Museomics: a window to past population history

Jérémy Gauthier

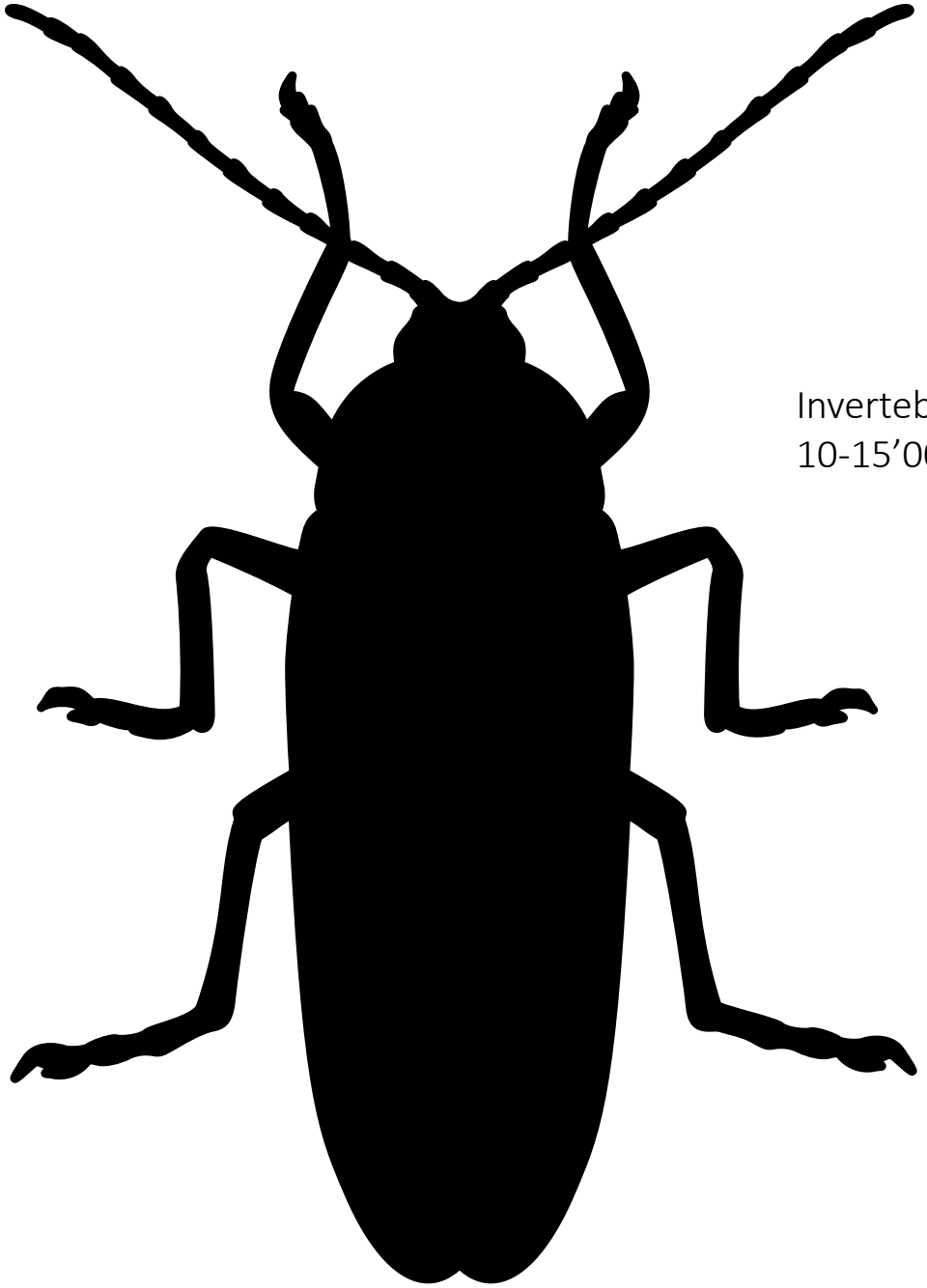
muséum genève

UNIVERSITÉ DE GENÈVE

2-3 billion specimens in museums !

Muséum d’histoire naturelle de Genève (MHNG)

15 million specimens



Invertebrates
10-15’000’000 (MHNG)

Vertebrates
330’000 (MHNG)

Minerals and Fossils
170’000 (MHNG)

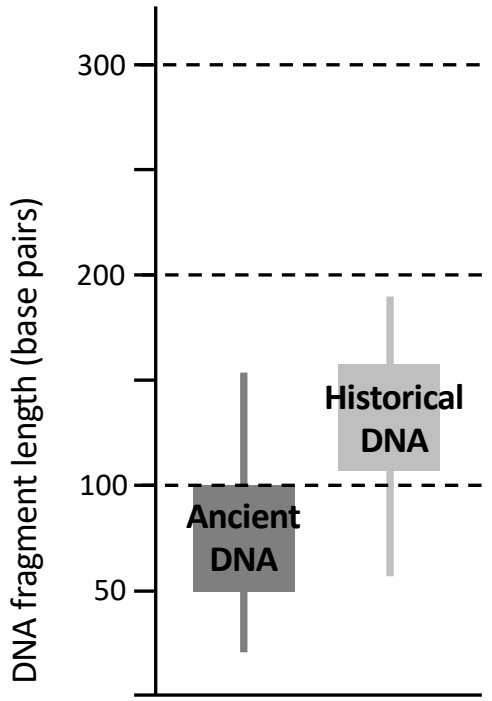
Main issues when working with historical DNA

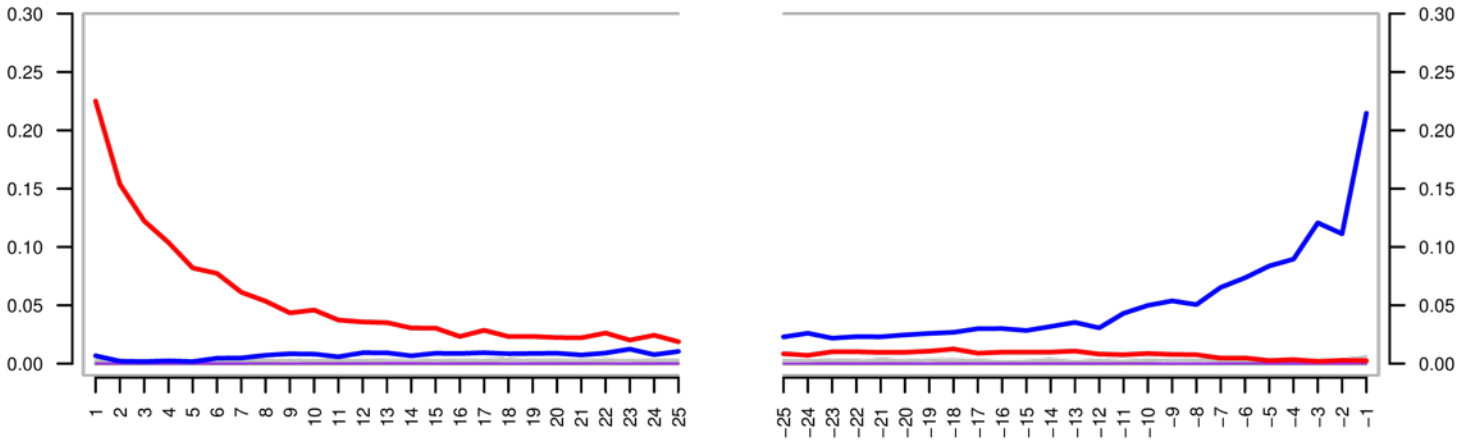
- Low quantity of DNA

- Contaminations

- Small fragments

- Chemical modifications: deamination





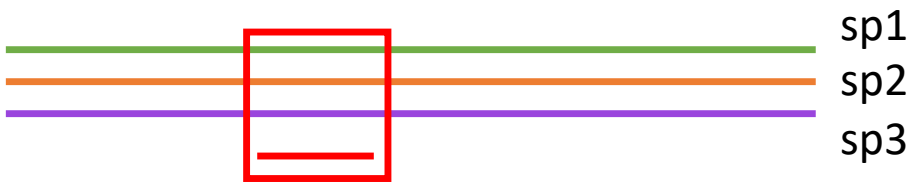
MapDamage2 results

What approaches to circumvent these problems?

- *Sequence capture using probes (exons, genome, UCE):*

  usually requires reference genomes

  in silico probe synthesis is expensive



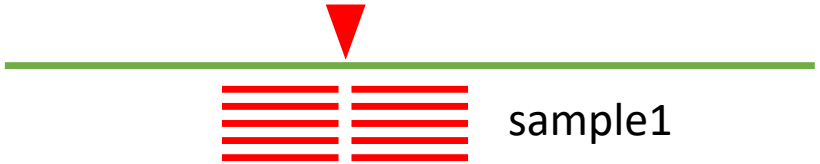
- *Shotgun sequencing, genome skimming:*

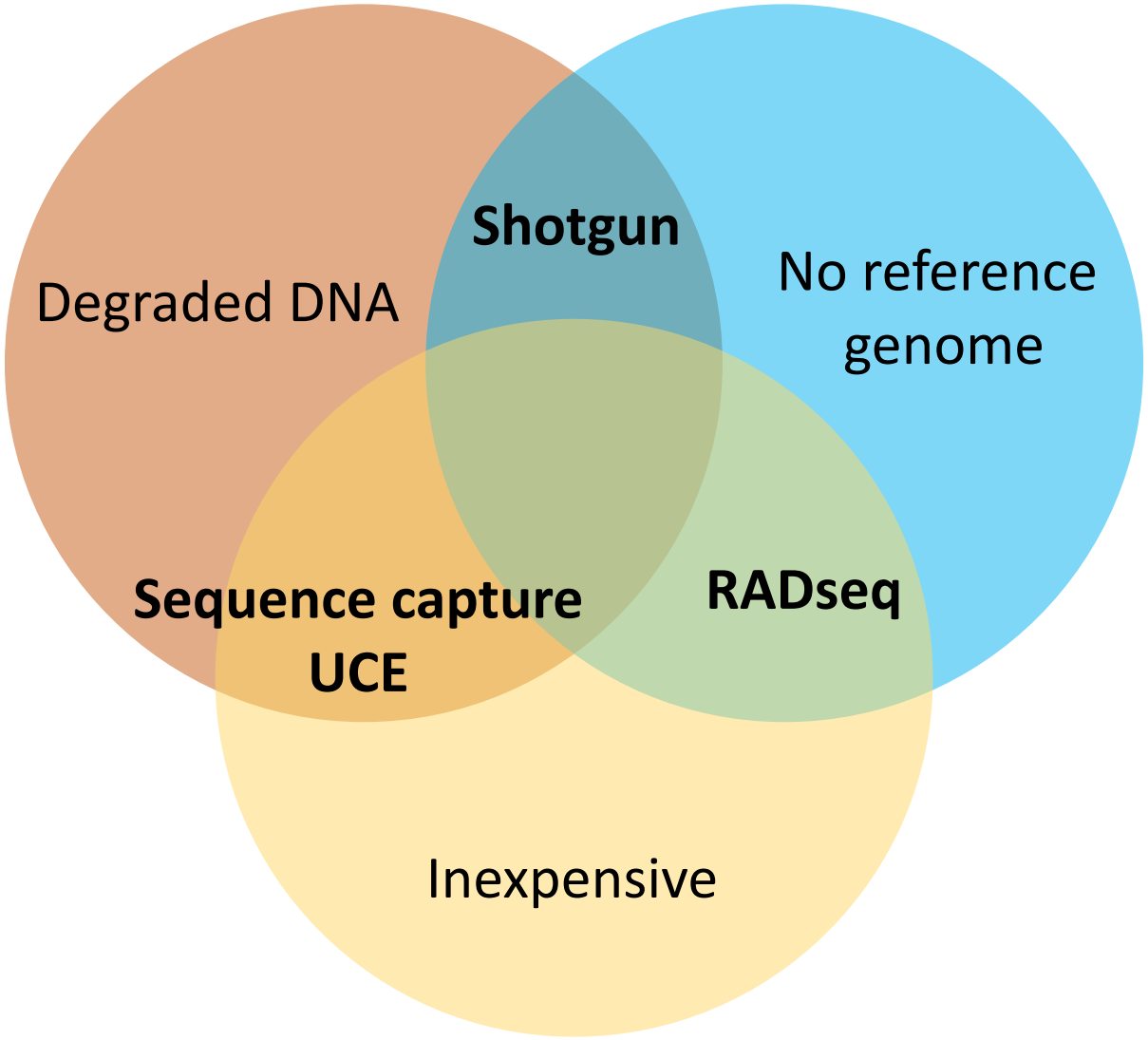
  expensive for many samples

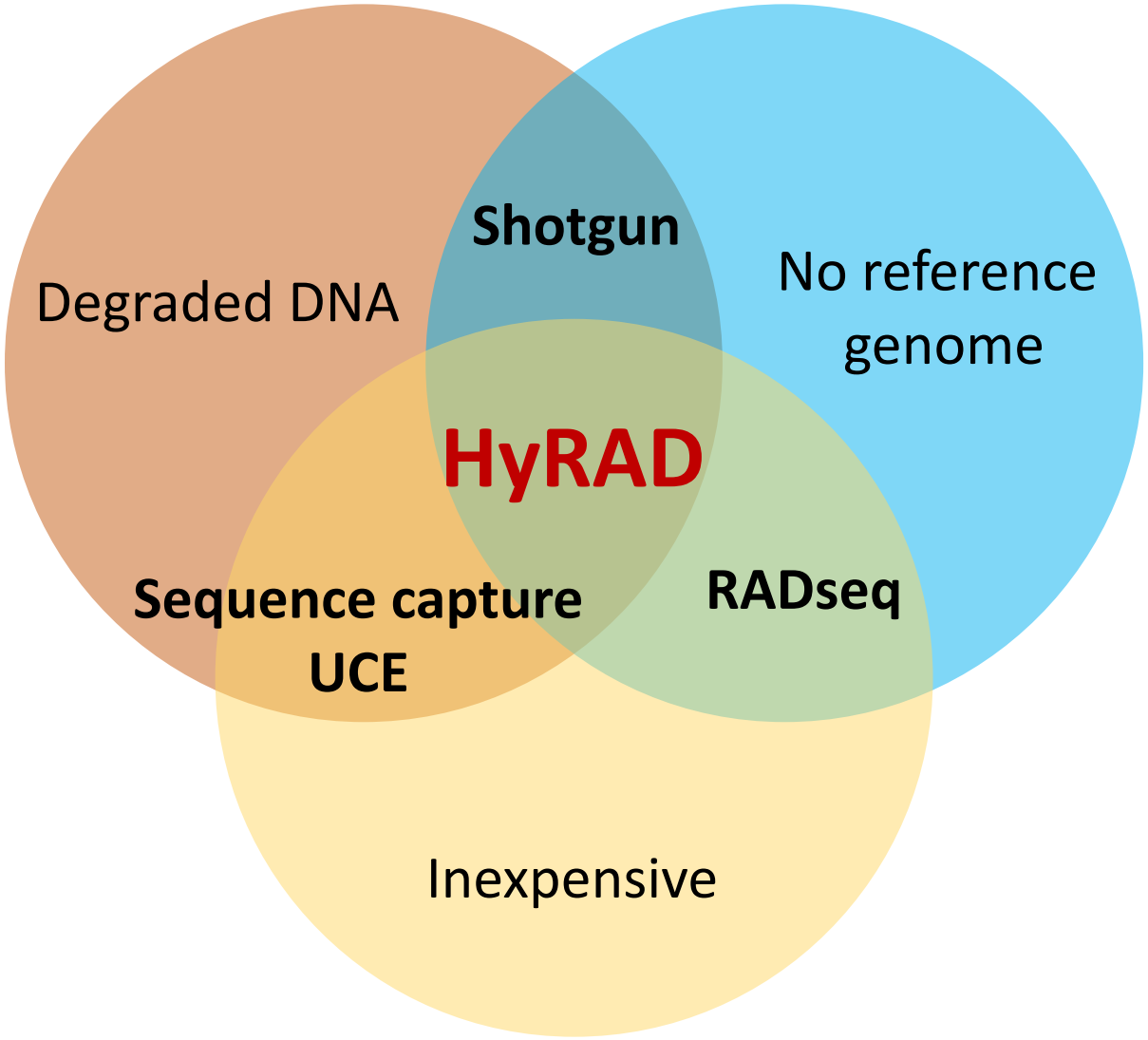
  number of shared loci is random

- *RADseq:*

  problematic with degraded DNA




Degraded DNA
Shotgun
No reference genome
Sequence capture UCE
RADseq
Inexpensive



Genome complexity reduction

+

hybridization capture

Synthesized commercial probes

RAPTURE (Ali et al. 2016)

GBS-capture (Barreiro et al. 2016)

RADcap (Hoffberg et al. 2016)

Bench-top produced probes

HyRAD (Suchan et al. 2016)

HyRAD-X (Schmid et al. 2017)

