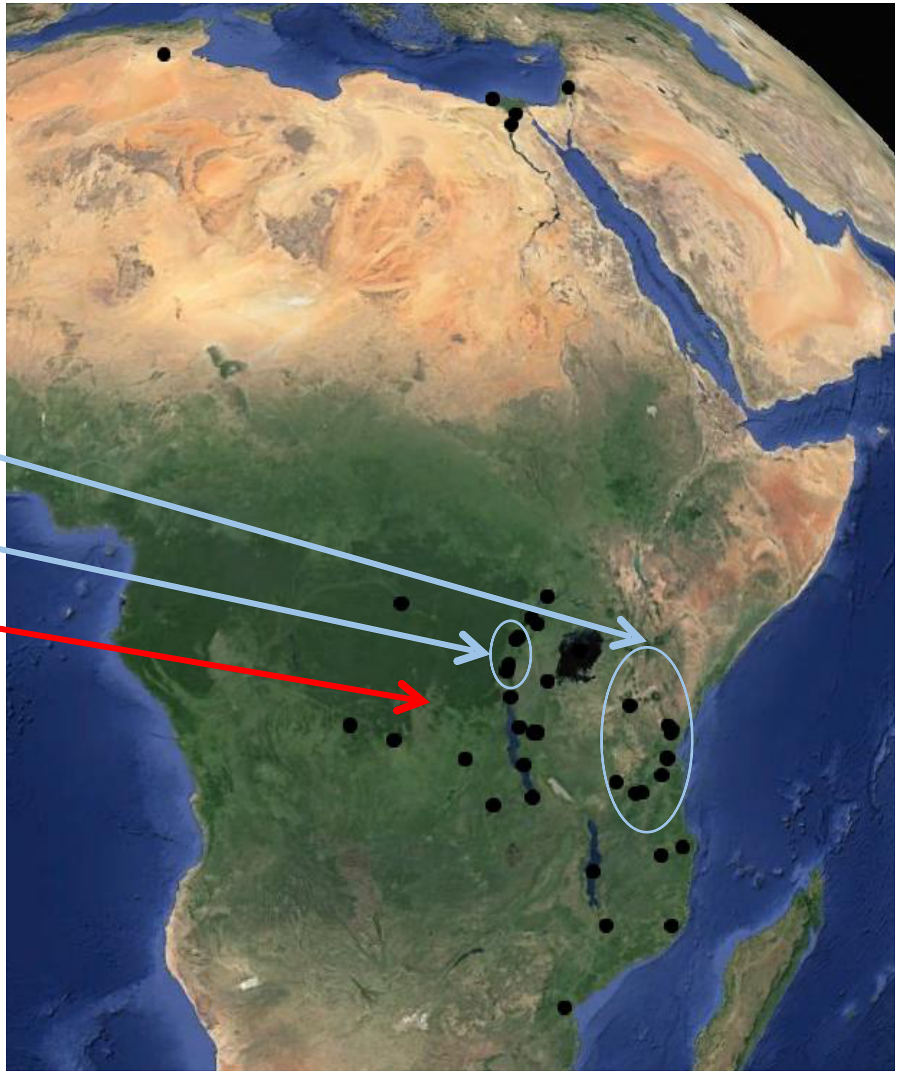
A. flavijosephi — outgroup

A. bloyeti
A. sparsidens
A. paludinosa
Wami river sp. — Eastern

T. pharyngalis
H. gracilior — Upper Nile

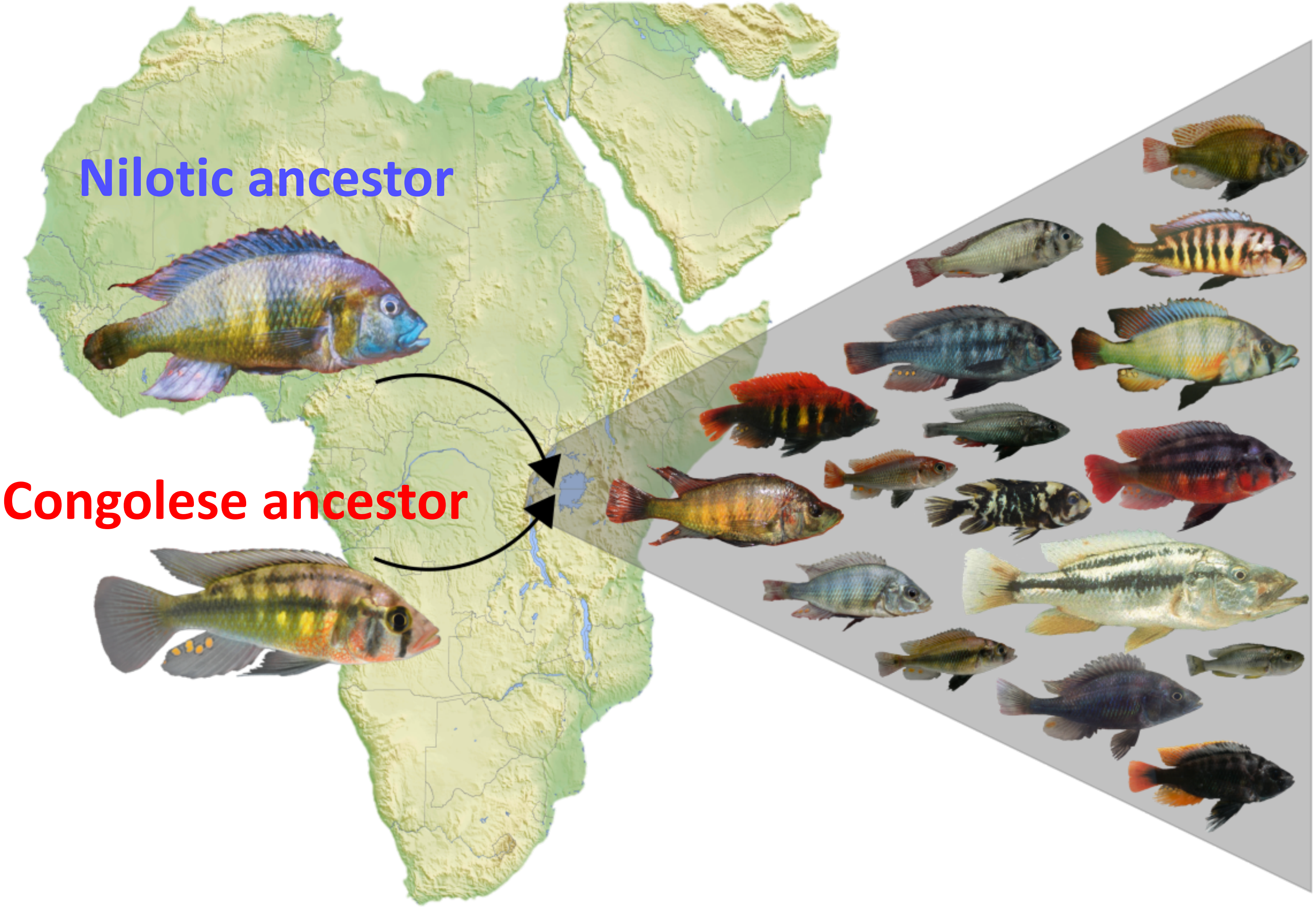
A. sp. Yaekama
A. stappersi — Congo

Lake Albert
Lake Edward
Lake Kivu
Lake Saka
Lake Victoria
Kagera Lakes — LVR radiations



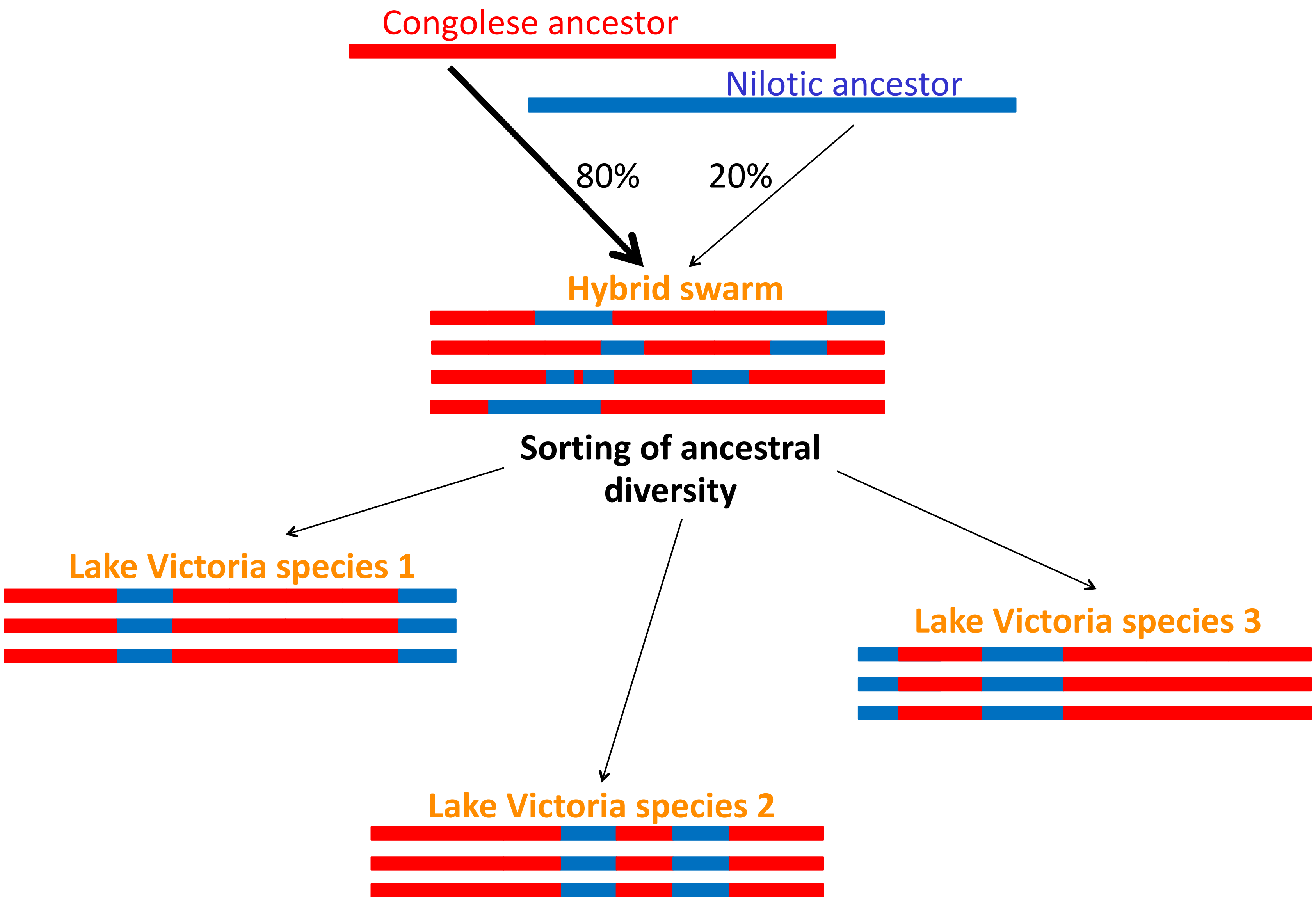
Meier *et al*. (2017) *Nat Commun*

Hybrid origin of the lineage that speciated rapidly



Meier *et al*. (2017) *Nature Commun*

Sorting of the parental lineage variation into different species



Congolese ancestor

Nilotic ancestor

80%

20%

Hybrid swarm

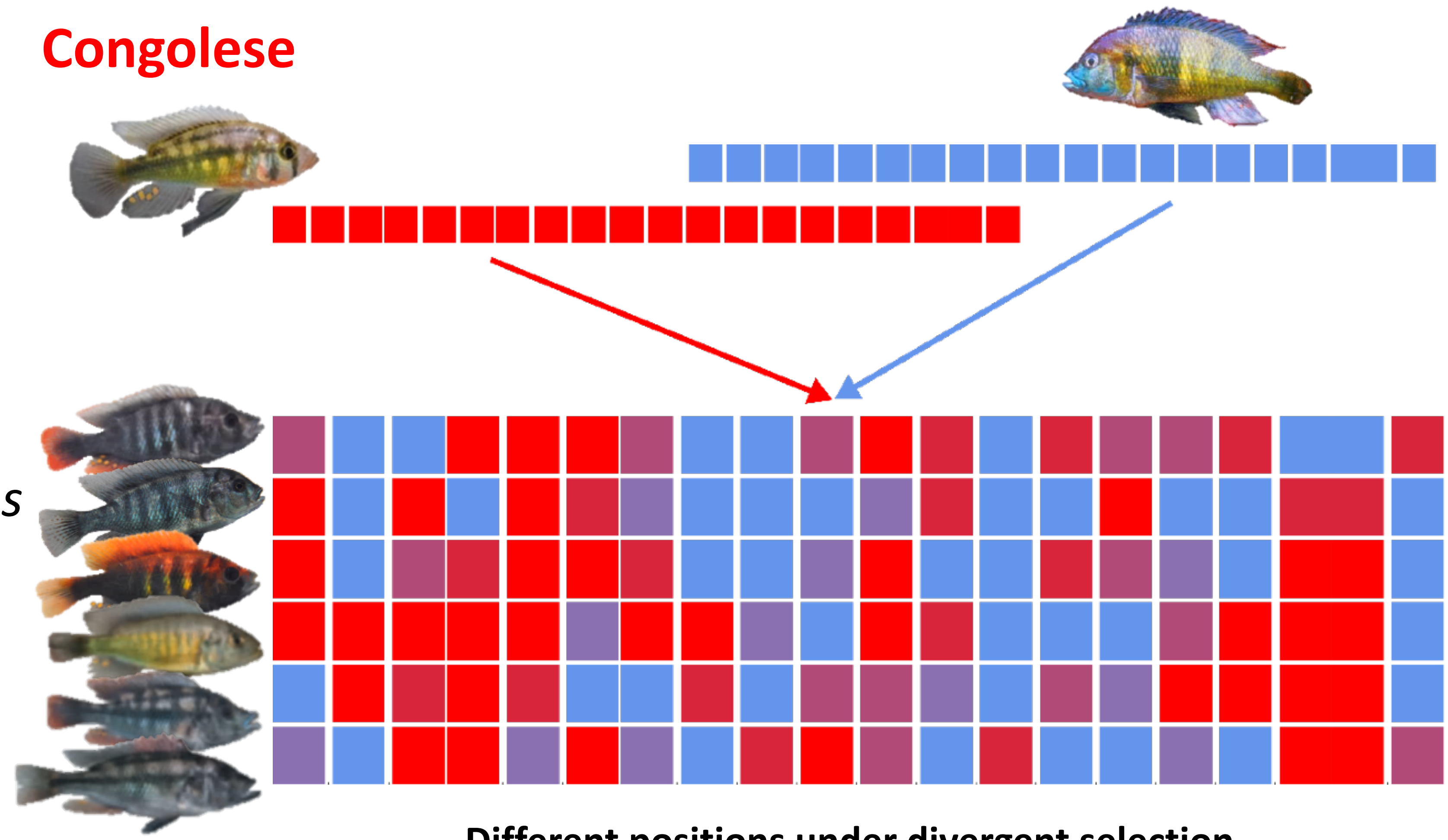
Sorting of ancestral diversity

Lake Victoria species 1

Lake Victoria species 2

Lake Victoria species 3

At sites under divergent selection, different species are different genomic mosaics of the parental lineages



