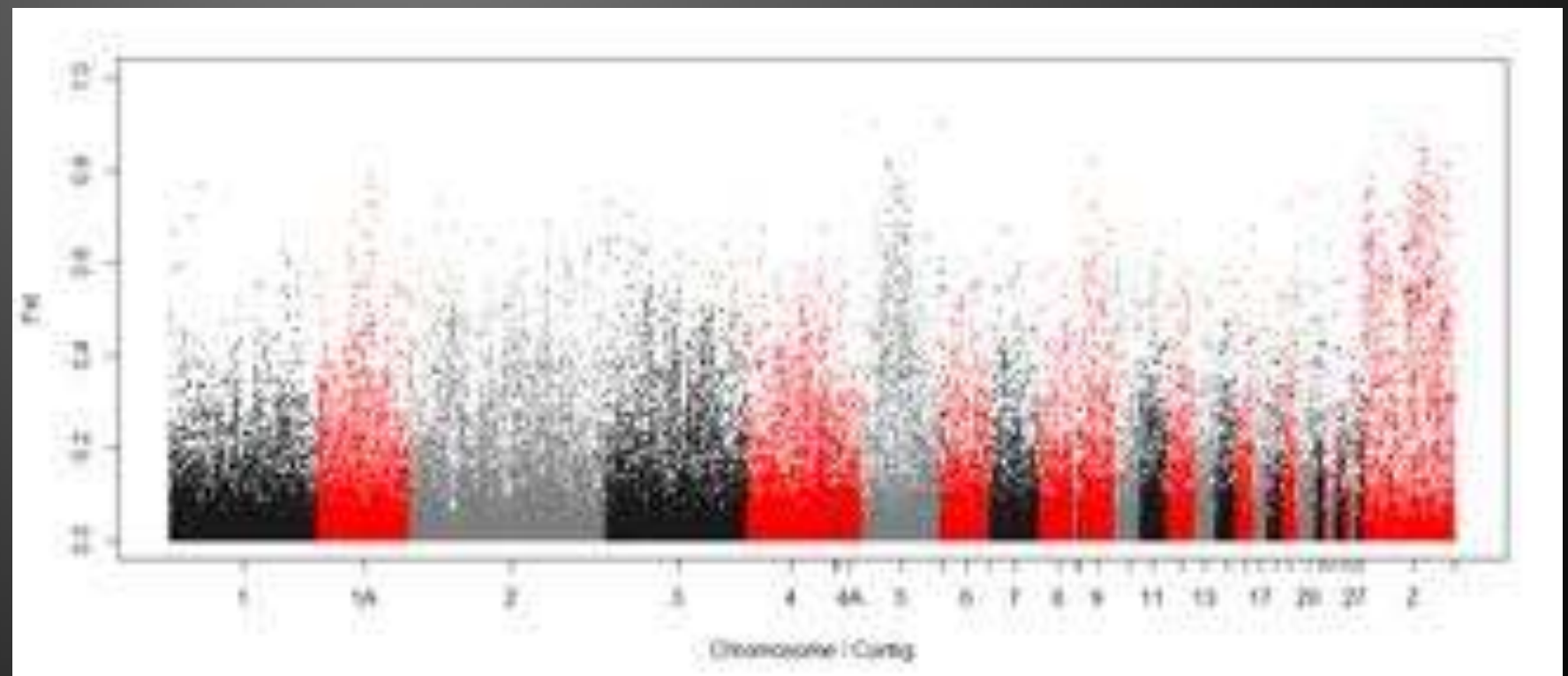


Participant Introduction



JASON SARDELL

University of Miami, USA





T.J. McGreevy, Ph.D.

Wildlife Genetics & Ecology Laboratory

Natural Resources Science Department

University of Rhode Island



Eastern Cottontail



PhotoCredit: Rand Herron

New England Cottontail



Photo Credit: Lou Perrotti



Bobcat



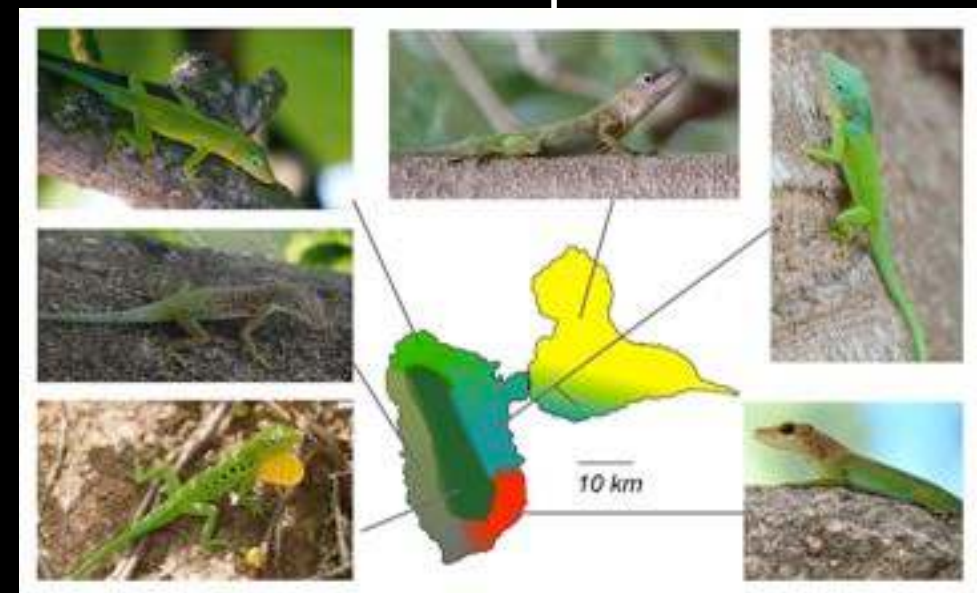
Photo: www.nhptv.org

American Black Bear

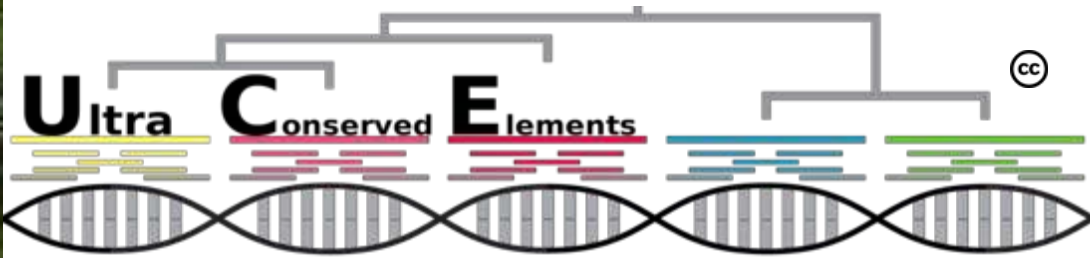


Photo: Westernwildlife.com

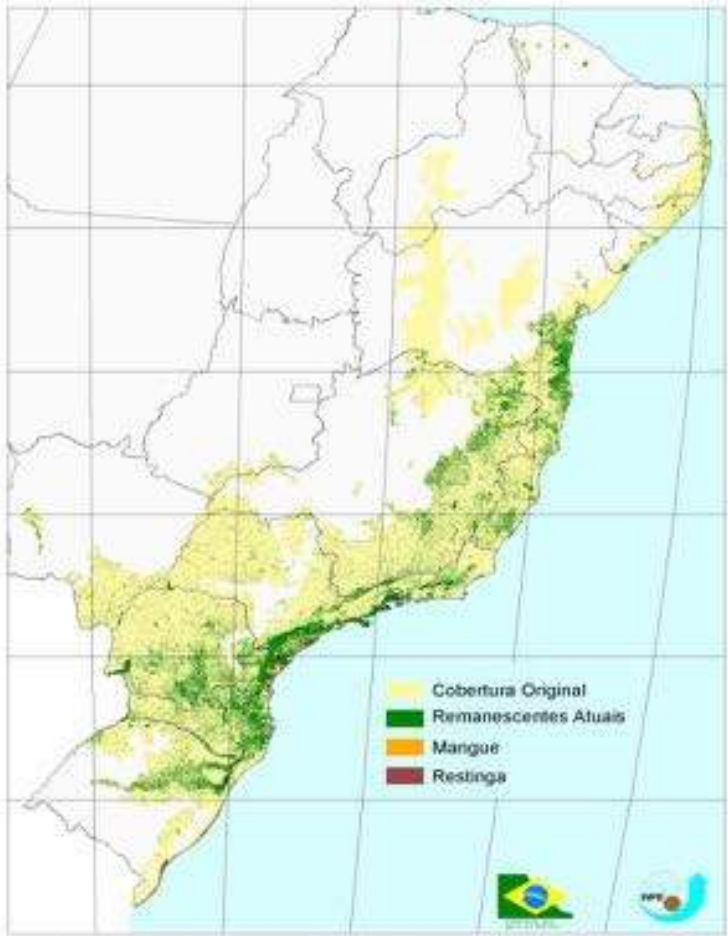
Guadeloupean anole



Patrícia Regina Ströher
working on
Phylogeography of Brazilian Atlantic Rainforest



© Alex Wild
www.alexwild.com



Laboratories:

Laboratório de
Dinâmica Evolutiva e
Sistemas Complexos

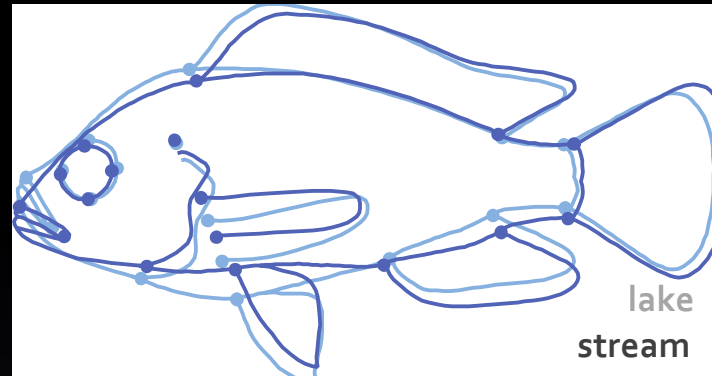
MOORE LABORATORY OF ZOOLOGY
OCCIDENTAL COLLEGE

EAGLE ROCK | LOS ANGELES | CA

Advisor: Prof. Dr. Marcio Pie
Contact: patricia.stroher@gmail.com

Support:

Adaptive divergence in the cichlid fish *Astatotilapia burtoni*

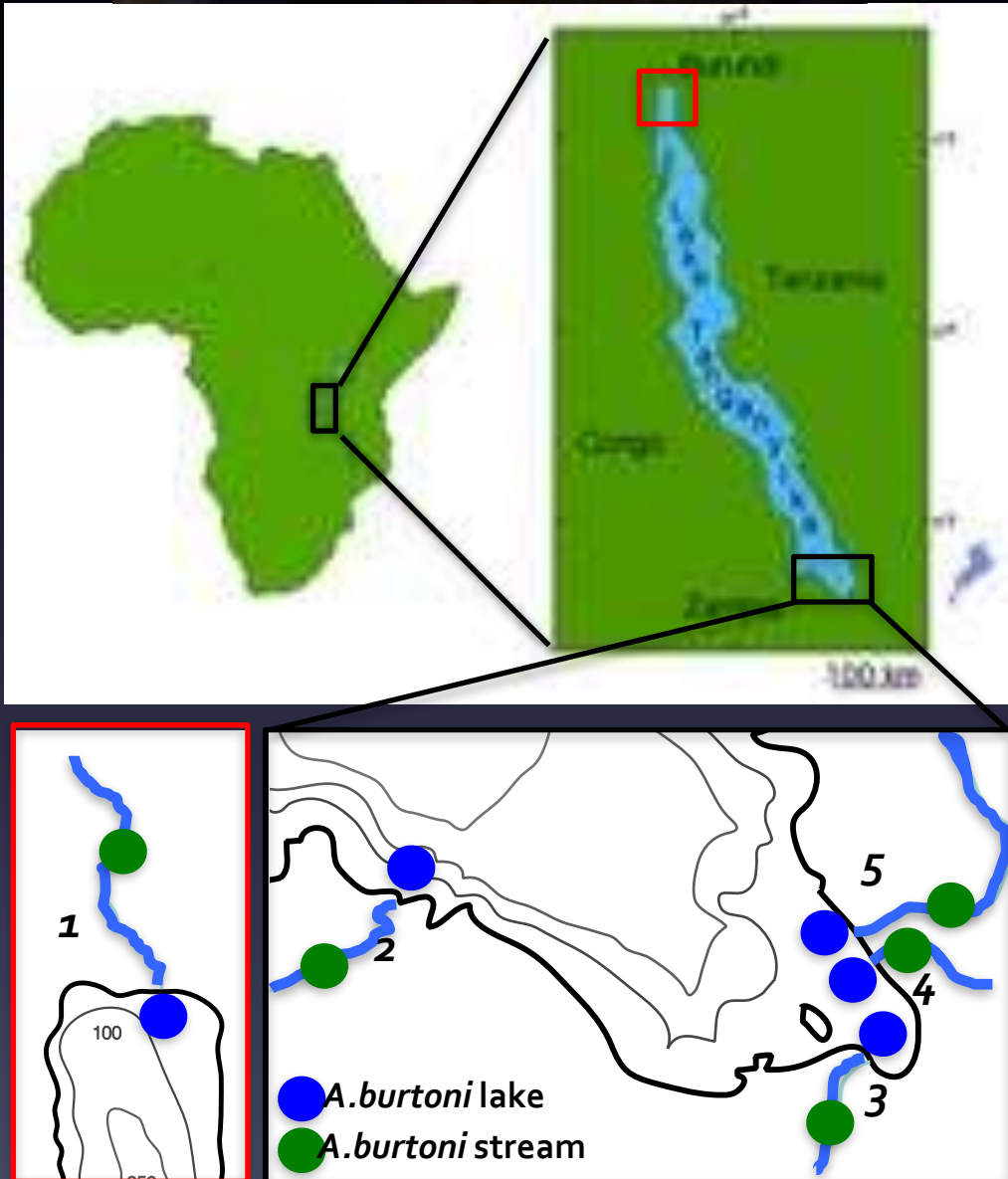


Morphological differences

- Body depth
- mouth position
- Trophic apparatus

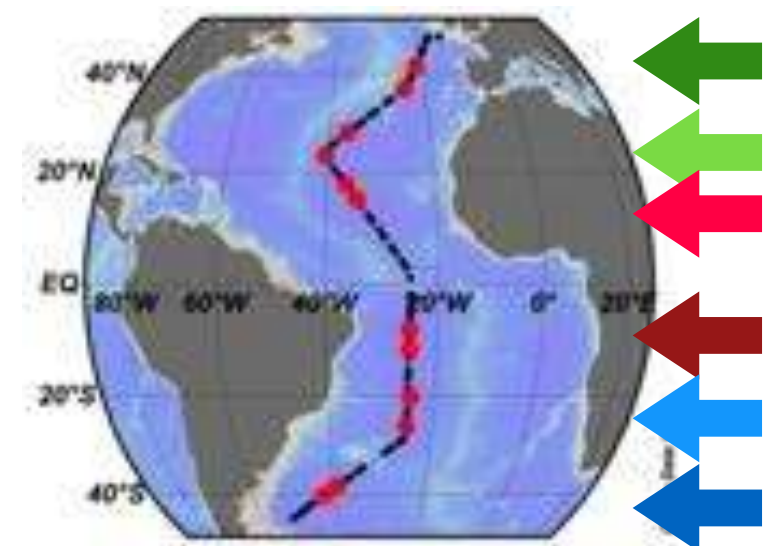
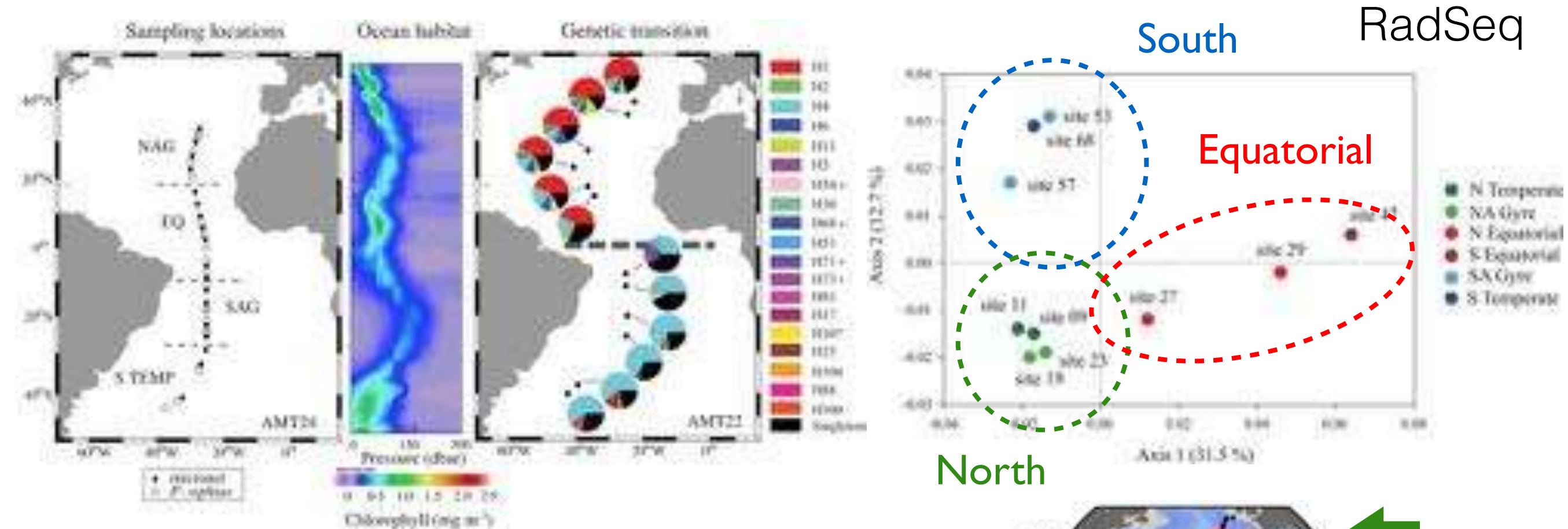
Genome divergence during speciation

- 5 « replicate » lake – stream systems (10 pop)
- Different stages of speciation continuum
- 12 individual genomes per pop (120 genomes)
- Genes involved in adaptation to different envt?
 - same among replicates?
 - local adaptation?



Adaptation in the open ocean

Erica Goetze, Department of Oceanography, University of Hawaii at Manoa



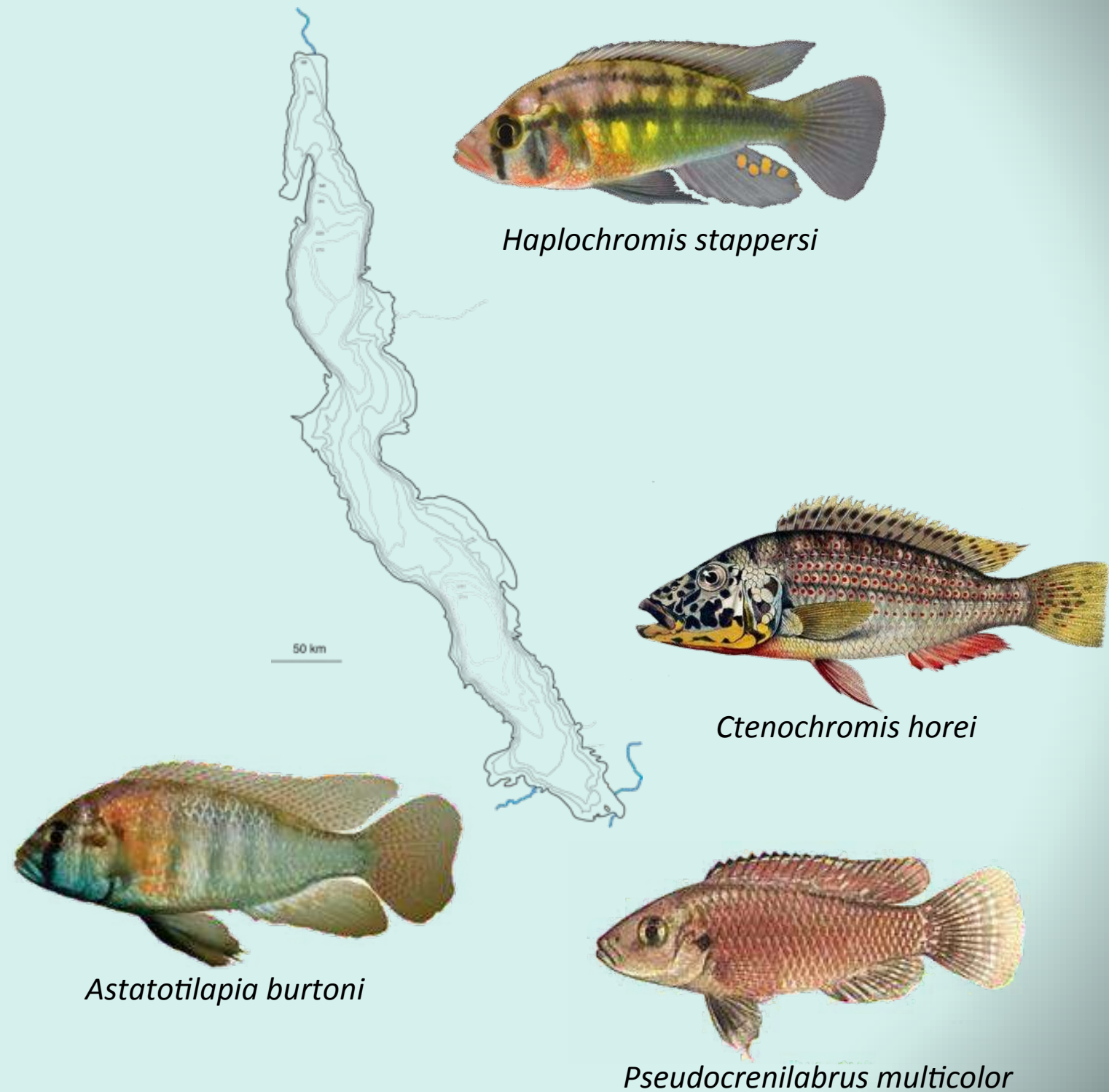
Adaptive divergence along a lake-stream environmental gradient in East African cichlid fishes: a comparative approach

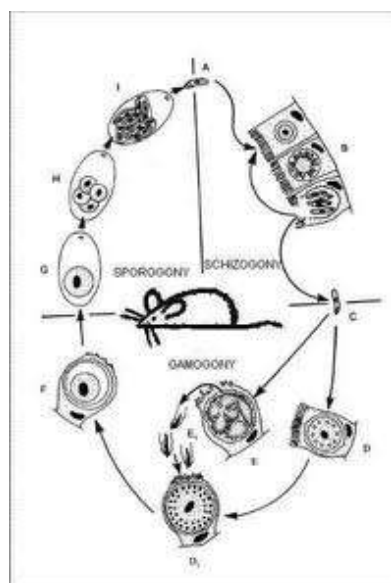


Lake Tanganyika



Affluent rivers

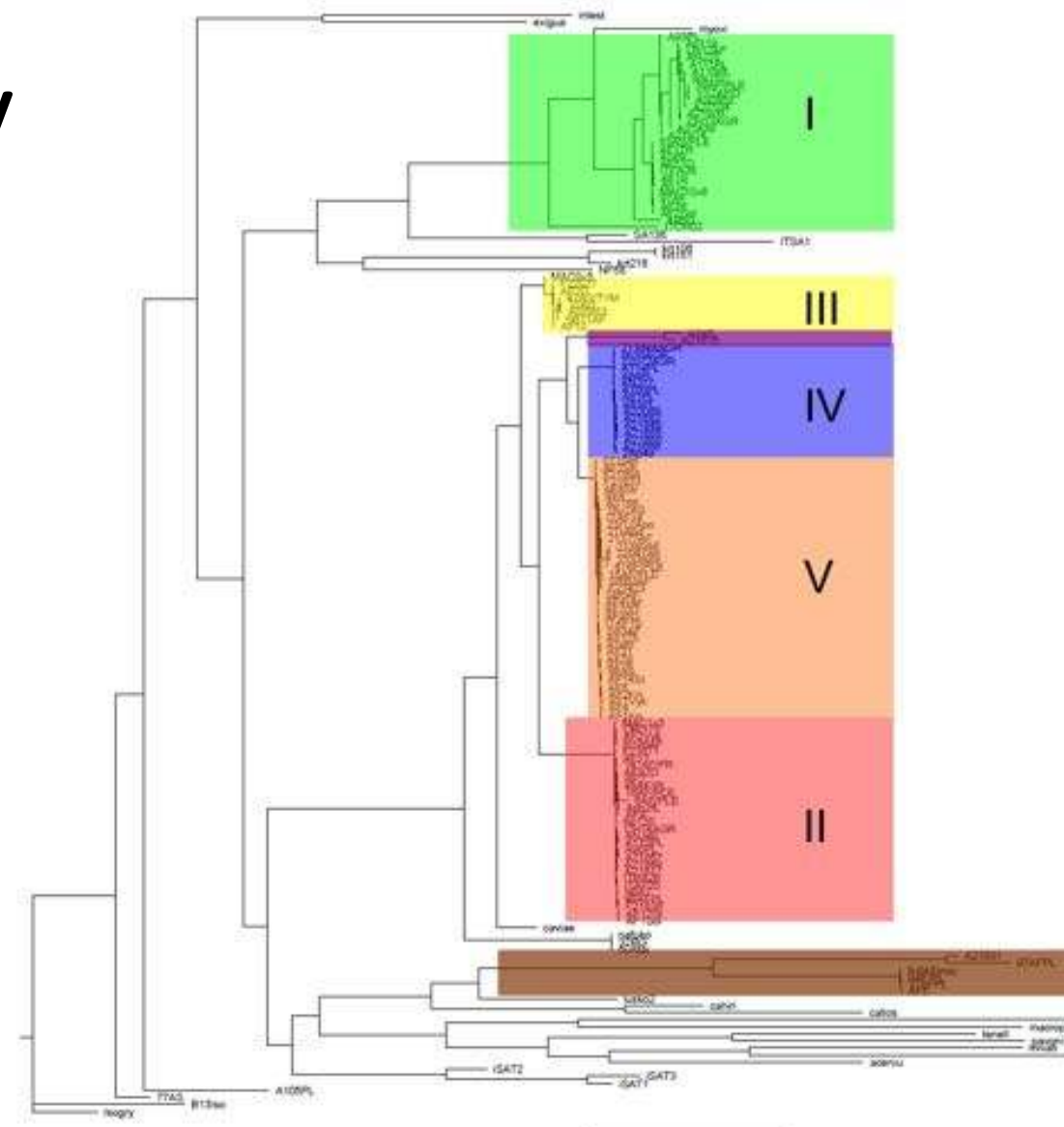
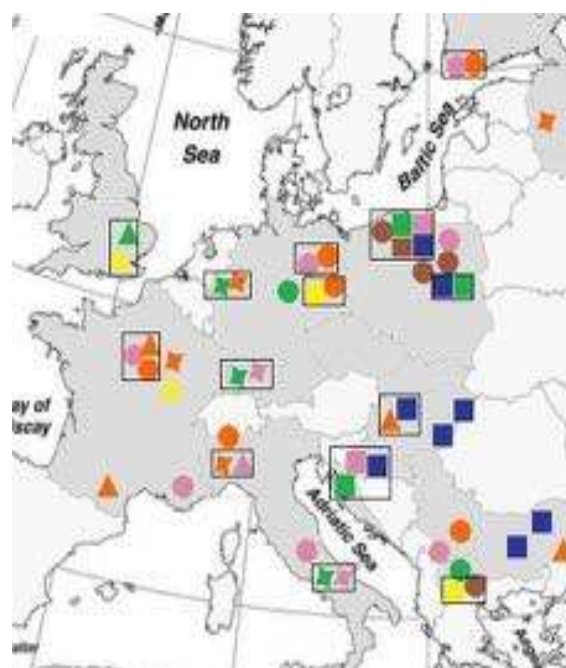




Evolution and phylogeny of *Eimeria* sp. infecting *Apodemus* sp.