HyRAD

Fresh sample DNA extraction

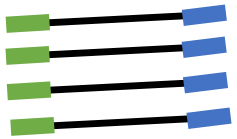
genomic DNA

HyRAD

Fresh sample DNA extraction

genomic DNA

ddRAD library

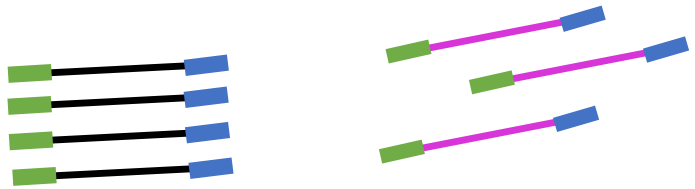


HyRAD

Fresh sample DNA extraction

genomic DNA

ddRAD library



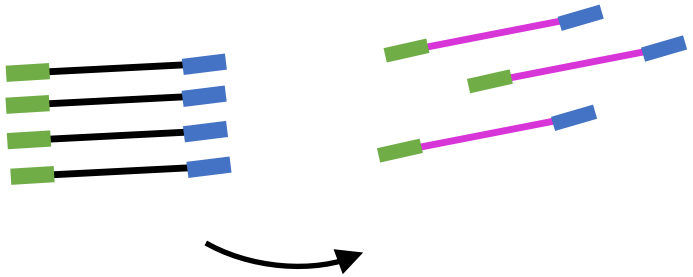
In vitro transcription into RNA probes

HyRAD

Fresh sample DNA extraction

genomic DNA

ddRAD library

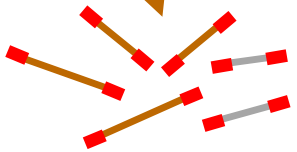


In vitro transcription into RNA probes

Historical DNA extraction

Including contaminant or untargeted loci

Shotgun library



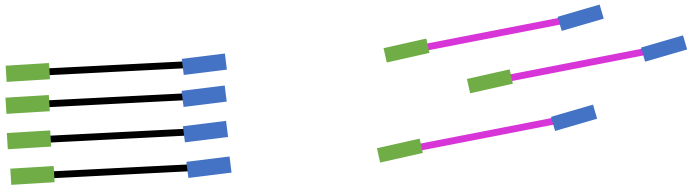
HyRAD

Fresh sample DNA extraction

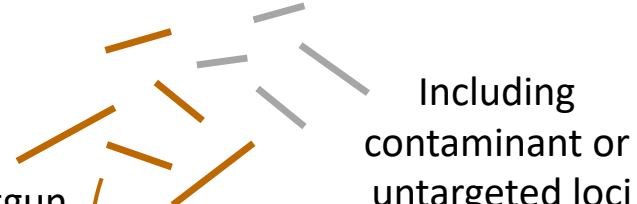
Historical DNA extraction

genomic DNA

ddRAD library

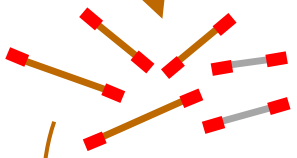


In vitro transcription into RNA probes

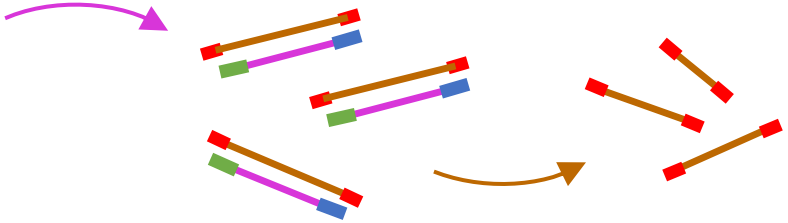


Including contaminant or untargeted loci

Shotgun library



Hybridization



Capture and wash

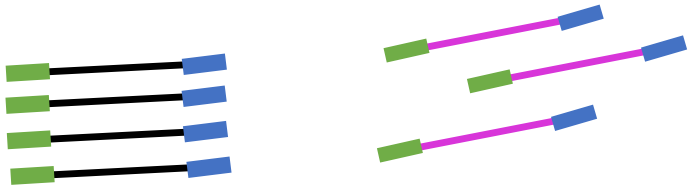
HyRAD

Fresh sample DNA extraction

Historical DNA extraction

genomic DNA

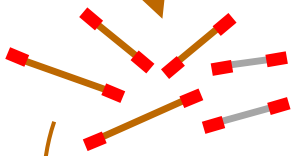
ddRAD library



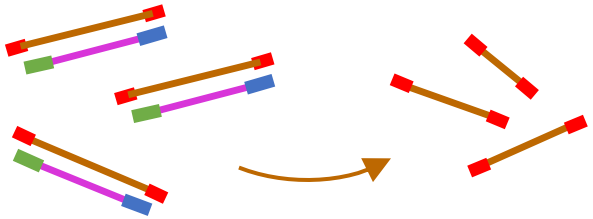
In vitro transcription into RNA probes

Including contaminant or untargeted loci

Shotgun library



Hybridization



Capture and wash

Sequencing

HyRAD

Fresh sample DNA extraction

Historical DNA extraction

genomic DNA

ddRAD library

Shotgun library

Including contaminant or untargeted loci

In vitro transcription into RNA probes

Hybridization

Probes sequencing

Sequencing

Capture and wash

Evolution of Carabinae: wing loss in Calosomes

Museomics

Collection samples
HyRAD-X protocol

Haplothorax burchellii

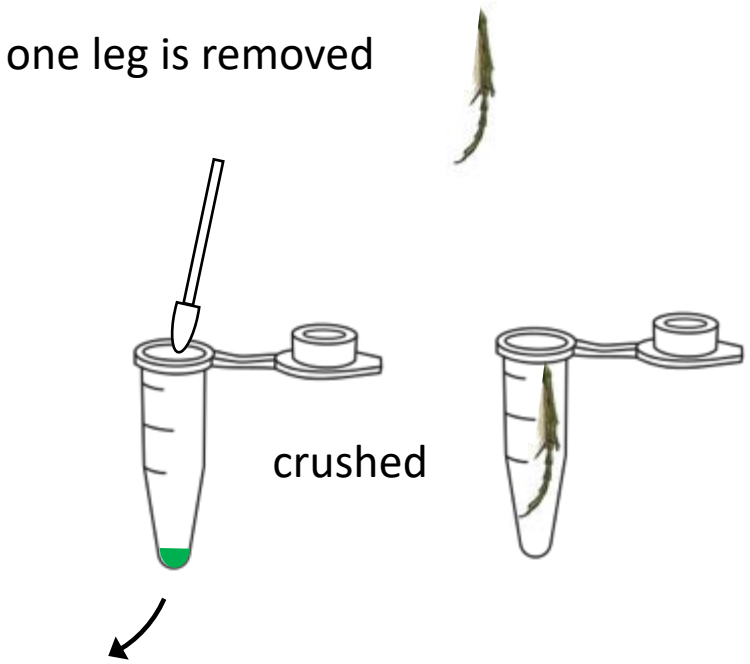
Toussaint*, Gauthier* et al. 2021 GBE

Evolution of Carabinae: wing loss in Calosomes

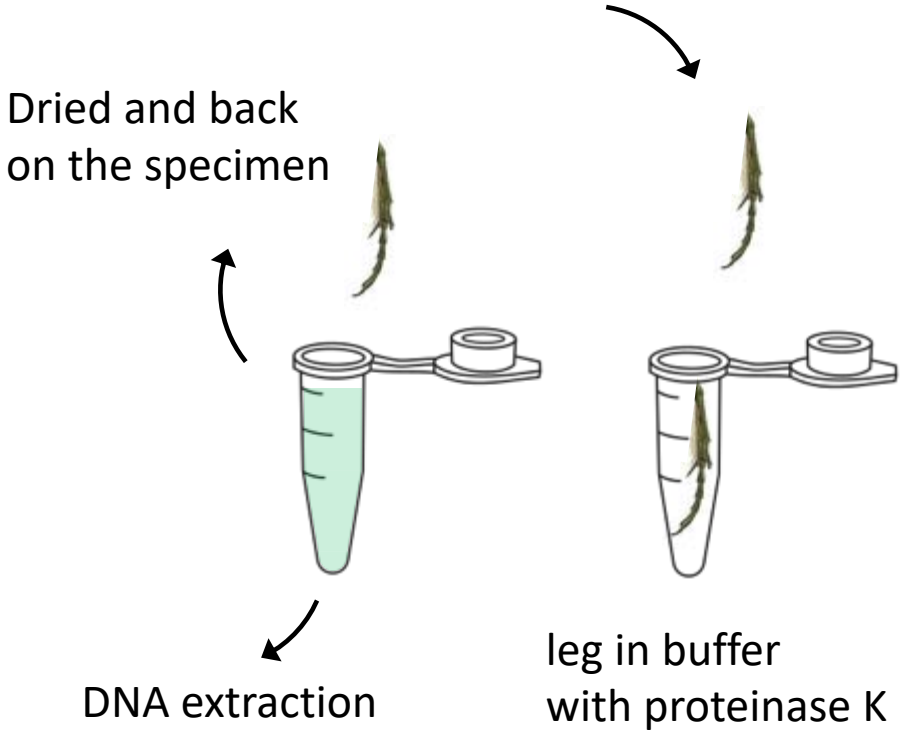
Museomics

Collection samples
HyRAD-X protocol

Classic DNA extraction



Non-destructive DNA extraction



Haplothorax burchellii

Toussaint*, Gauthier* et al. 2021 GBE

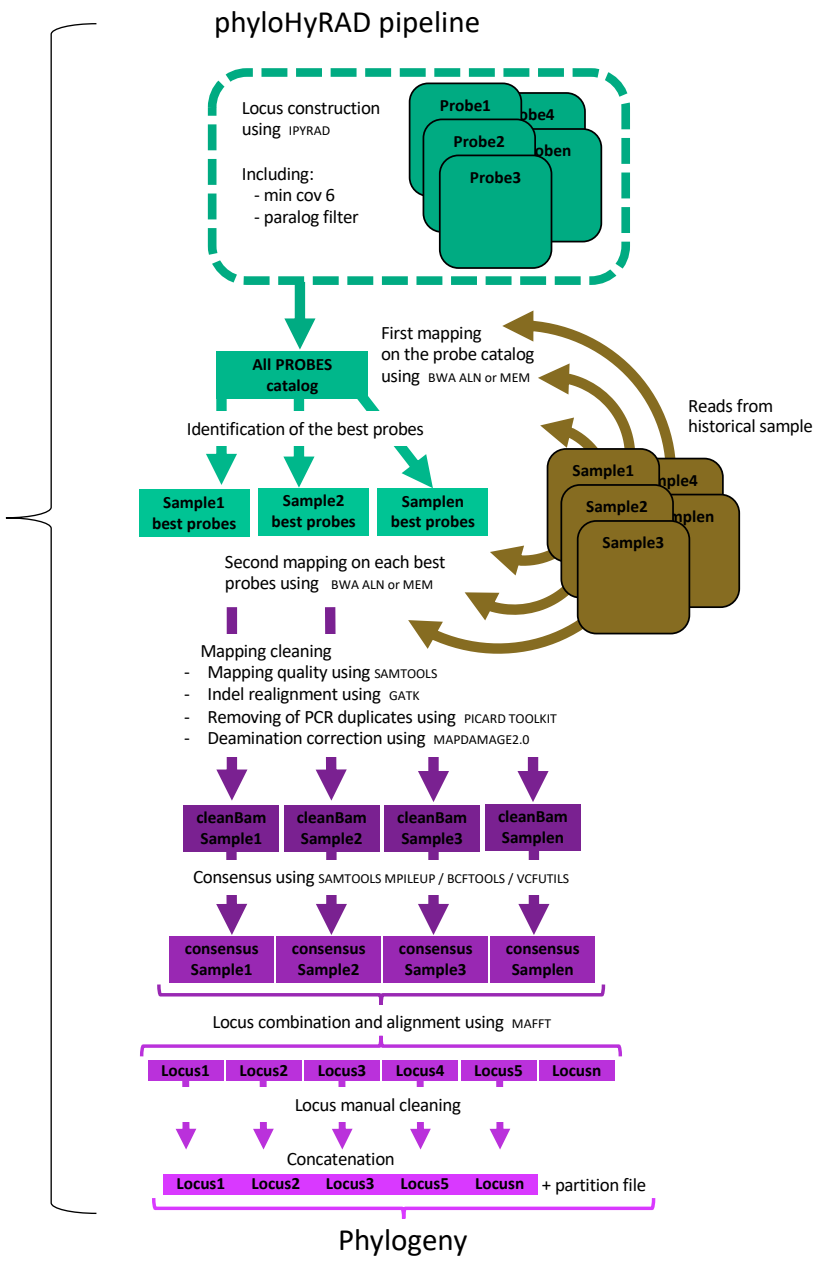
Evolution of Carabinae: wing loss in Calosomes

Museomics

Collection samples
HyRAD-X protocol

↓

`phyloHyRAD` pipeline



Toussaint*, Gauthier* et al. 2021 GBE

Evolution of Carabinae: wing loss in Calosomes

Museomics

Collection samples
HyRAD-X protocol

↓

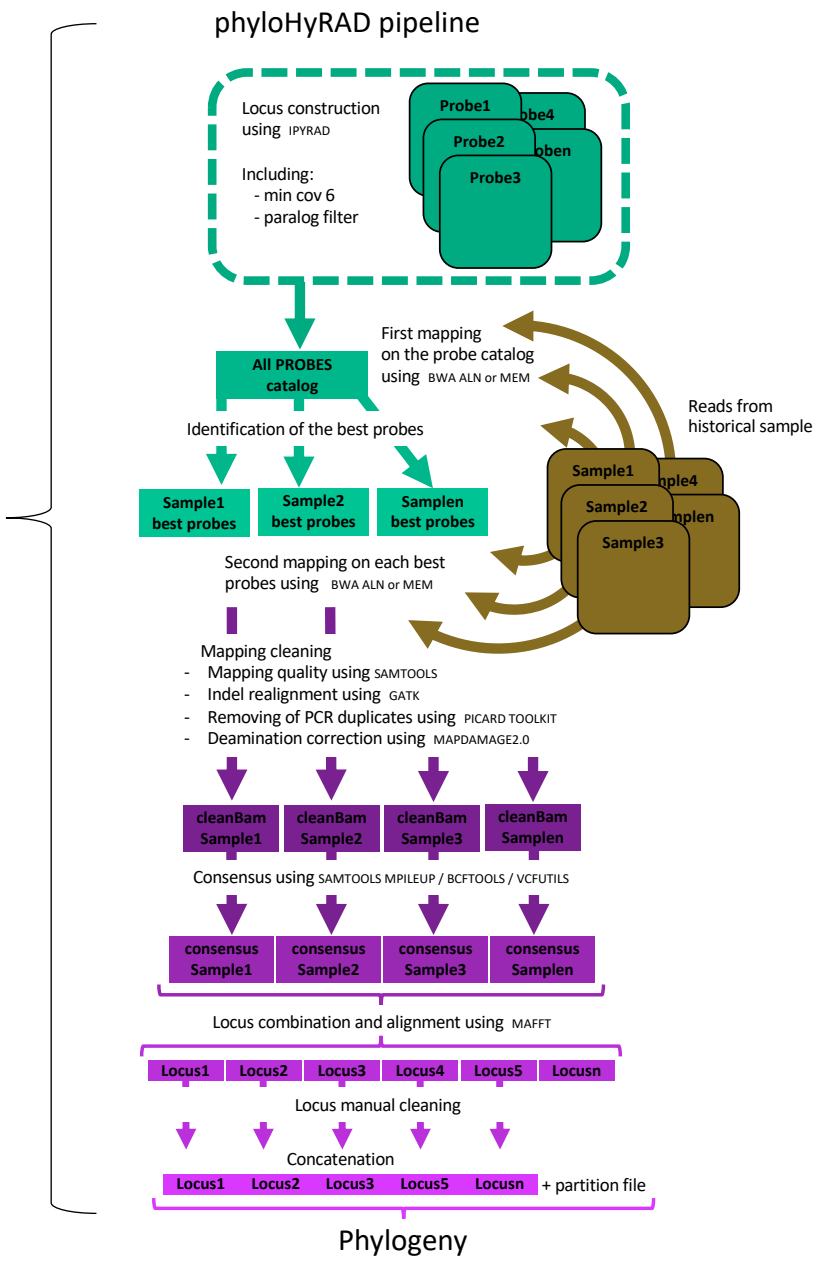
phyloHyRAD pipeline

↓

2945 shared loci

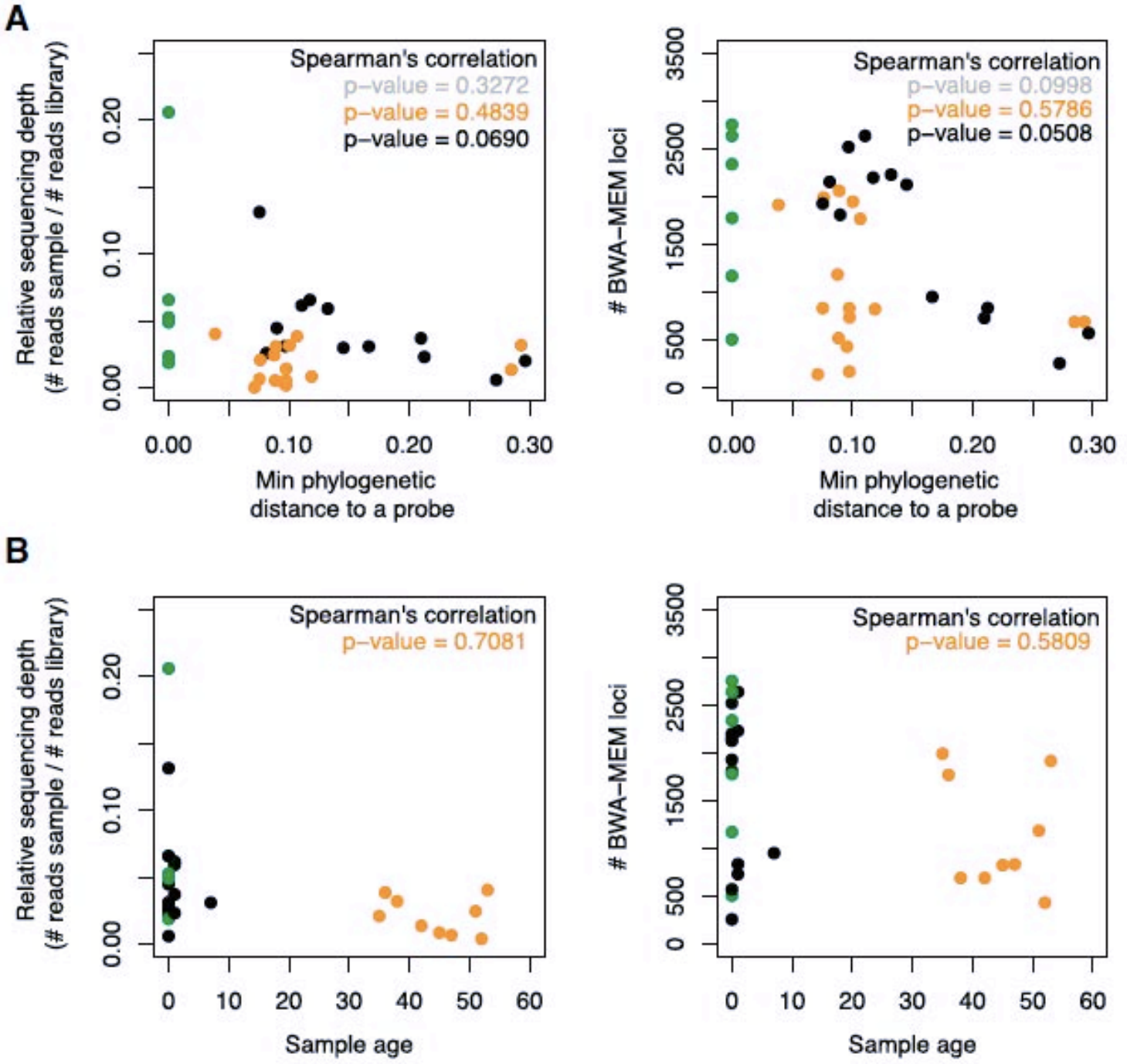
↓

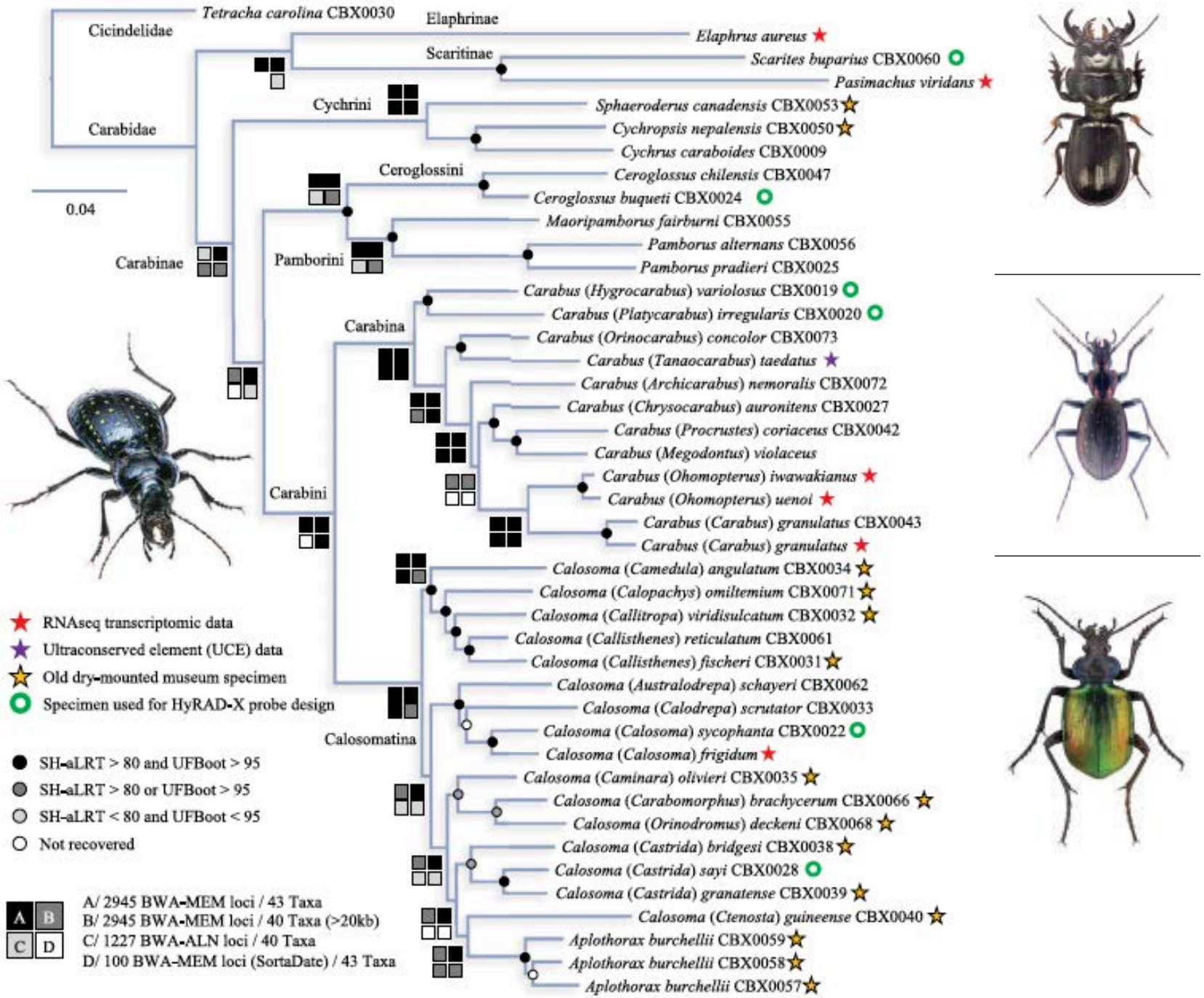
Phylogenomic inferences



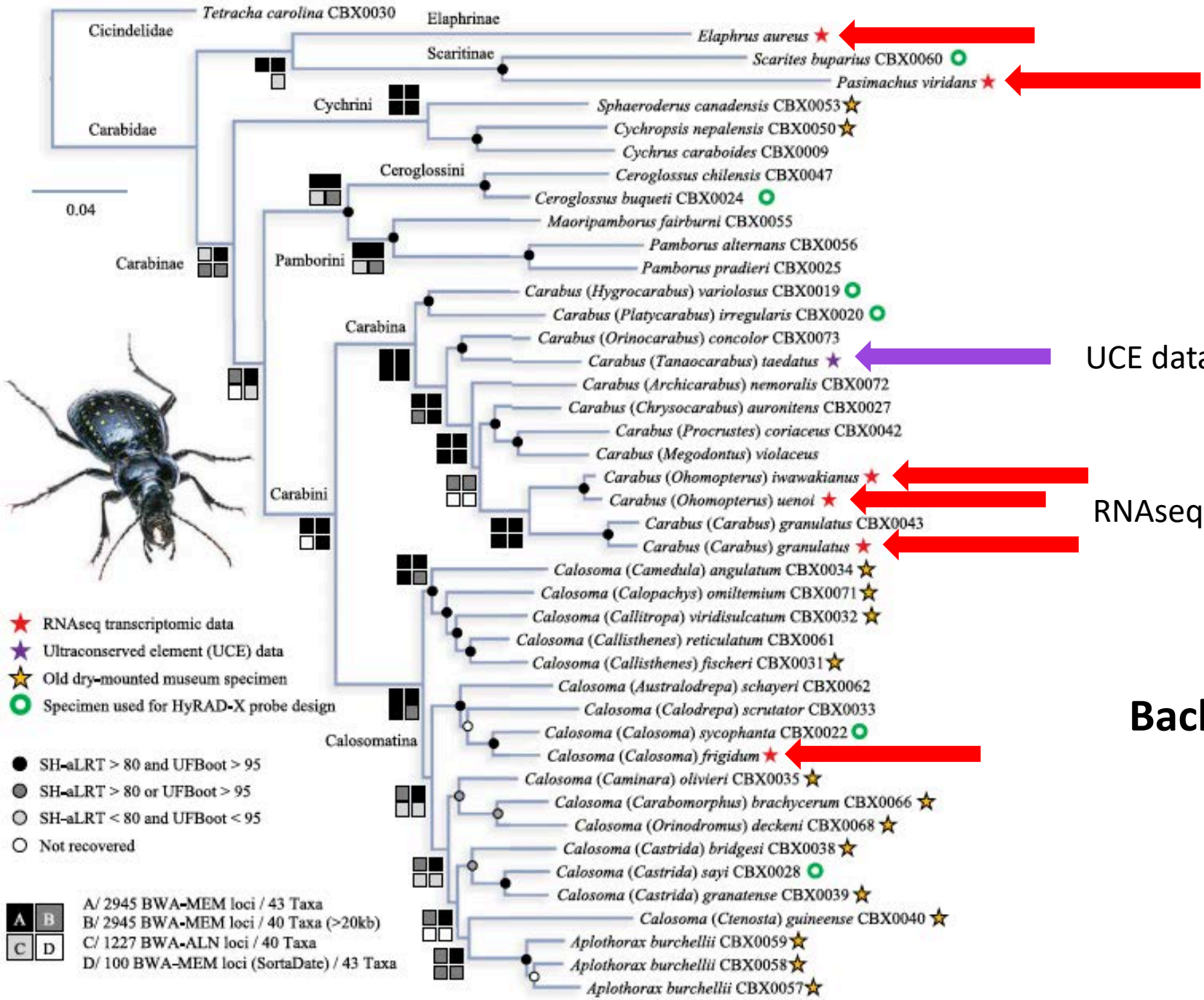
Toussaint*, Gauthier* et al. 2021 GBE

Putative biases ?





Toussaint*, Gauthier* et al. 2021 GBE

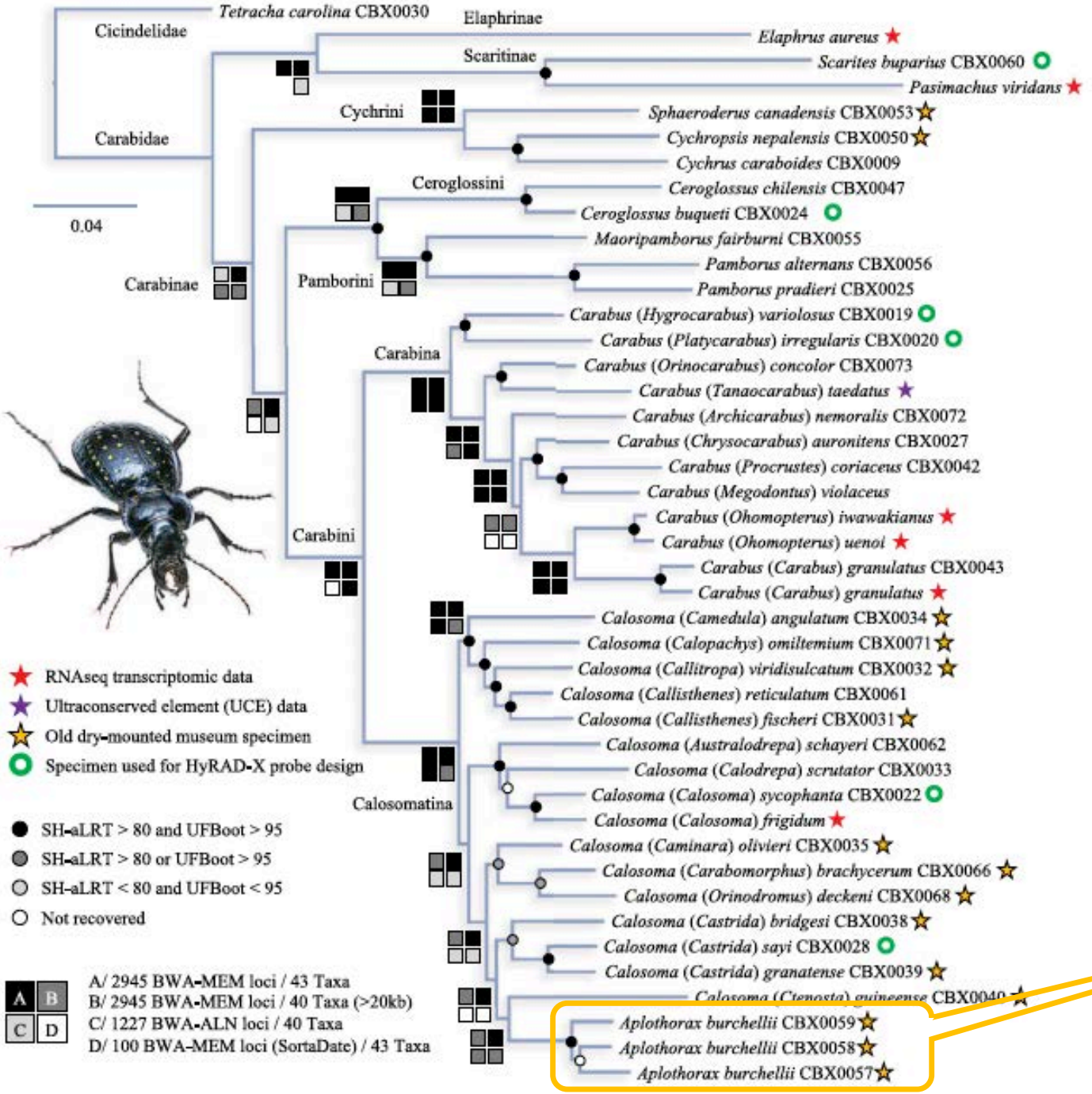


UCE data from Baca et al. 2017 Syst Entomol

RNAseq data from 1KITE project

Backwards compatibility with existing data

Toussaint*, Gauthier* et al. 2021 GBE



St Helena endemic species
Extinct since 1968

Haplothorax burchellii

Toussaint*, Gauthier* et al. 2021 GBE

Diversification of *Oreina* species

naturhistorisches museum Basel

Oreina alpestris

Oreina speciosa

Oreina speciosissima

- Monophyly of *Oreina* ?
- Mecanisms involved in diversification ?