Upper Nile

Congolese

Pu. pundamilia

N. omnicaeruleus

Pu. nyererei

L. melanopterus

Pa. chilotes

H. cf. serranus

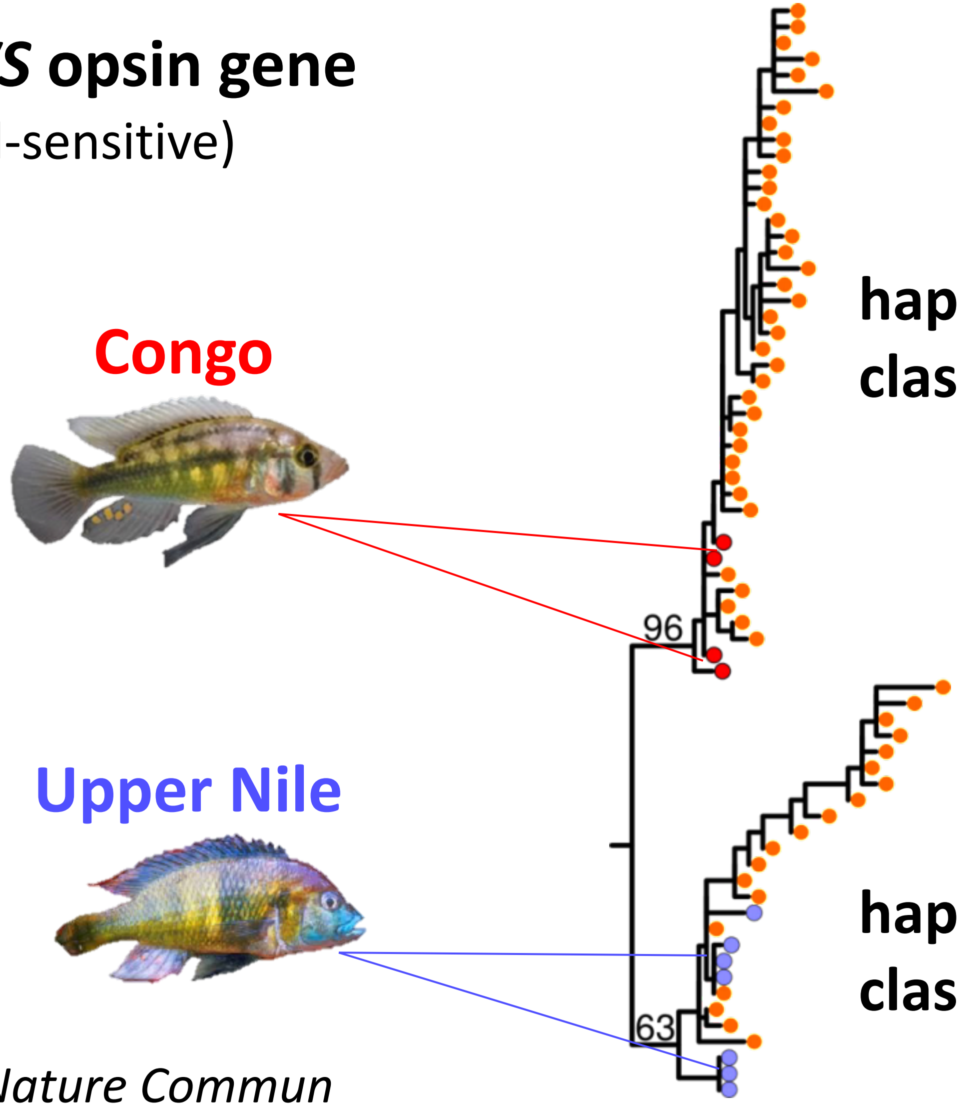
Different positions under divergent selection

Meier *et al*. (2017) *NatComm*

Admixture provided key genetic variation

***LWS* opsin gene**

(red-sensitive)



haplotype class I

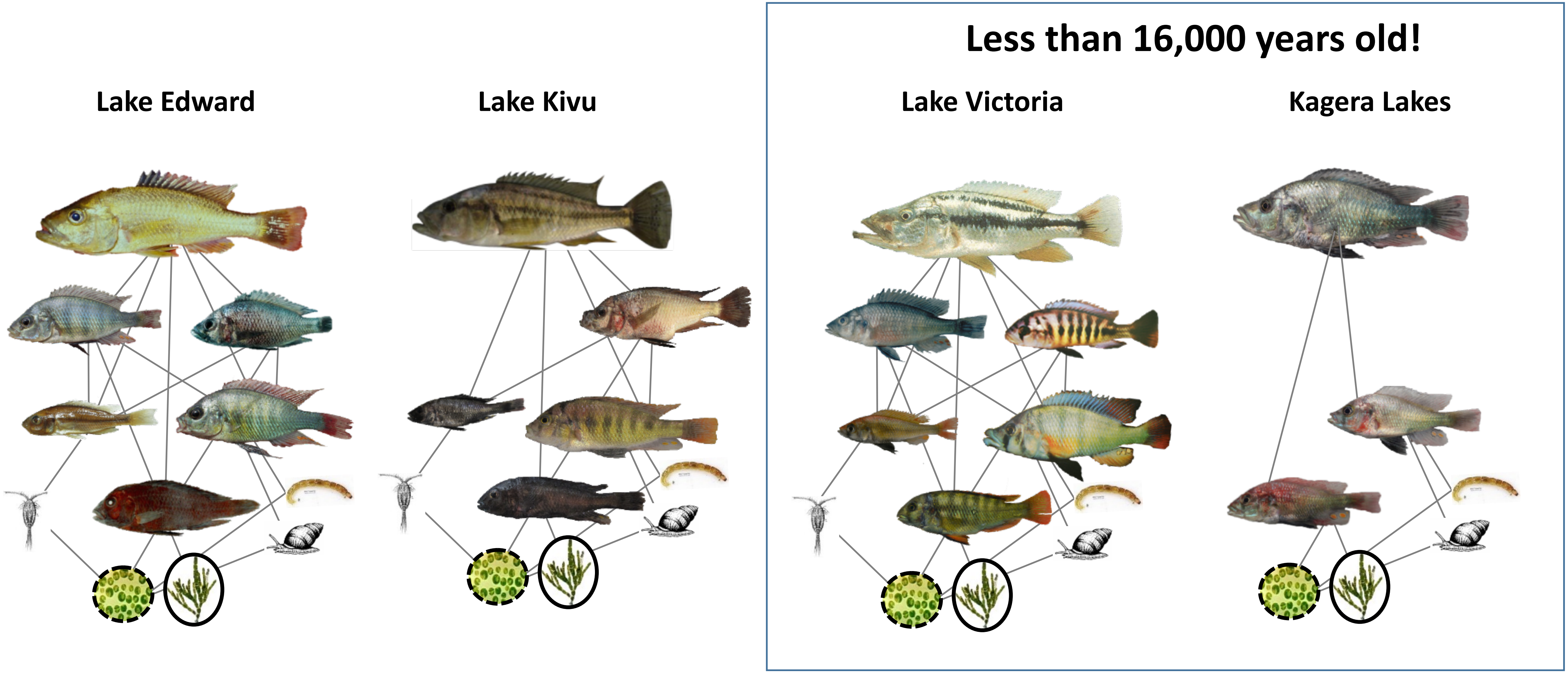
e.g. clear shallow water algivores

haplotype class II

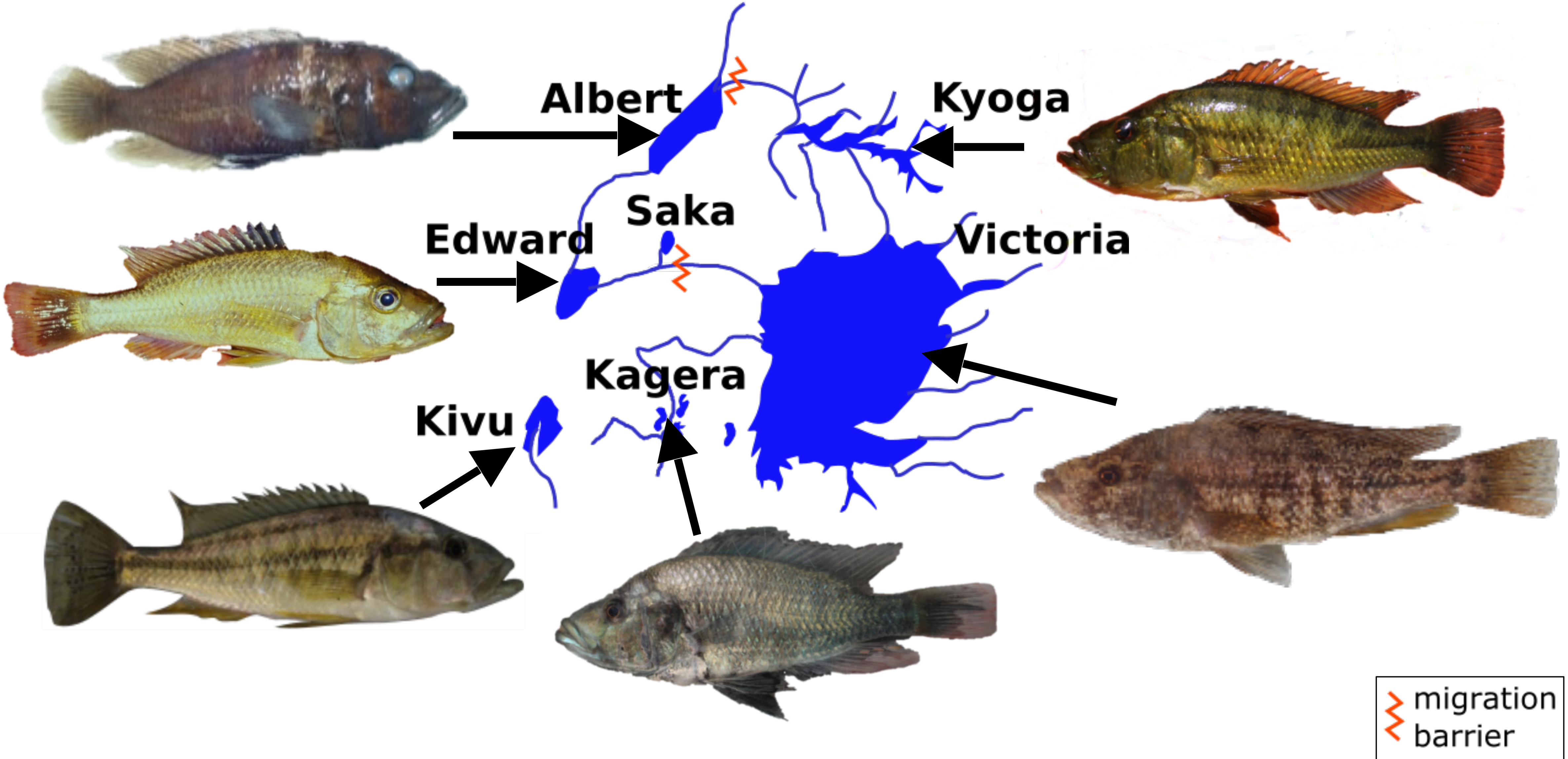
e.g. turbid deep water detritivores

Meier *et al*. (2017) *Nature Commun*

How did this admixture variation of 150 kya contribute to the origin of the much younger radiations after the Pleistocene dry period?