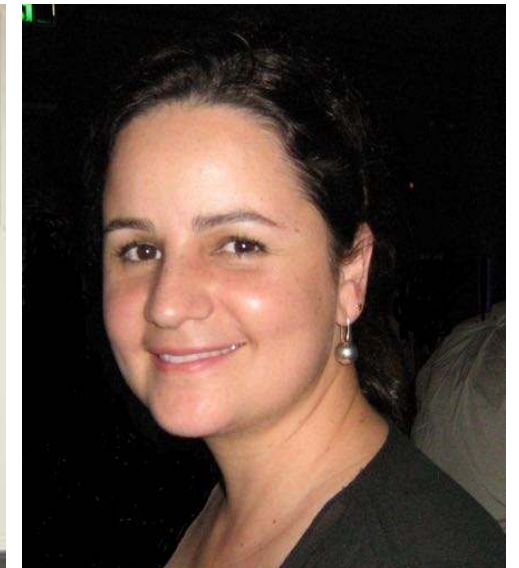
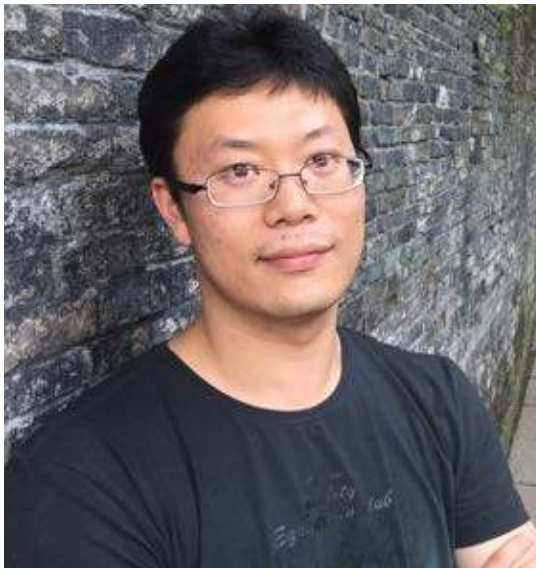
Anna Mácová



University of South Bohemia, Faculty of Science, České Budějovice, Czech Republic

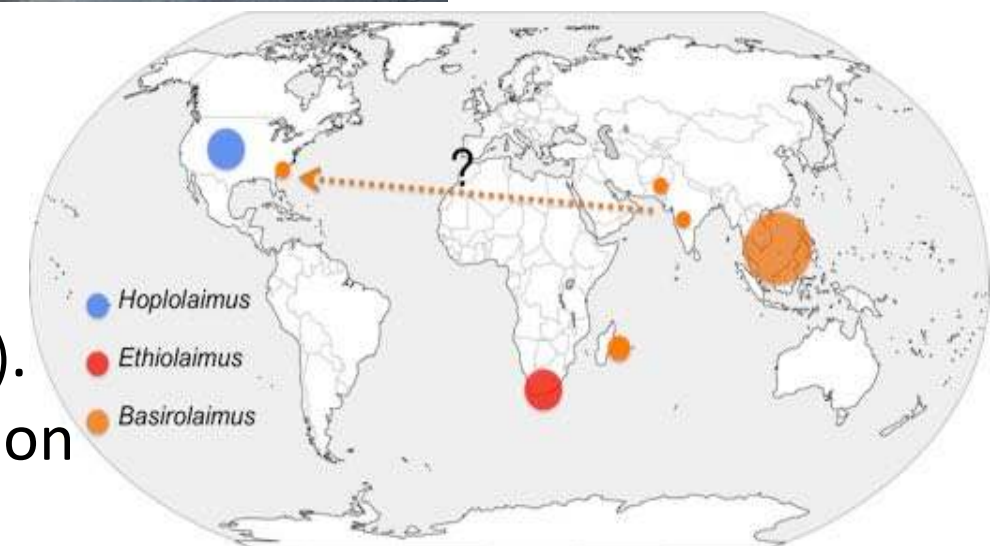
Academy of Sciences of the Czech Republic, Institute of Parasitology, České Budějovice, Czech Republic

Xinyuan Ma "Max" PhD student, Plant and Environ. Sciences. Clemson University. Clemson, SC. USA
Plant Nematology Lab. Advisor: Dr. Paula Agudelo



LAB RESEARCH FOCUS: Biology and ecology of lance nematodes in agroecosystems.

PERSONAL INTERESTS: Speciation and phylogenetic relationships among lance nematodes (*Hoplolaimus* spp.). Biogeographic patterns. Genetic diversity and population structure.



Michael Matschner

Konstanz → Basel → Auckland → Oslo



Tandem



CladeAge

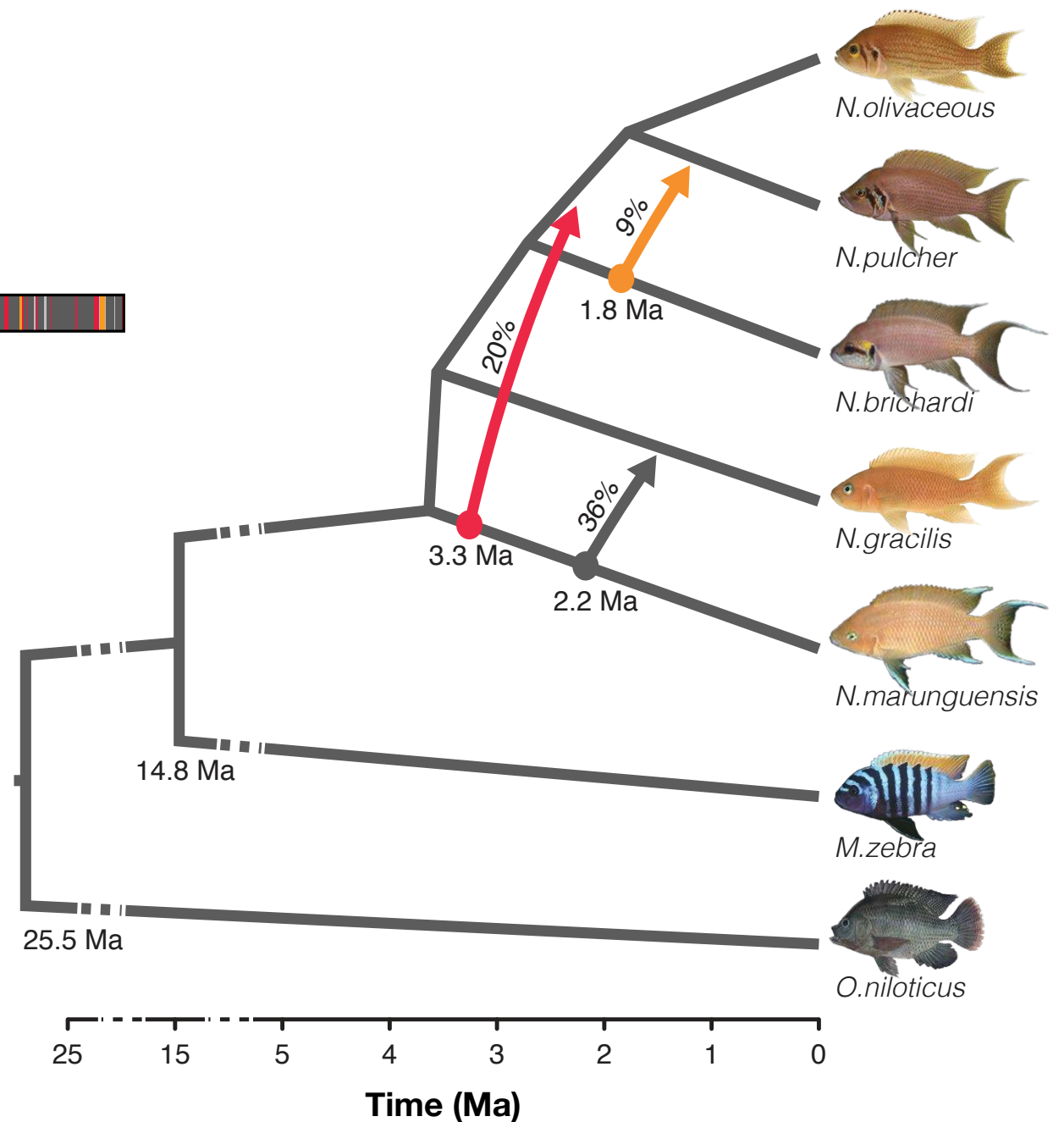
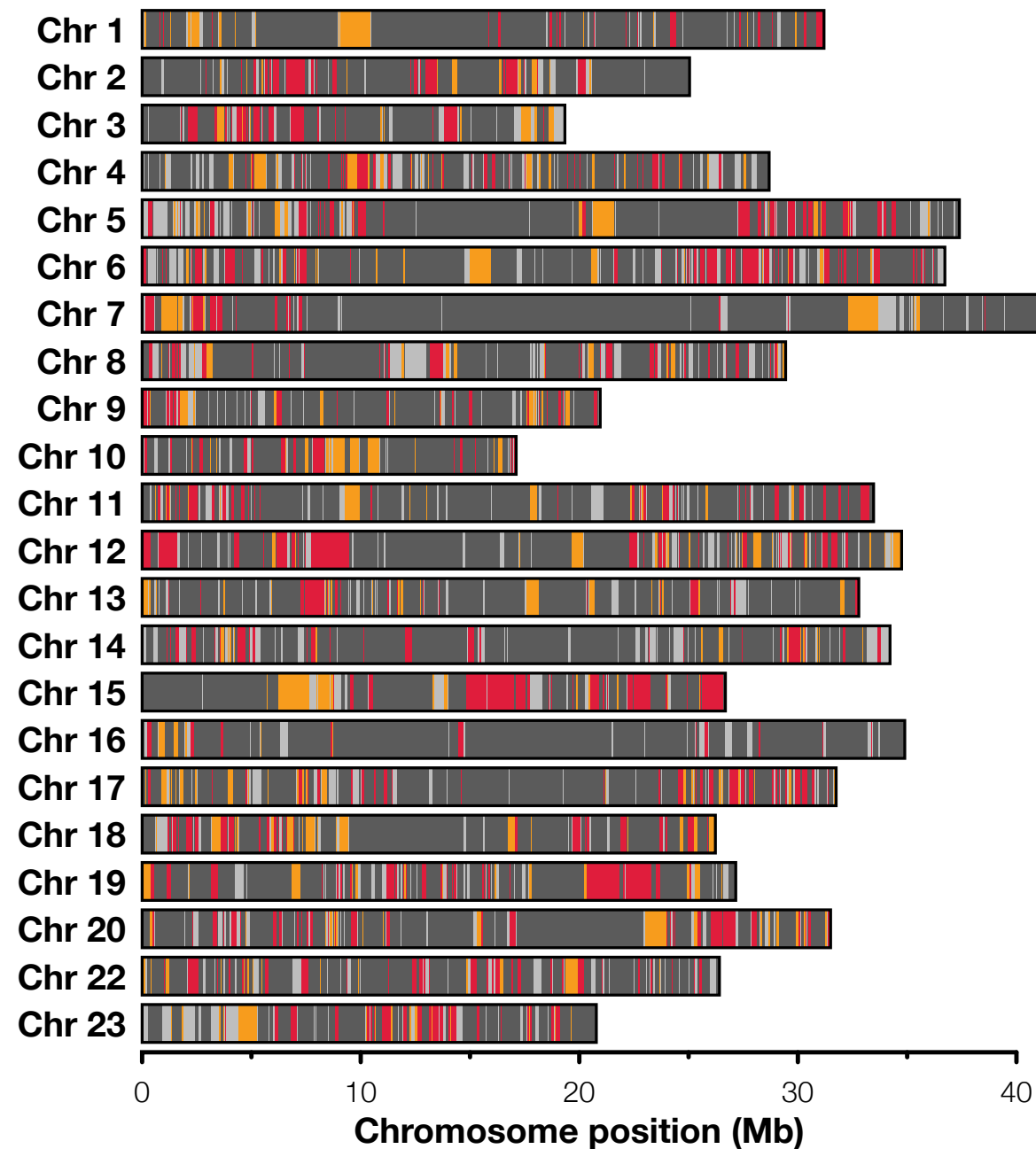


Fitchi



F4

Introgression in cichlid fishes:



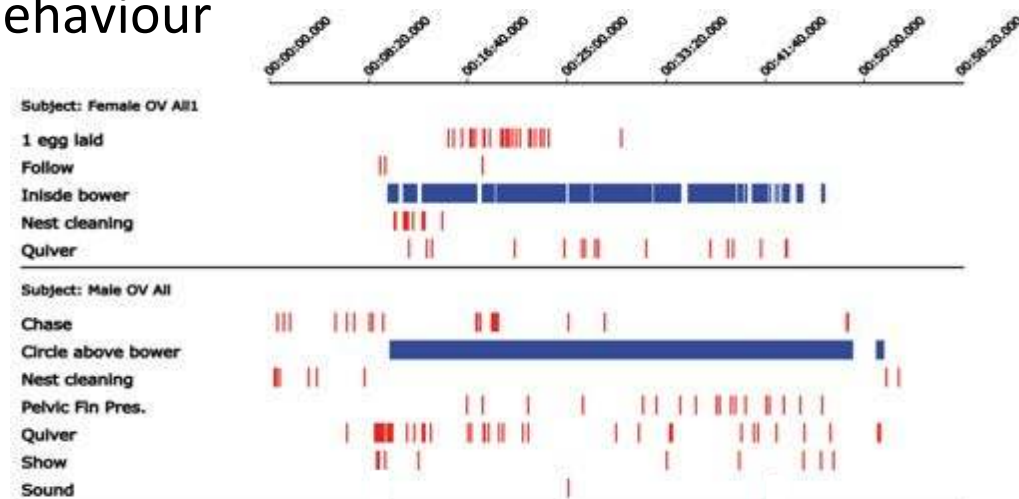
Derycke Sofie
Verheyen Erik

GENBAS: GENomic BAsis of Speciation



From left to right: *O. ventralis*, *O. nasuta* and *O. boops*. Pictures courtesy of Ad Konings and Siegfried Loose.