Credit : Matthias Borer

Gauthier*, Borer* et al. in prep

Diversification of *Oreina* species

HyRAD (Hybridization RAD) protocol

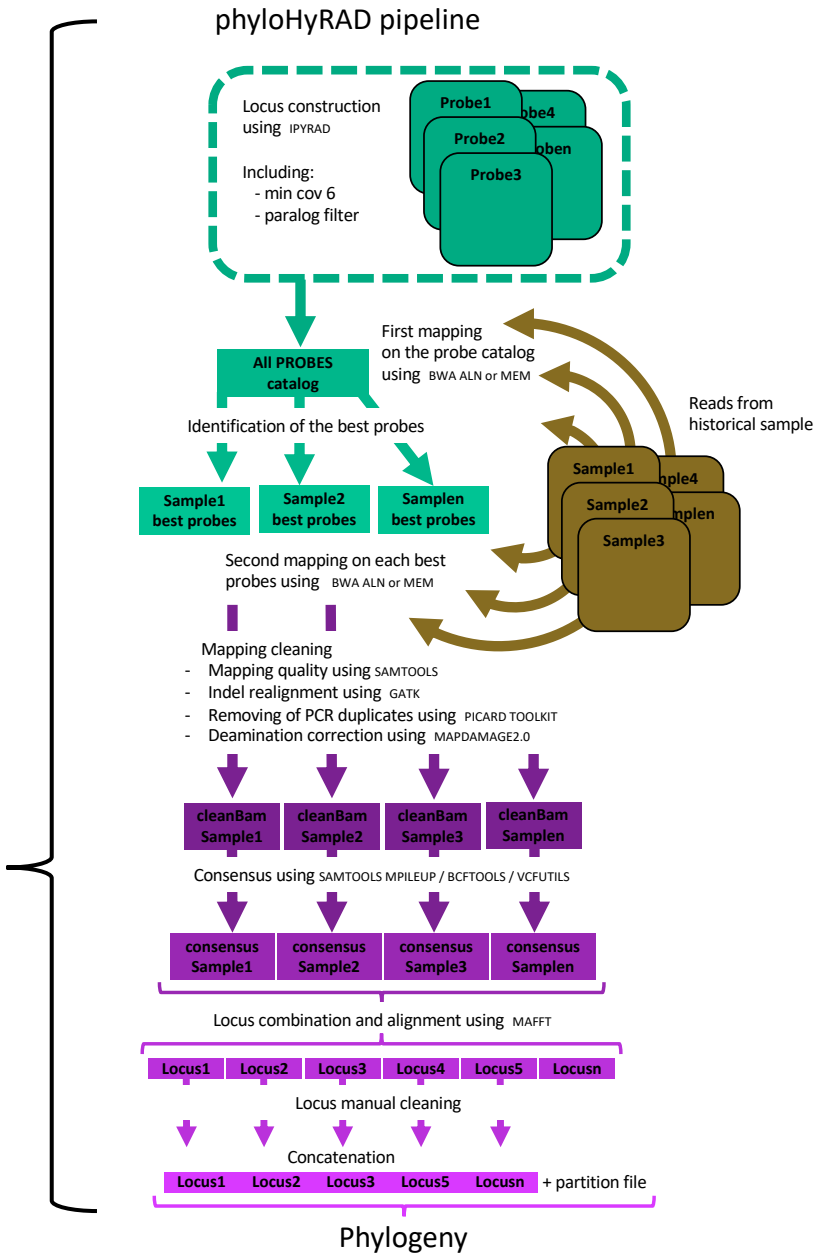
Gauthier*, Borer* et al. in prep

Diversification of *Oreina* species

HyRAD (Hybridization RAD) protocol

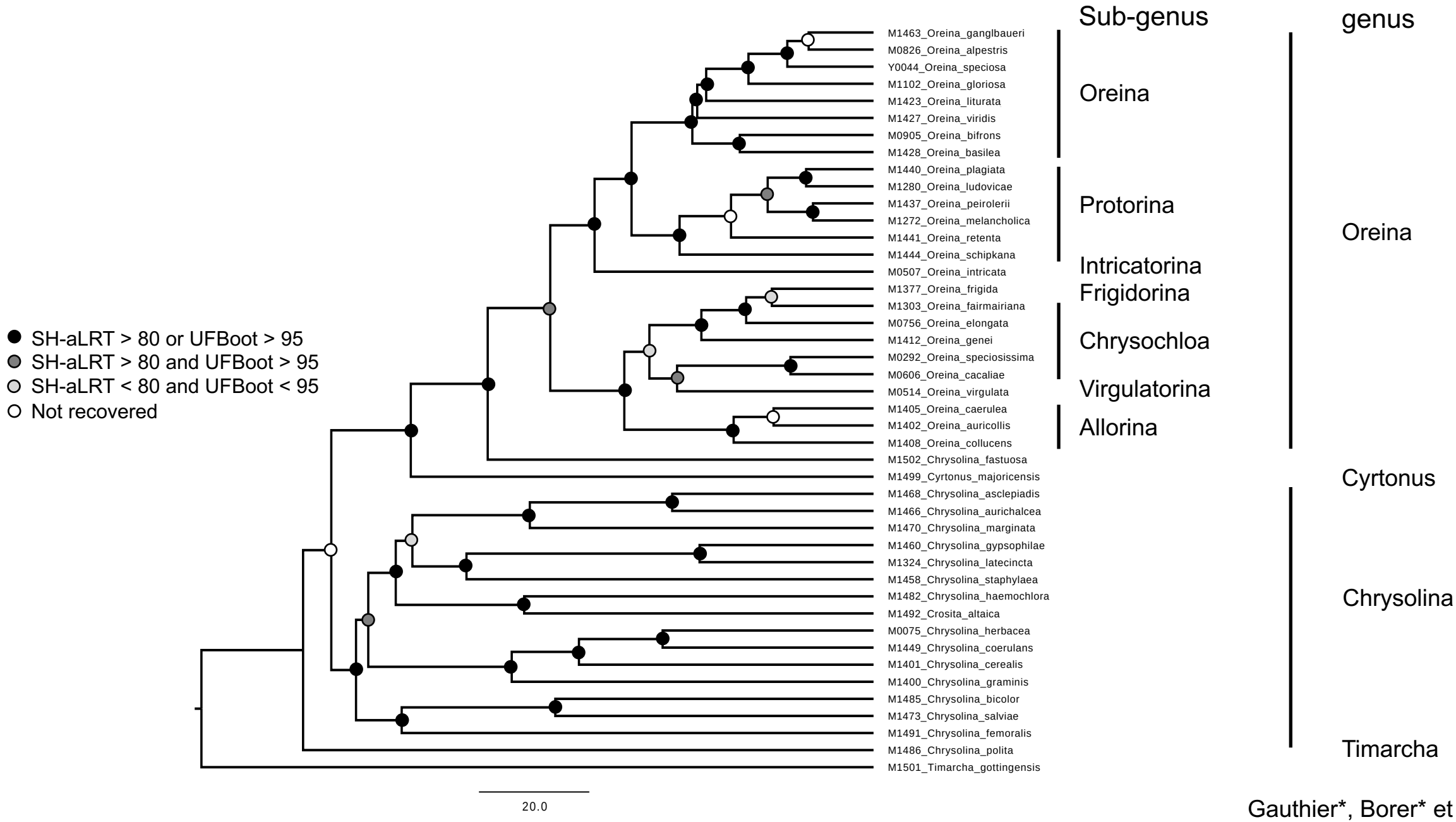
phyloHyRAD pipeline

2235 shared loci



Gauthier*, Borer* et al. in prep

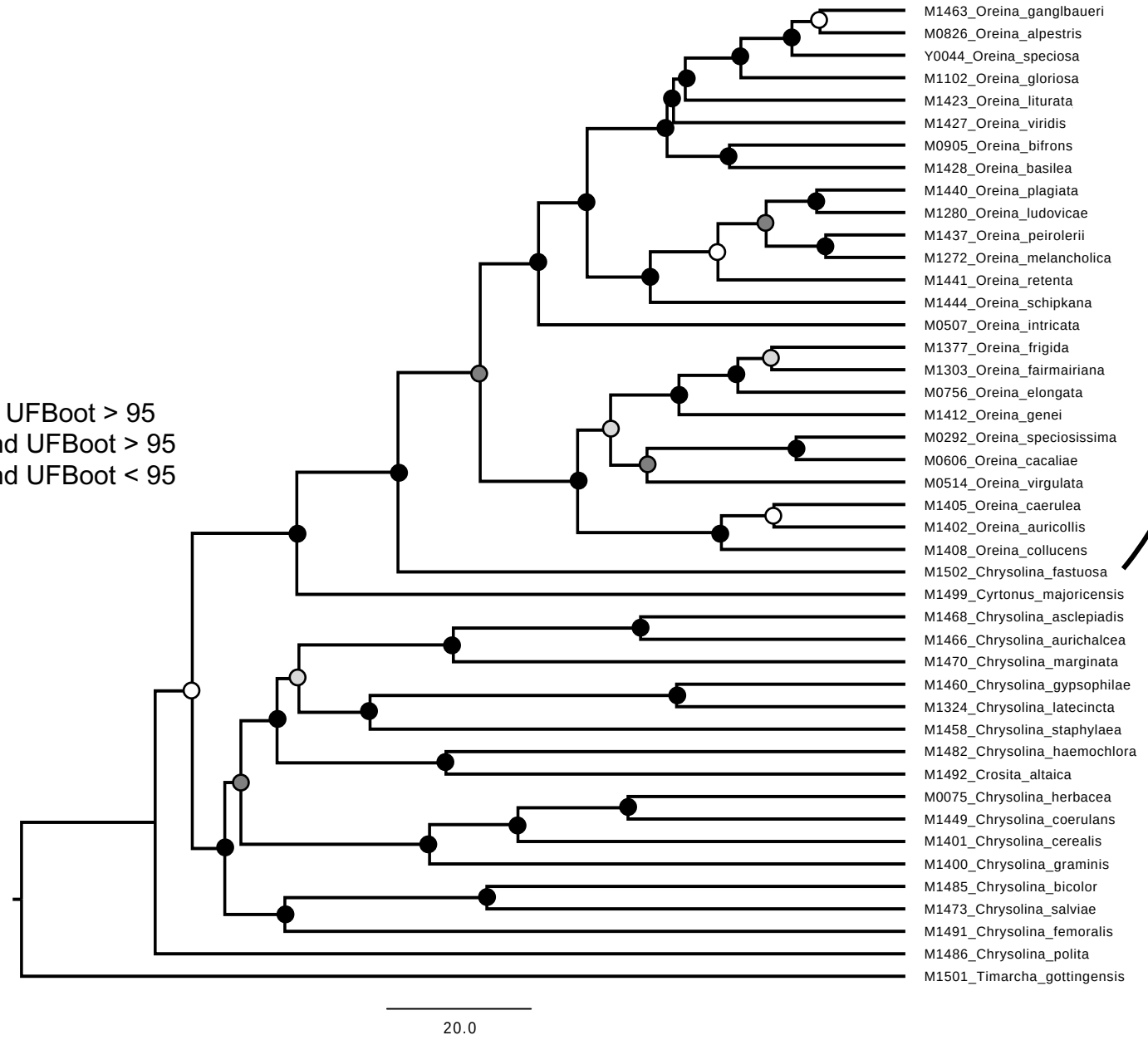
Diversification of *Oreina* species



Gauthier*, Borer* et al. in prep

Diversification of *Oreina* species

- SH-aLRT > 80 or UFBoot > 95
- SH-aLRT > 80 and UFBoot > 95
- SH-aLRT < 80 and UFBoot < 95
- Not recovered



Chrysolina fastuosa

New genus : *Fasta fastuosa*

Cyrtonus

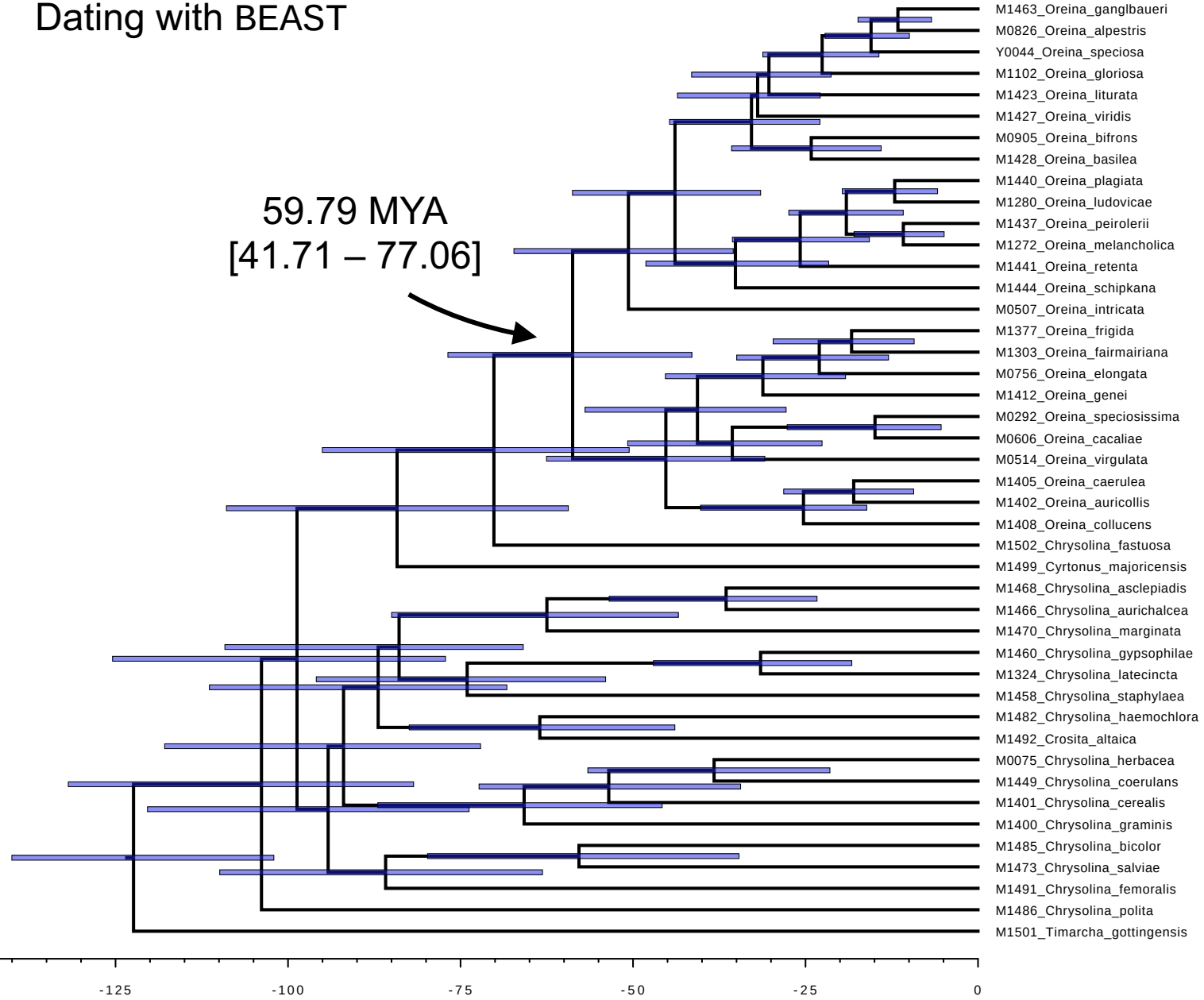
Chrysolina

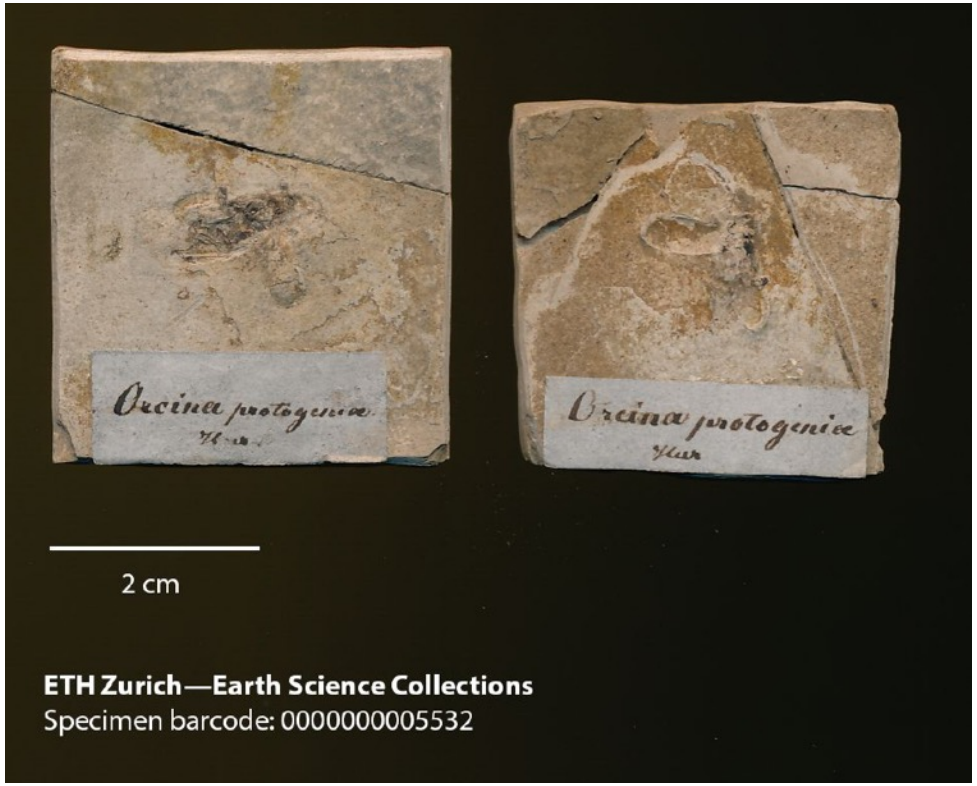
Timarcha

Gauthier*, Borer* et al. in prep

Diversification of *Oreina* species

Dating with BEAST





Oreina fossils

Oreina amphyctionis (Heer, 1847)

Oreina hellenis (Heer, 1847)

Oreina protogeniae (Heer, 1847)

Sarmatian deposits in Germany

dated to **11.6-12.7** Ma ago

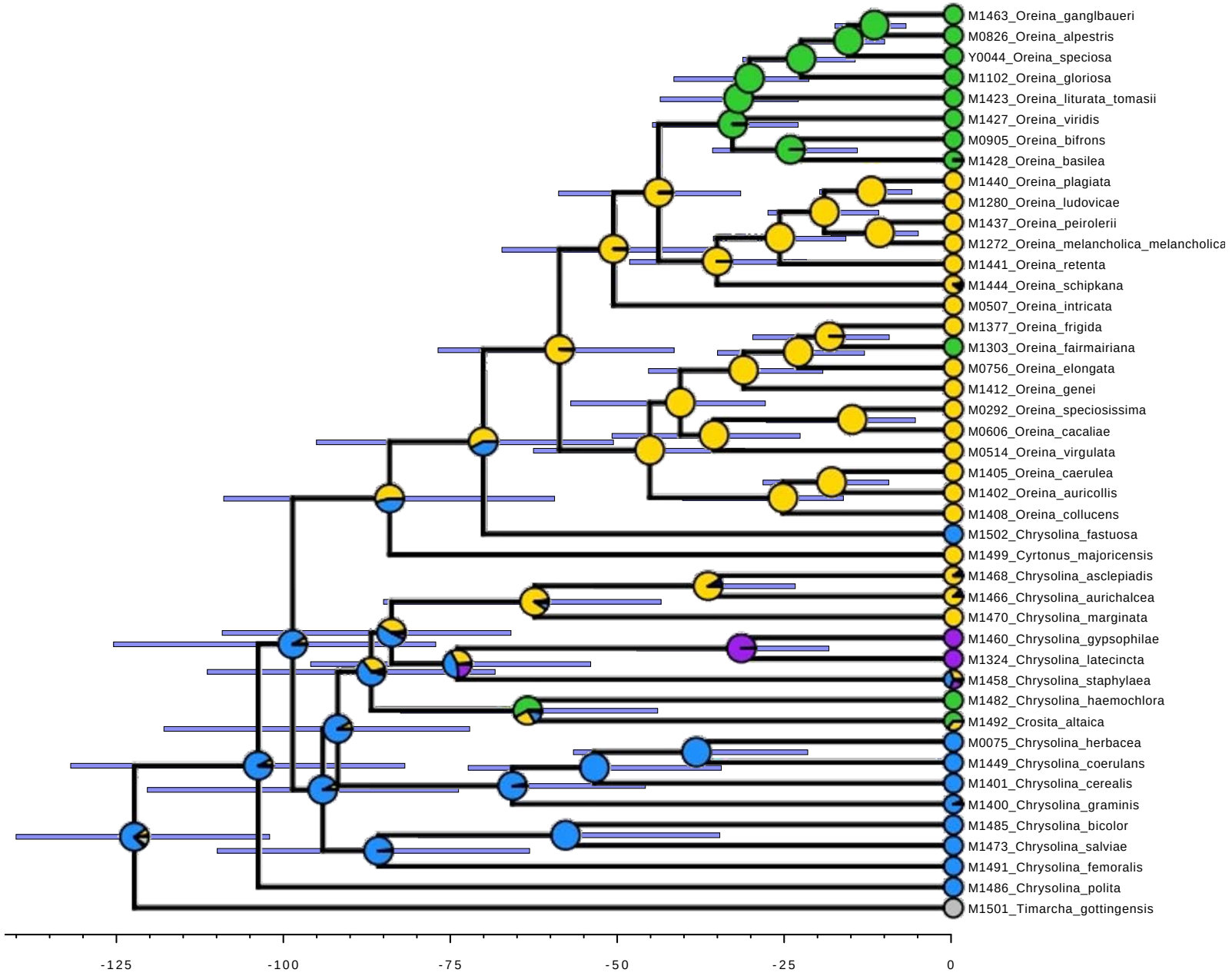
Oreina pulchra (Förster, 1891)

Brunstatt (France) and Kleinkembs (Germany)

dated to **28.4-33.9** Ma ago

Gauthier*, Borer* et al. in prep

Diversification of *Oreina* species



- Apiaceae
- Asclepiadaceae
- Asteraceae
- Lamiaceae
- Plantaginaceae
- Ranunculaceae
- Rubiaceae

Gauthier*, Borer* et al. in prep

Diversification of *Oreina* species

Asteraceae

genus

Oreina

- Apiaceae
- Asclepiadaceae
- Asteraceae
- Lamiaceae
- Plantaginaceae
- Ranunculaceae
- Rubiaceae