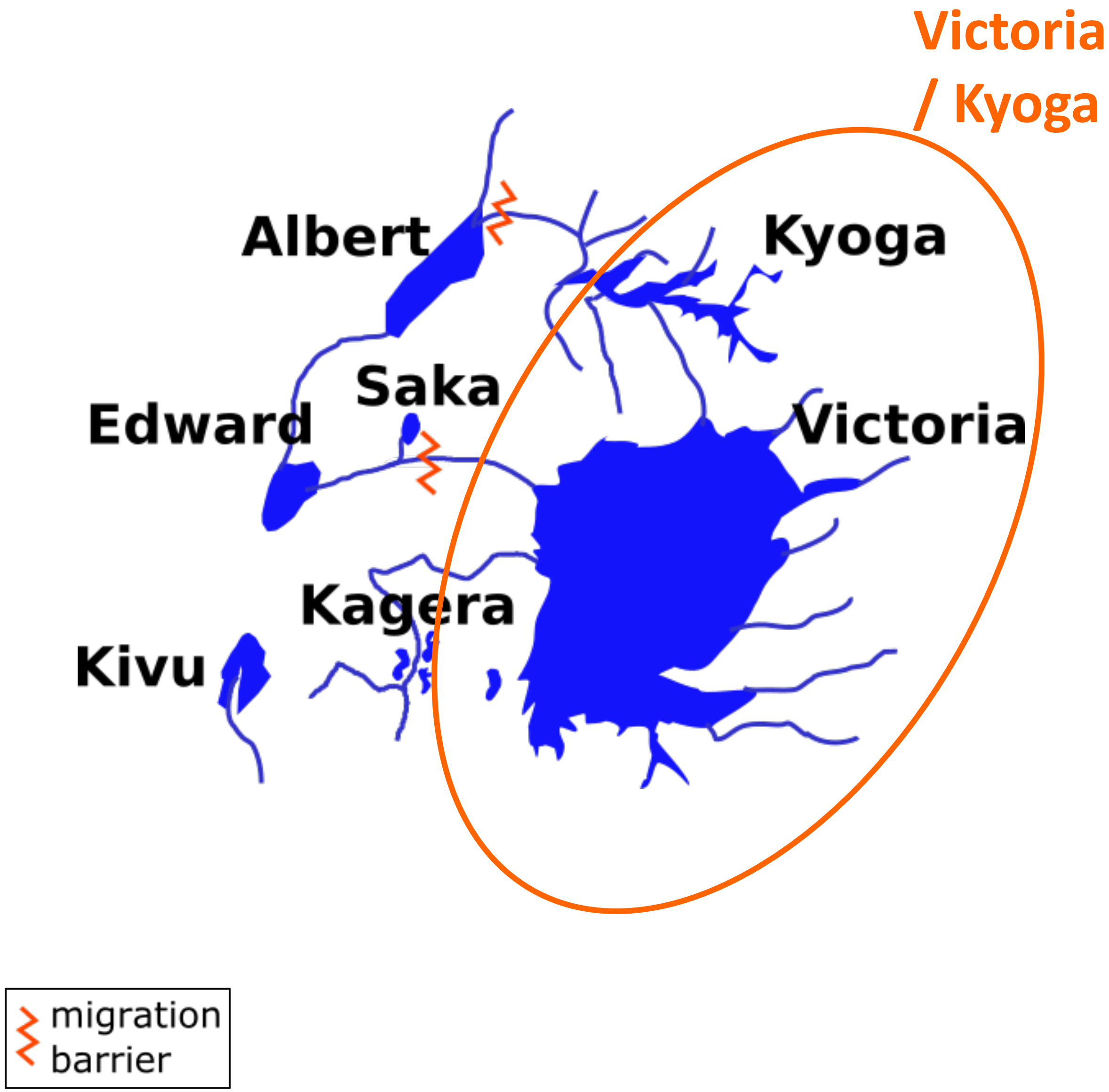


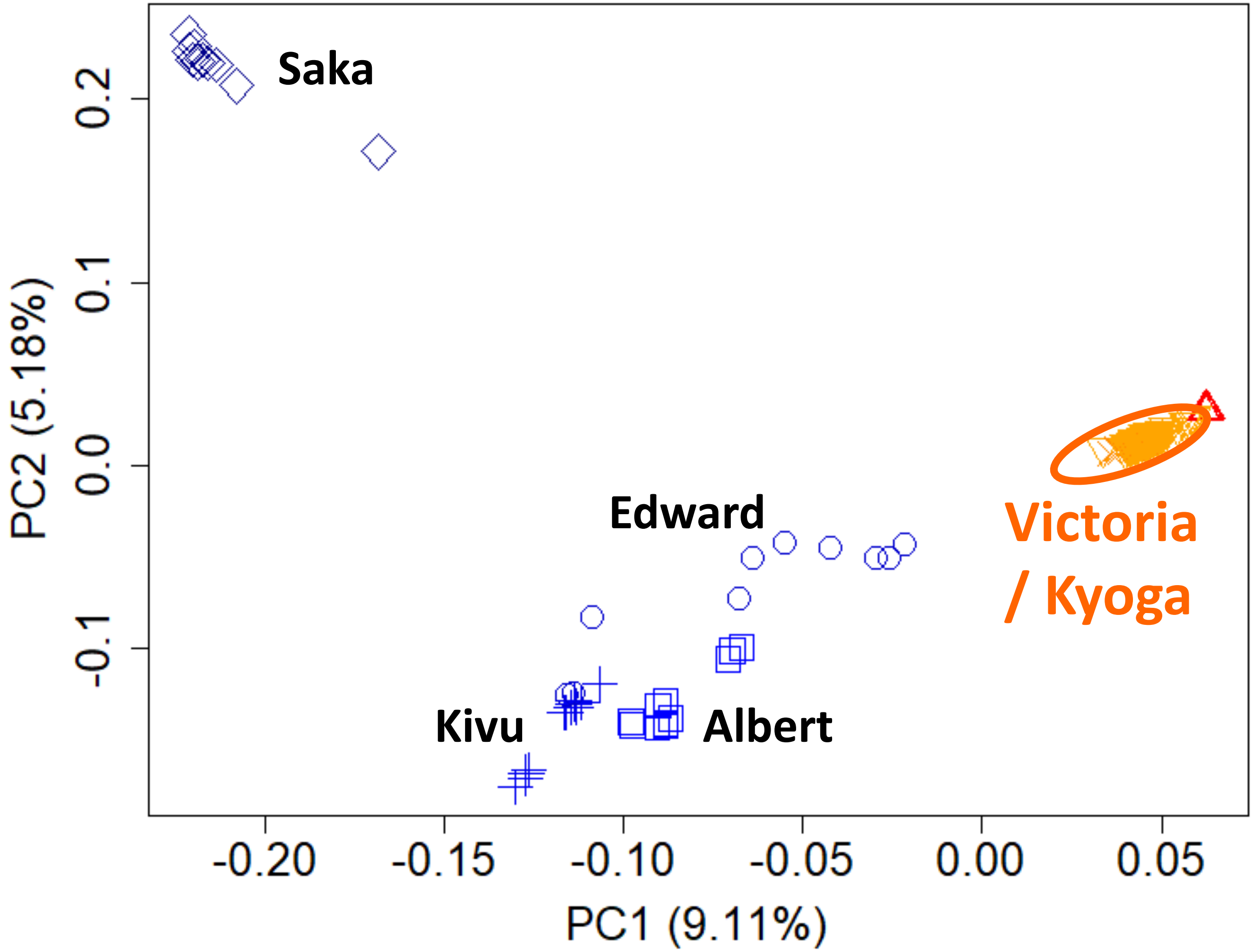
Predators across different lake radiations are extremely similar in morphology



PCA on whole-genomes separates Lake Victoria/Kyoga cichlids from others

(152 genomes, 1.6M LD-pruned SNPs)





Meier *et al*. (2023) *Science*

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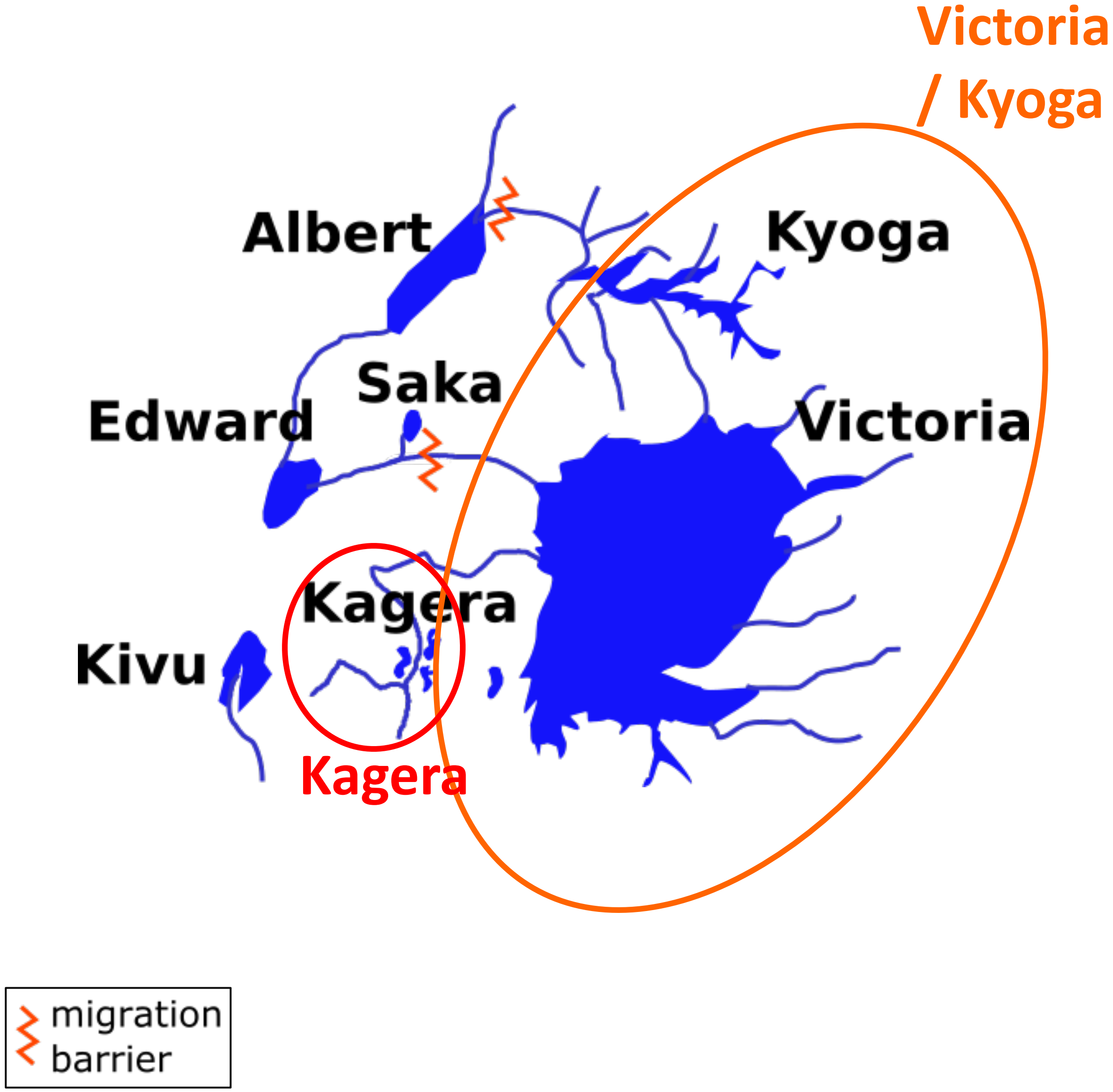

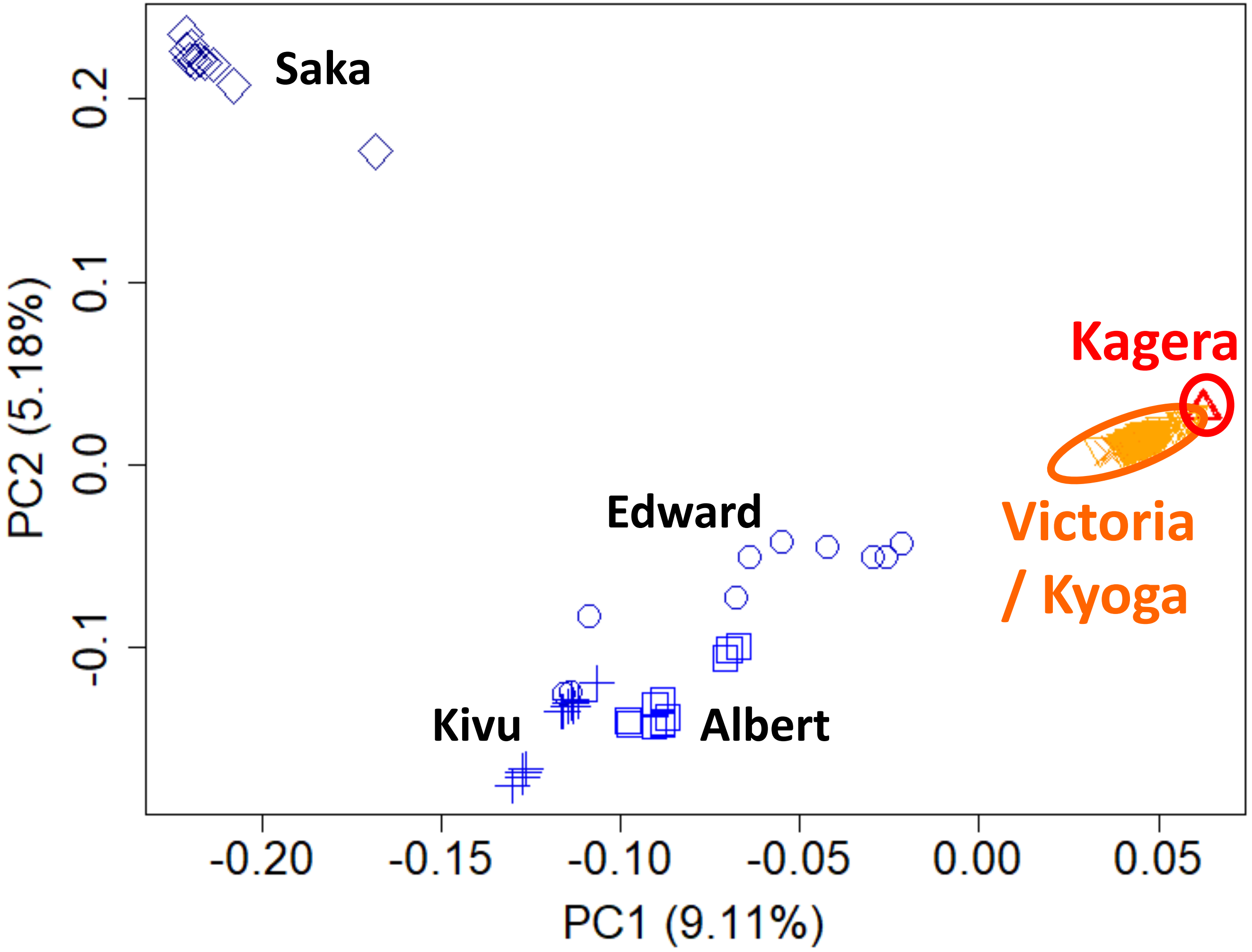

Meier *et al*. (2023) *Science*

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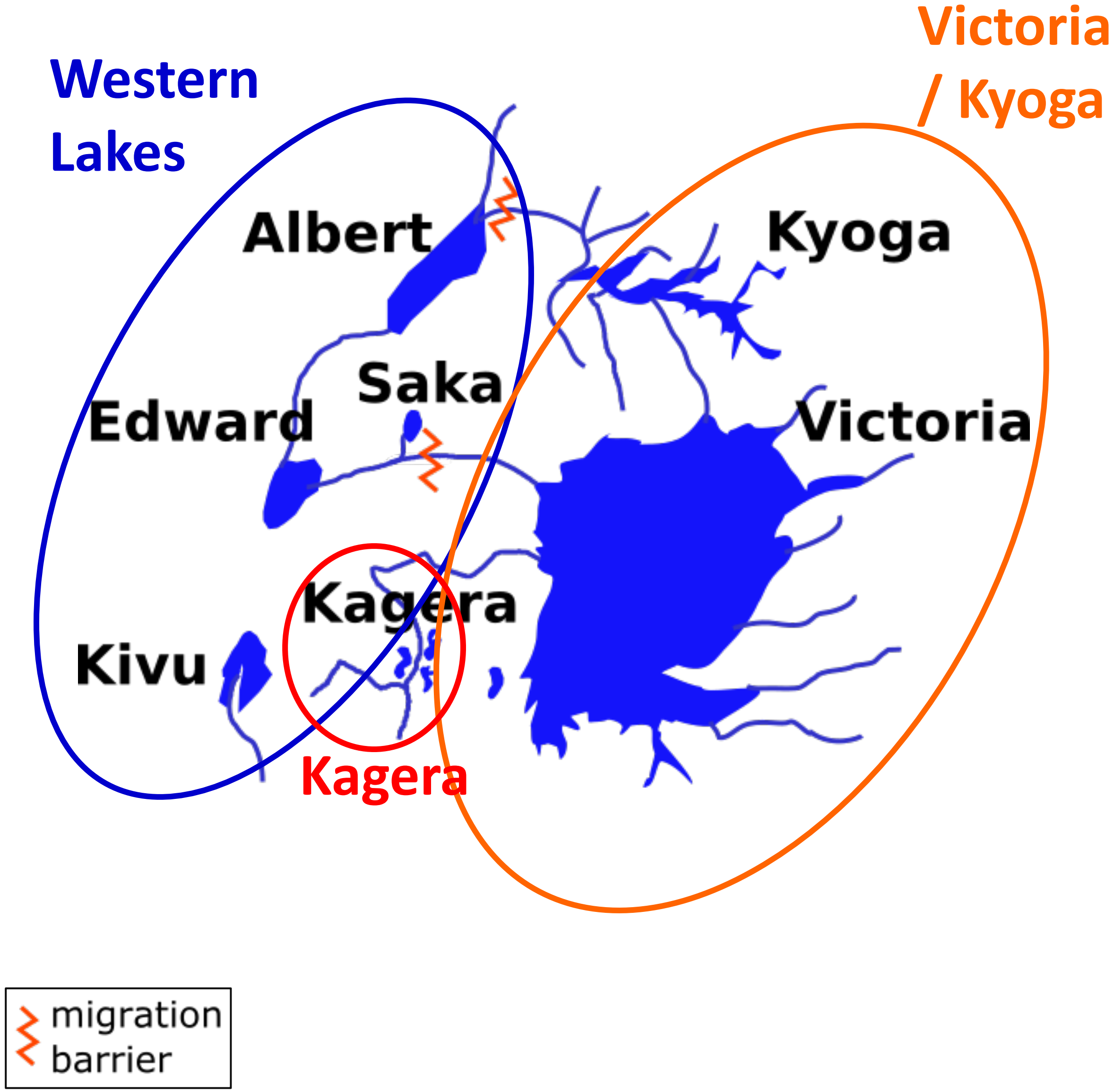