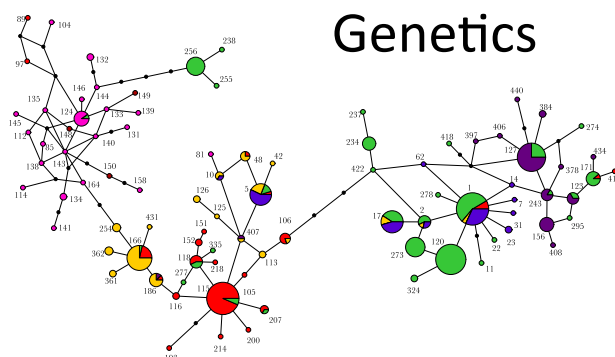
Behaviour



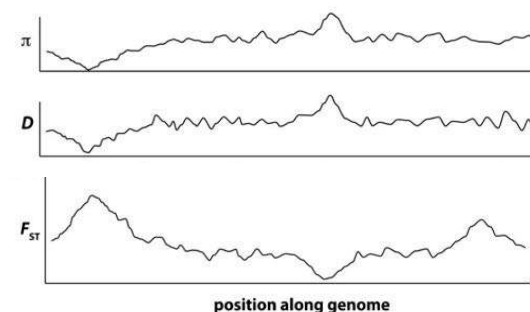
Transcriptomics – Quantseq 3' mRNA seq



Genetics



Population genomics - GBS



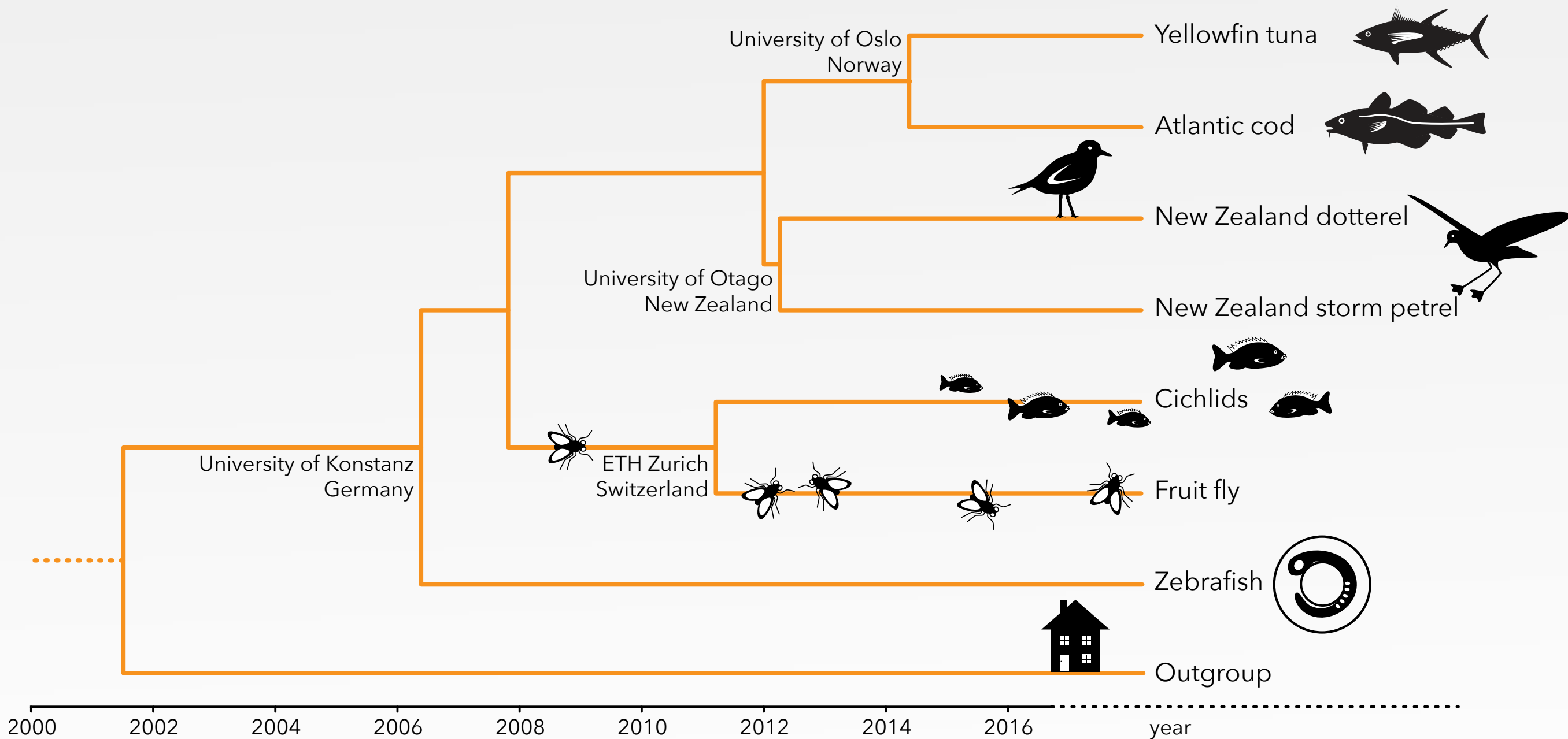
Royal Belgian Institute
for Natural Sciences

museum



JULIA M.I. BARTH

University of Oslo



Postcopulatory sexual selection: the genetics of sperm traits and female extrapair mate preferences

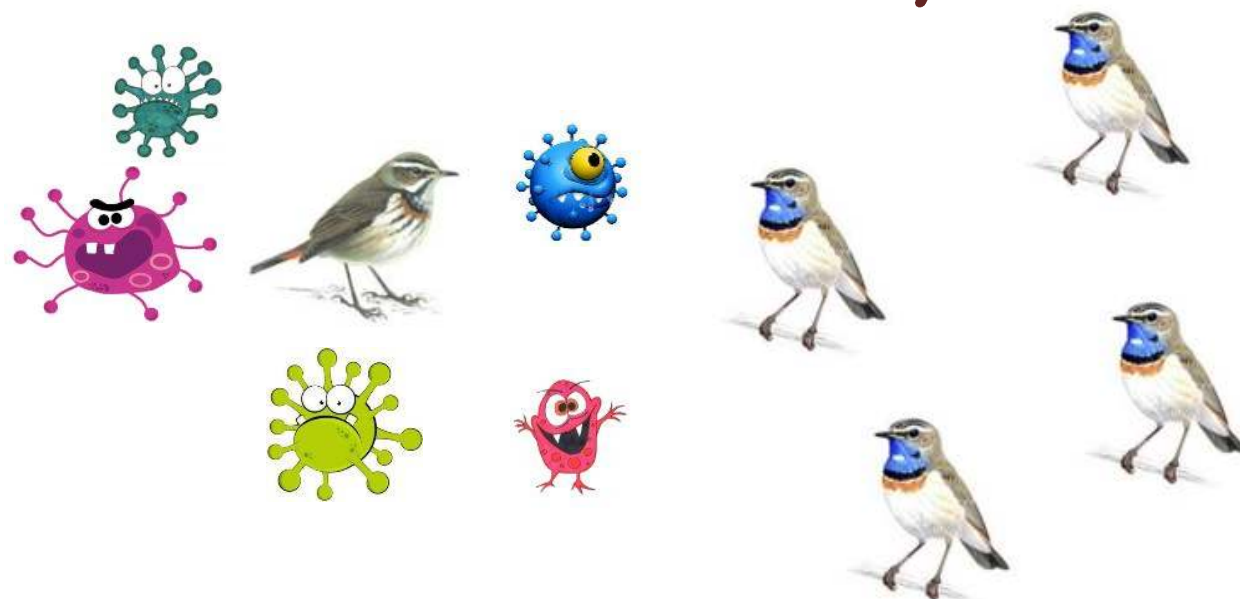
Part I – SPERM COMPETITION: genetic bases for sperm traits



willow warbler (*Phylloscopus trochilus*)

- Variation in sperm traits
- Genome-wide SNPs
- Identification of related genomic regions (GWAS)
- Linkage map

Part II – CRYPTIC FEMALE CHOICE: Extra pair mate preferences and MHC diversity



bluethroat (*Luscinia svecica*)

- MHC diversity
- Relation to mating systems (EPY vs WPY)
- Amplicon sequencing (Ion Torrent)

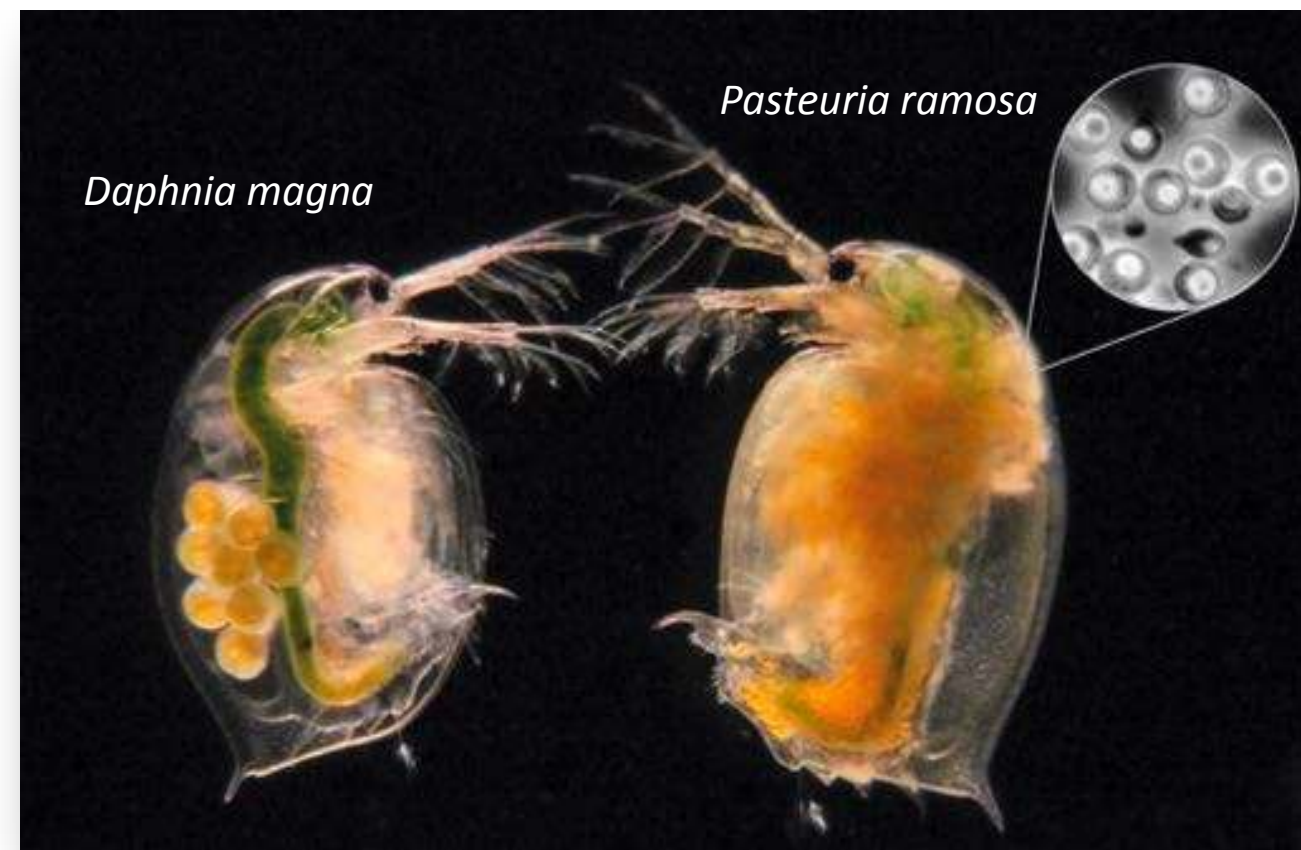
→ sexual selection and the resulting evolutionary consequences

Camille Ameline, PhD

Zoological Institute, Evolutionary Biology
Dieter Ebert group
Basel, Switzerland



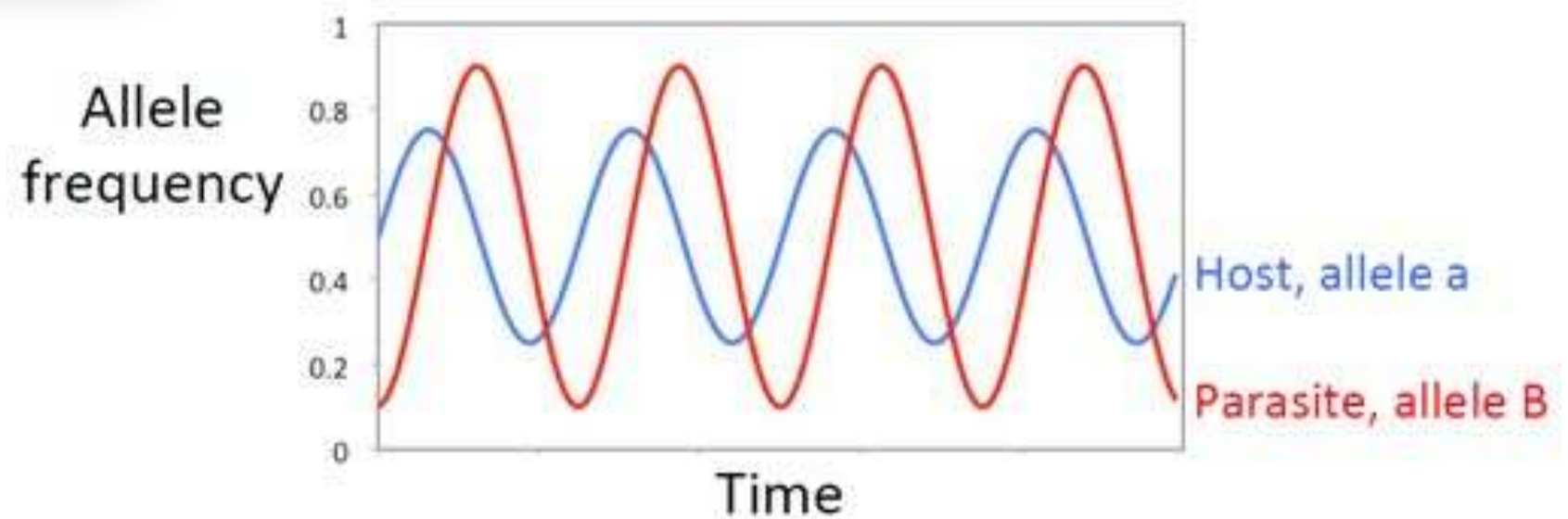
The Swiss pond



Coevolution of Host – Parasite interactions

- Dynamics of resistance/infection alleles in the populations

- ❖ Red Queen hypothesis
- ❖ Negative Frequency Dependant Selection
- ❖ Matching Allele Model



Cong Liu

Okinawa Institute of Science and Technology Graduate University



Research interests:

Ant systematics, Community ecology/phylogeny, Phylogeography, and Population genetics

Current project:

Phylogeny, population genomics, speciation and adaptation of ant genus *Camponotus* in the Pacific archipelagoes using RADseq.



System of study: plant genus *Cochlearia*.

European alpine population

- Arctic alleles fixed or high frequency.

COLONIZATION AND RADIATION

ECOLOGICAL SPECIATION
FUELED BY SGV

Arctic metapopulation

- Cold adapted. Source of SGV.