Gauthier*, Borer* et al. in prep

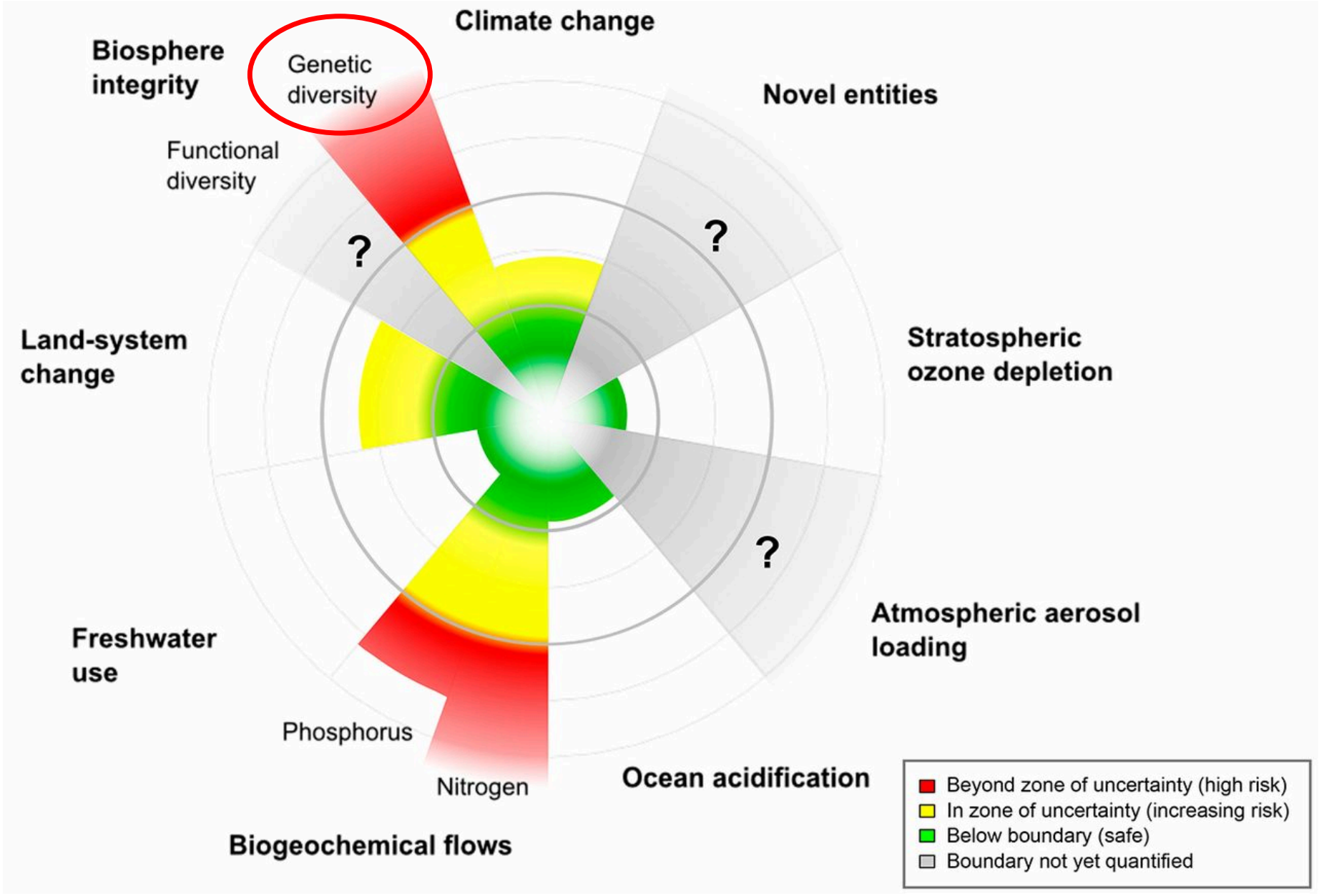
Diversification of *Oreina* species

Apiaceae

Gauthier*, Borer* et al. in prep

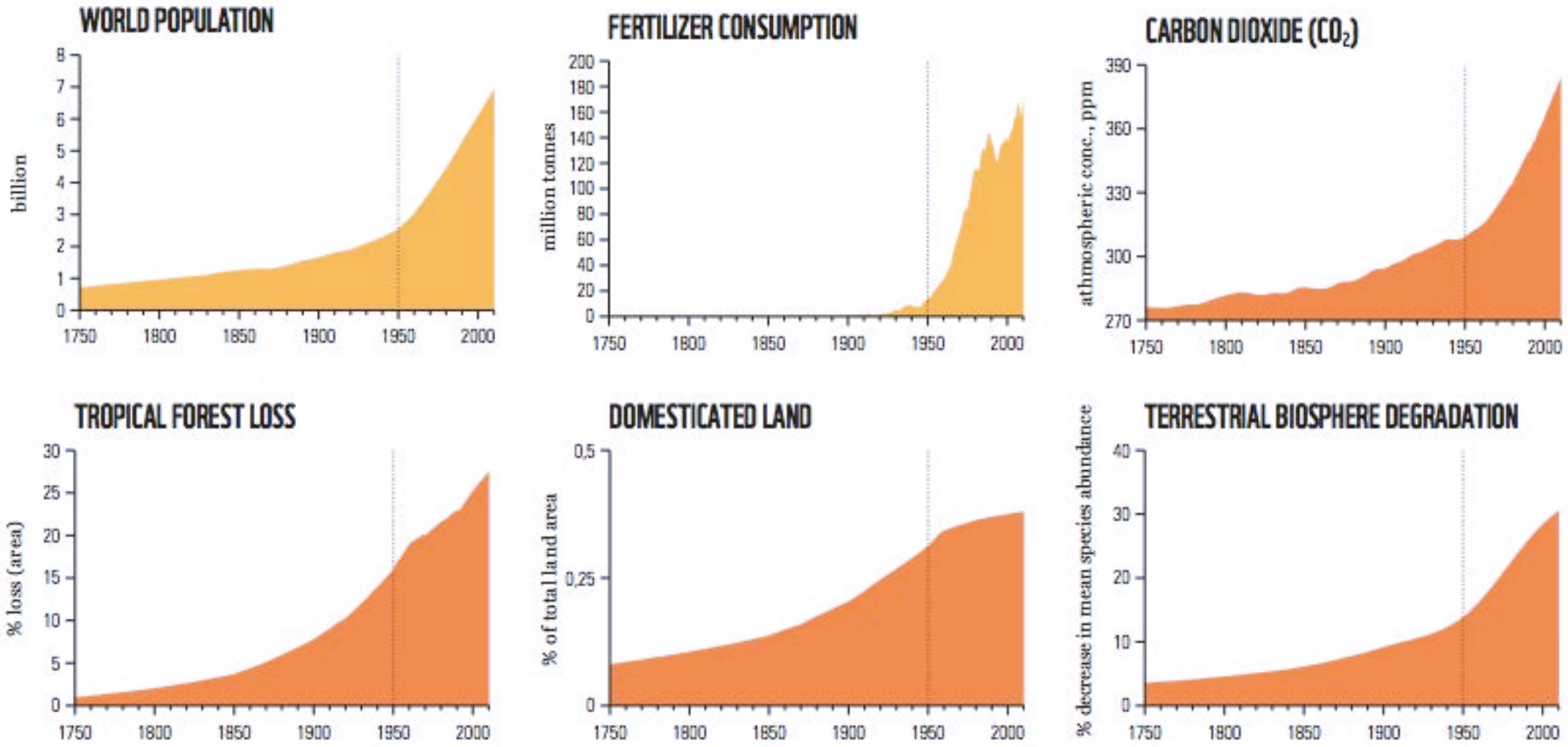

An incredible biobank to track
the recent history of populations

Biodiversity crisis



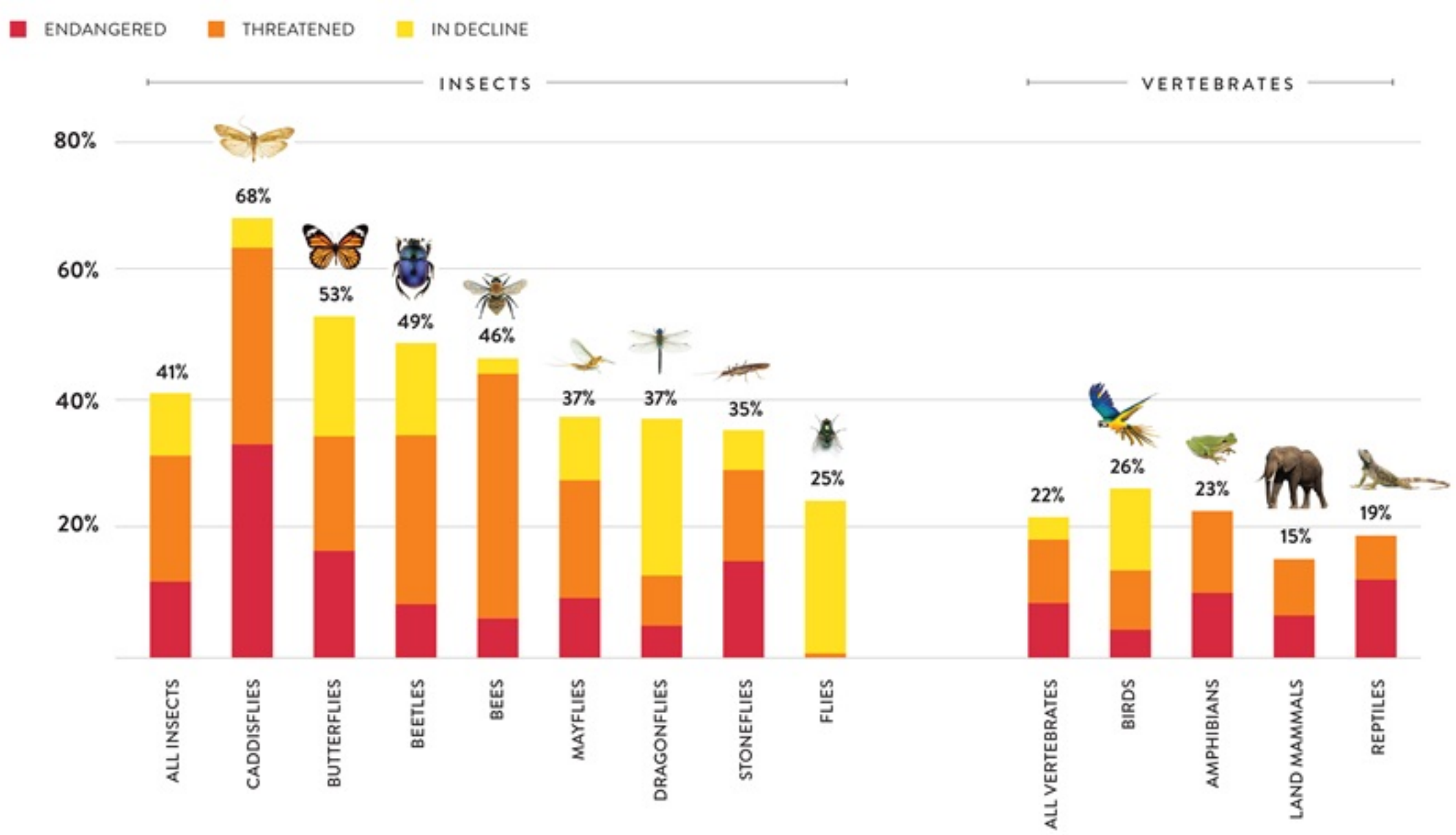
Steffen et al. 2015 Science

The Great Acceleration



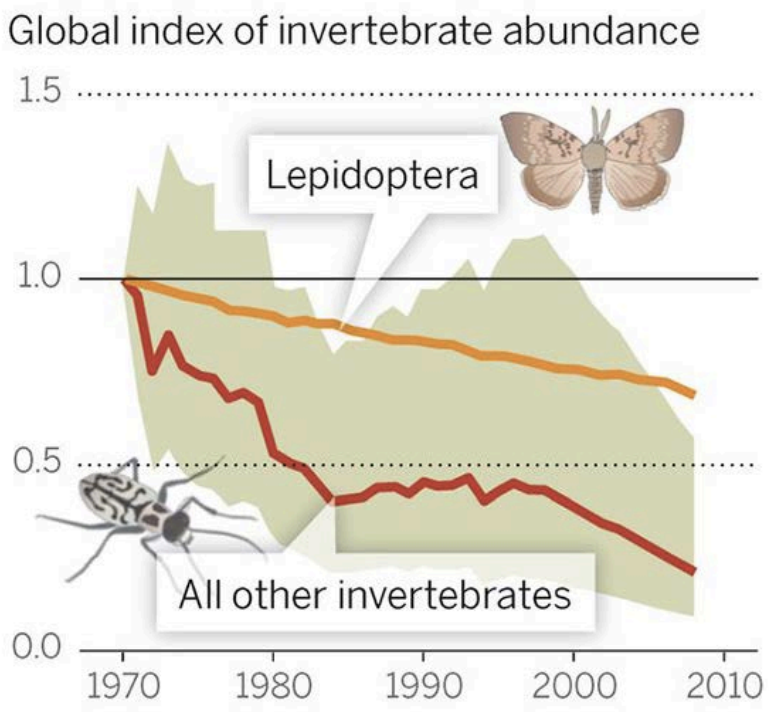
Steffen et al. 2015 The Anthropocene Review

Insect decline



IUCN

Insect decline



Diszo et al. 2014 Science

PLOS ONE

RESEARCH ARTICLE

More than 75 percent decline over 27 years in total flying insect biomass in protected areas

Caspar A. Hallmann[1]*, Martin Sorg[2], Eelke Jongejans[1], Henk Siepel[1], Nick Hofland[1], Heinz Schwan[2], Werner Stenmans[2], Andreas Müller[2], Hubert Sumser[2], Thomas Hörren[2], Dave Goulson[3], Hans de Kroon[1]

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Over a century of data reveal more than 80% decline in butterflies in the Netherlands

Arco J. van Strien[a,*], Chris A.M. van Swaay[b], Willy T.F.H. van Strien-van Liempt[c], Martin J.M. Poot[a], Michiel F. WallisDeVries[b,d]

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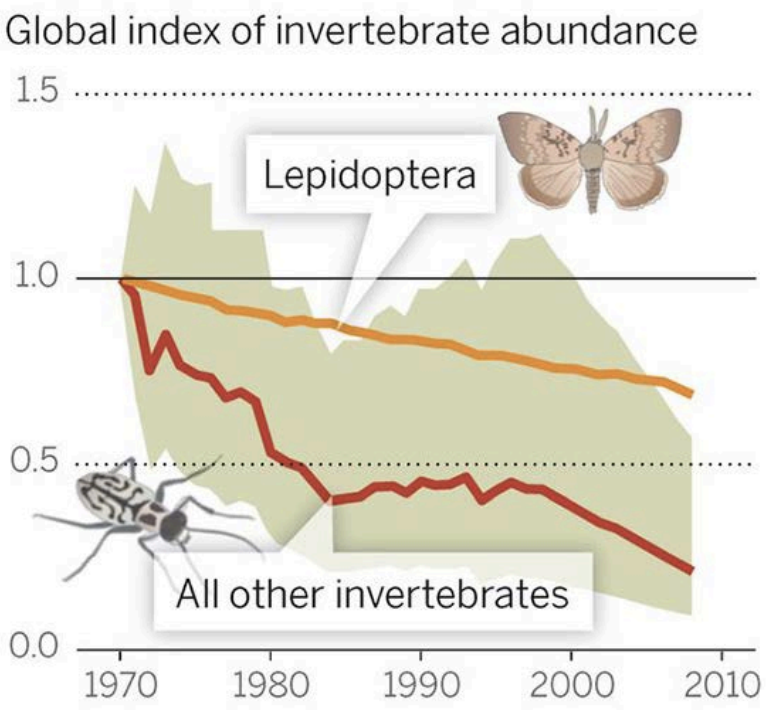
ELSEVIER

Review

Worldwide decline of the entomofauna: A review of its drivers

Francisco Sánchez-Bayo[a,*], Kris A.G. Wyckhuys[b,c,d]

Insect decline



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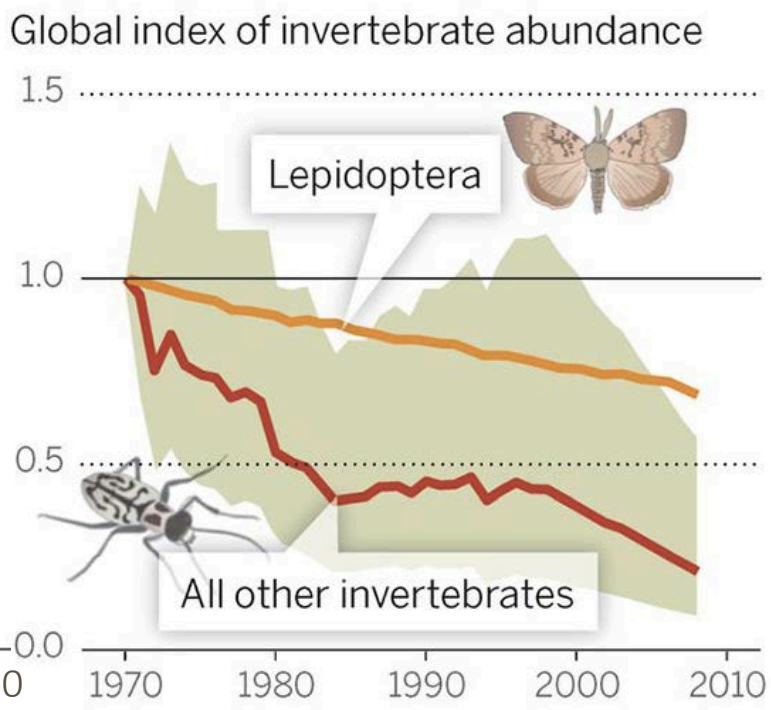
Diszo et al. 2014 Science

Insect decline

?



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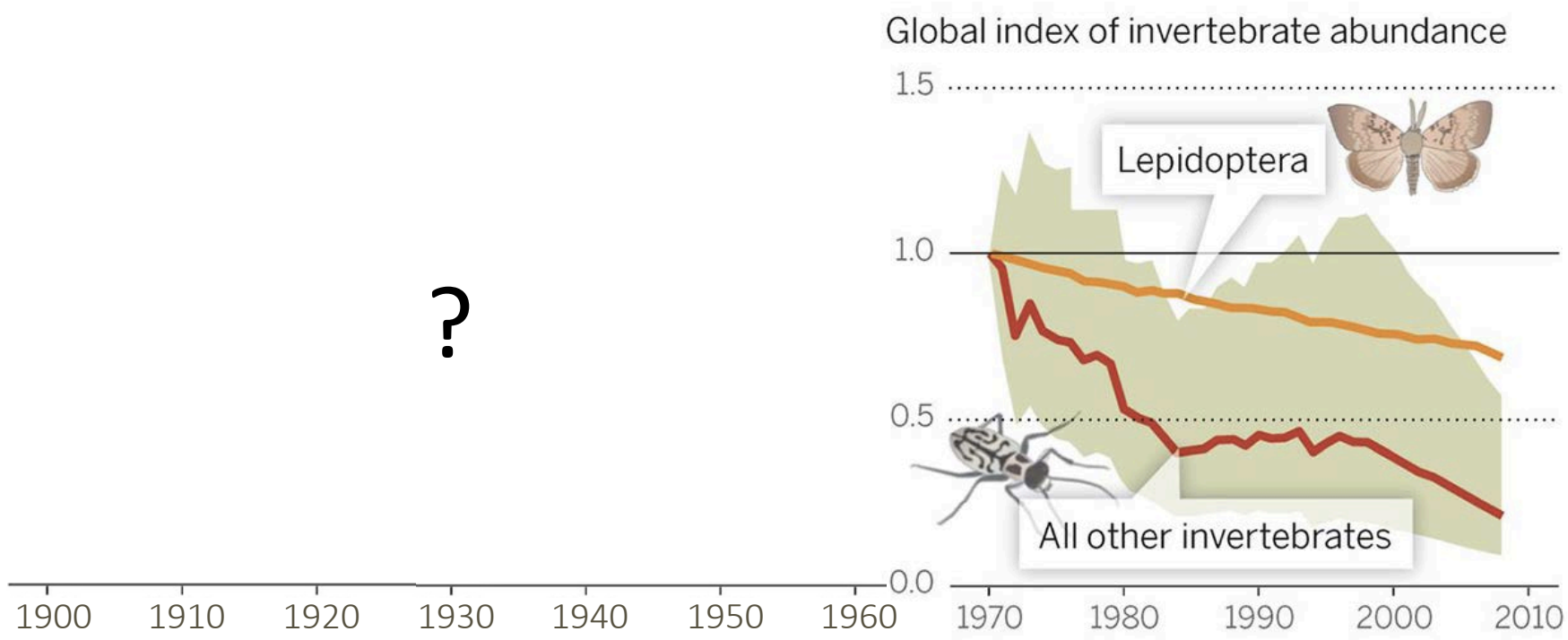

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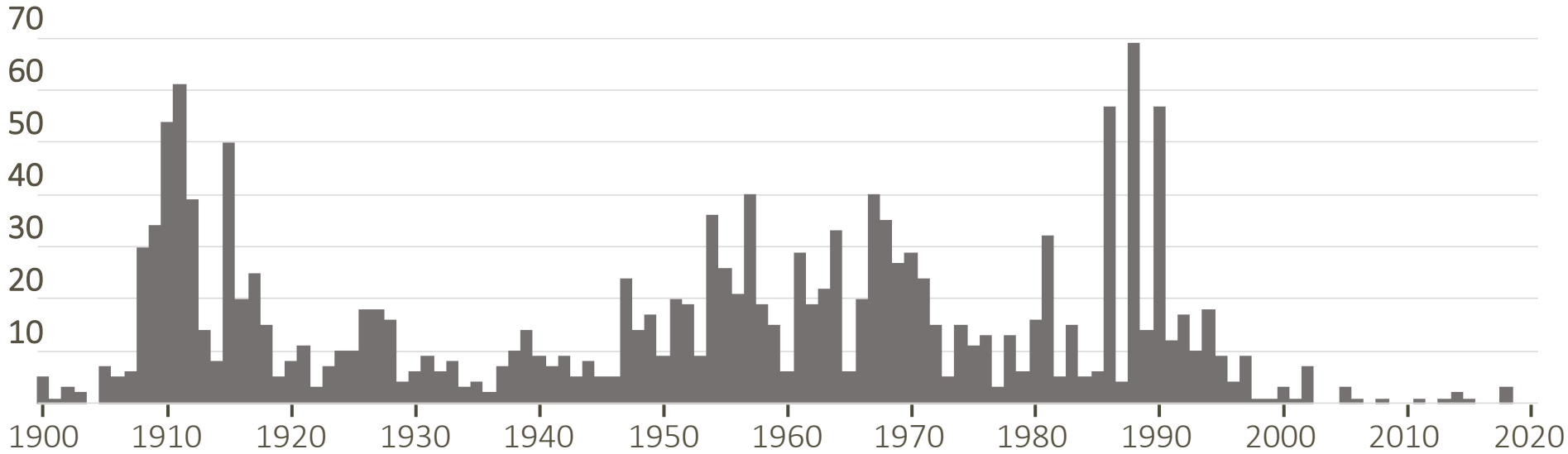
Diszo et al. 2014 Science



Pieris napi
in swiss collections

Representative of the genetic state
of their population of origin at the time they were caught

HyRAD

Fresh sample DNA extraction

Ancient DNA extraction

genomic DNA

ddRAD library

Shotgun library

Including contaminant or untargeted loci

In vitro transcription into RNA probes

Hybridization

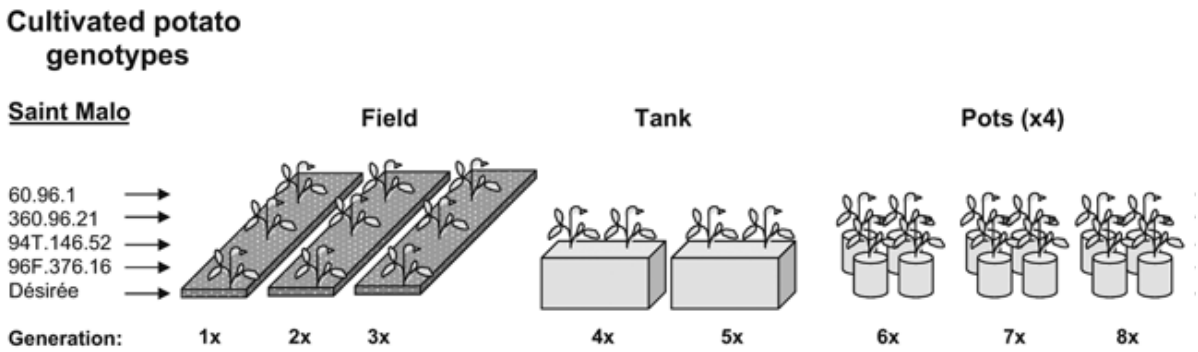
Probes sequencing

Sequencing

Capture and wash

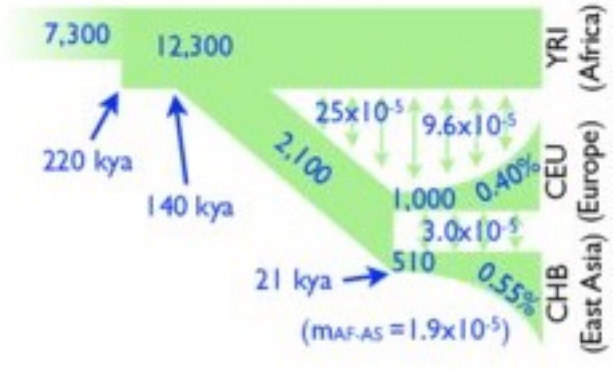
A new way in evolutionnary biology

Experimental evolution



Time series
Tracking allelic frequency changes

Population genomics on current populations



Demographic inferences
Genome scan

Museomics

Time series on natural populations

Sampling

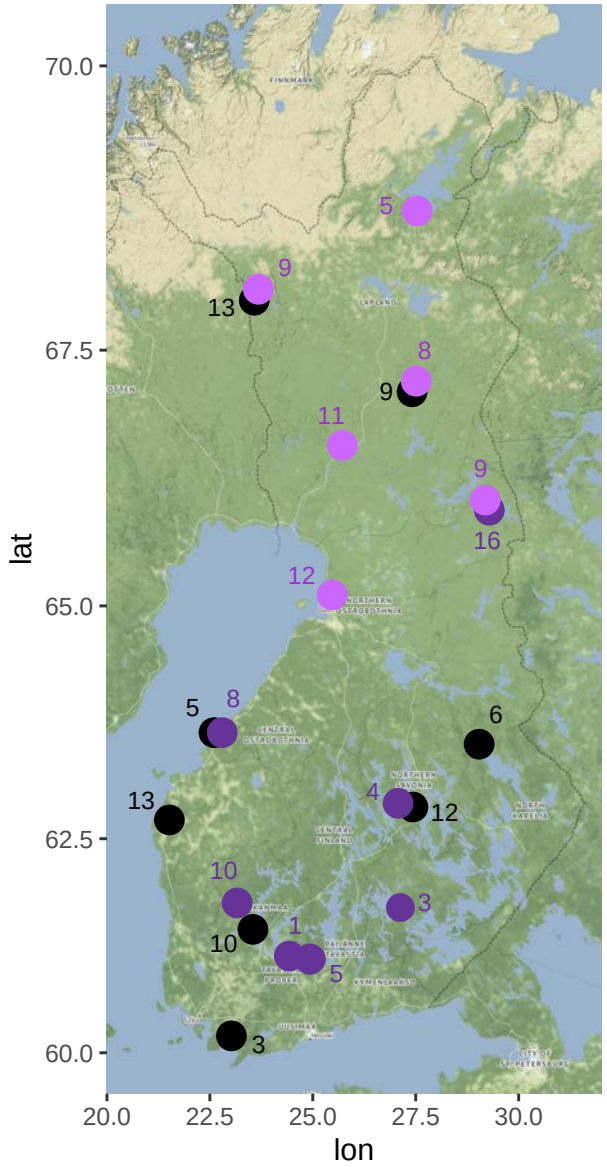
LUOMUS
FINNISH MUSEUM OF NATURAL HISTORY

Sampling

Erebia embla N = 169

a.