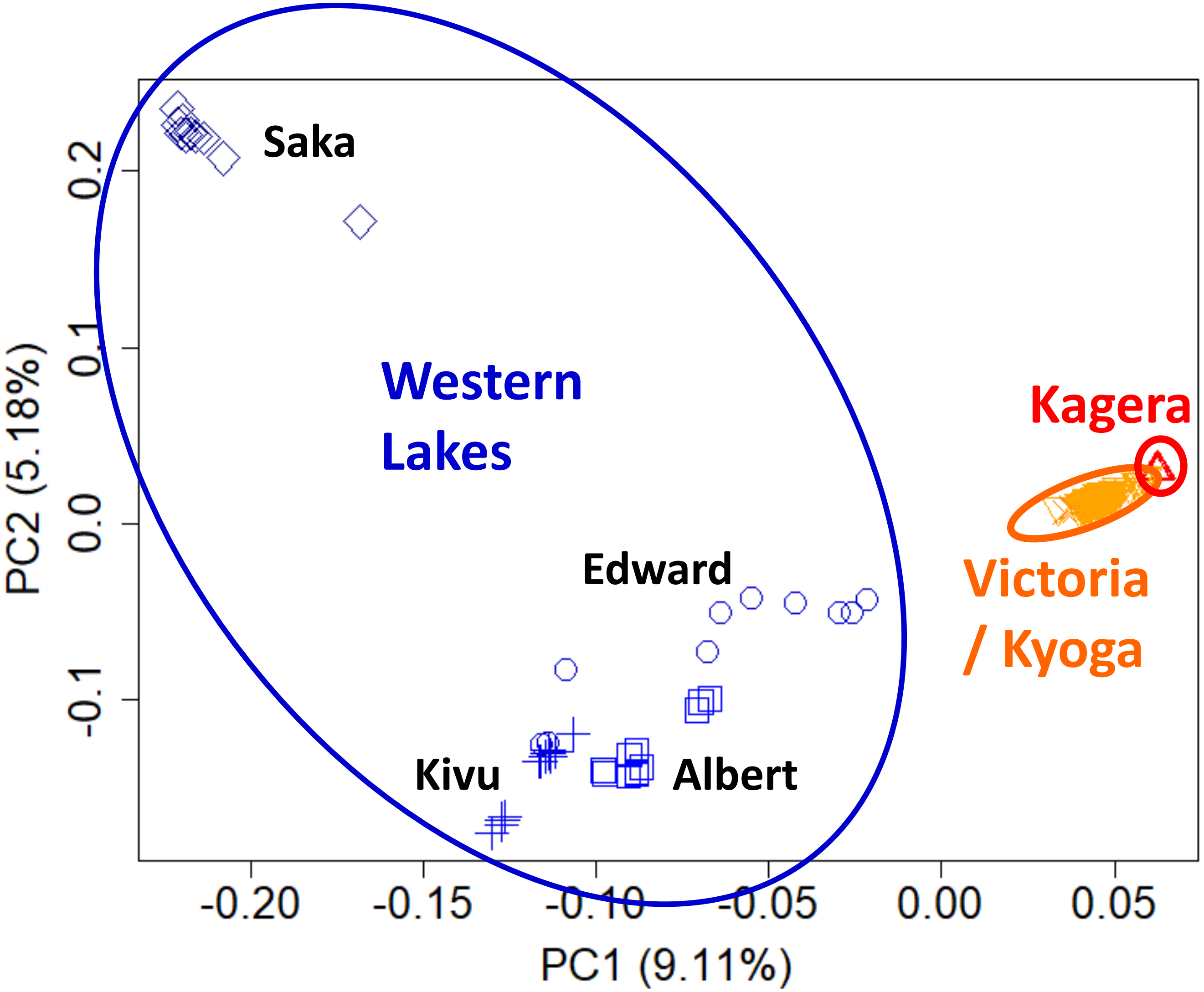

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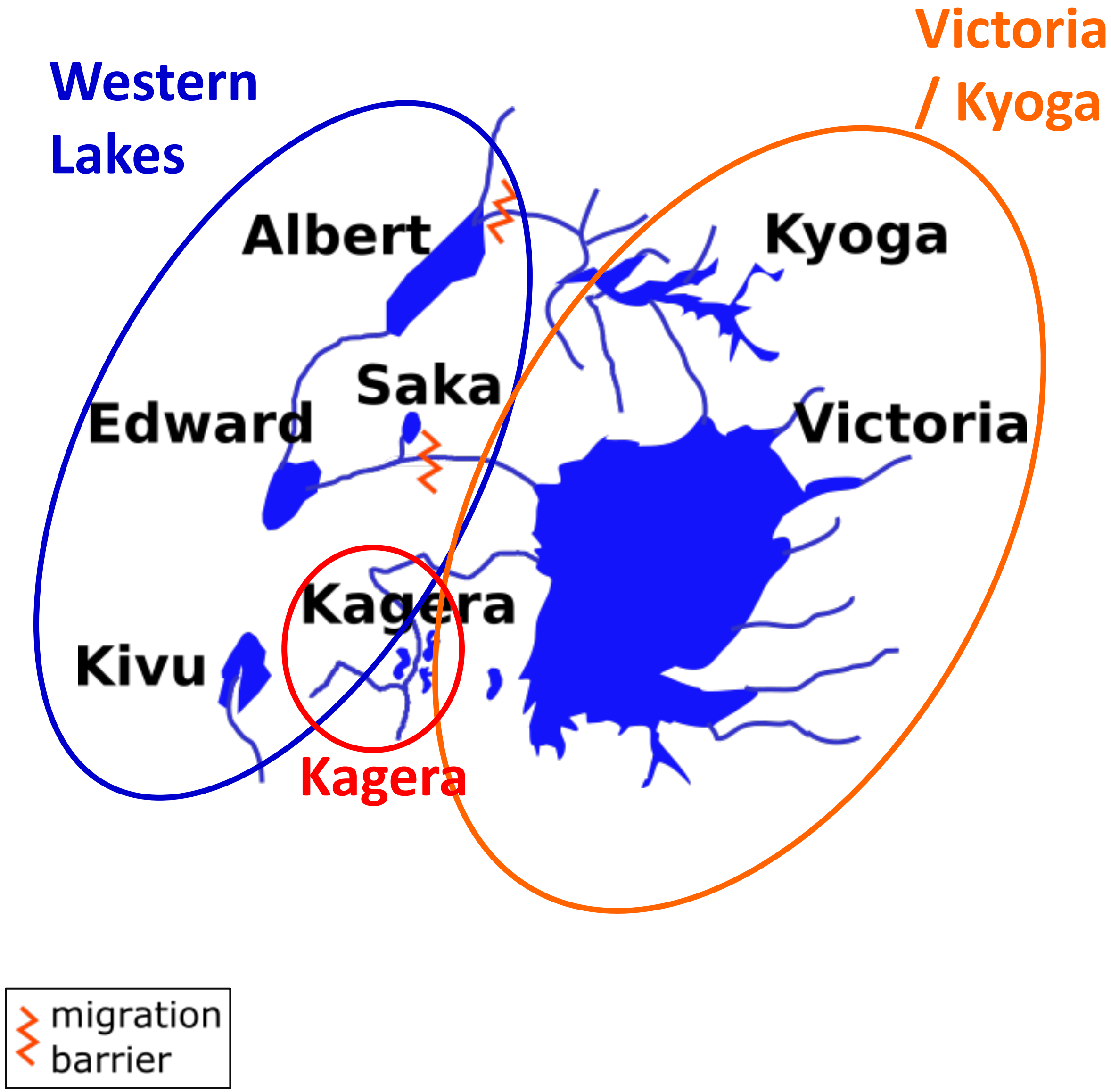