European lowland population

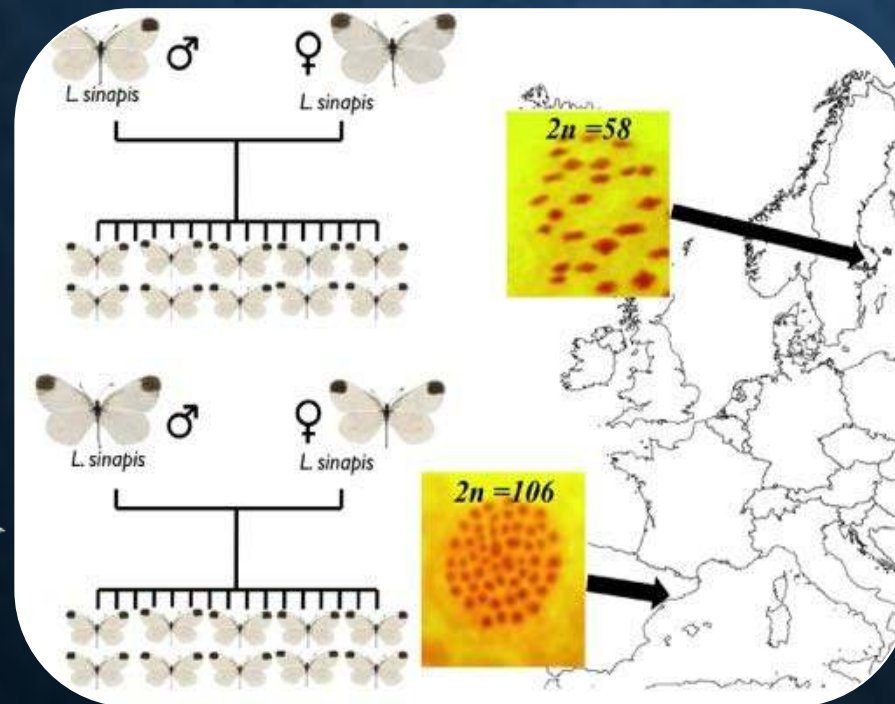
- Arctic alleles low frequency.



THE “CRYPTIC” CASE OF EUROPEAN WOOD WHITE BUTTERFLIES

Venkat Talla

Niclas Backström





Walter Salzburger

Zoological Institute
University of Basel, Switzerland



Unraveling the ecological and genetic basis of adaptive divergence in two hybridizing songbirds

Camille Sottas, PhD student

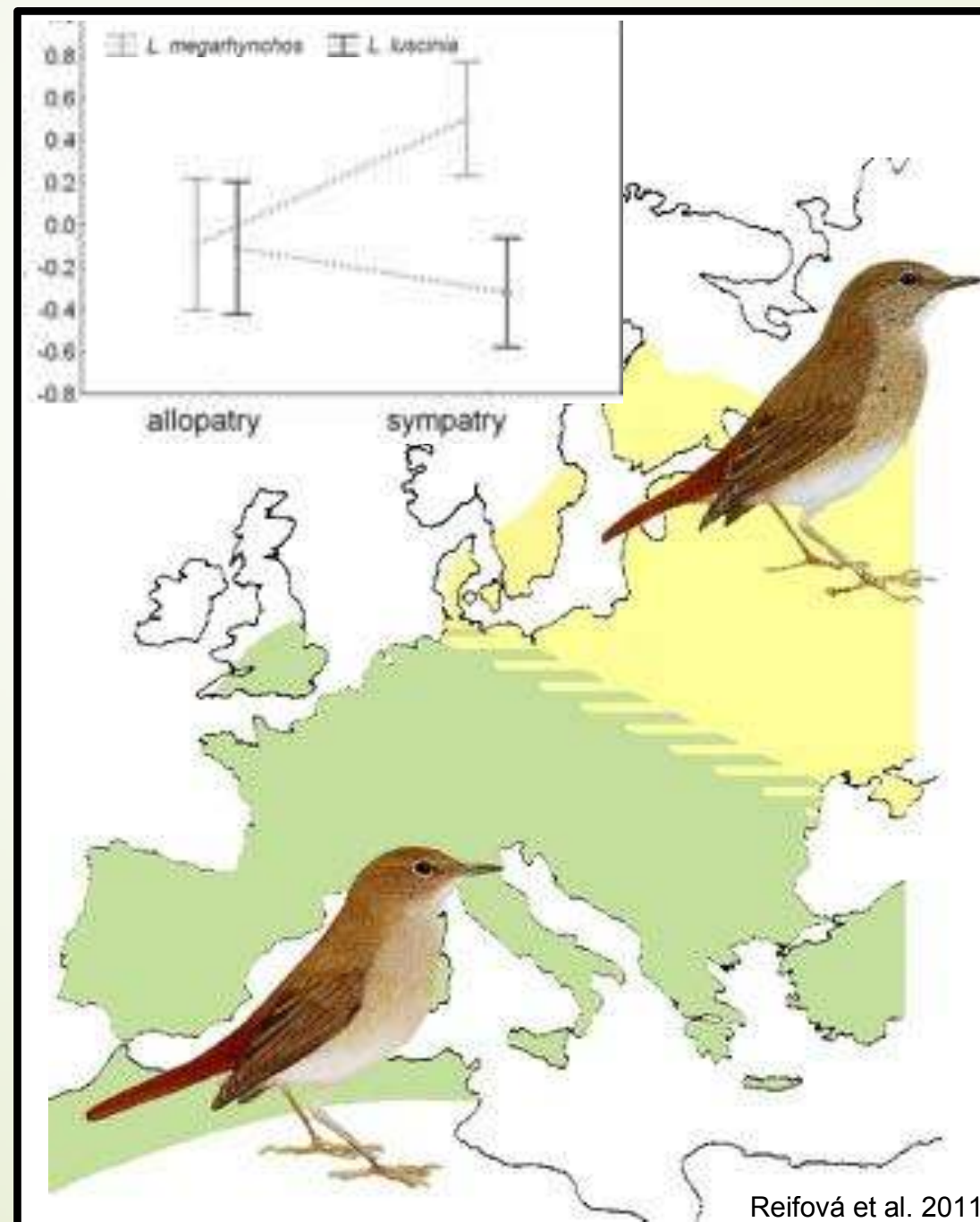
Supervisor: Radka Reifová

Faculty of Science, Charles University in Prague

Department of Zoology – Biodiversity Research Group



Common Nightingale
(*Luscinia megarhynchos*)



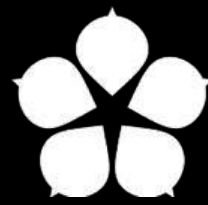
Reifová et al. 2011



Trush Nightingale
(*Luscinia luscinia*)



Lubomír Piálek
České Budějovice (Budweis)
Czech Republic



Faculty of Science
University of South Bohemia
in České Budějovice

Lab of Oldřich Říčan (USB)
Jorge Casciotta (Museo de La Plata)
Adriana Almirón (Museo de La Plata)
Klára Dragová (USB)

Research interests:

Evolution of Neotropical cichlids (and other fishes..)

Faunistic field work in Argentina (Iguazú/Paraná/Uruguay basins)

- 9 new fish species discovered & described (so far)
- new species flock of *Crenicichla* discovered in the Iguazú River:
piscivore – grazer – picker – thick lips



River 1

River 2

River 3

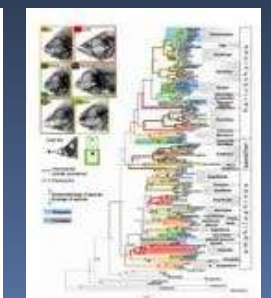
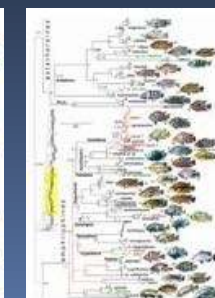


Parallel speciation in two unrelated *Crenicichla* species flocks from different basins

- distinct 'ecomorphospecies' are polyphyletic
- repeated diversification also in different subbasins?
- evolutionary mechanisms being studied based on *ddRAD* genomic markers

Diversity & evolution of Middle American cichlids

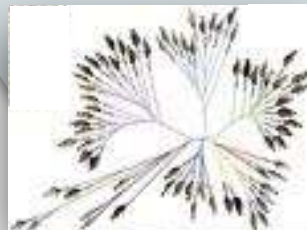
- new phylogenetic inference & taxonomy
- general principles of ecomorphological diversification



genomics, morphology and ecology of the Tanganyikan cichlid radiation ~250 species

whole genome sequencing

~570 ind.



μ CT - scanning



stable isotopes



Population genomics and demographic history of non-Midas

Aim:

Population genomic analysis using SNP markers in non-Midas Cichlid fish to investigate their genetic diversity and population structure to reconstruct the demographic history of species inhabiting Nicaraguan crater lakes



A. longimanus



H. nematopus



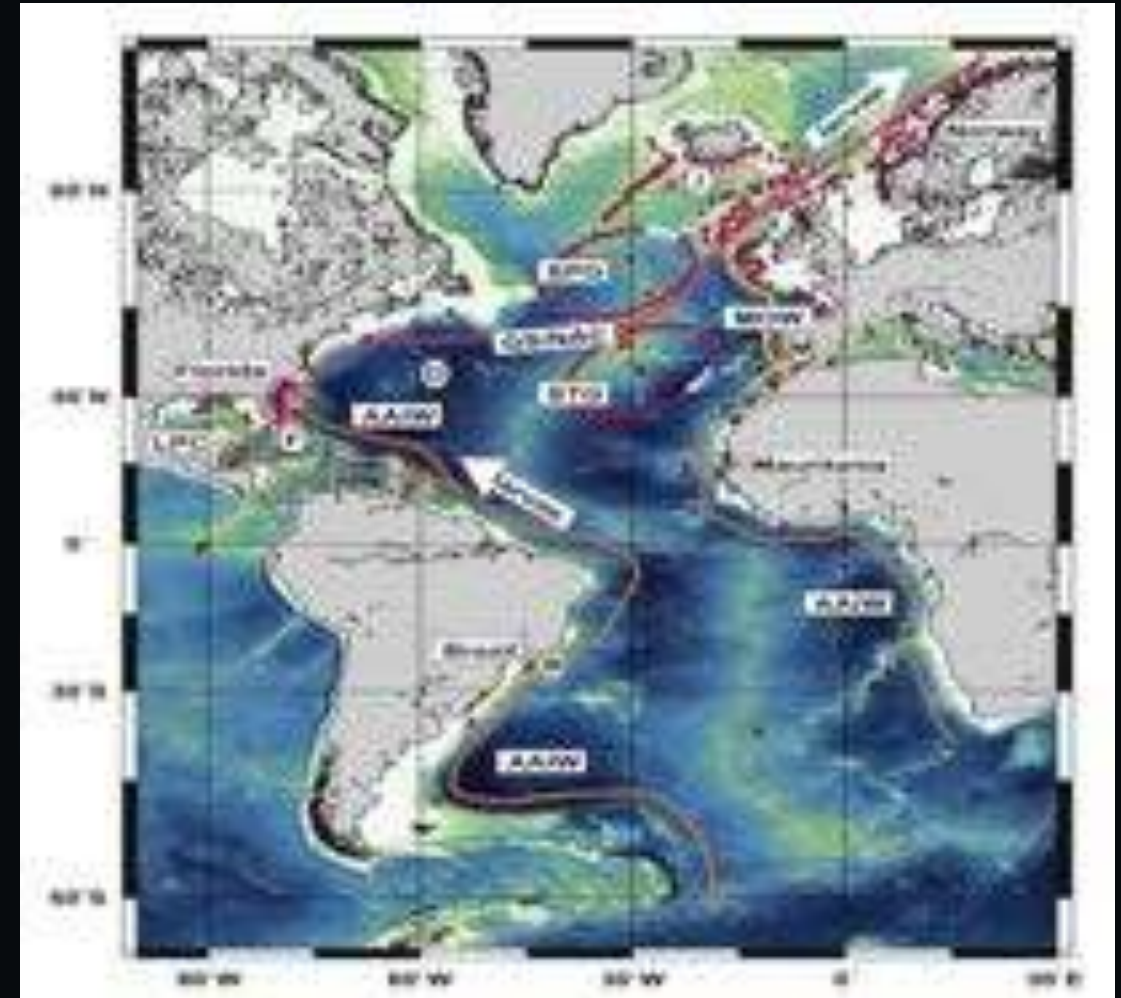
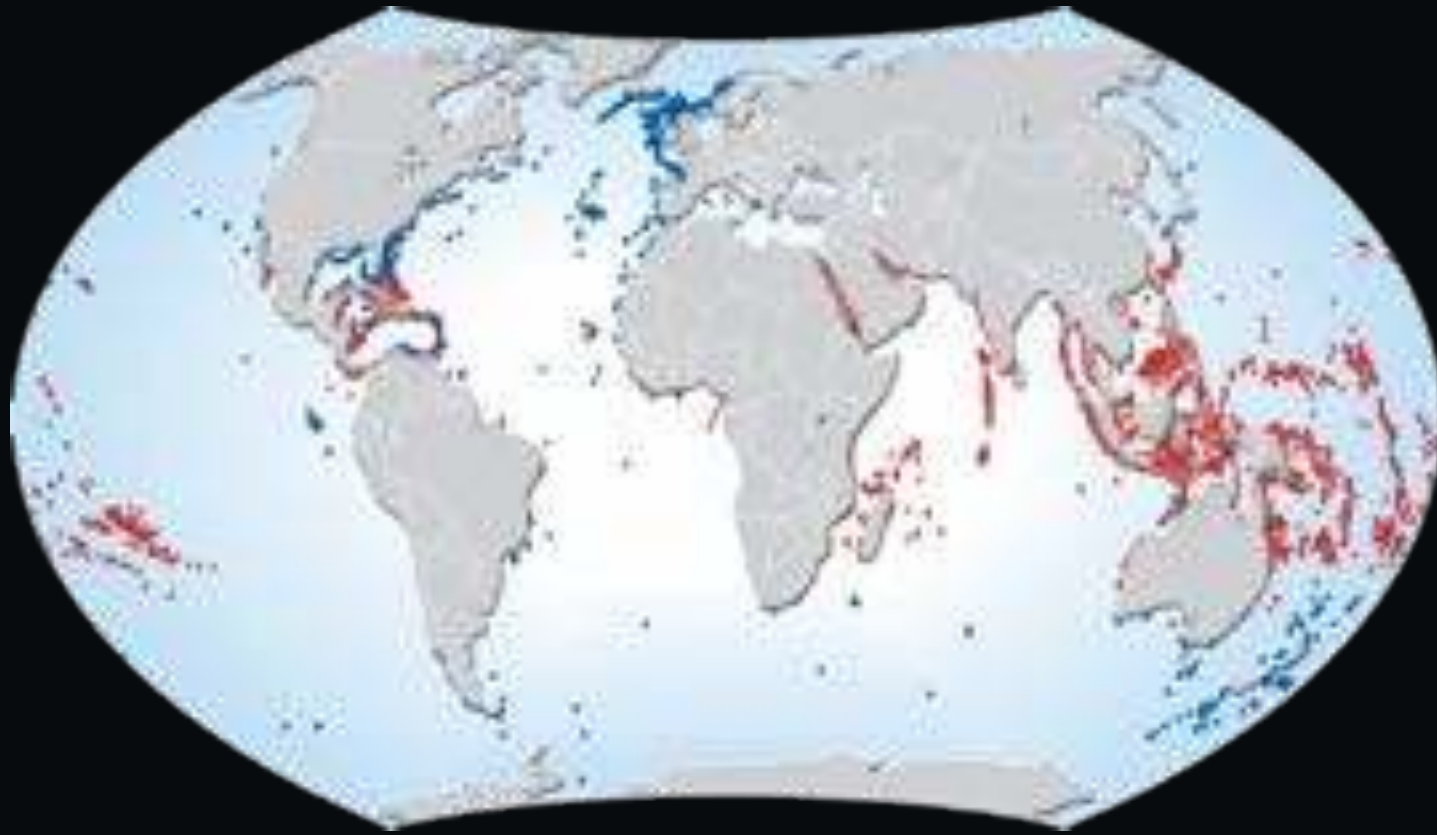
P. managuensis