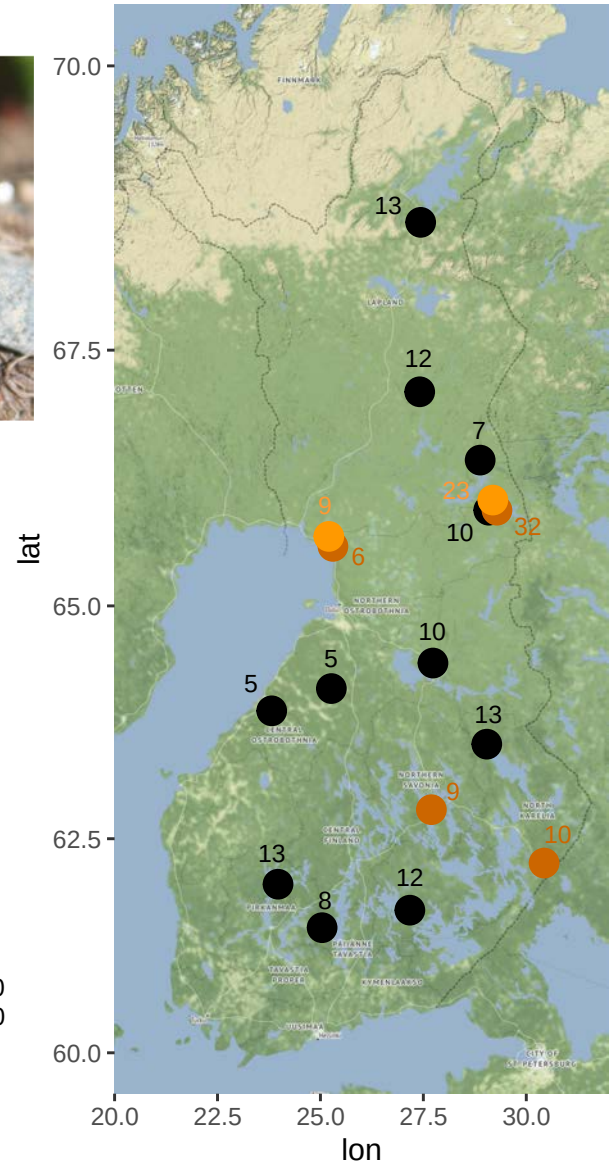
b.



Lycaena helle N = 197

c.

d.



Gauthier et al. 2020 Mol Ecol Res

HyRAD

Fresh sample DNA extraction

Ancient DNA extraction

genomic DNA

ddRAD library

Shotgun library

Including contaminant or untargeted loci

In vitro transcription into RNA probes

Hybridization

Probes sequencing

Sequencing

Capture and wash

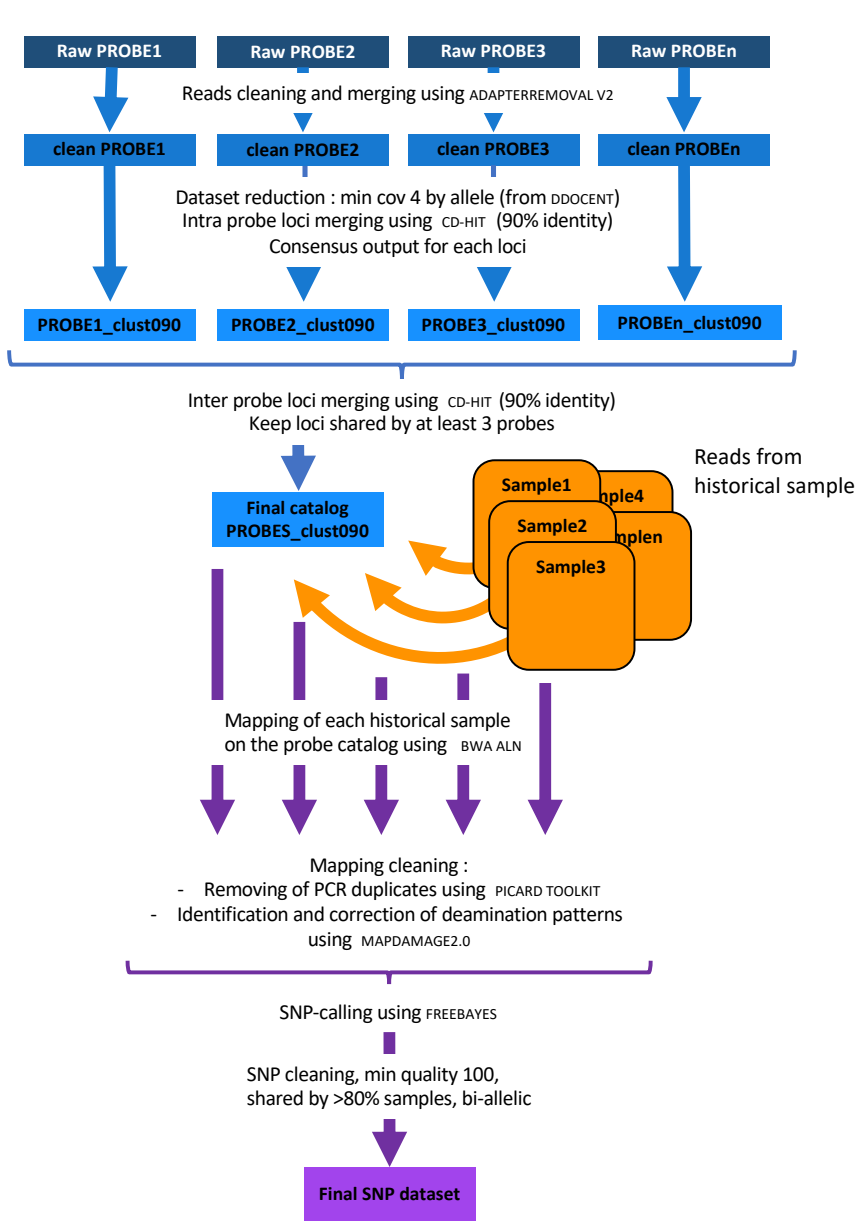
HyRAD (Hybridization RAD) protocol

↓

popHyRAD pipeline

↓

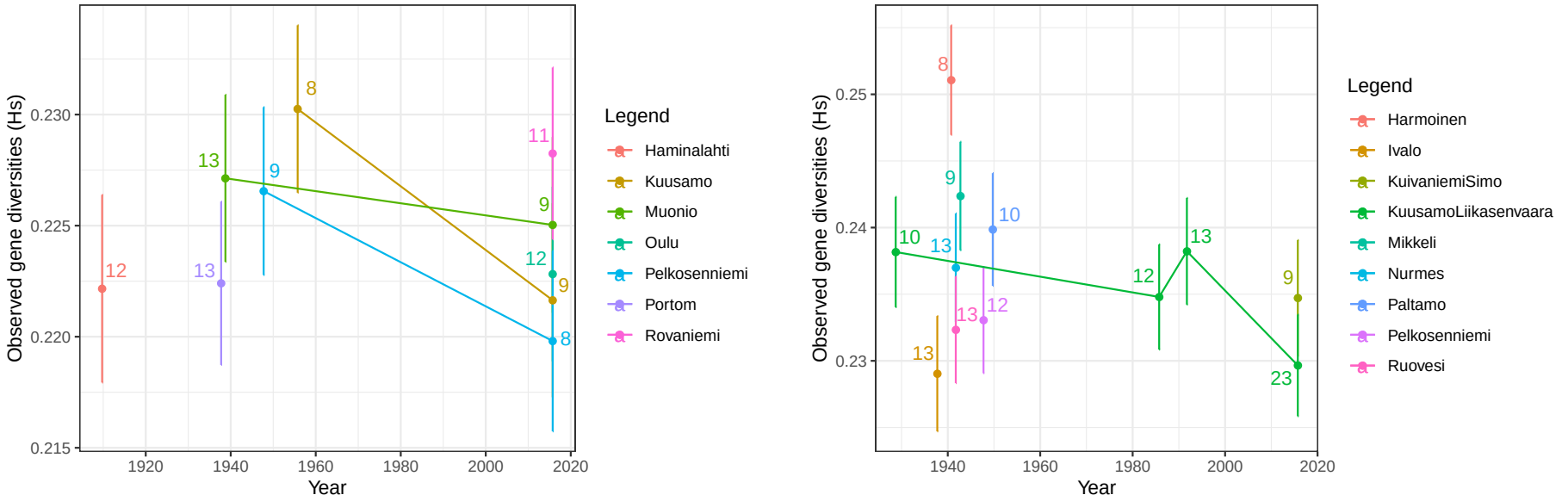
Erebia embla	1,015 loci	2,549 SNPs
Lycaena helle	869 loci	2,742 SNPs