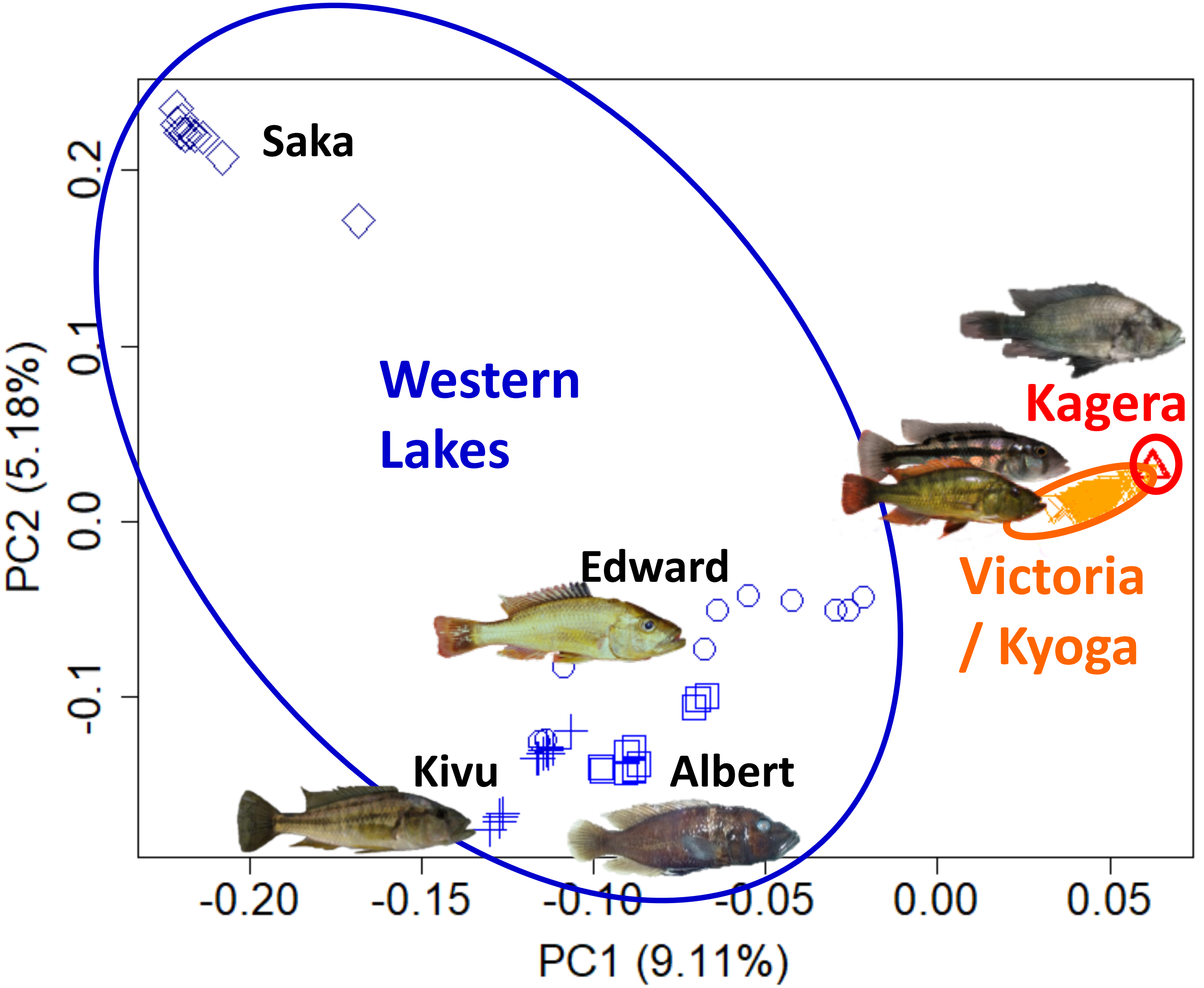

Meier *et al*. (2023) *Science*

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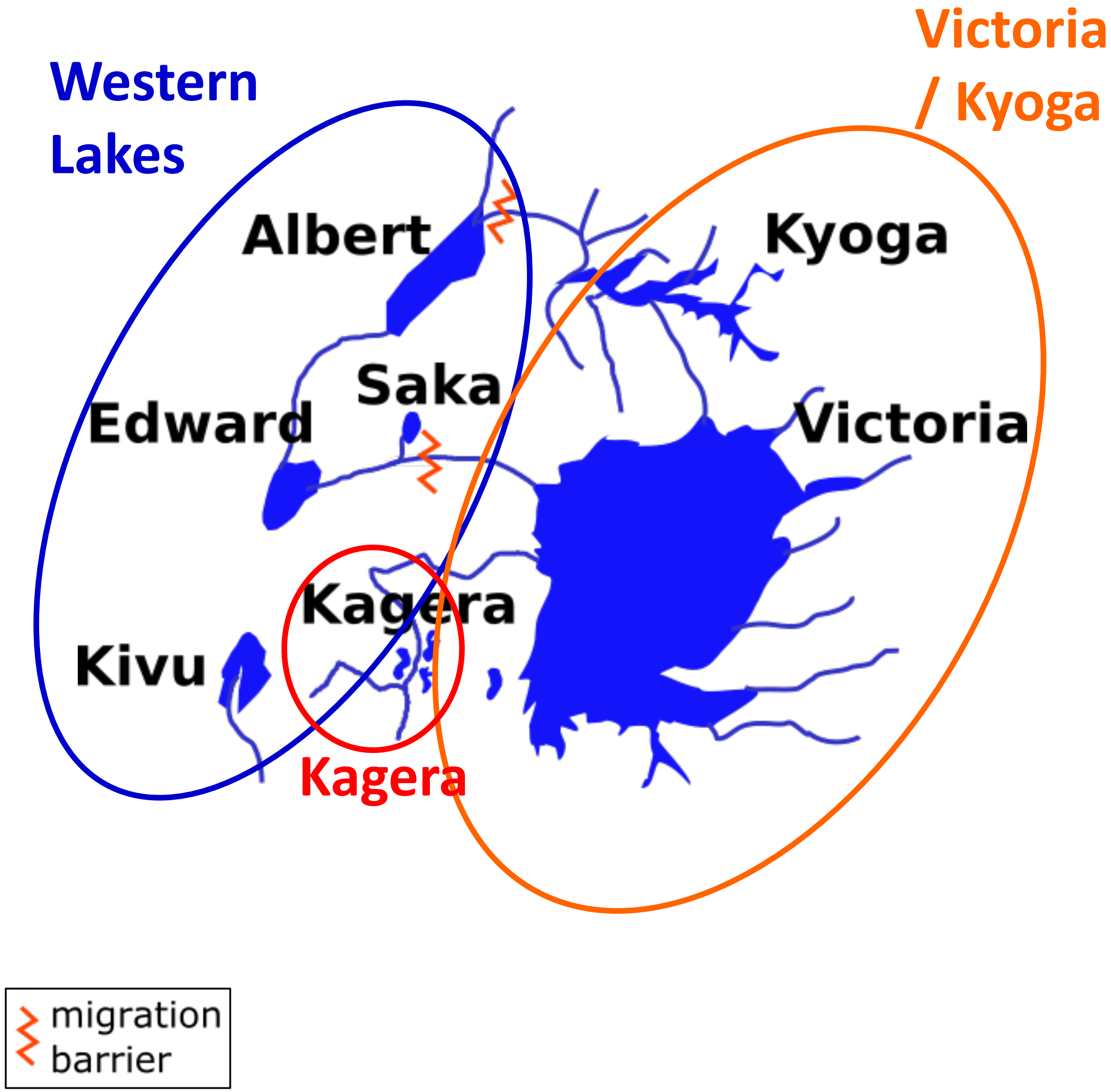
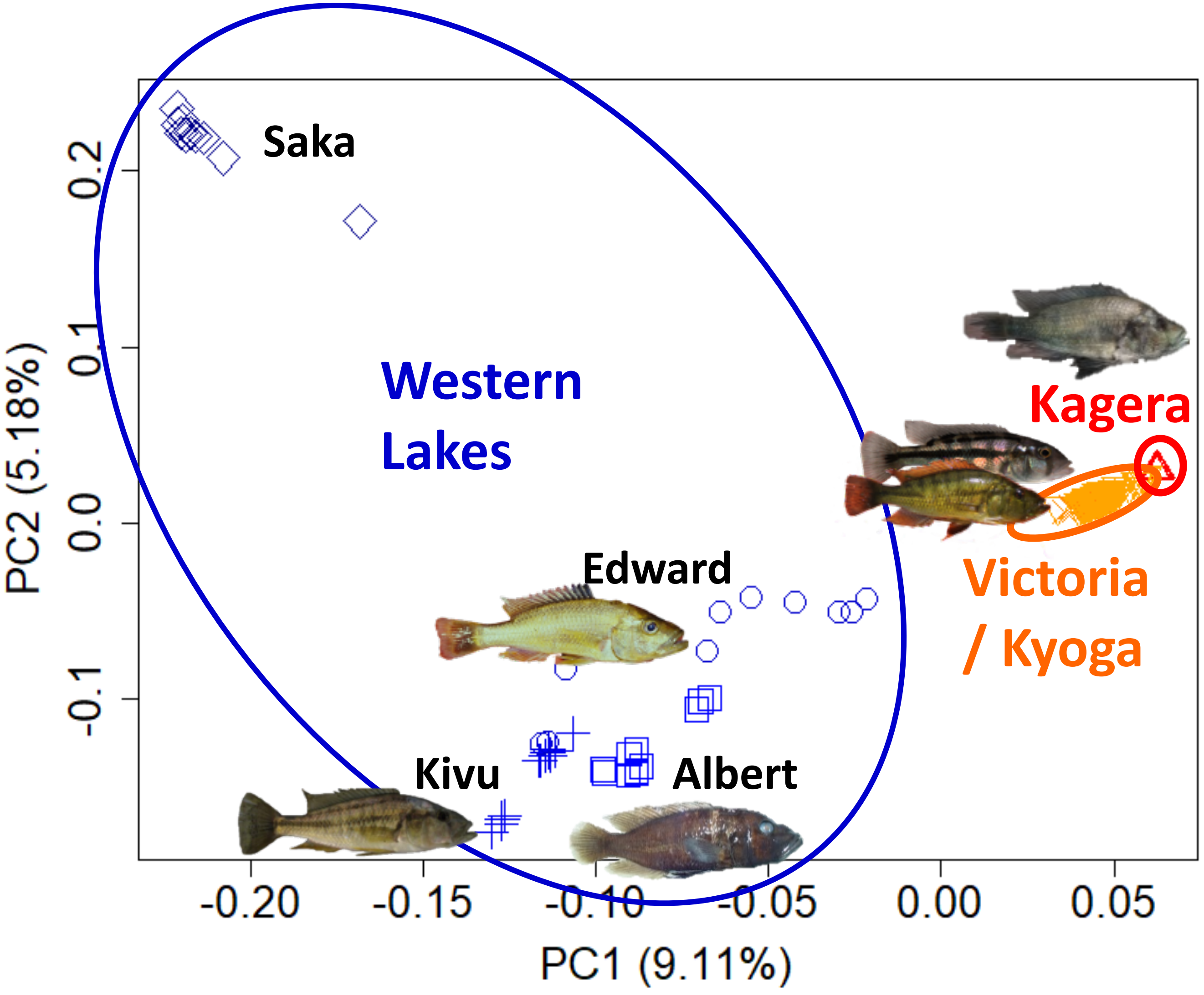
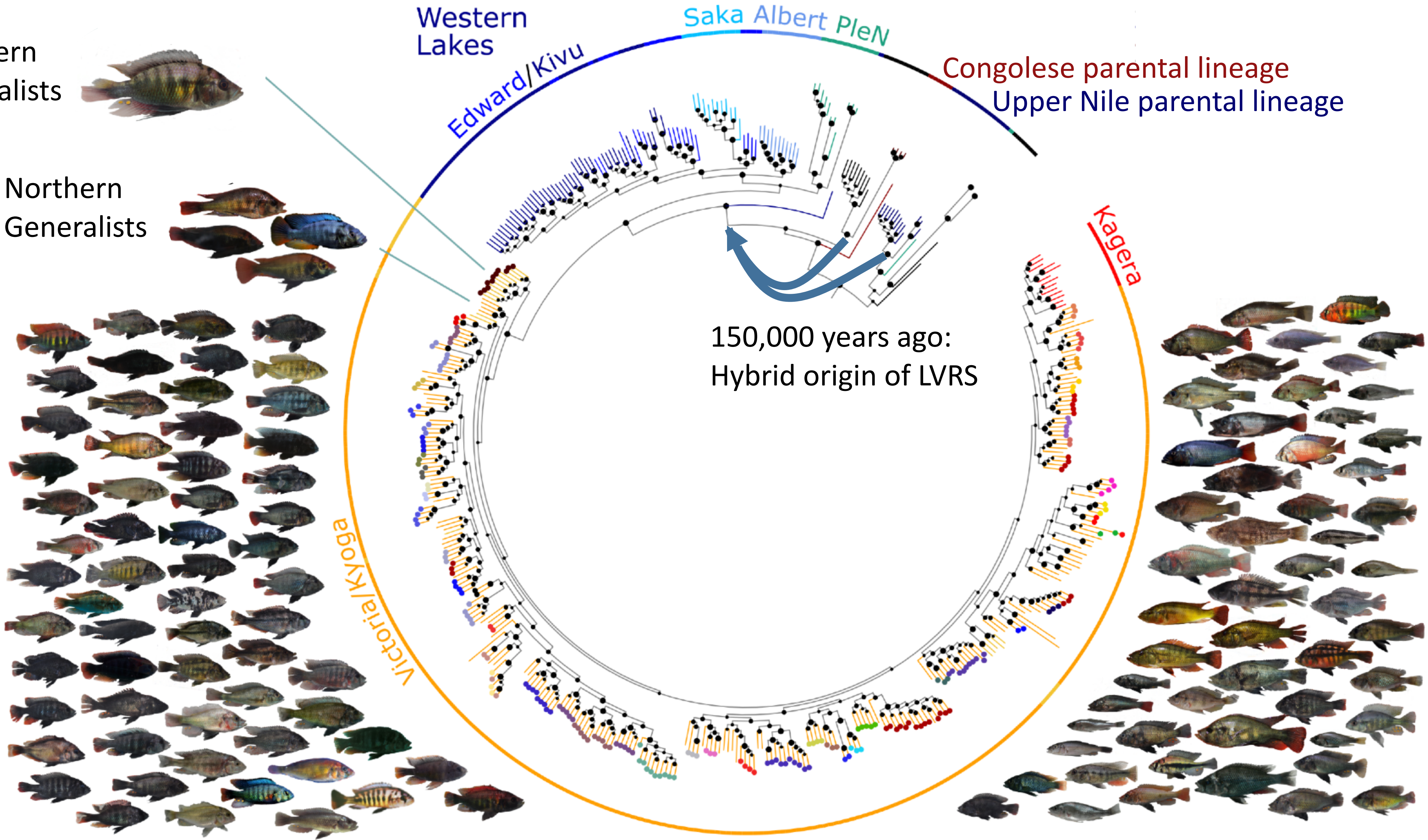




Meier *et al*. (2023) *Science*

Phylogeny of 474 genomes reveals two lineages of generalists as closest relatives



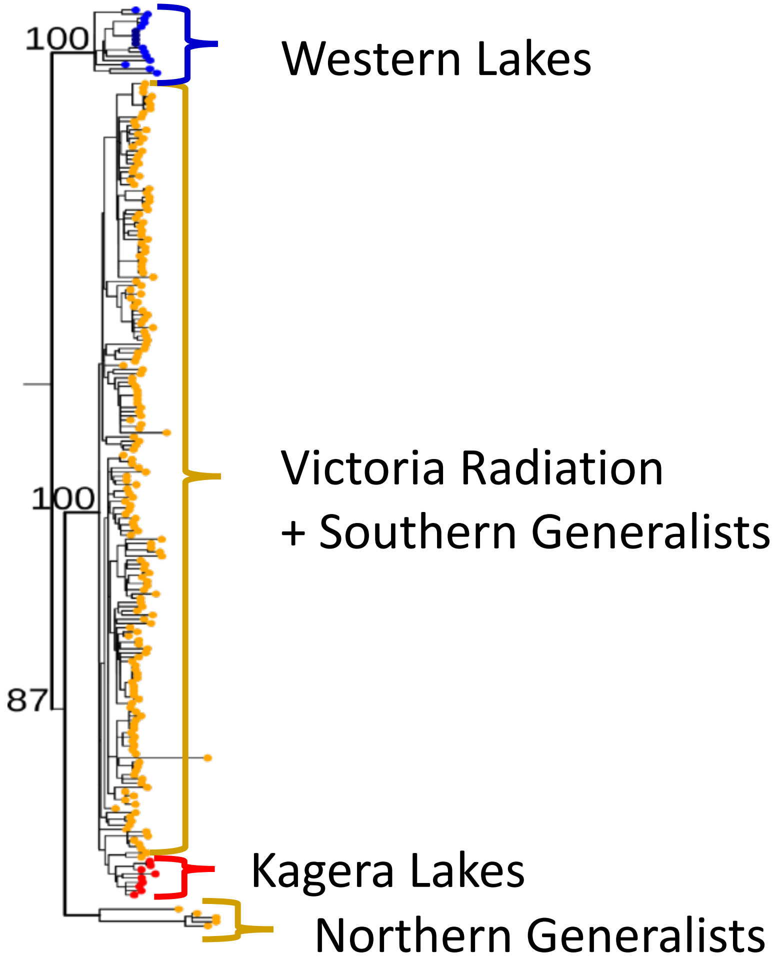
Southern Generalists

Northern Generalists

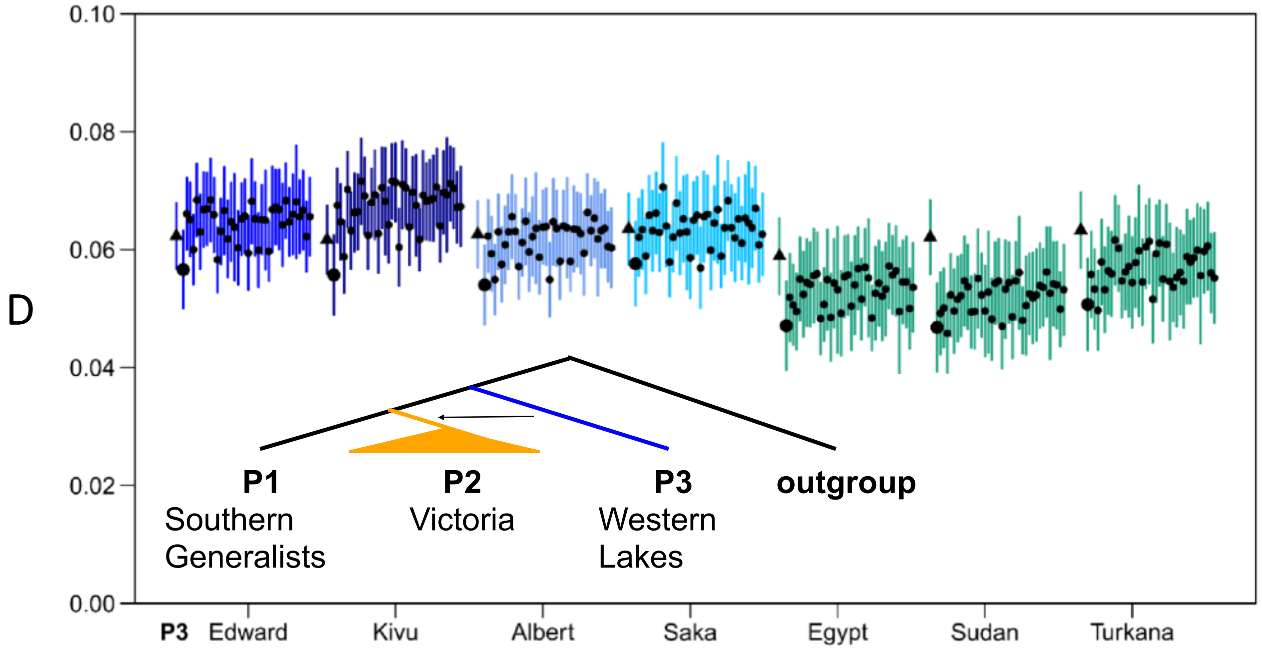
150,000 years ago:
Hybrid origin of LVRS

Multiple lines of evidence for another hybrid origin

Deep mitochondrial divergence not reflected in the nuclear phylogeny

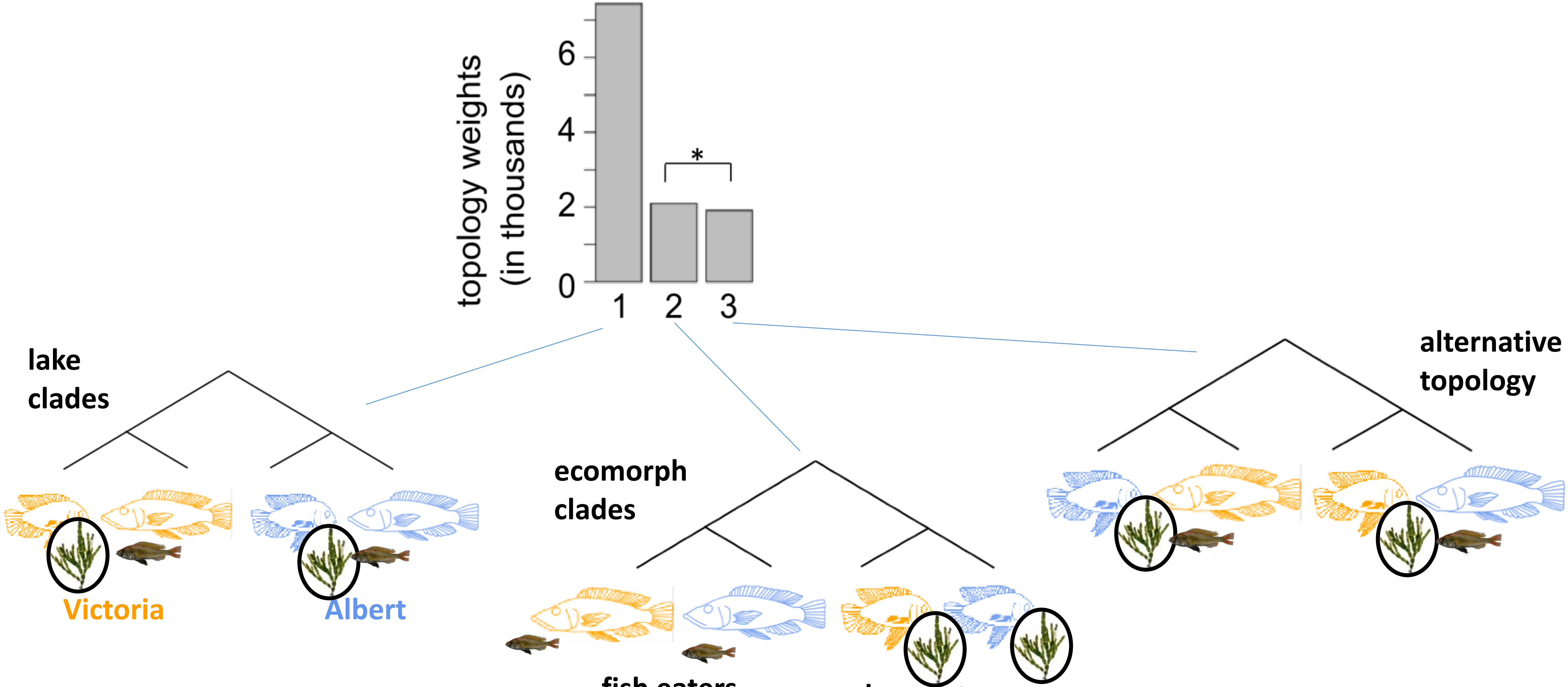


Tests of admixture reveal an additional ancestry contribution of a relative of the Western Lake radiations