Poecilia mexicana



Cold-water Coral Genome Project



Jaqueline Hess

Postdoctoral Researcher – University of Oslo, Norway

Computational Biologist in the team of Inger Skrede



“Genome evolutionary mechanisms and their role in ecological transitions”

Evolution of symbiosis



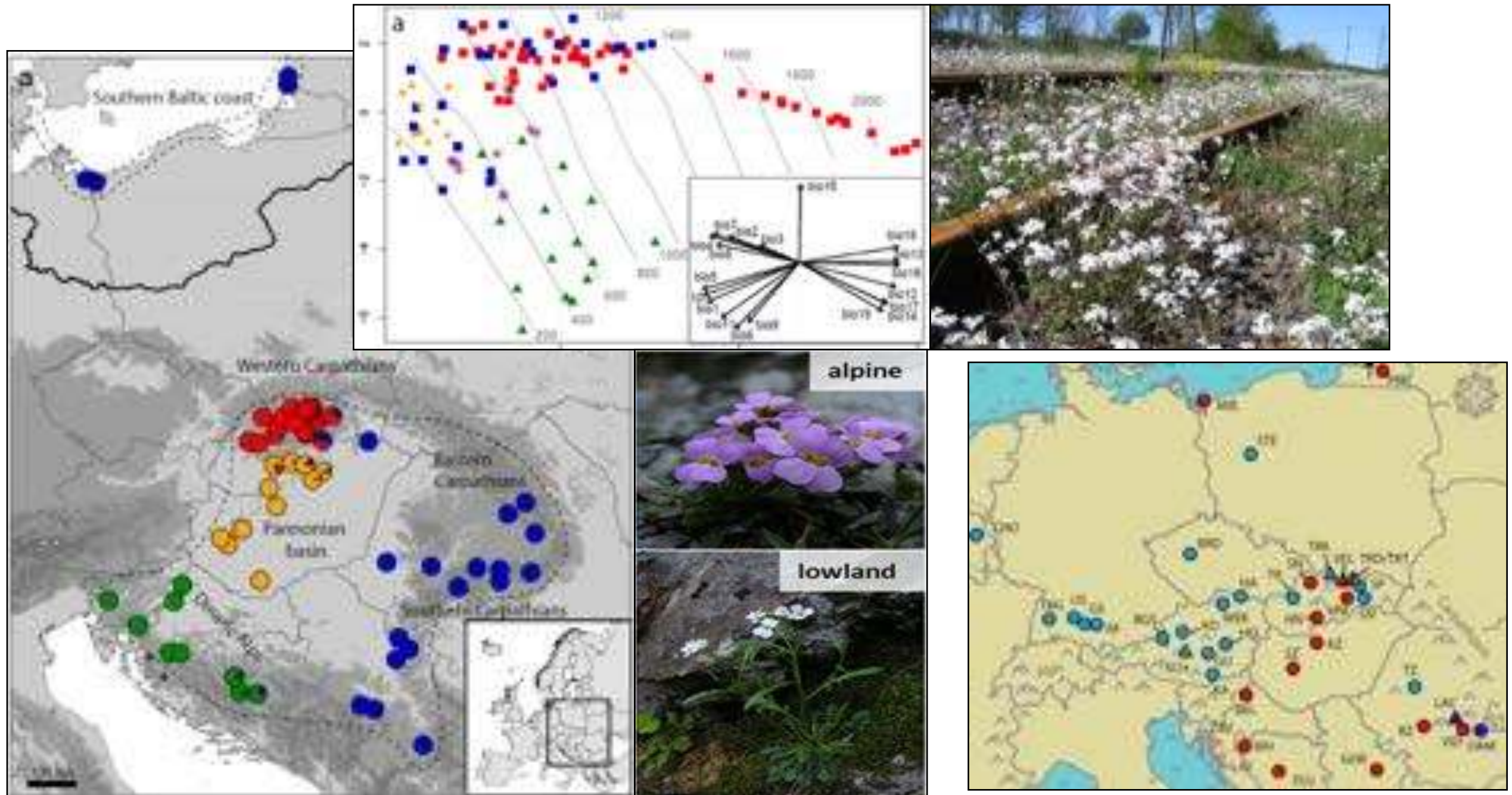
Invasive species



Transposable elements and their role in facilitating an early adaptive response to a change in environments

Ecological and historical drivers of range-wide genomic differentiation in *Arabidopsis arenosa*

Filip Kolář, University of Oslo & Charles University in Prague



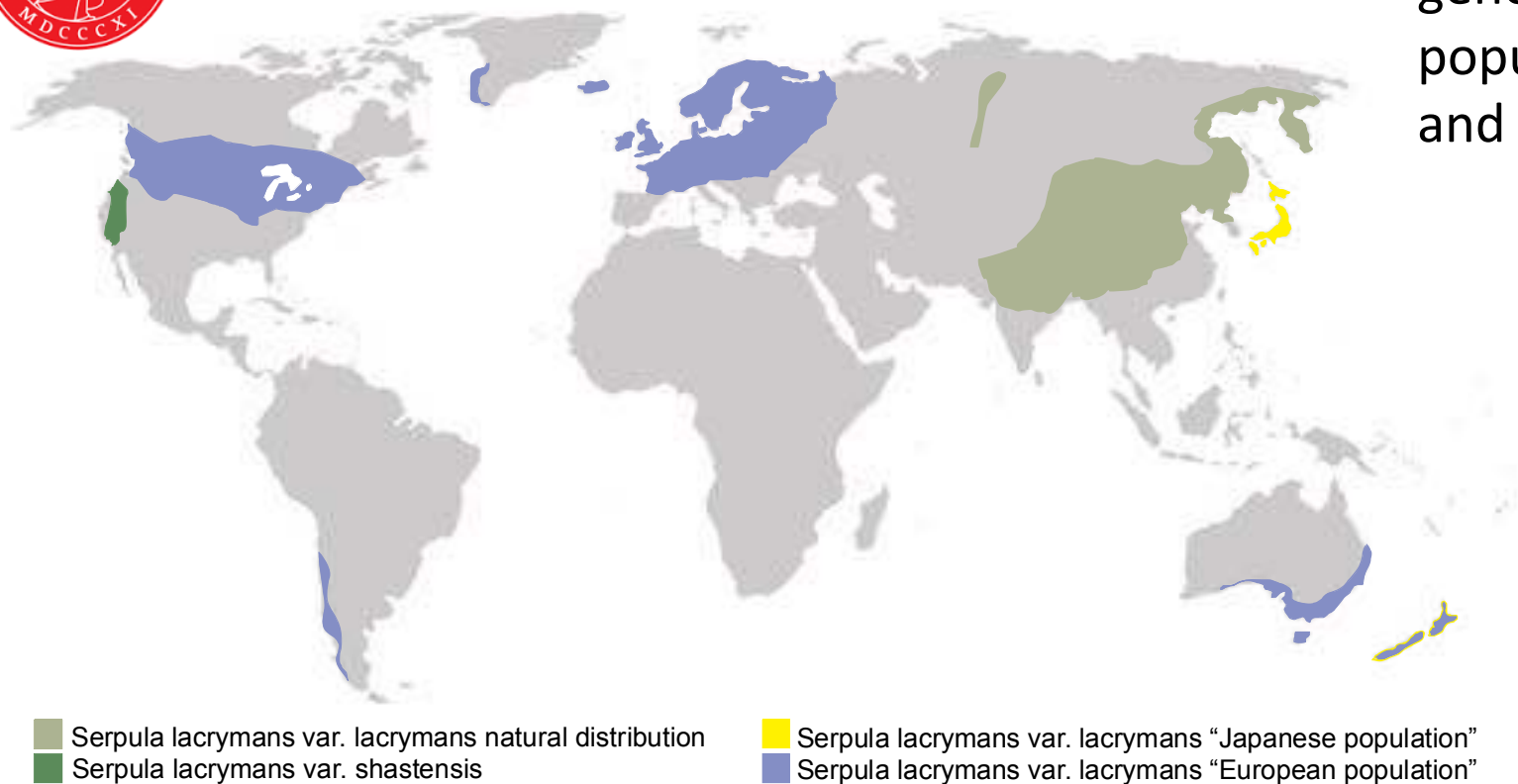
Genetic structure (> 2000 SNPs), niche and phenotypic variation of diploid *A. arenosa*

Range-wide resequencing of ~ 300 indivs.
(collaborative project with L. Yant & K. Bomblies, John Innes Centre, Norwich, UK)



Inger Skrede, University of Oslo

Research topics: population genetics, comparative genomics, population genomics, fungi, ecology and evolution



Current population genomic project:

- Identify genes/functions important for colonization of new habitat/human made habitat?
- Divergence, diversity and demographic history of populations from Japan, Europe and New Zealand?

37 genomes (about 100X coverage)