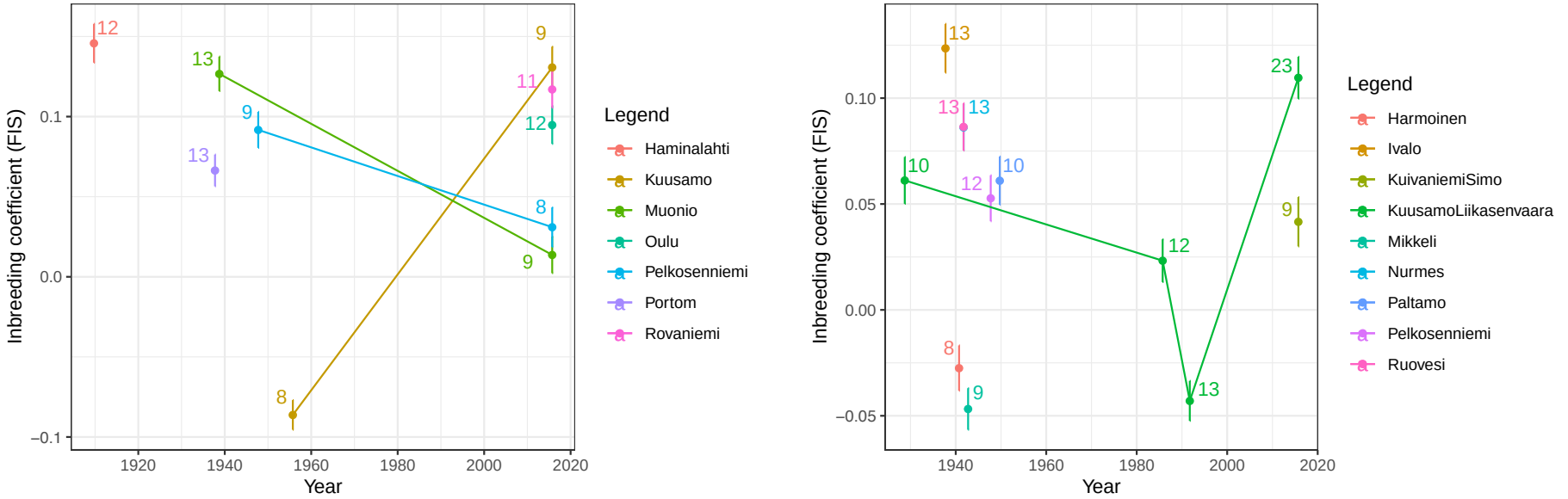
Gauthier et al. 2020 Mol Ecol Res

Genetic statistics evolution

Erebia embla

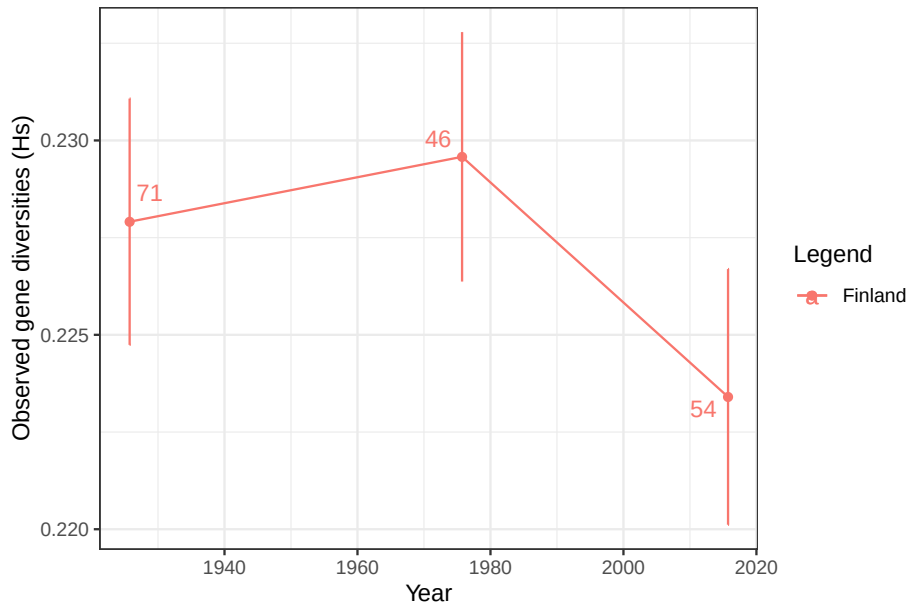


Lycaena helle

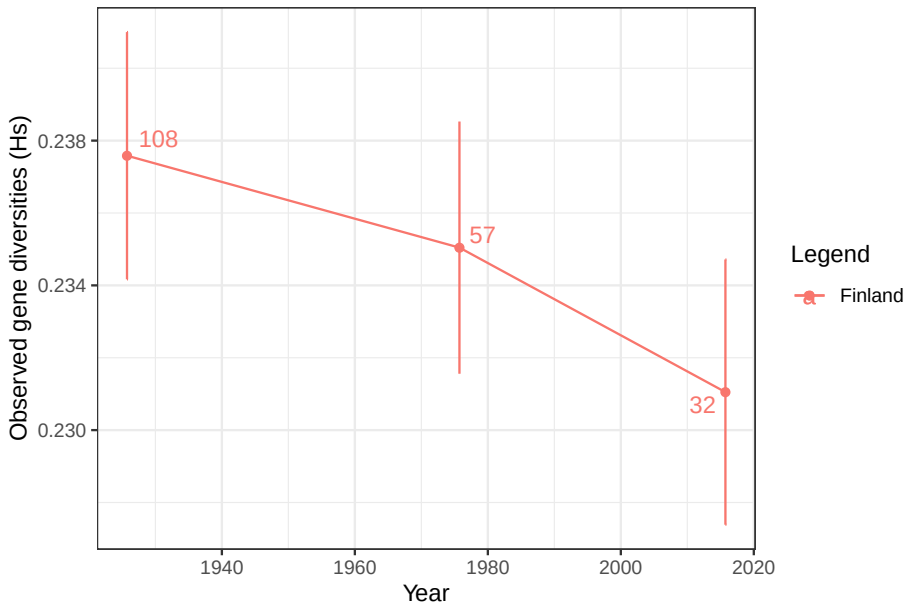


Finland patterns

Erebia embla

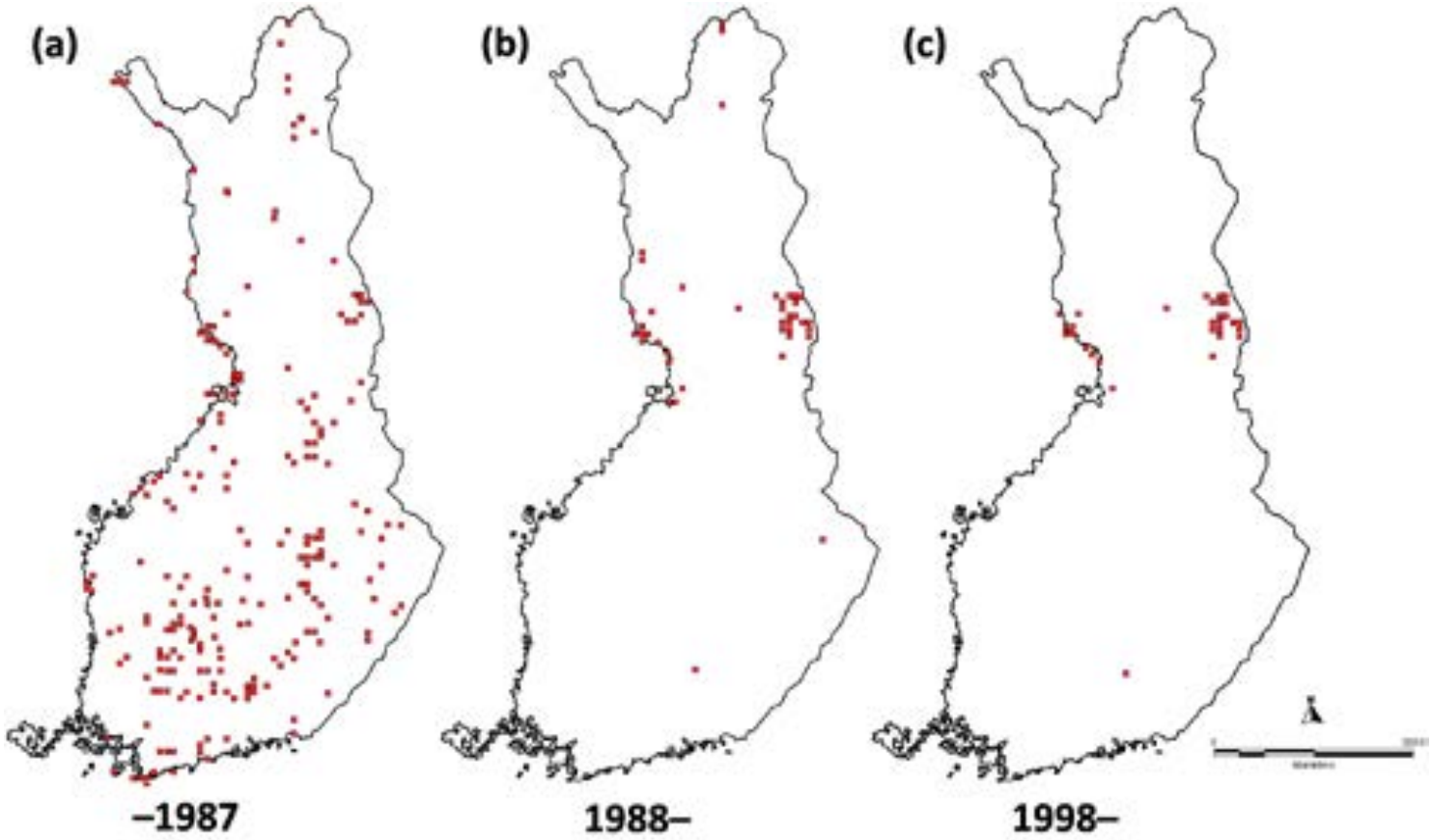


Lycaena helle



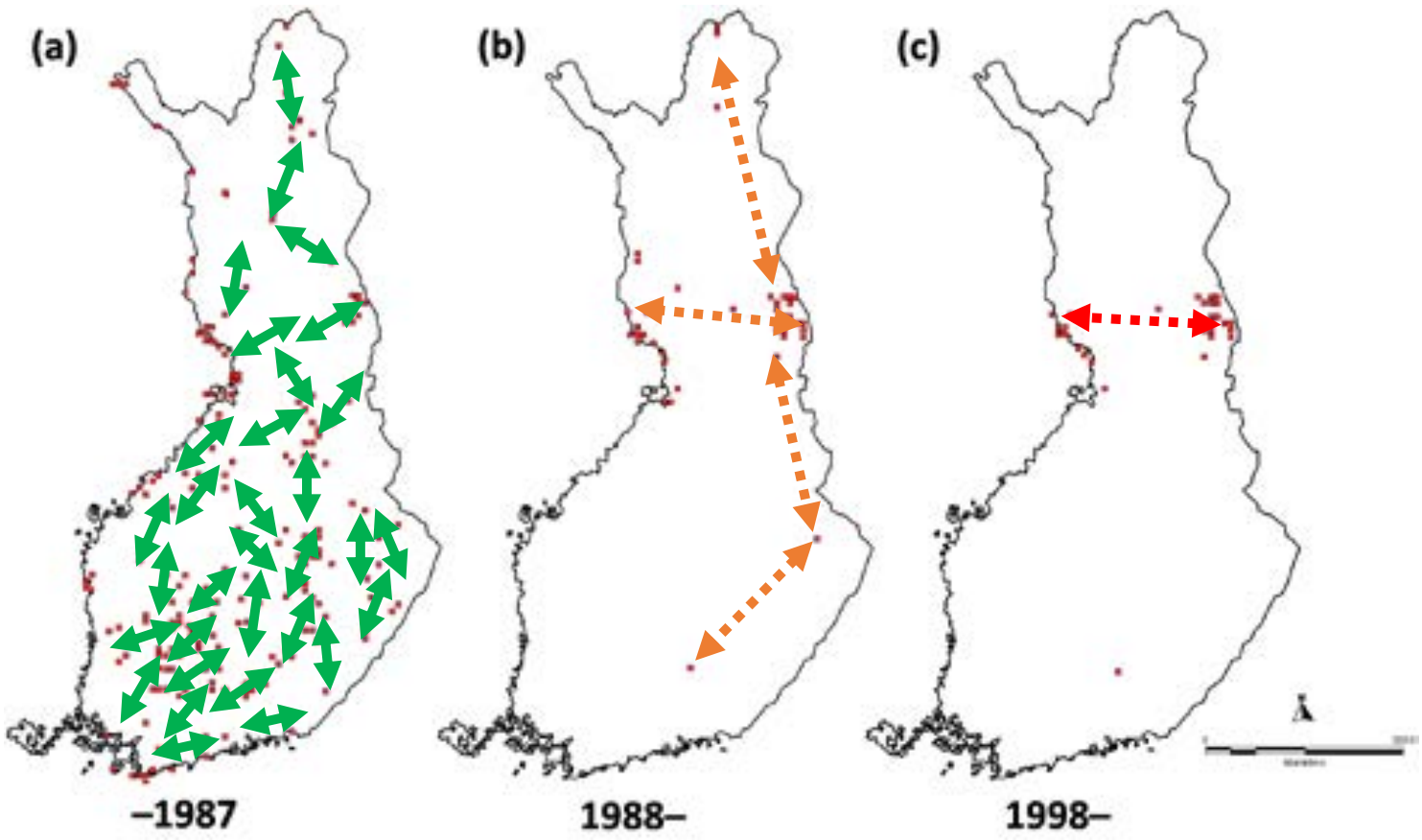
Comparison with field records

Lycaena helle

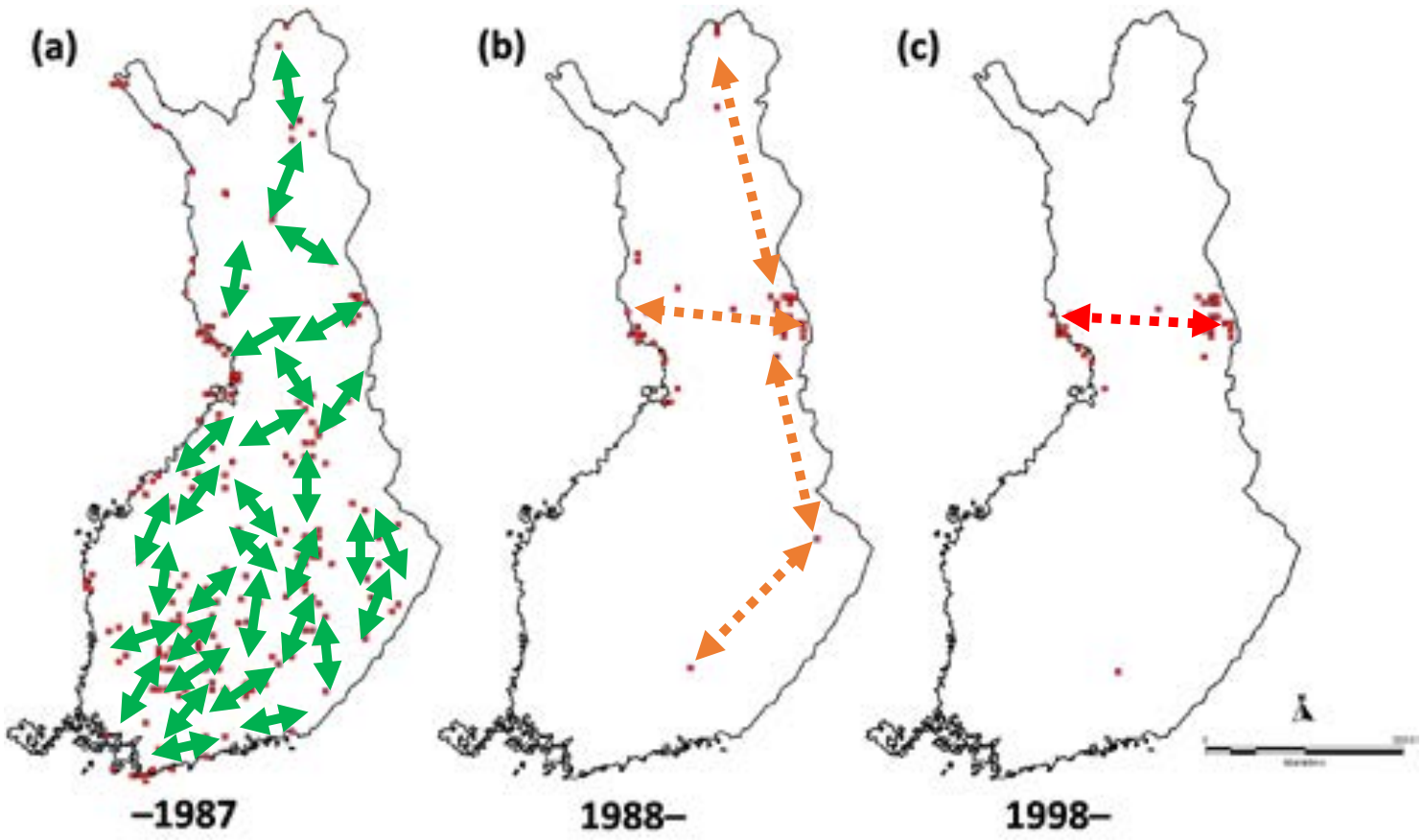


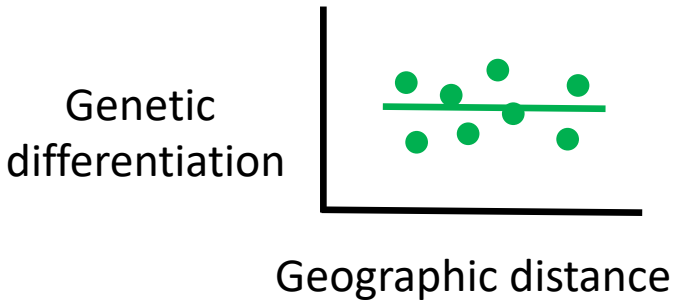
Habel et al. 2014

Isolation by Distance

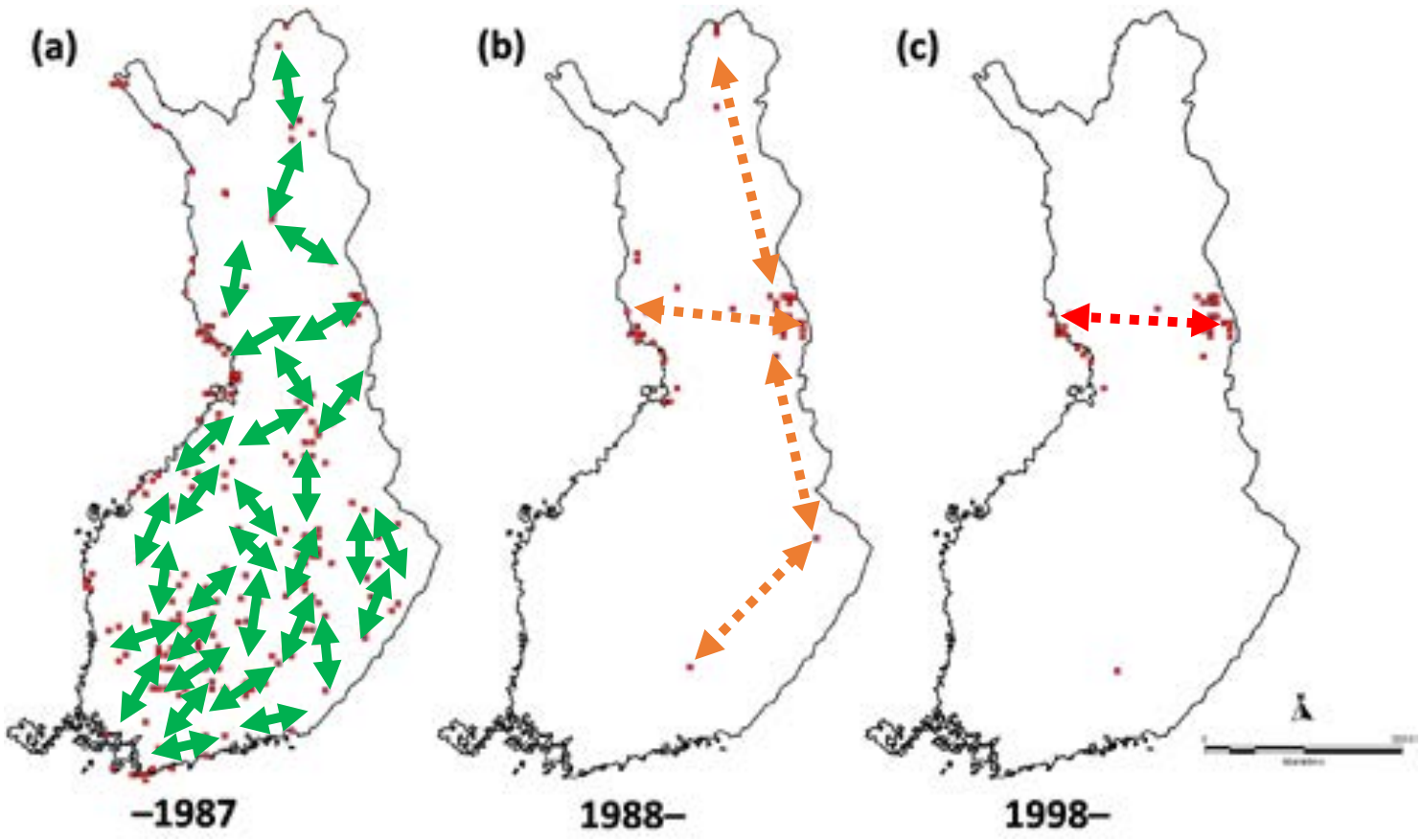


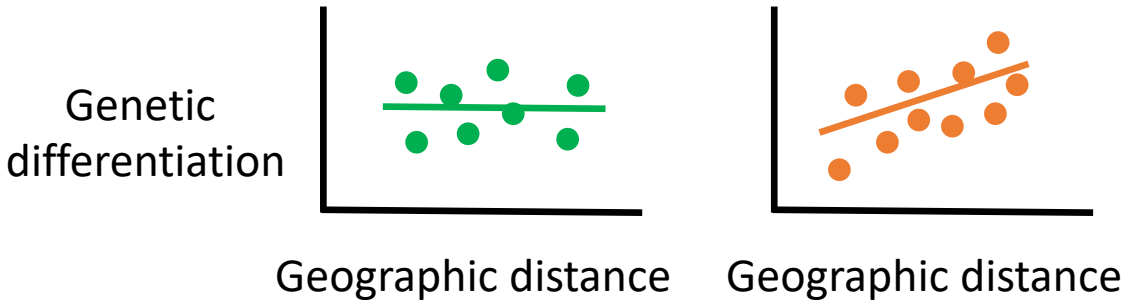
Isolation by Distance



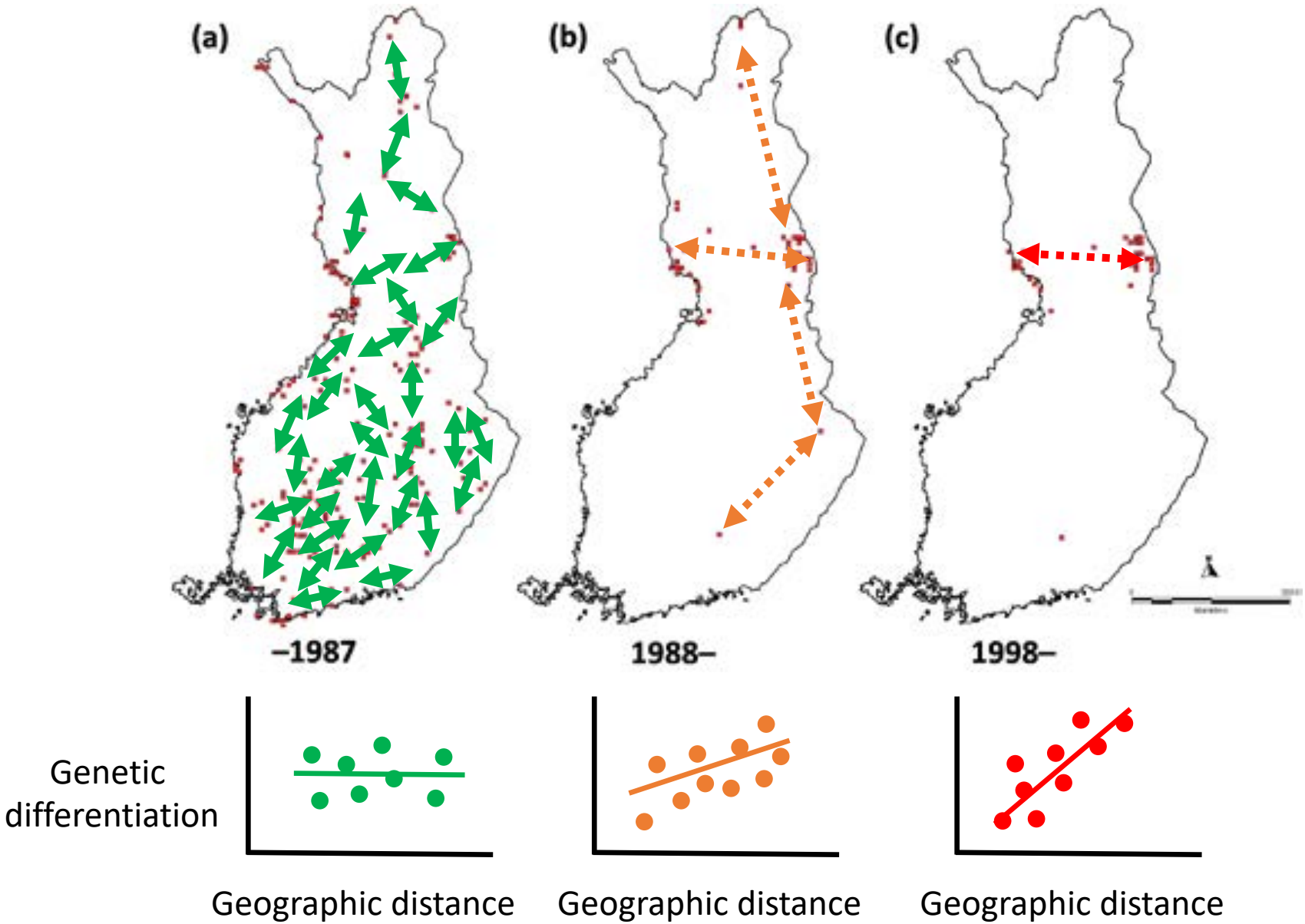


Isolation by Distance



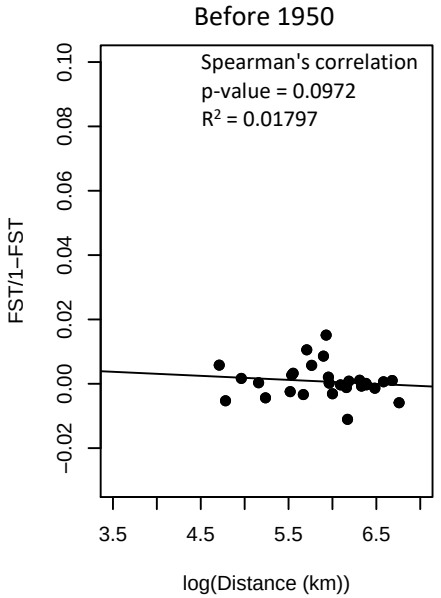


Isolation by Distance



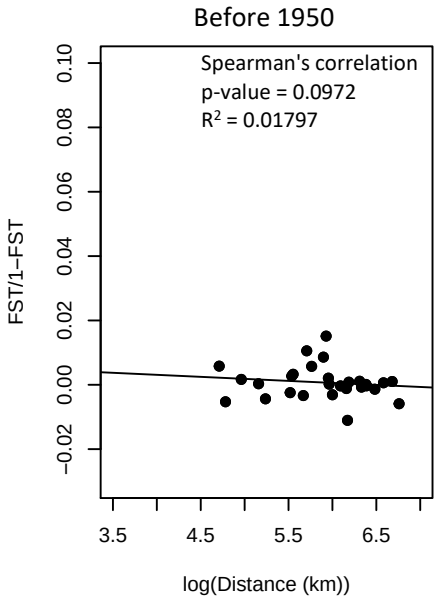
Isolation by Distance

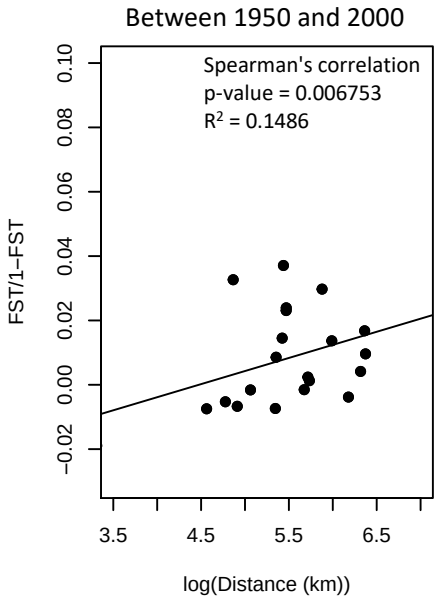
Erebia embla

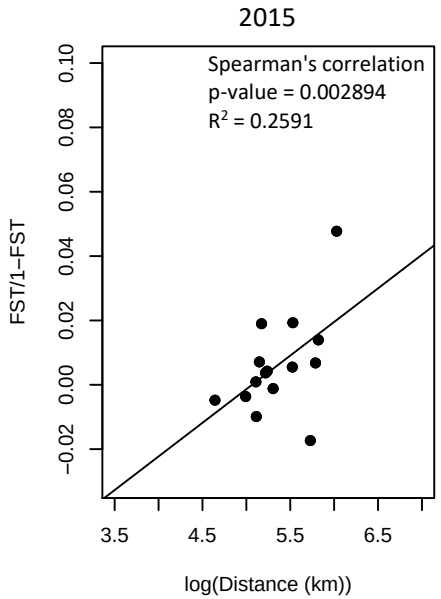


Isolation by Distance

Erebia embla

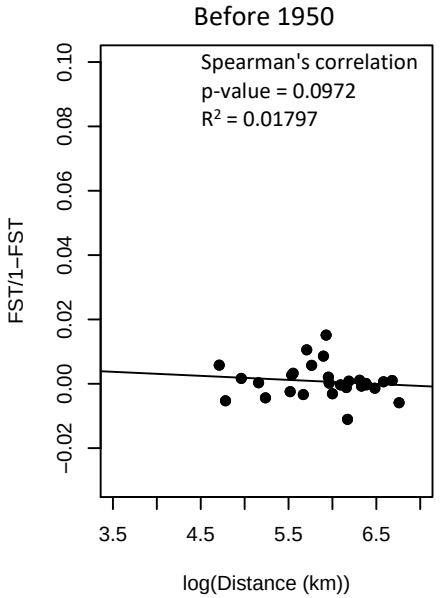


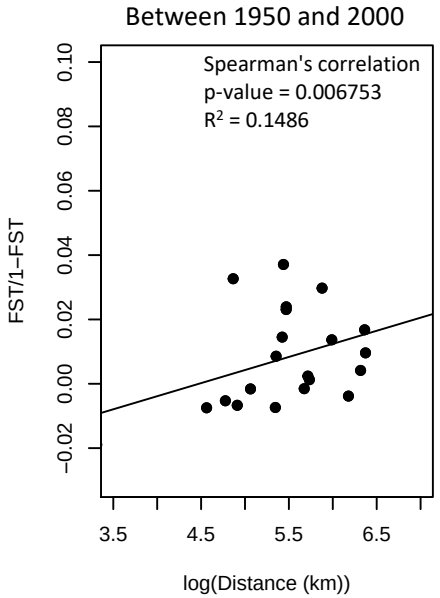


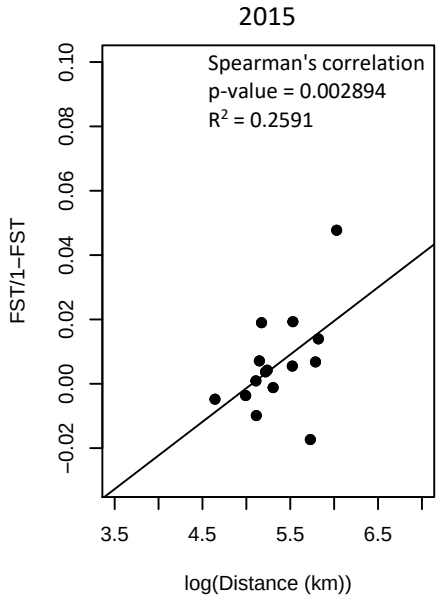


Isolation by Distance

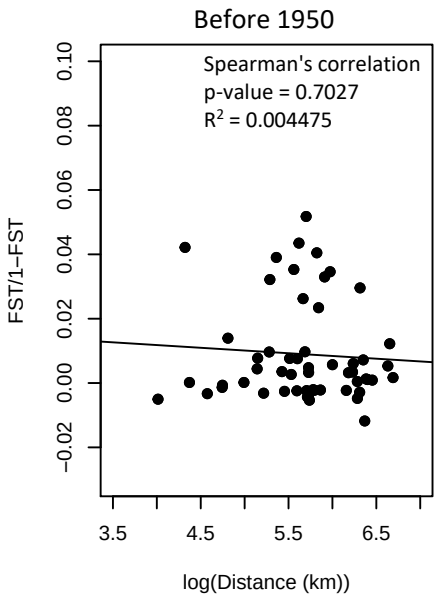
Erebia embla

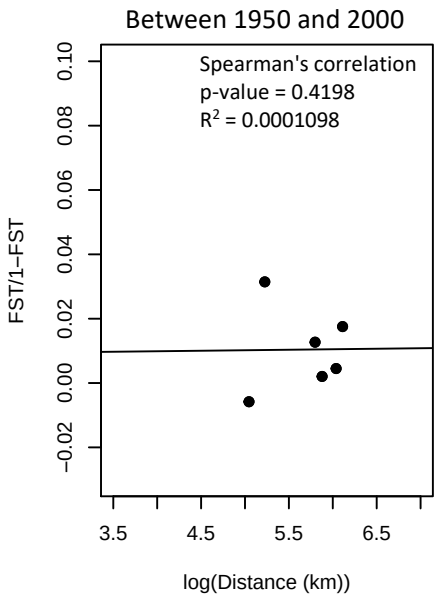


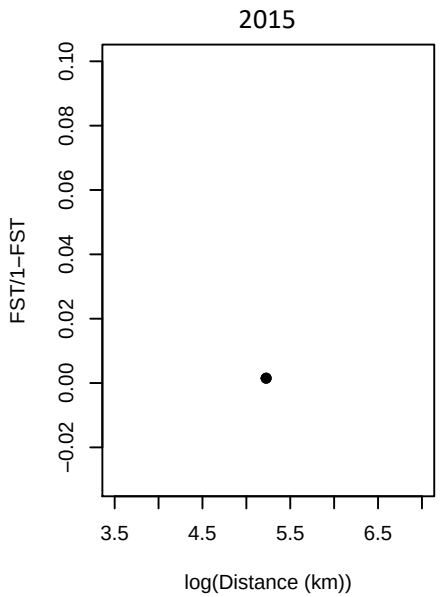




Lycaena helle







Swiss Confederation

Federal Office for the Environment FOEN

10 insect species from different orders at the Swiss scale

(Lepidoptera Coleoptera EPT Orthoptera Hymenoptera)

Pieris napi

Polyommatus icarus

Cetonia aurata

Baetis alpinus

Serratella ignita

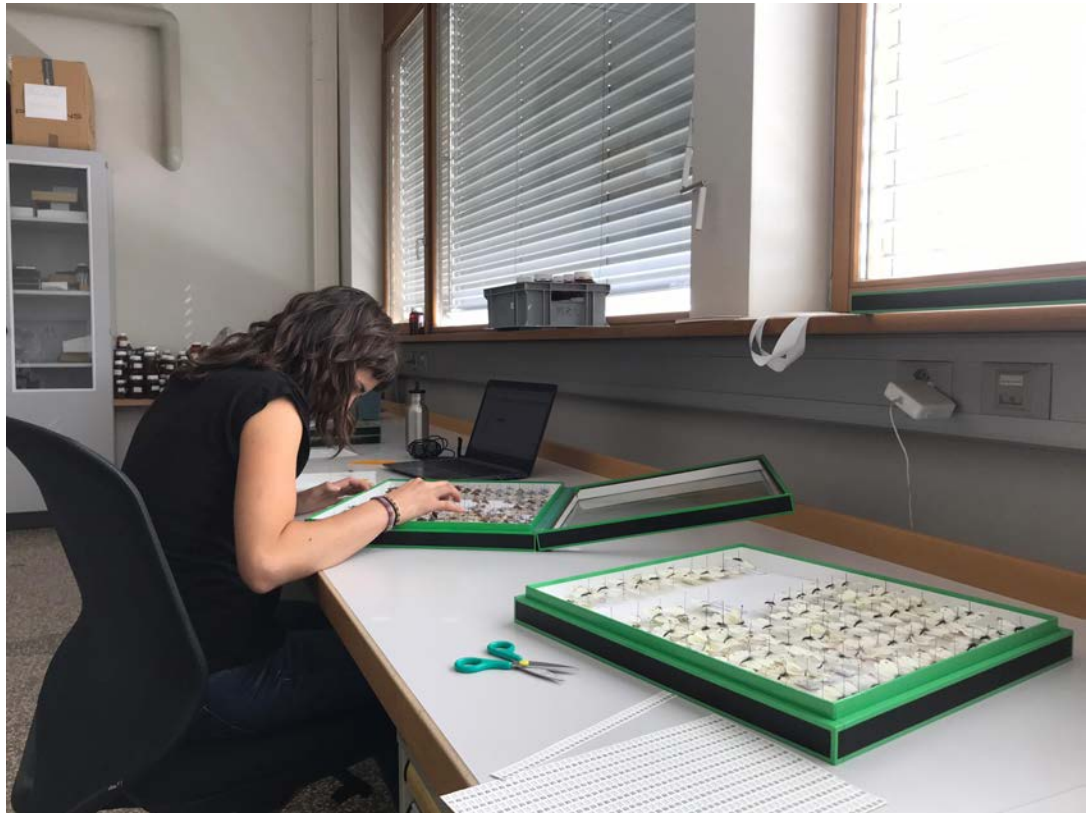
Miramella alpina

Chorthippus parallelus

Omocestus viridulus

Bombus humilis

Bombus pascuorum



Databasing

1. Gathering of extant databases

2. Digitalisation of collection specimens

Specimen
Metadata
DNA extraction

Final database of 12 769 entries

8 608 (67%) entries newly produced

X

Historic population identification

Year
Location

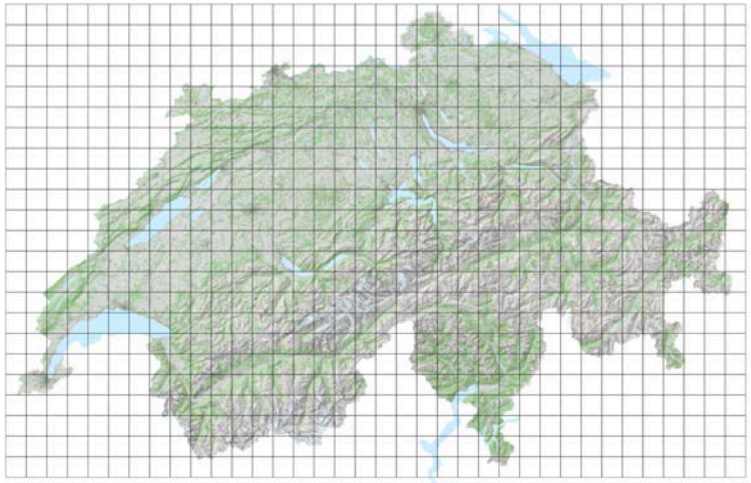
x, y

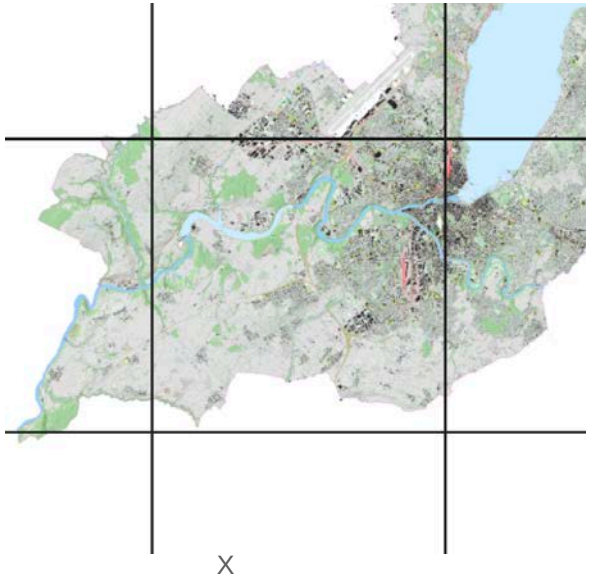
Grid cell (10x10km; infoFauna)