Meier *et al*. (2023) *Science*

Slight excess allele sharing between ecologically similar species of different lake radiations



lake clades

ecomorph clades

alternative topology

fish eaters

algae eaters

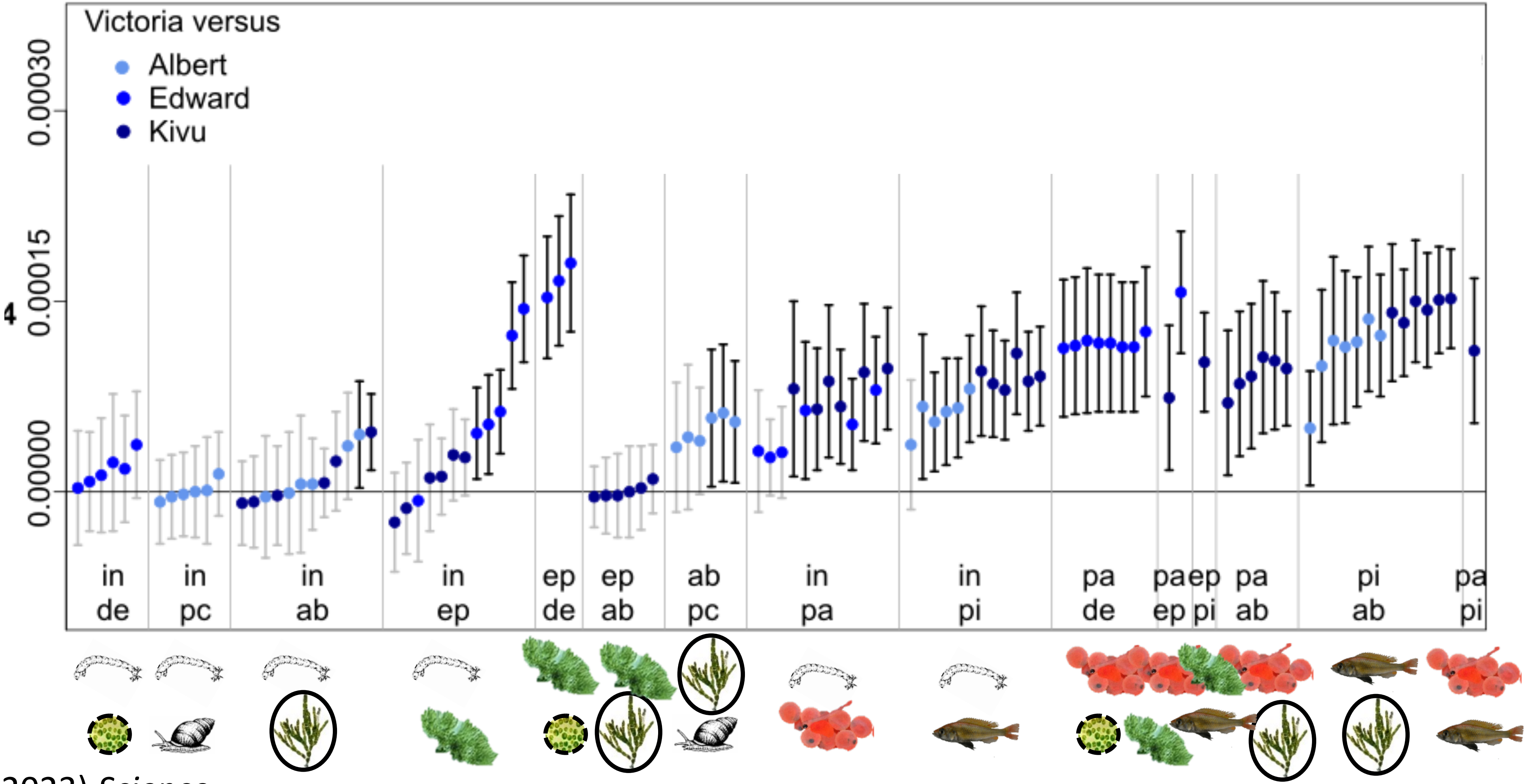
Meier *et al*. (2023) *Science*

Victoria ecomorphs share alleles with the corresponding ecomorphs of the other radiations

Meier *et al*. (2023) *Science*

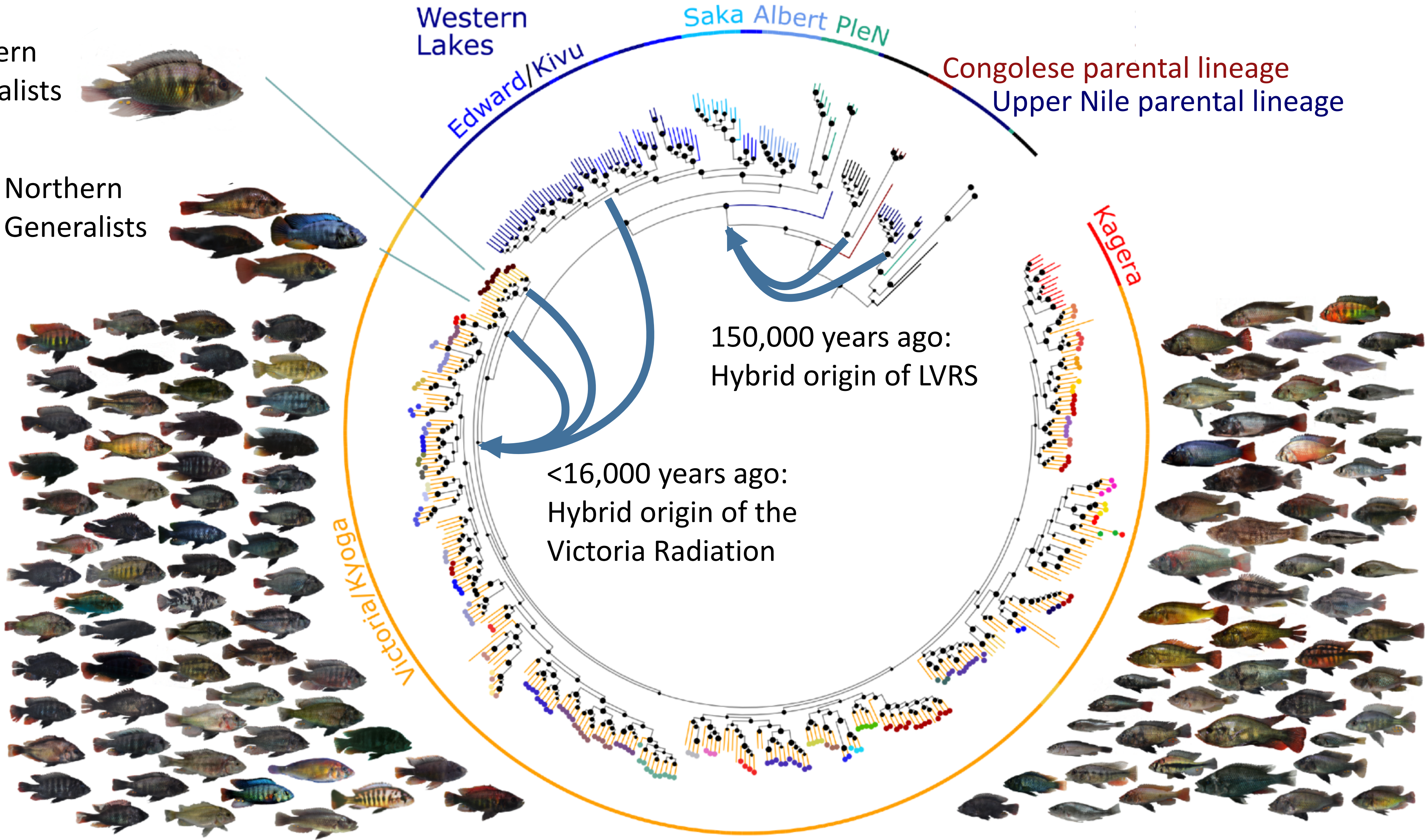
Victoria ecomorphs share alleles with the corresponding ecomorphs of the other radiations

f4 test
(excess
allele
Sharing)



Meier *et al*. (2023) *Science*

Hybrid origin at the base of the Victoria Radiation



Southern Generalists

Northern Generalists

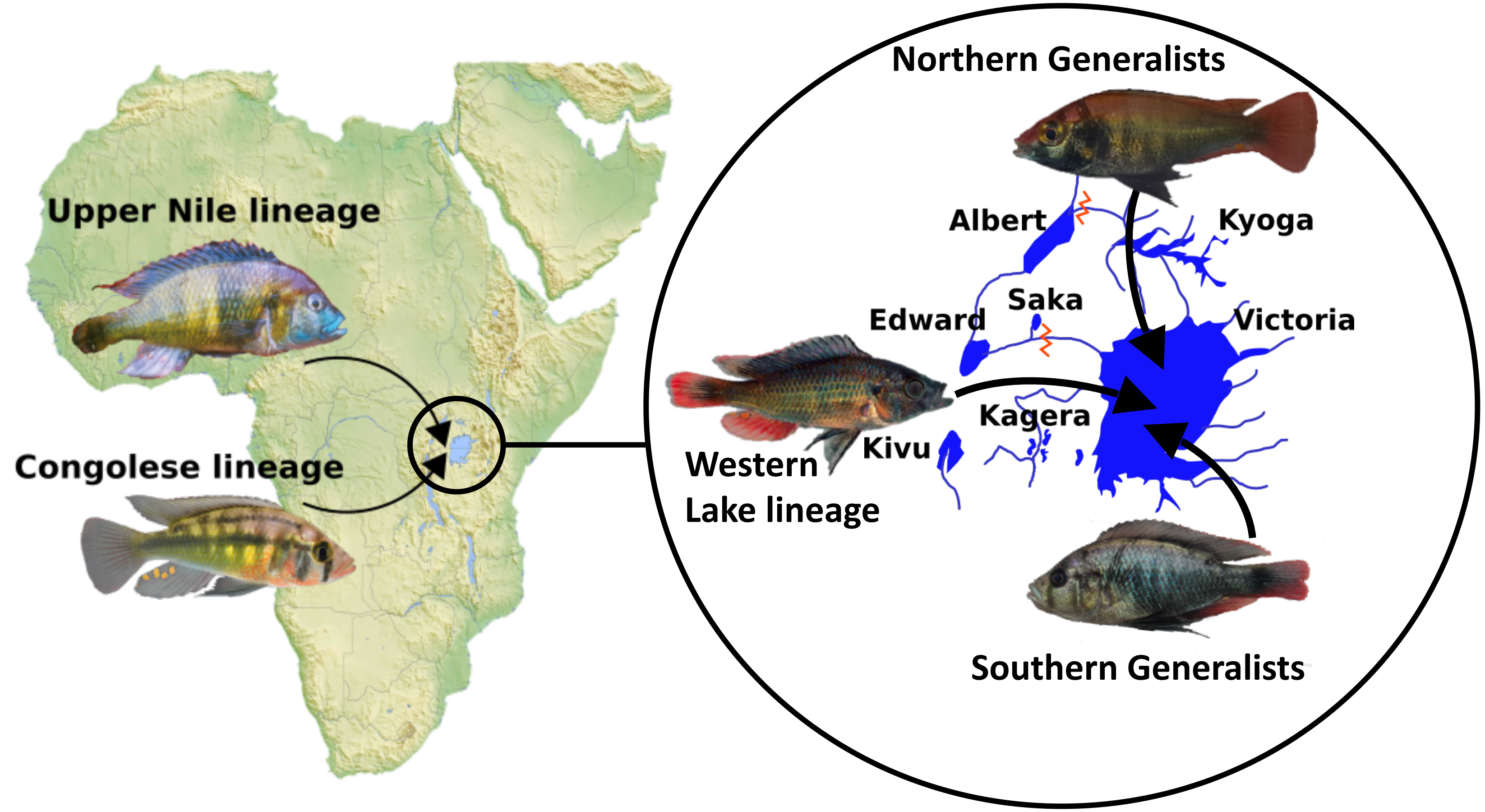
150,000 years ago:
Hybrid origin of LVRS