~500,000 SNPs





NTNU
Norwegian University of
Science and Technology

- ▶ Avian brood parasitism – WGS
- ▶ Ecosystem services – eDNA

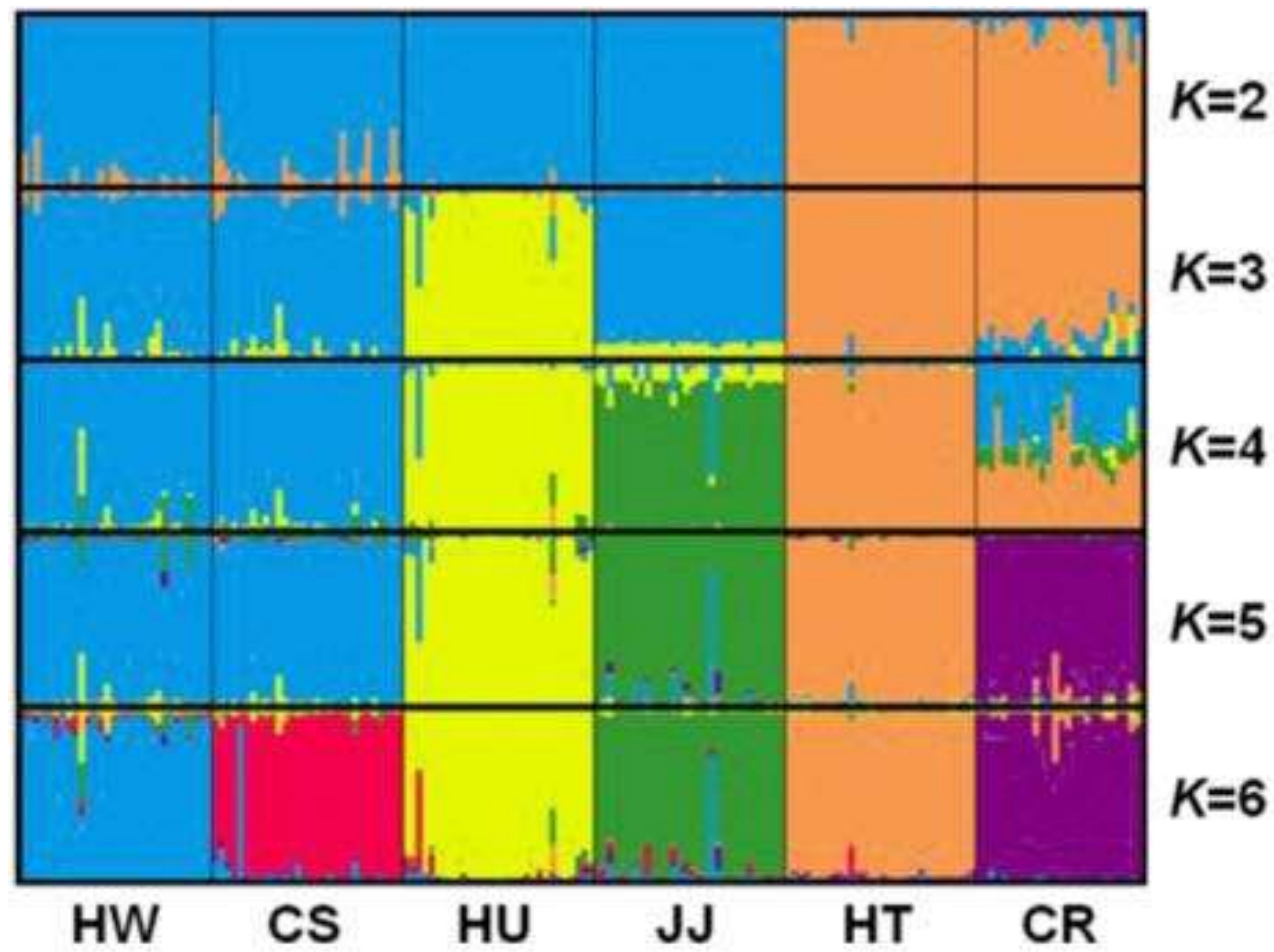


- ▶ Metabarcoding, eDNA
- ▶ RADSeq

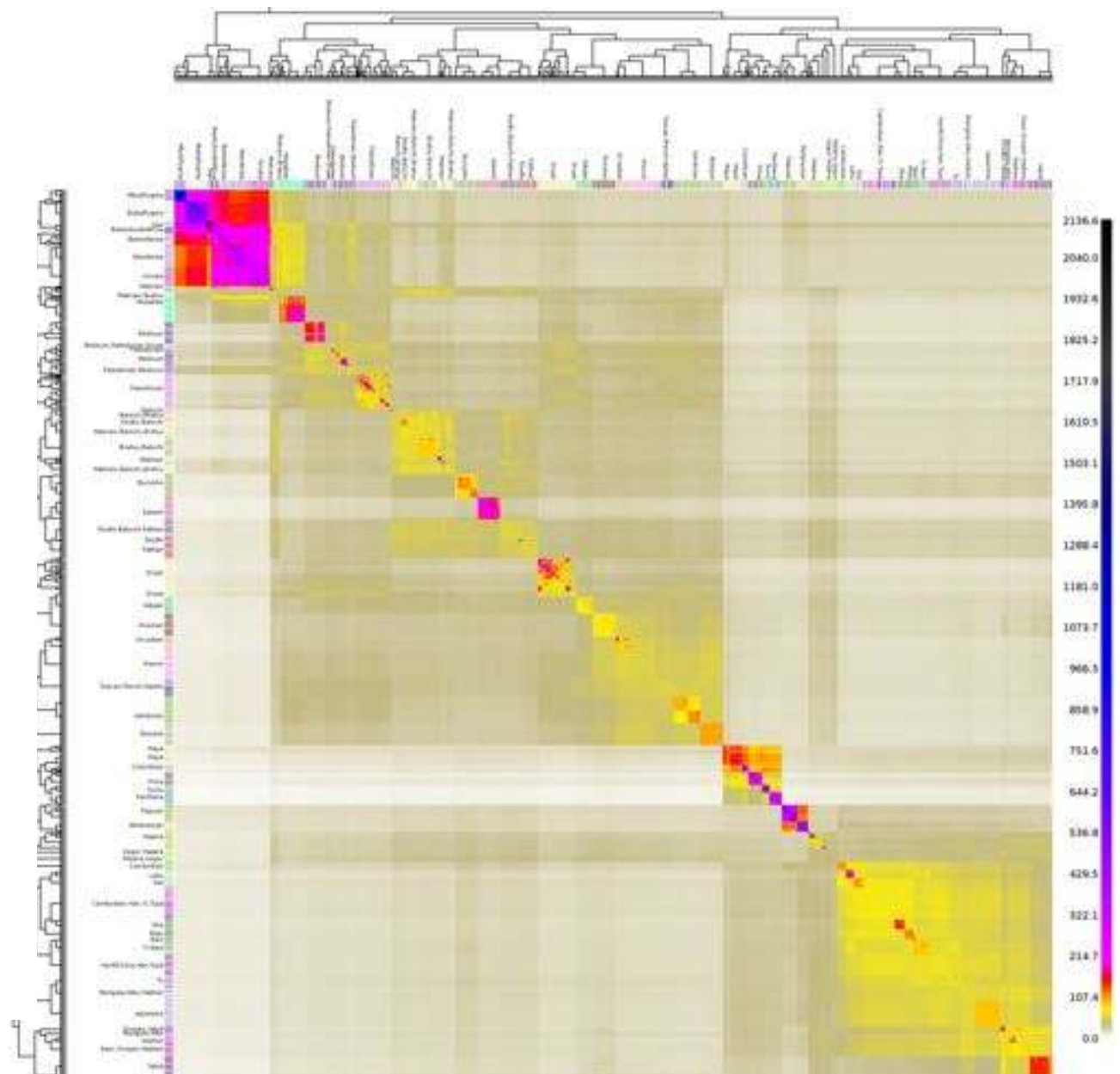
AfricanBioServices 



STRUCTURE



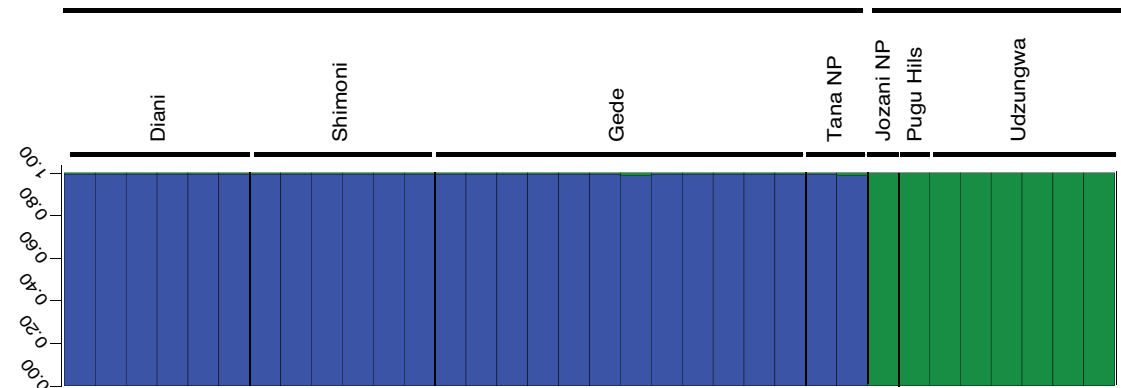
fineSTRUCTURE



finerSTRUCTURE?



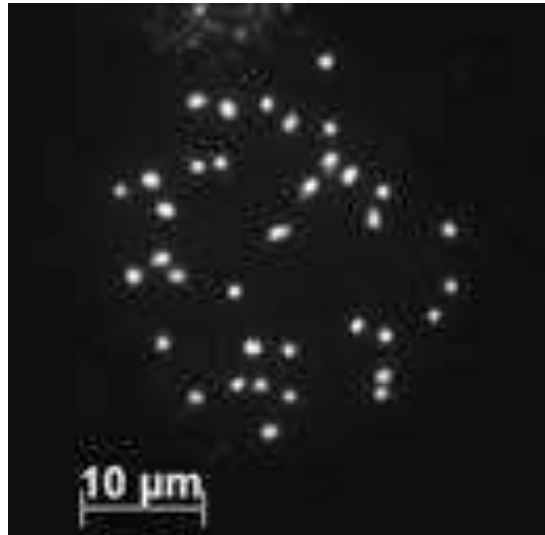
CRYPTIC DIVERSITY & SPECIATION



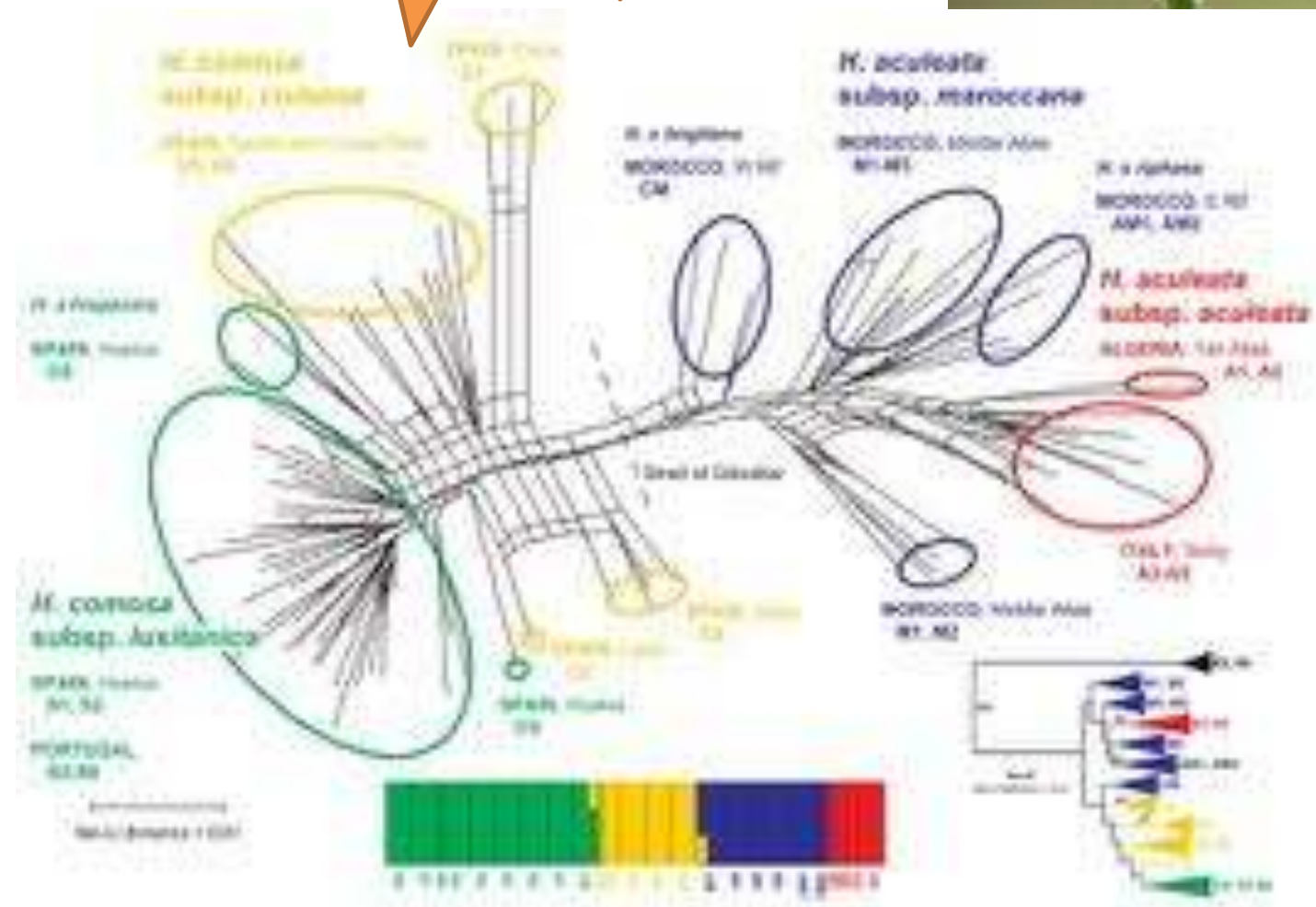
Polyploidy

Plant evolution

Incomplete lineage
sorting vs.
hybridization



Soil seed
bank



Karin Tremetsberger
University of Natural Resources and Life Sciences, Vienna, Austria

Natalia Díaz Arce
PhD Student 2015-2019

Marine Research Division AZTI
(Sukarrieta, Spain)

PhD Supervisors:
Dra. Naiara Rodríguez-Ezpeleta
Haritz Arrizabalaga



Oscar Gaggiotti

Scottish Oceans Institute

University of St Andrews



University of
St Andrews | FOUNDED
1413



- Statistical inference of the demography and ecology of species from the spatial patterns of *neutral* genetic diversity
- Study of *local adaptation* to understand the molecular bases of phenotypic variation



Vikings as Vectors



University of Oslo

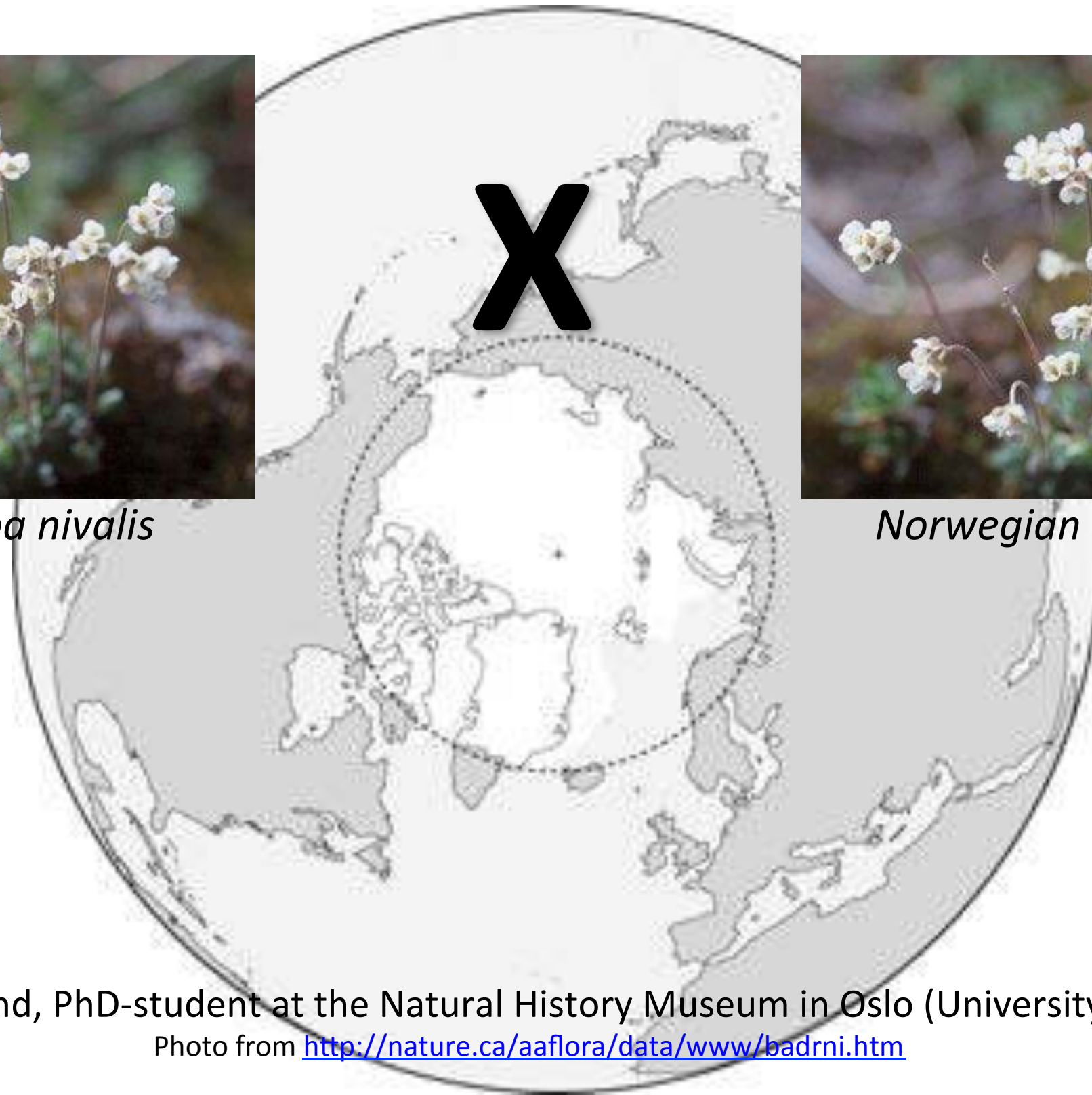
Heidi Nistelberger

SpArc

Speciation genetics in Arctic plants and searching for cryptic species in the Mediterranean flora