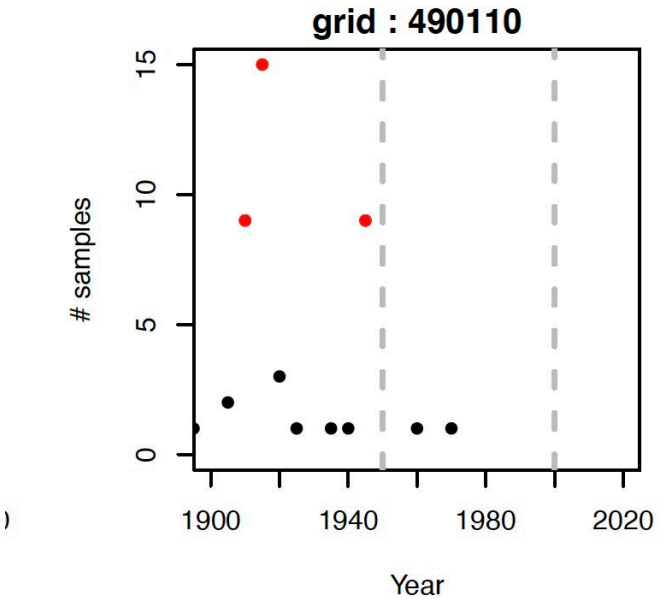
Location accuracy

Sum of individuals
of the same grid
in a period of 5 years

≥ 6 before 1950







Collection’s sampling

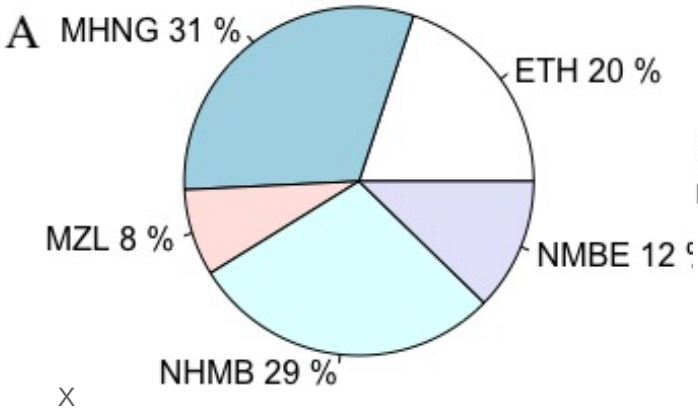
Total nb collection specimens: 2 739

Sampled so far: 1 301 (47.5%)

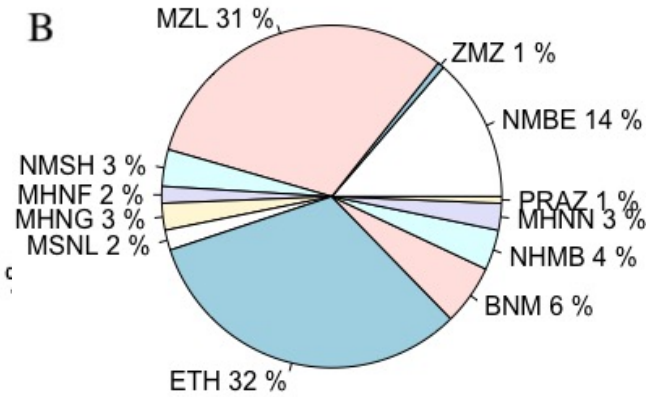
1 leg

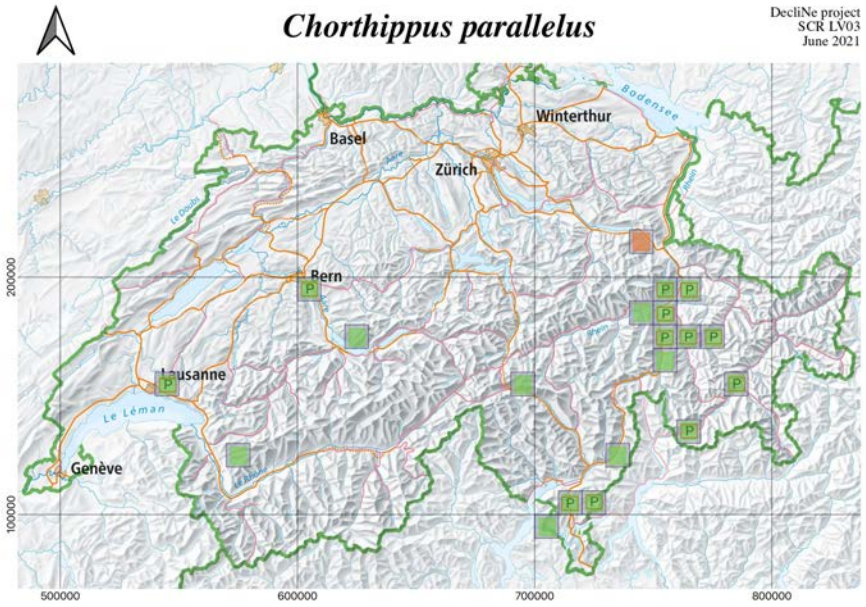
Avoid cross contamination

Non-Hymenoptera species



Hymenoptera species





Field campaing

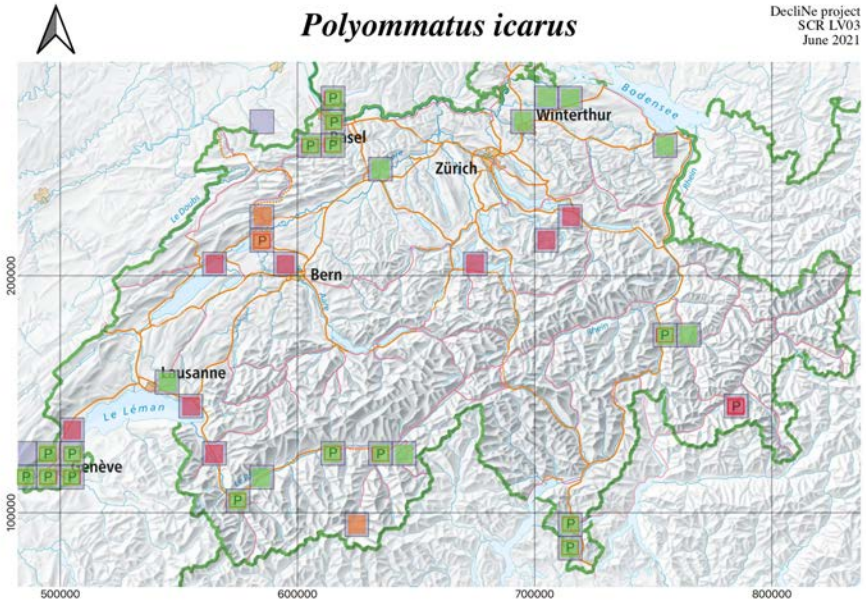
161 locations to sample

756 samples

72 localities

1 locality ⟶ 1 complete individual

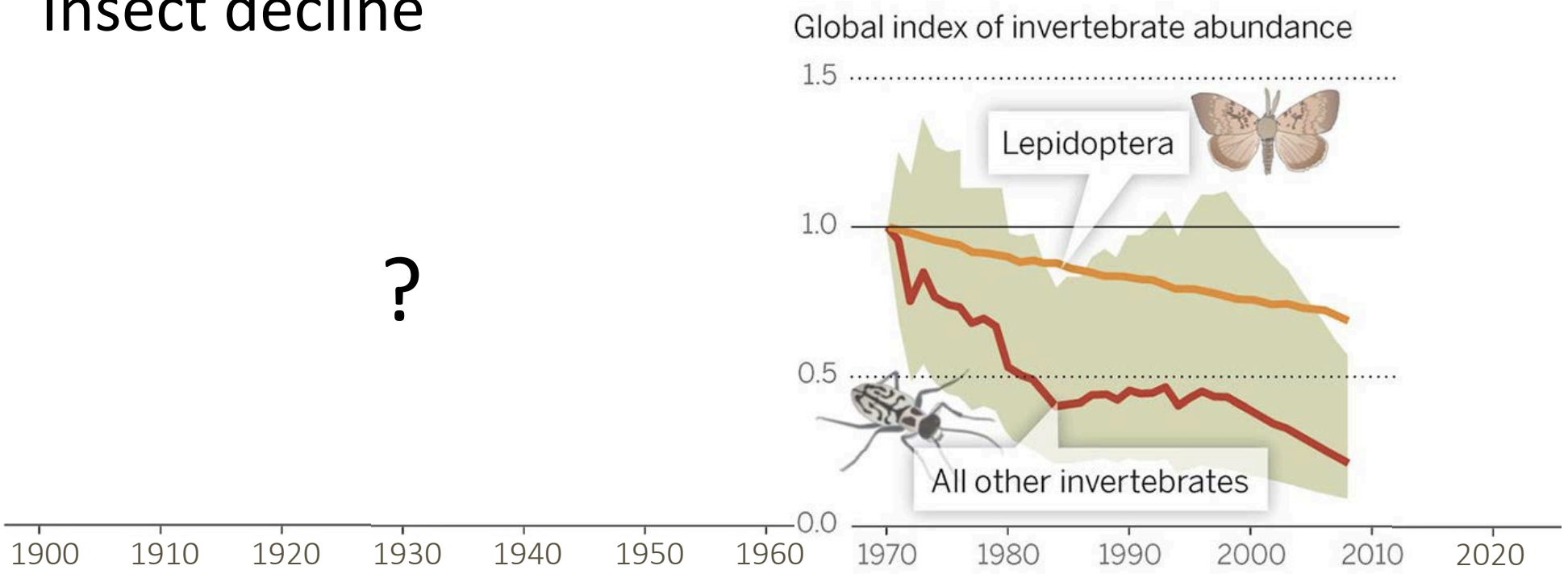
9 legs



X

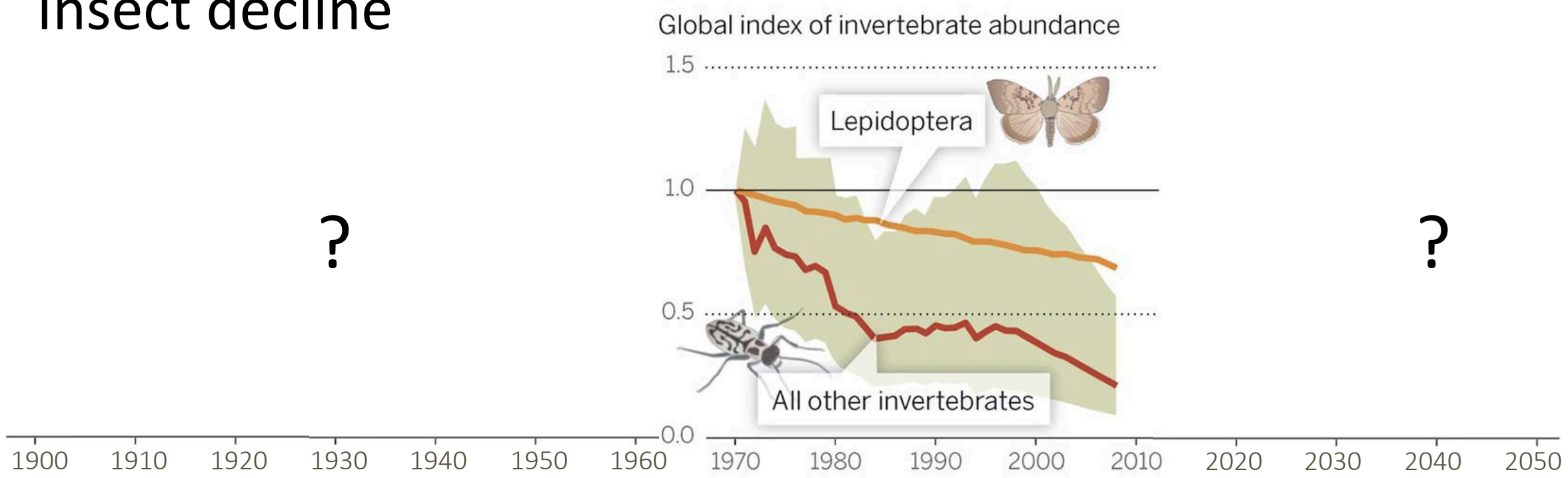
Insect decline

?



Past diversity
Museomics

Insect decline



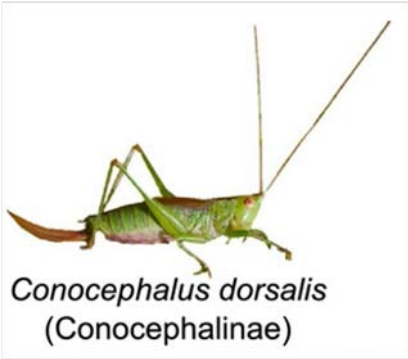
?

?

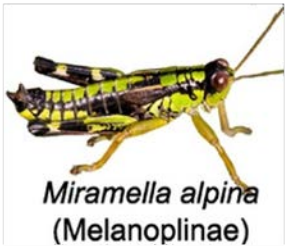
Past diversity
Museomics

Tracking the evolution
of the diversity

Development of a multi-locus marker for swiss orthoptera

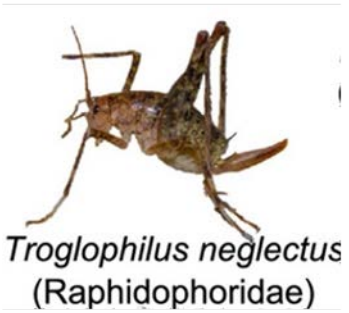

Conocephalus dorsalis
(Conocephalinae)

OrthoSwissBOL project


Miramella alpina
(Melanoplinae)

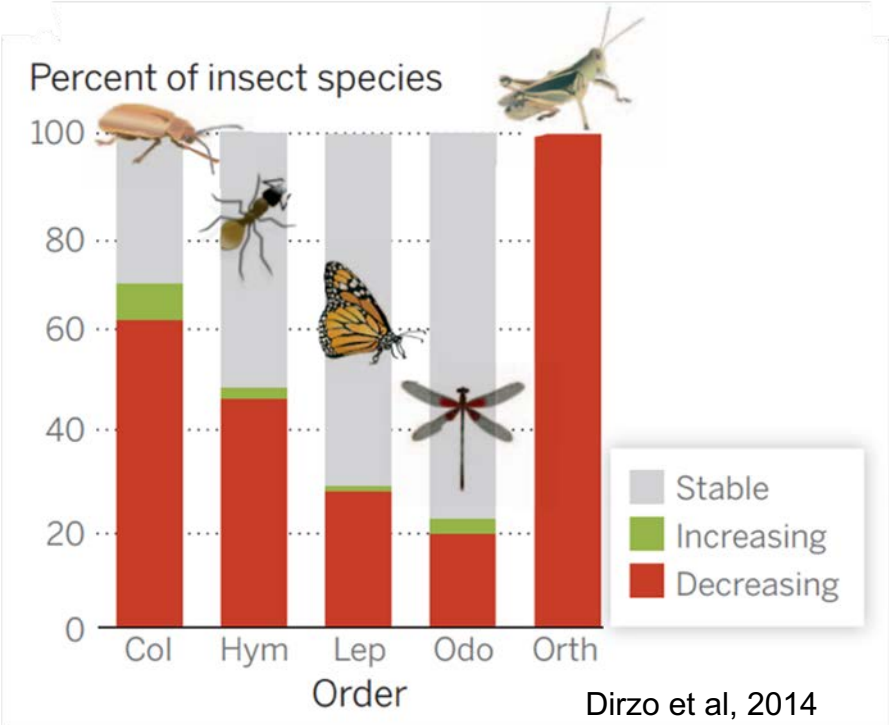

Gryllotalpa gryllotalpa
(Gyllotalpidae)


Xya variegata
(Tridactylidae)


Troglophilus neglectus
(Raphidophoridae)

+ SwissBOL

Orthopteran species



Dirzo et al, 2014

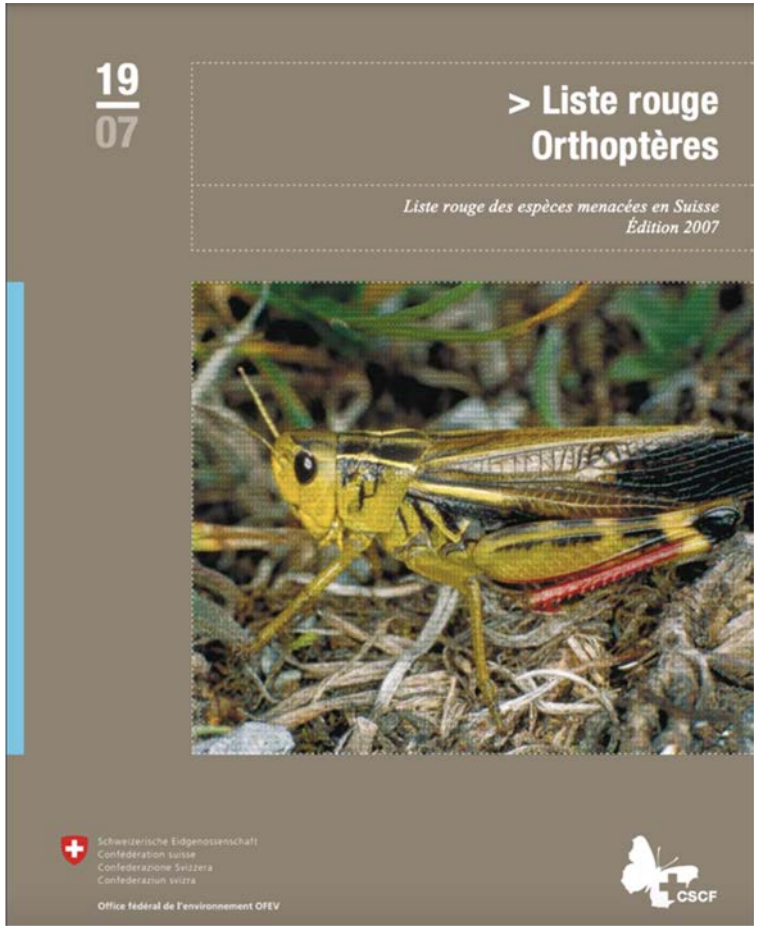
Bioindicator species

- pioneer areas in river alluvial zones
-secondary pioneer areas
-marshes and wet meadows
- scorched lawns, dry meadows and pastures
- semi-forest

Swiss Orthoptera

105 species

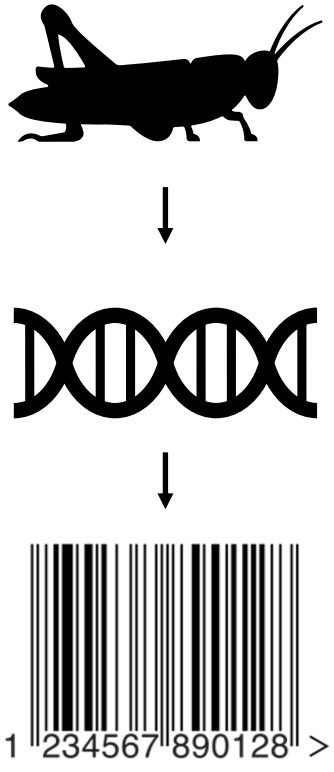
7 families



- Red List of Swiss Orthoptera 2007:
  40% are threatened

- Ongoing update

Single-locus barcode



Define trophic networks

Define species boundaries

Species monitoring

Undercover cryptic species

DNA barcoding of crickets, katydids and grasshoppers (Orthoptera) from Central Europe with focus on Austria, Germany and Switzerland

O. HAWLITSCHEK,*,† J. MORINIÈRE,* G. U. C. LEHMANN,‡ A. W. LEHMANN,§ M. KROPF,¶ A. DUNZ,* F. GLAW,* M. DETCHAROEN,* S. SCHMIDT,* A. HAUSMANN,* N. U. SZUCSICH,** S. A. CAETANO-WYLER†† and G. HASZPRUNAR*,‡‡

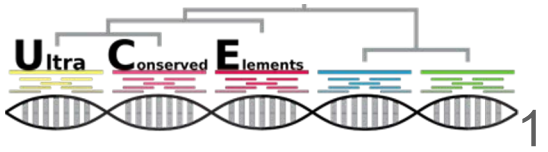
40% of Caelifera can not be identified using COI barcode

-Lack of variation at the interspecies level

-Incomplete lineage sorting

-Nuclear Mitochondrial DNA Segments (*numts*)

-Negligible variation within-species

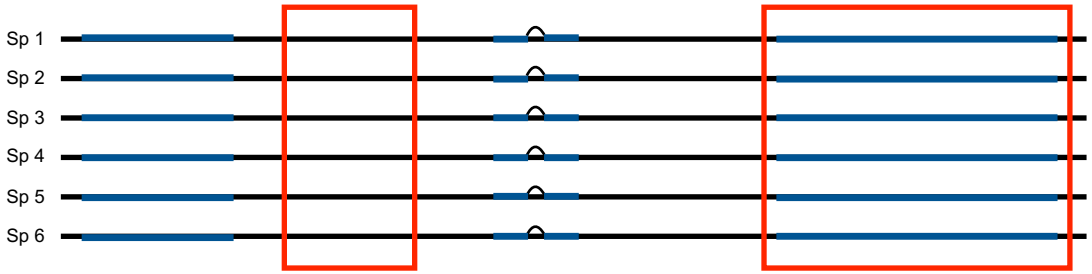


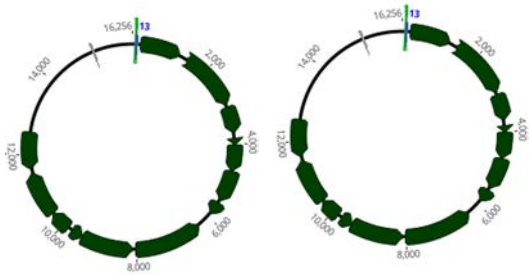
1

2

Ribosomal DNA 3

Mitogenome 4

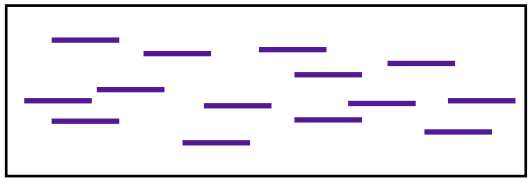




Alignment

Probes design

Probe set *de novo* synthesis



Ribosomal DNA

NCBI

Complete rDNA sequences

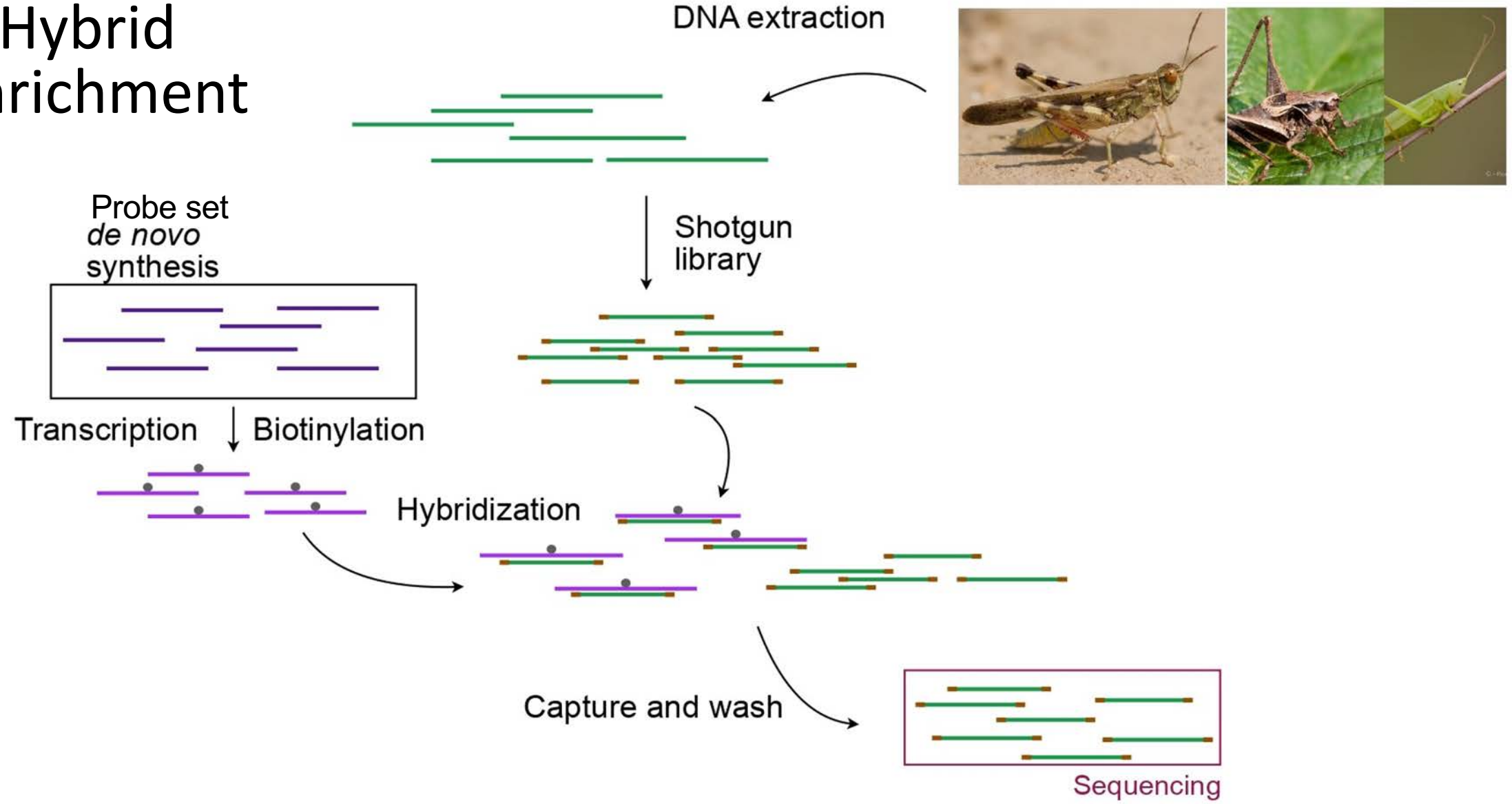
2 - Caelifera
0 - Ensifera

Universal eukaryote primers Krehenwinkel et al. 2018

Ribosomal DNA sequences for 13 new species!