<16,000 years ago:
Hybrid origin of the Victoria Radiation

Repeated cycles of admixture and diversification

1. level: ~150,000 years ago:
Hybrid origin of the entire LVRS

2. level: ~16,000 years ago:
Hybrid origin of the Victoria Radiation



Meier *et al*. (2023) *Science*

Hybrid origin of pelagic dwarf predators

pelagic
dwarf predators

Meier *et al*. (2023) *Science*

Hybrid origin of pelagic dwarf predators

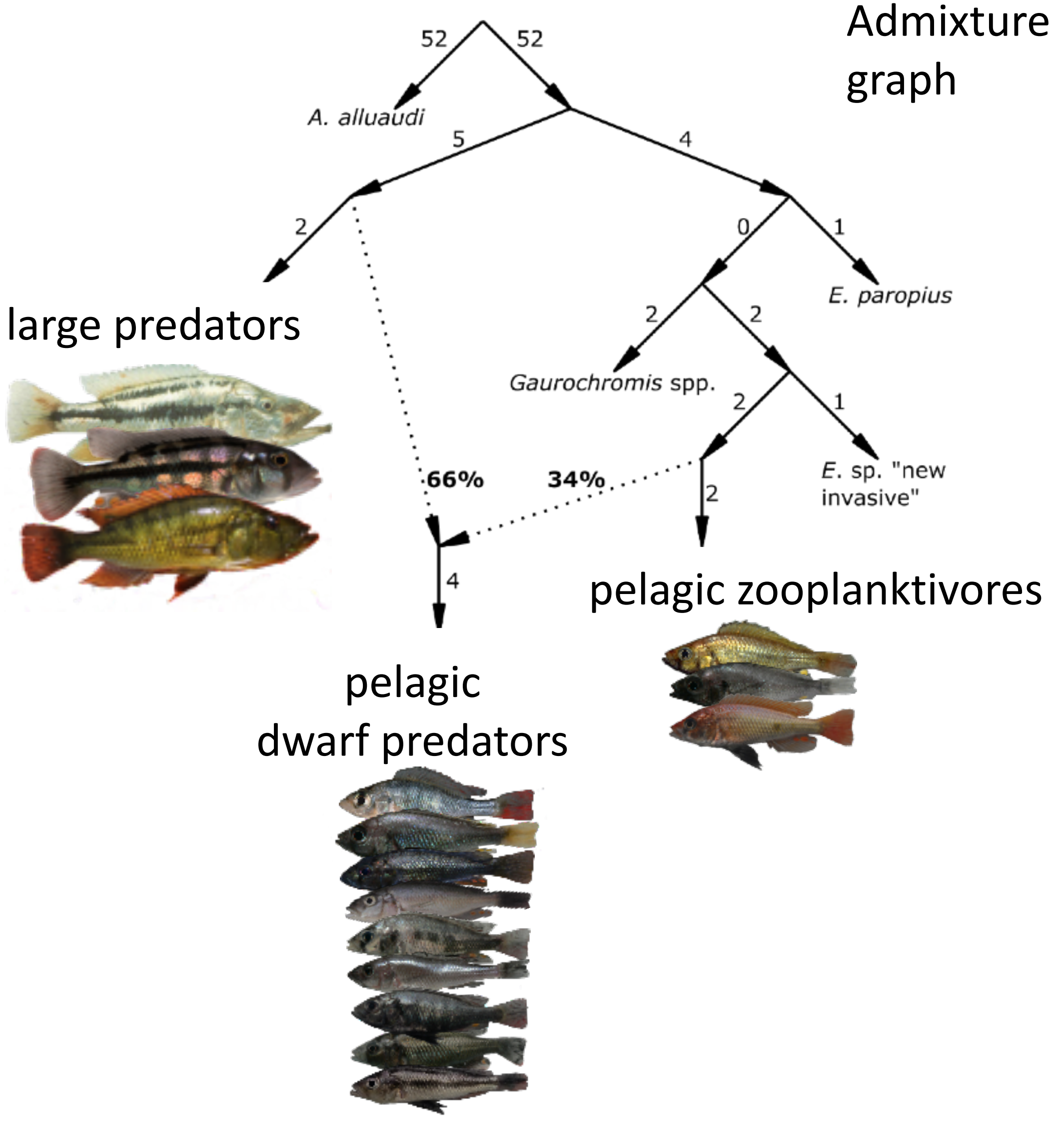
large predators

pelagic zooplanktivores

pelagic
dwarf predators

Meier *et al*. (2023) *Science*

Hybrid origin of pelagic dwarf predators



Admixture graph

large predators

pelagic zooplanktivores

pelagic
dwarf predators

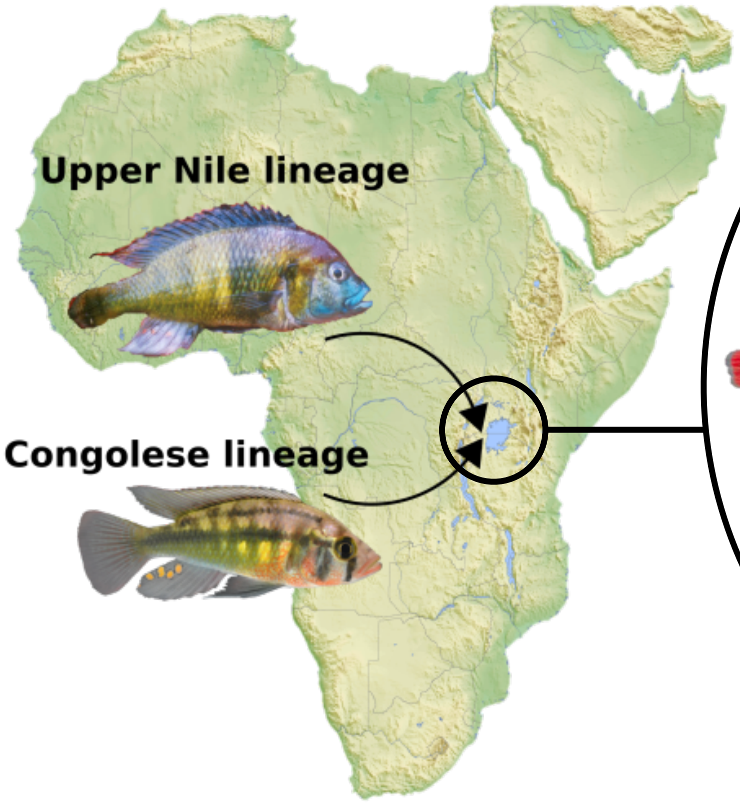
Meier *et al*. (2023) *Science*

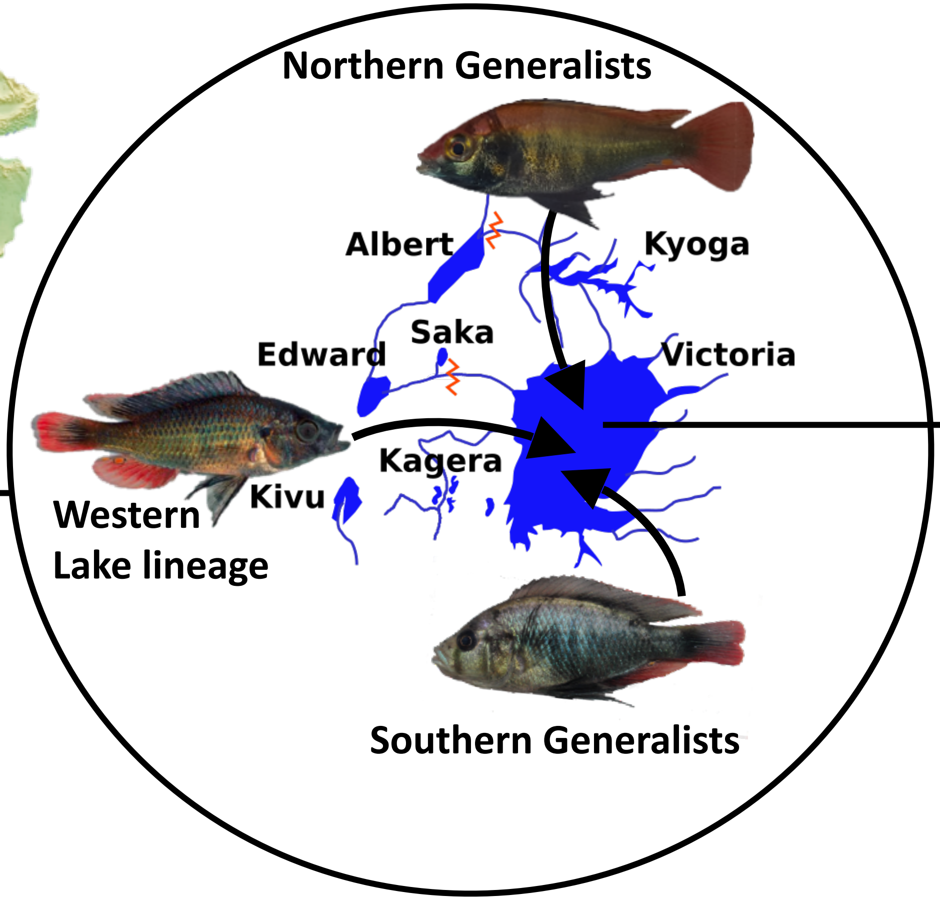
Repeated cycles of admixture and diversification

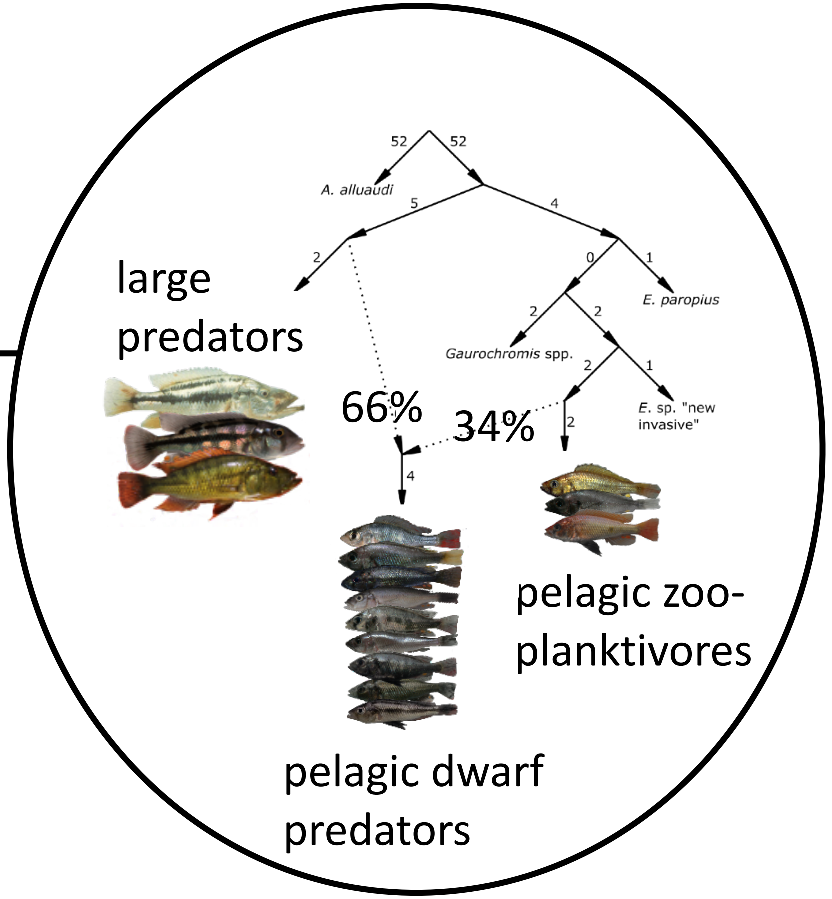
1. level: ~150,000 years ago:
Hybrid origin of the entire LVRS

2. level: ~16,000 years ago:
Hybrid origin of the Victoria Radiation

3. level: <16,000 years ago:
Hybrid origin of dwarf predators and other species

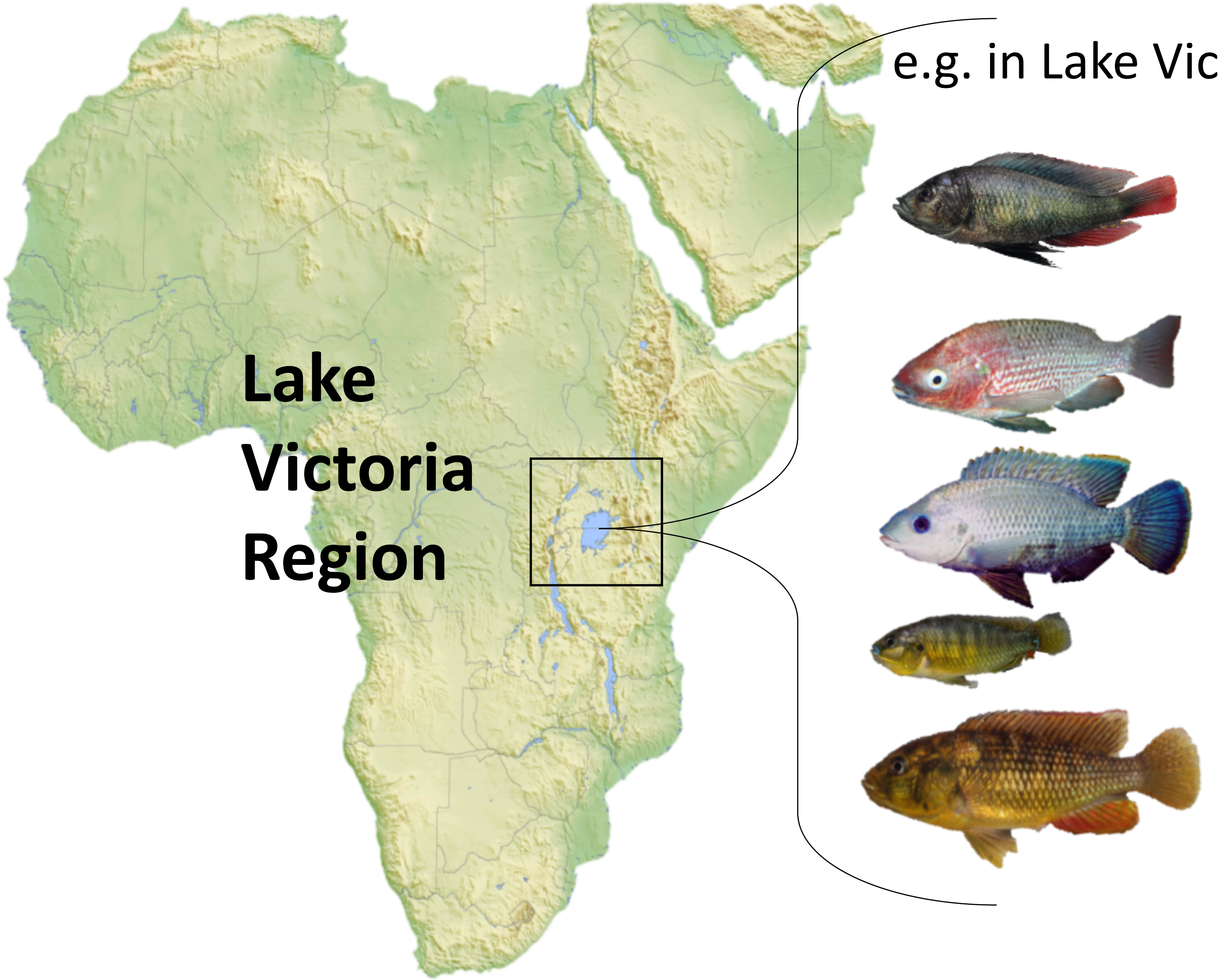






Meier *et al*. (2023) *Science*

Did the other lineages not hybridize?