Oxford NANOPORE Technologies

Anchored Hybrid Enrichment



Lemmon et al., 2012

Perspectives

- Update of the Orthoptera Red List
- Application of the multi-locus marker approach to other groups

Thank you for your attention

Science et recherche au Muséum de Genève

Inés Carrasquer
Camille Pitteloud
Julia Bilat
Nadir Alvarez

Monitoring

Development of a multi-purpose and multi-locus marker for (Swiss) Orthoptera

OrthoSwissBOL project

Schweizerische Eidgenossenschaft
Confédération suisse
Confederazione Svizzera
Confederaziun svizra

Swiss Confederation

Federal Office for the Environment FOEN

Multi-locus marker: Species delimitation

Groupe *Chorthippus biguttulus*

C. brunneus

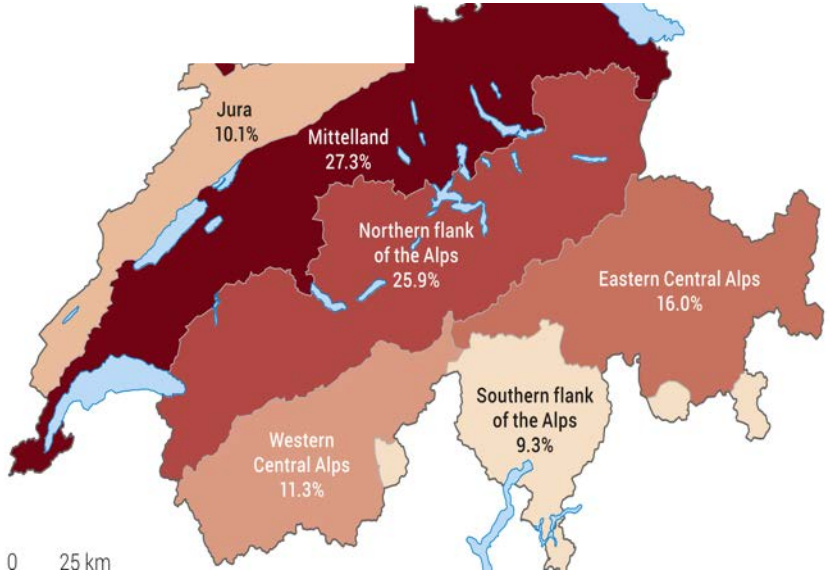
C. mollis

C. biguttulus

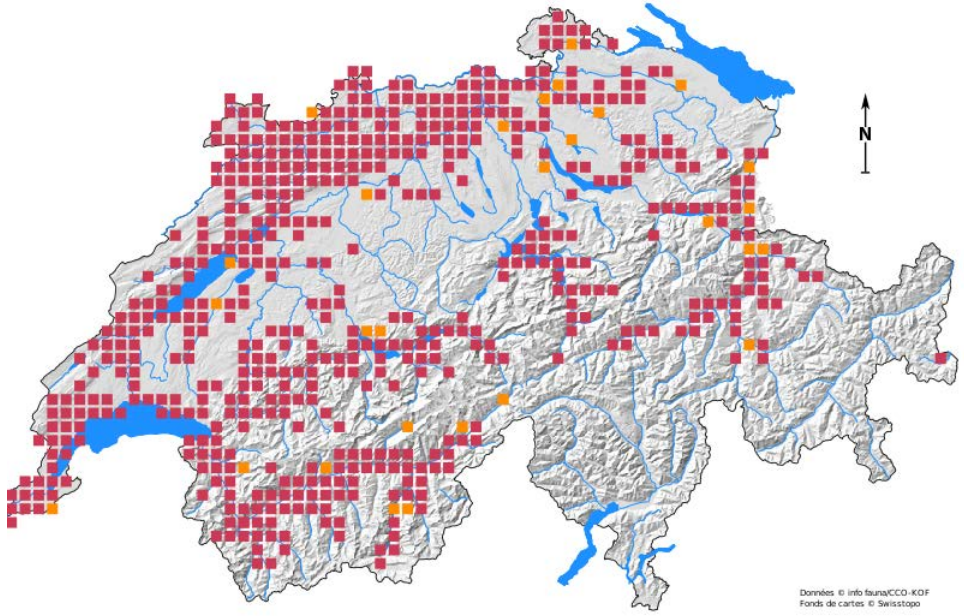
C. eisentrauti

Platycleis albopunctata
ssp. *albopunctata*
ssp. *grisea*

Multi-locus marker: Genetic diversity inference

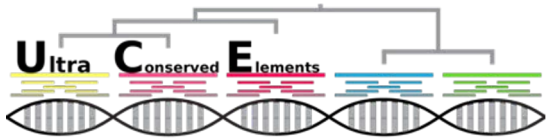


ESPECE	JU	PL	NA	AiOc	AiOr	SA	Total général
nus barbarus	3						
nus italicus	4	6		4	1	3	
nus siciliae						3	
pus albomarginatus	8	5	1				
pus apricarius	3		5		4		
pus biguttulus	8	5	9	2	3		
pus brunneus	6	5	1	2	3	6	
pus dorsatus	4	8	4	1	3	5	
pus eisentrauti			3	2	2	4	
pus mollis	2	8		3	3	3	
pus montanus	11	2	14	1	2		
pus parallelus	14	6	8	4	3	4	
pus pullus				1	3		
pus vagans	4			8		3	



Platycleis albopunctata
ssp. *albopunctata*

Genomic components



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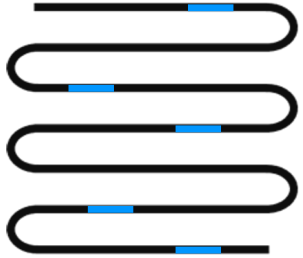
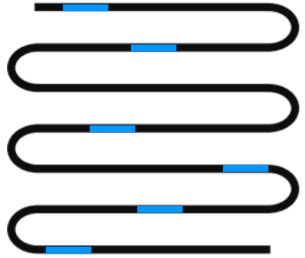
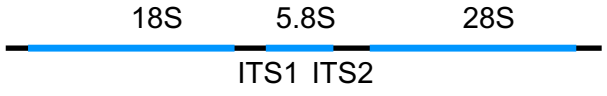
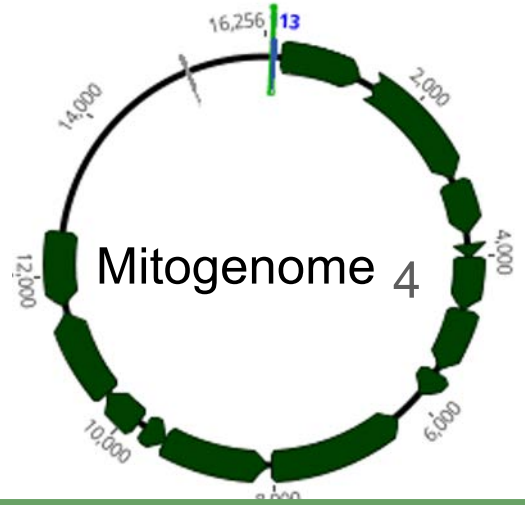


2



Ribosomal DNA 3

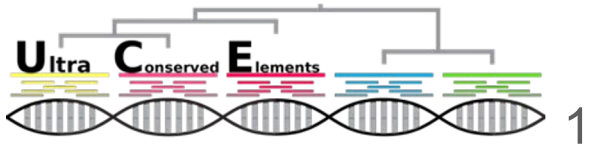




Mitogenome 4

Genomic components

- Informativeness
- Universality
- Backward compatibility
- Standardization



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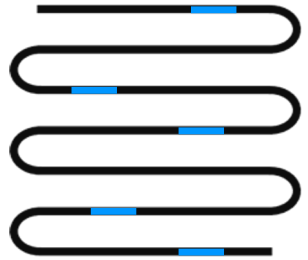

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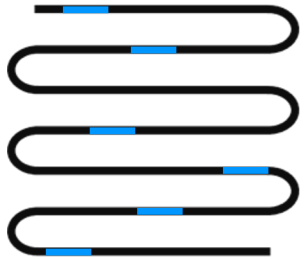
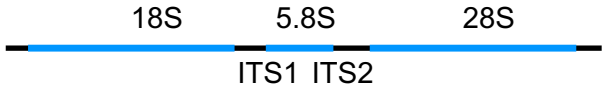
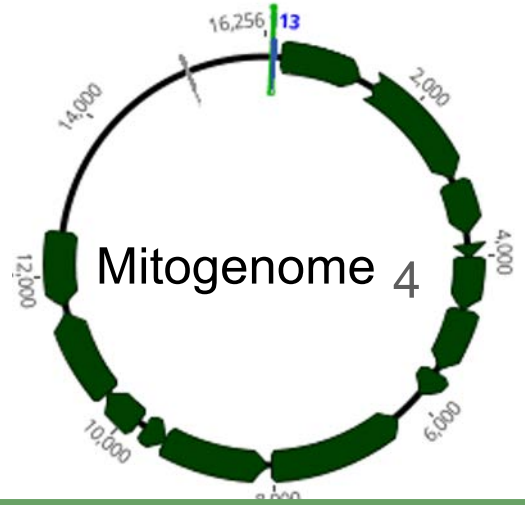


Ribosomal DNA 3





Mitogenome 4

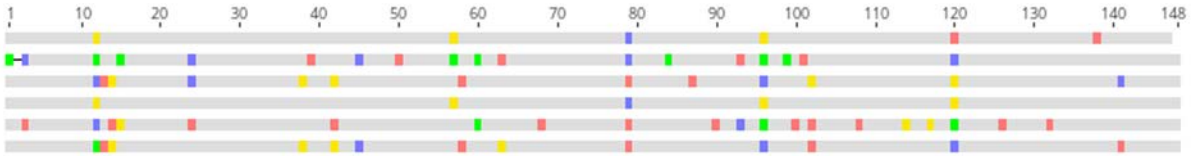
Conserved genetic regions

Reference genomes
3 x Ensifera
3 x Caelifera
1 outgroup

290 loci

[1]

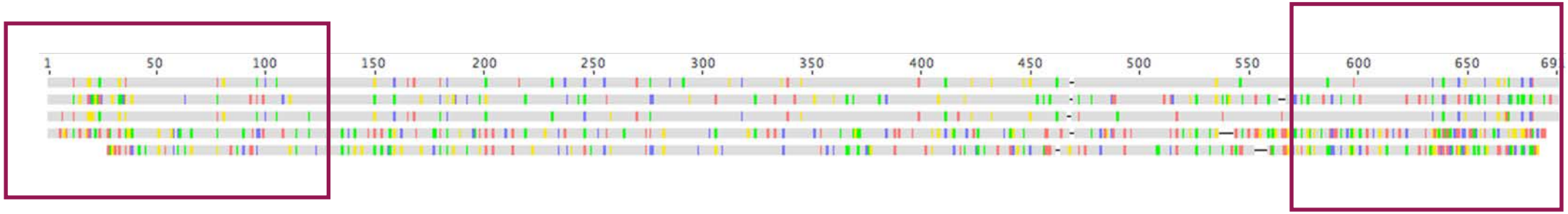
PHYLUCE Faircloth, 2016



64 loci

[2]

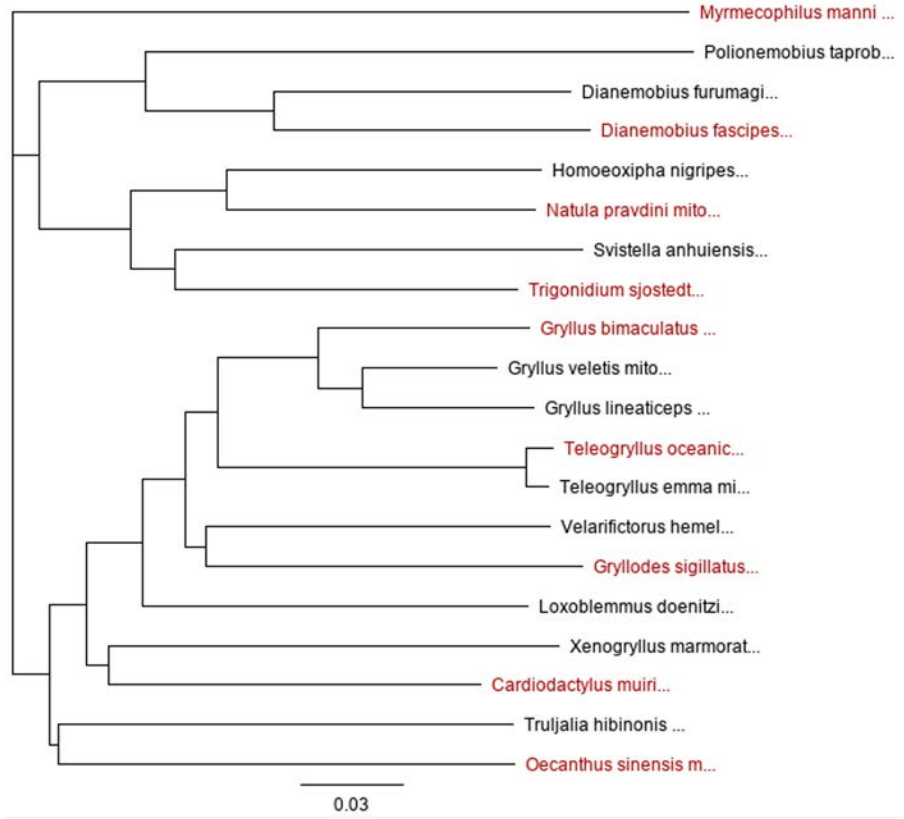
BUSCO v.4 Manni et al., 2021

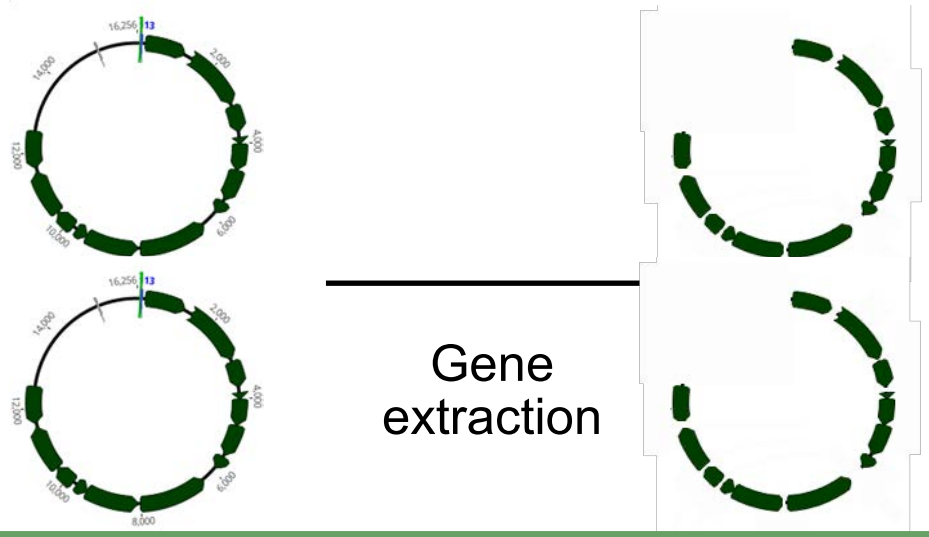


Mitogenome$_4$

NCBI 240 complete mitochondrion

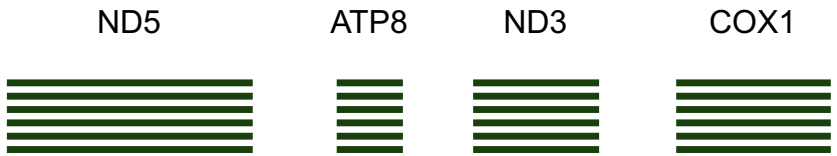
42 selected mitogenomes
evenly distributed in the phylogeny



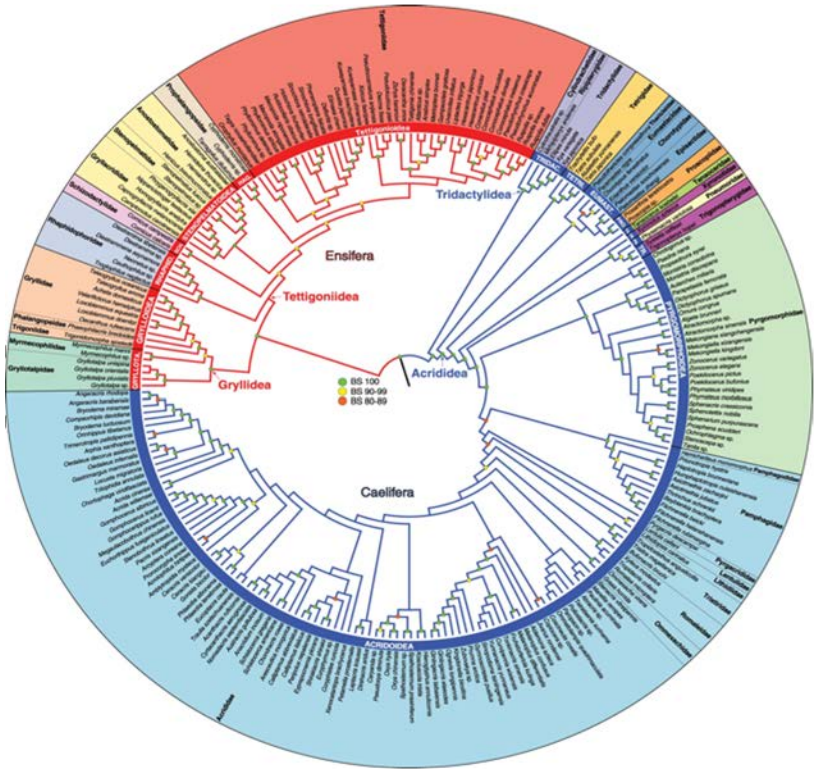


Gene extraction

Alignment

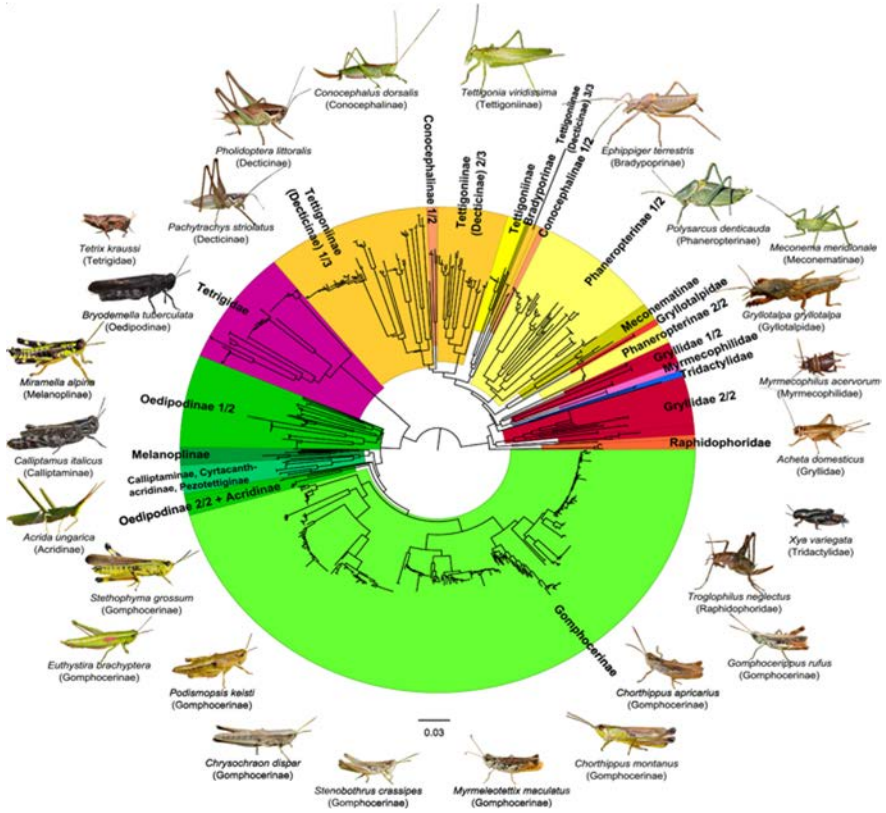


Multi-locus marker: Phylogenetic reconstruction



Transcriptomes

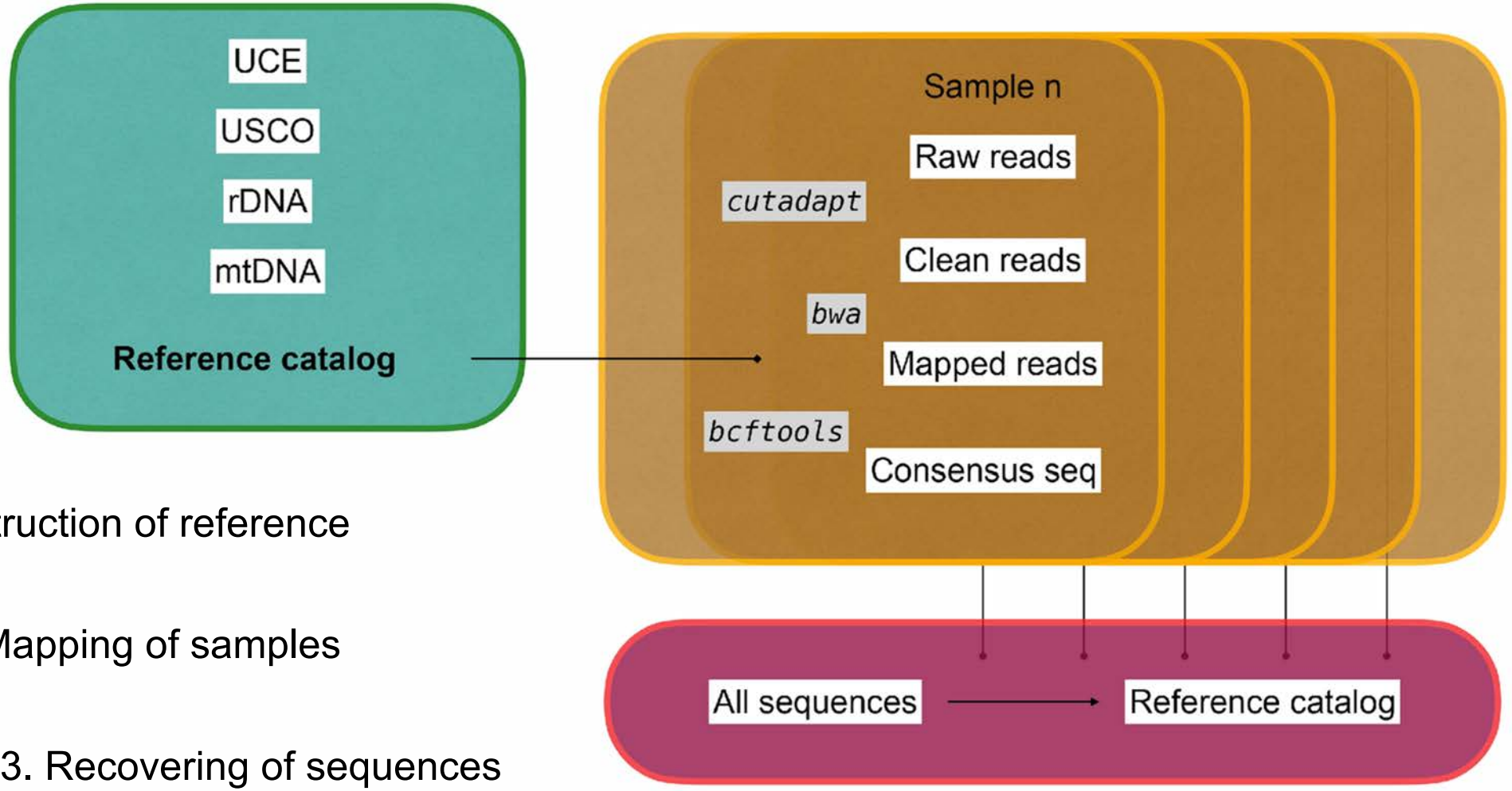
Song et al., 2020



mtDNA

Hawlitschek et al., 2020

Data treatment



1. Construction of reference

2. Mapping of samples

3. Recovering of sequences

Selection of the best combination of loci

Species delimitation
Phylogenetic power
Within-species diversity

Multi-locus barcode

Extinction vortex