Lake Victoria Region

e.g. in Lake Victoria

500 species

Hybrid origin + radiation

no new species

no new species

no new species

no new species

no close relatives to hybridise with

Repeated in multiple lakes

Did the other lineages not hybridize?

e.g. in Lake Victoria

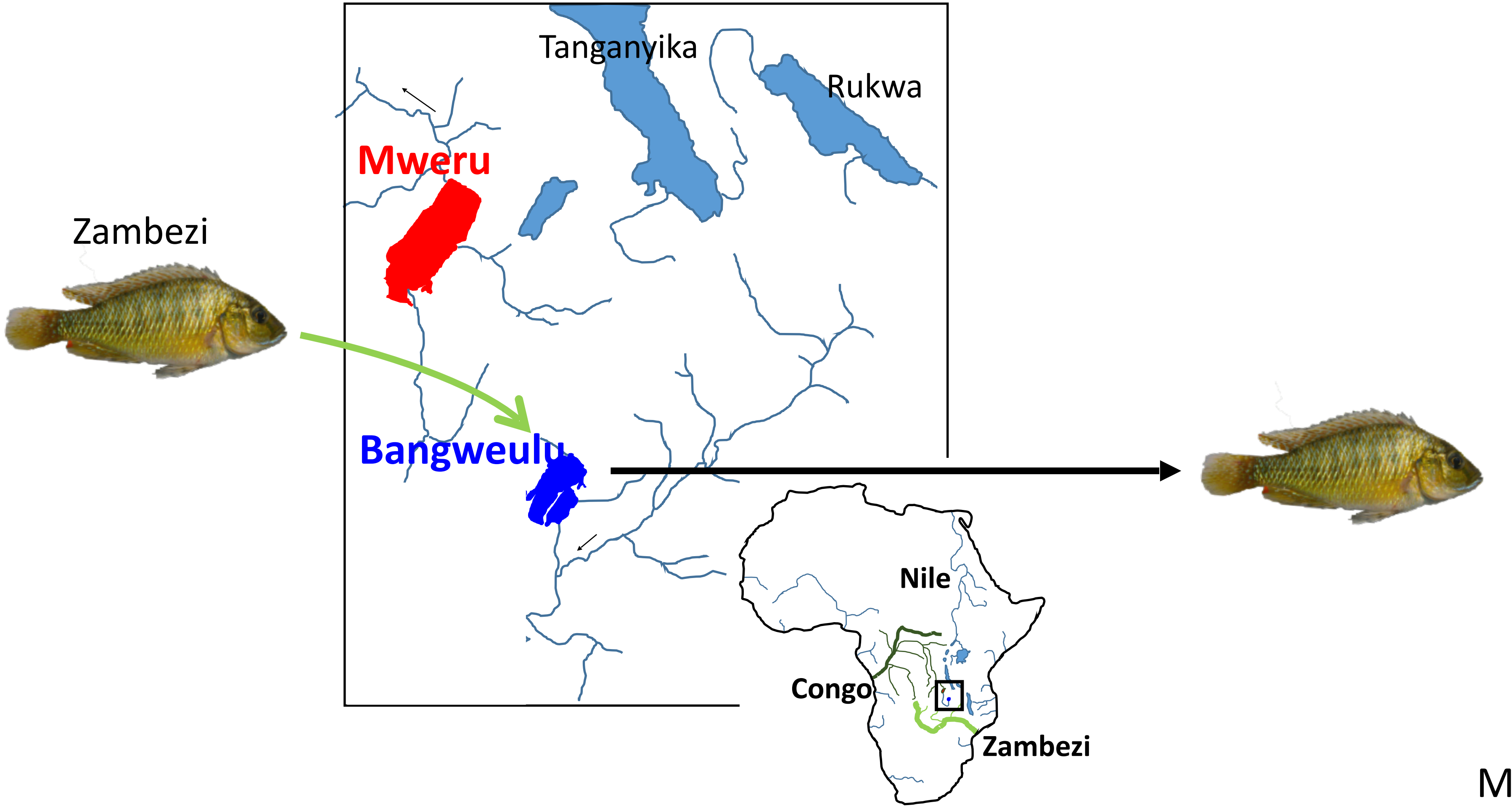
500 species (LVRS)

Hybrid origin
+ radiation

Pseudocrenilabrus

no new species
in 5 lakes

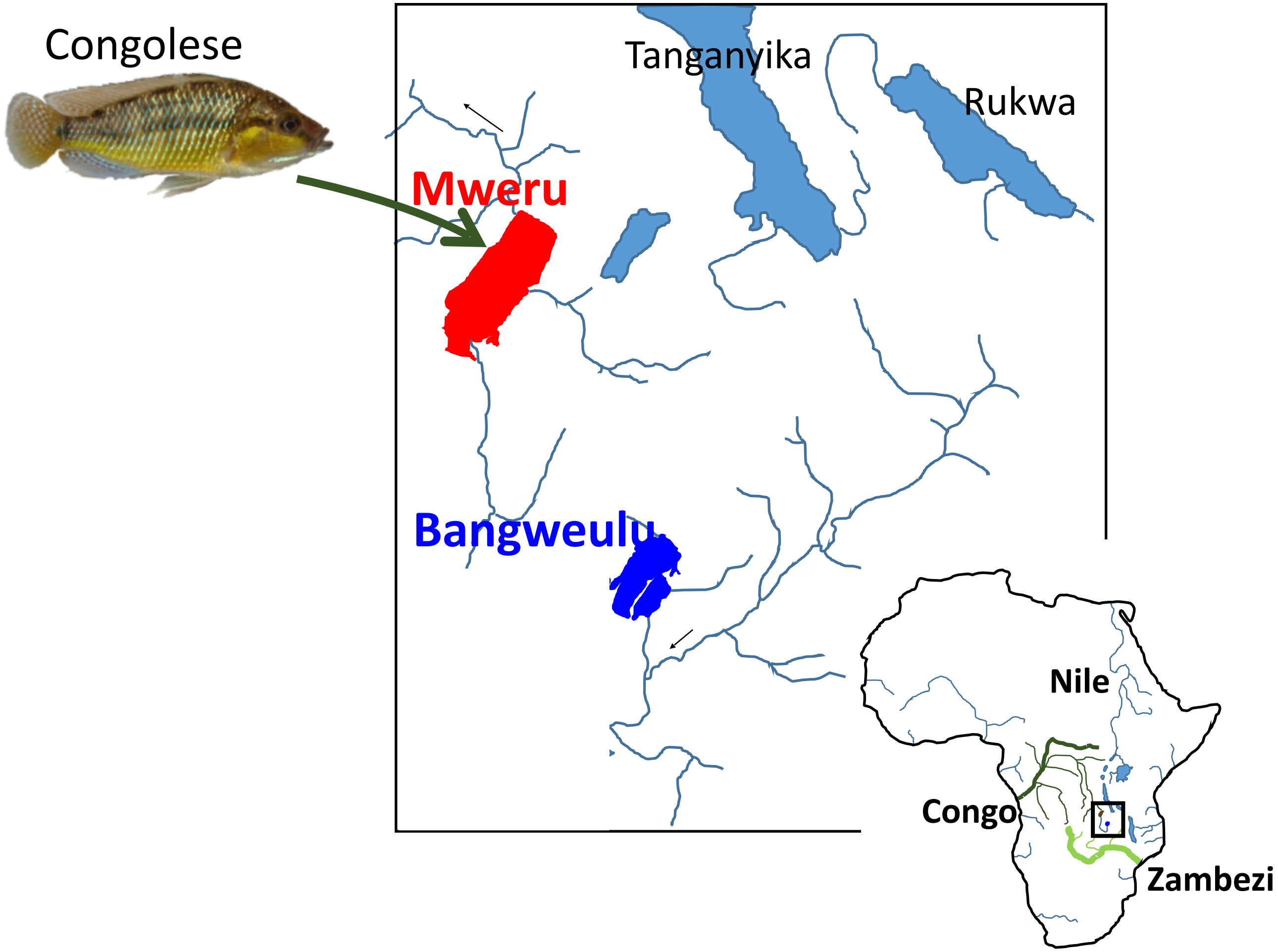
Lake Bangweulu contains a single generalistic Zambezian *Pseudocrenilabrus* species



P. philander (1 species)

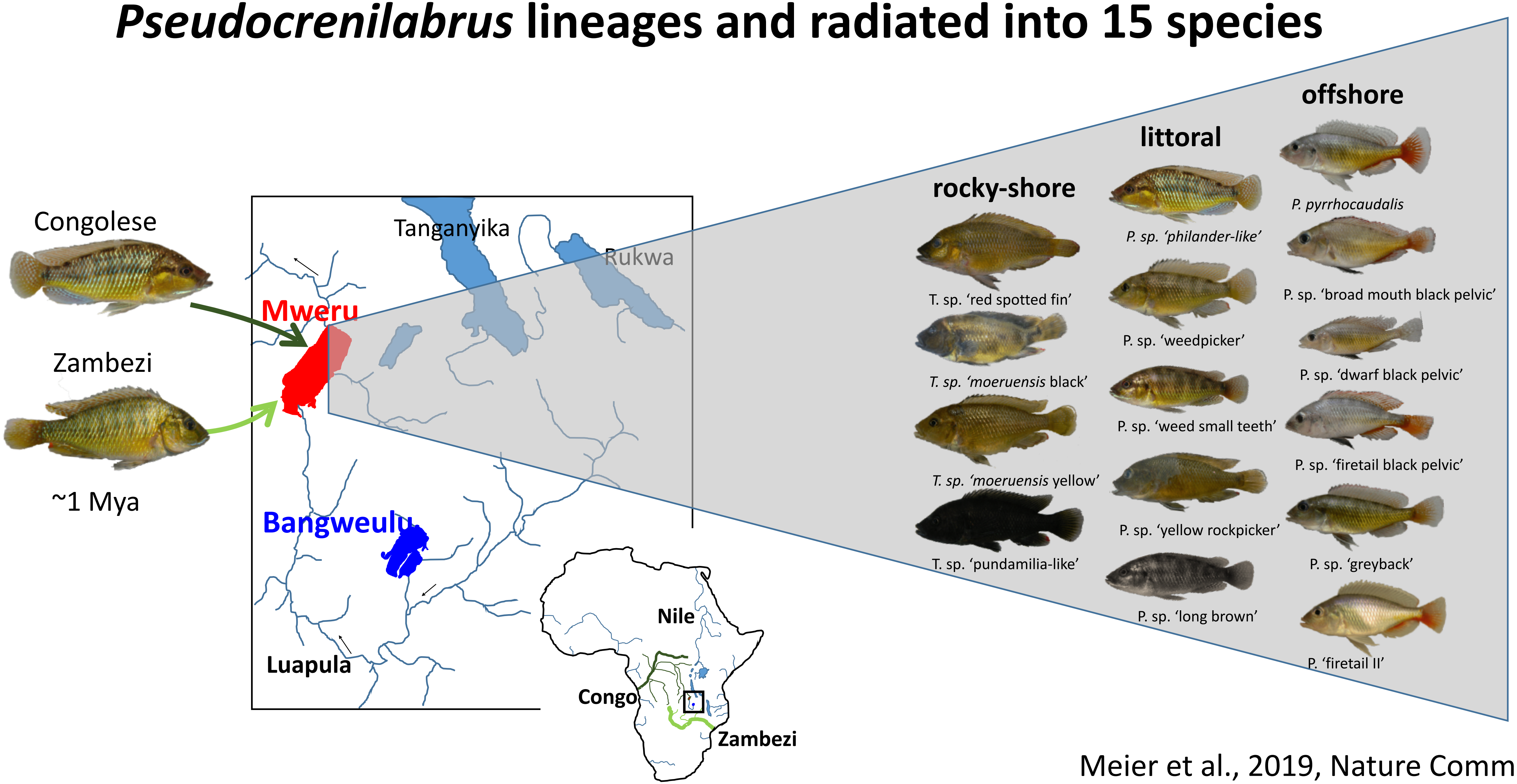
Meier et al., 2019, Nature Comms

Lake Mweru was colonized by Zambezian and Congolese *Pseudocrenilabrus* lineages and radiated into 15 species



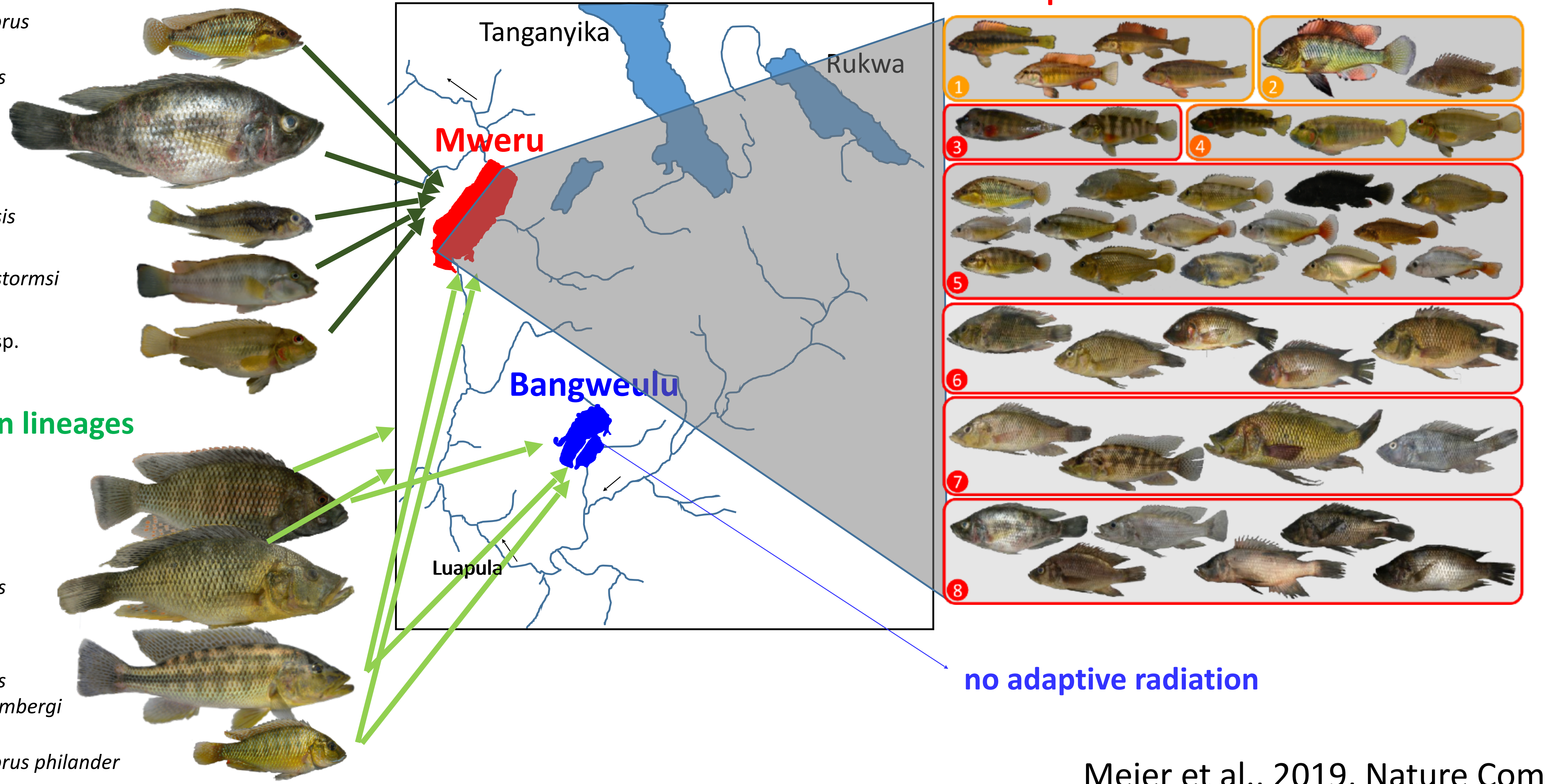
Meier et al., 2019, Nature Comms

Lake Mweru was colonized by Zambezian and Congolese *Pseudocrenilabrus* lineages and radiated into 15 species



Meier et al., 2019, Nature Comms

In Lake Mweru ~40 new species evolved from hybrid origin between Zambezian and Congolese lineages



Congolese lineages

Pseudocrenilabrus

Serranochromis lineage

Orthochromis kalungwishiensis

Orthochromis stormsi

Orthochromis sp.

Zambezian lineages

Sargochromis mellandi

Serranochromis altus & angusticeps

Serranochromis robustus & thumbergi

Pseudocrenilabrus philander

~40 species evolved in 8 radiations

no adaptive radiation

Meier et al., 2019, Nature Comms

Slow evolution through new mutations

Boost of diversity through hybridisation