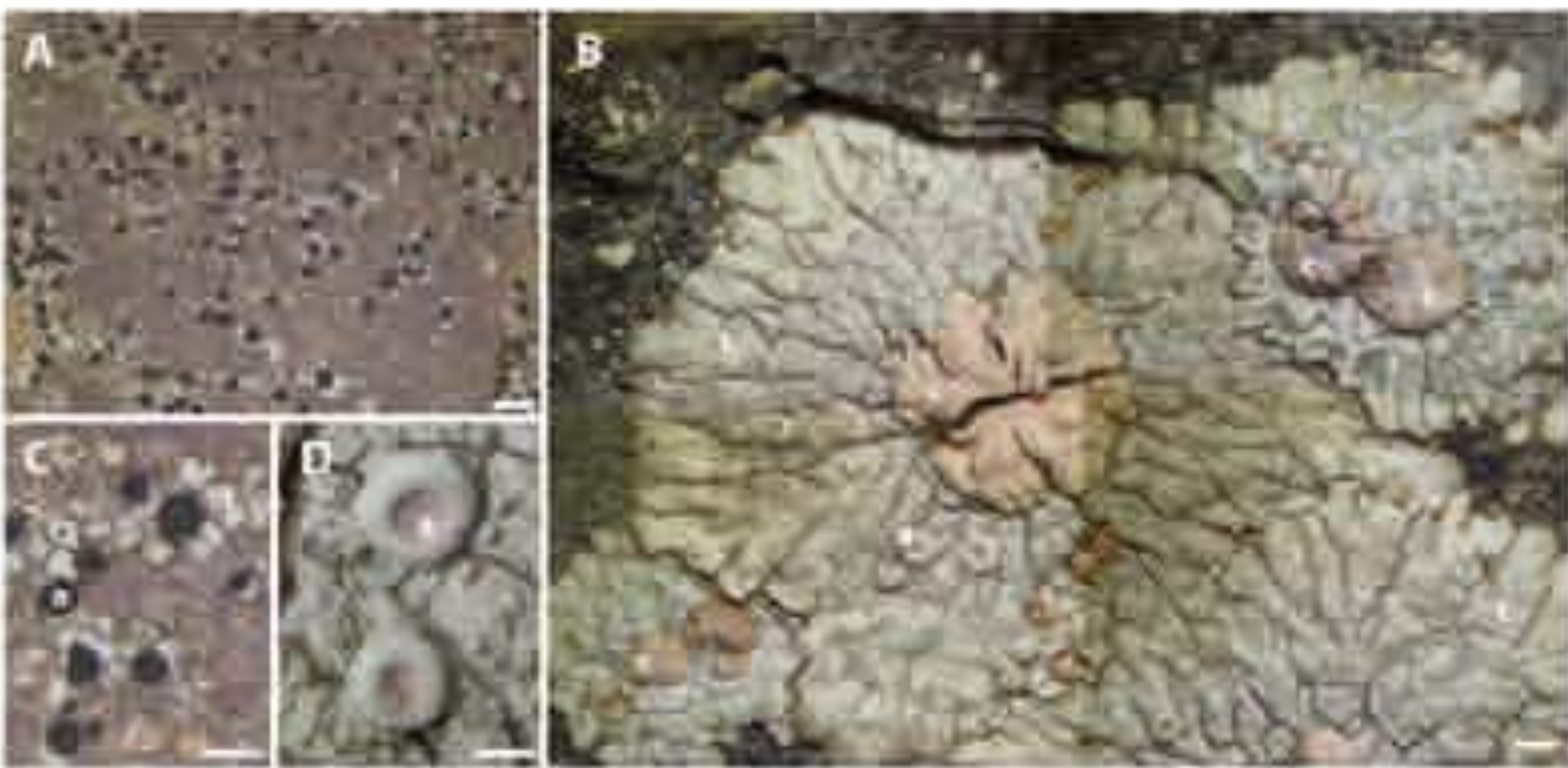
American Draba nivalis



Norwegian Draba nivalis

Siri Birkeland, PhD-student at the Natural History Museum in Oslo (University of Oslo)

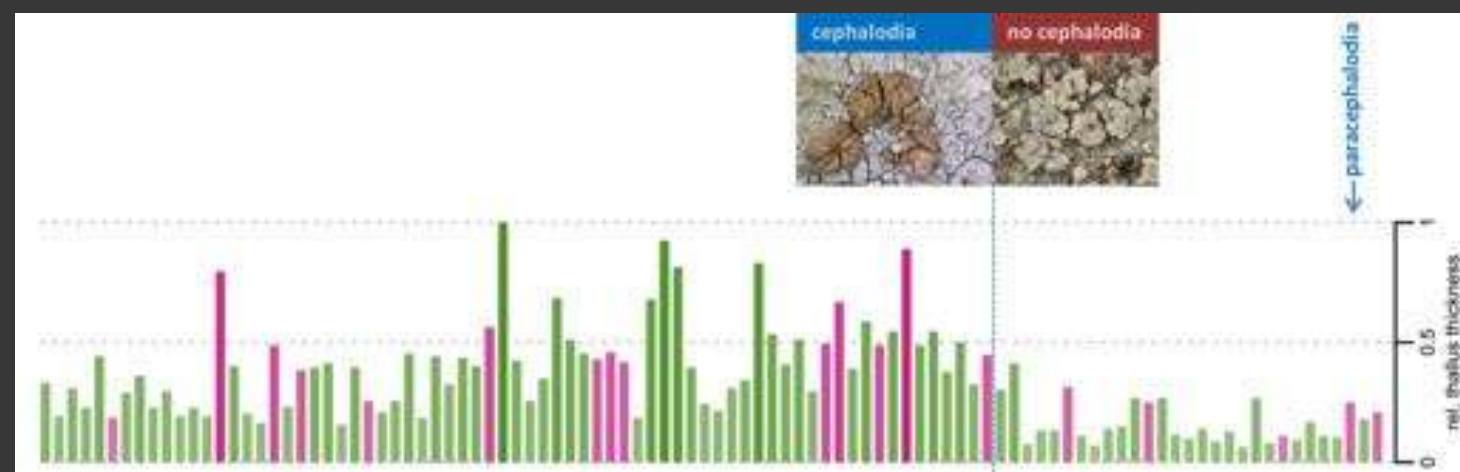
Photo from <http://nature.ca/aaflora/data/www/badrni.htm>



Escape from the cryptic species trap: lichen evolution on both sides of a cyanobacterial acquisition event

Kevin Schneider

University of Graz, Austria





Adam Bazinet

Post-Doctoral Associate
Laboratory of Molecular Evolution
Center for Bioinformatics and Computational Biology

3122 Biomolecular Sciences Building #296
University of Maryland, College Park, MD 20742-3360
8314 Paint Branch Dr.
E-mail: adam.bazinet@umiacs.umd.edu
Office: (301) 405-7408
CV 

Advisor: Dr. Michael Cummings

RESEARCH PROJECTS



Grid computing – The Lattice Project

lattice.umiacs.umd.edu |
molecularevolution.org



Lepidopteran molecular phylogenetics – "Leptree"

PLOS ONE (December 2013 | March 2013)
| BMC Evolutionary Biology (2009)



Sequence classification programs – A comparative evaluation

BMC Bioinformatics (2012)



Species differentiation – Genealogical Sorting Index

molecularevolution.org

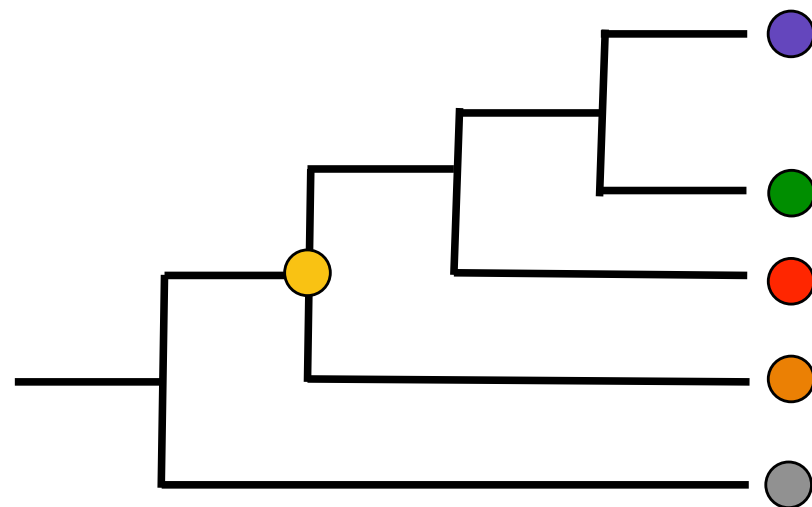
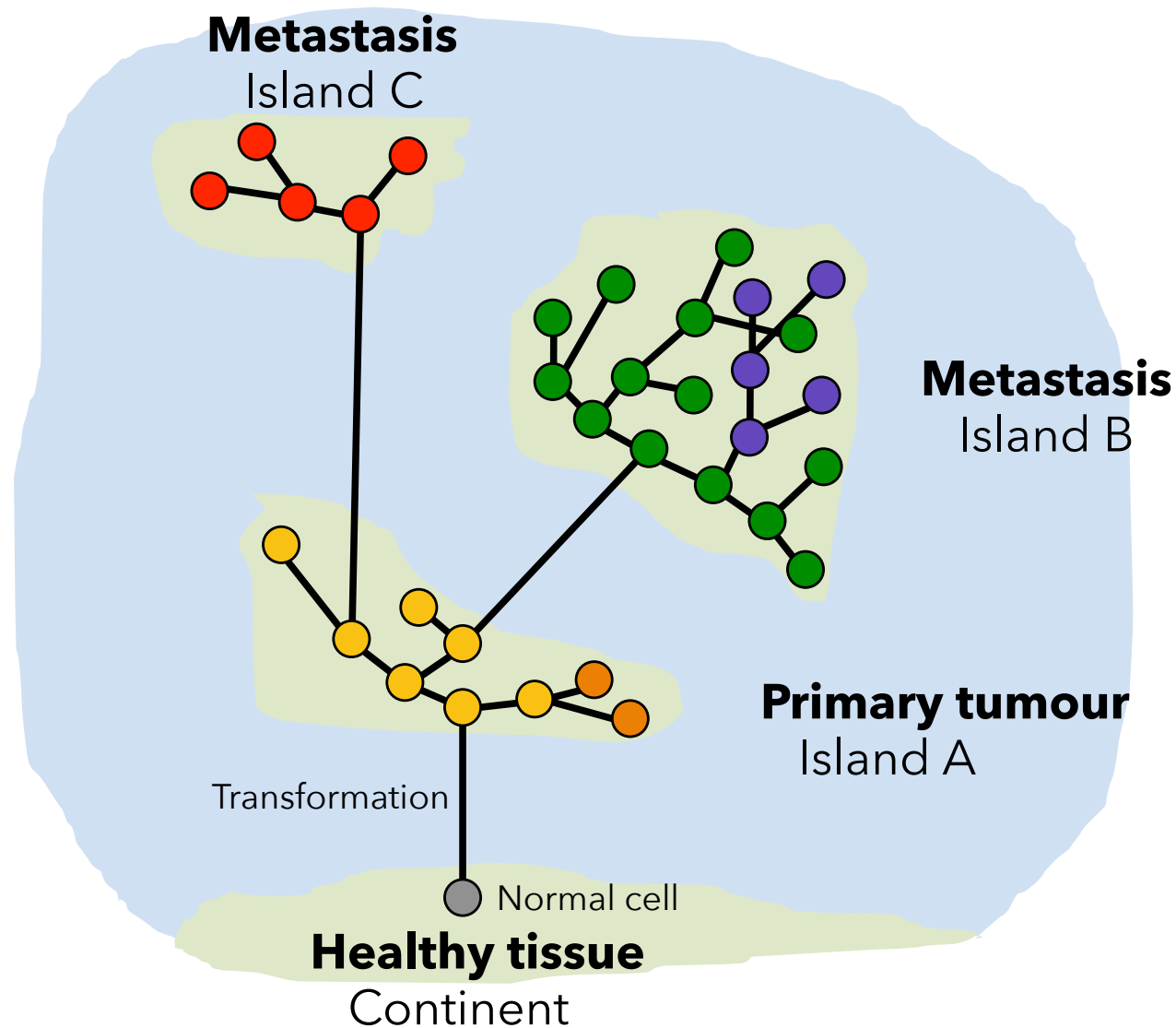
After the Ice: hybrid male sterility in a grasshopper hybrid zone



Ricardo J Pereira
ricardojn.pereira@gmail.com

Natural History Museum of Denmark
University of Copenhagen

PHYLOCANCER



Aim

Reconstructing tumor evolution

Data

WGS / WES

Bulk-seq / SC-seq

Bioinformatic analysis

Somatic variant calling

Evolutionary analysis

Population growth

Population structure

Population effective size

Divergence time

Selection vs neutral

Tamara Prieto



phylocancer



Biology Centre CAS
Institute of Entomology

&

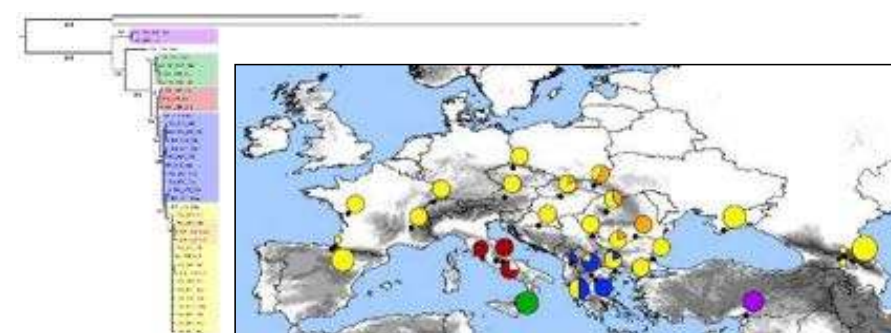
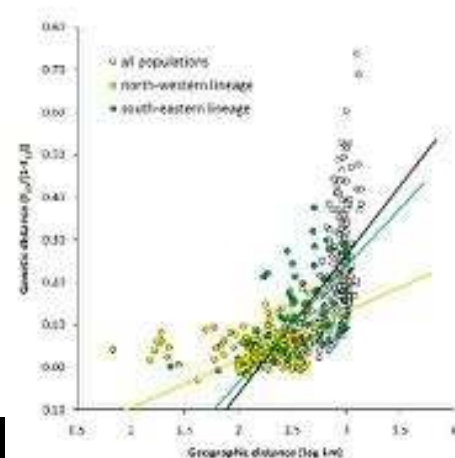
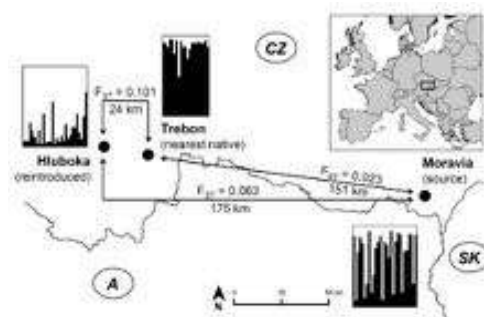
University of South Bohemia
Faculty of Science



České Budějovice, Czech Republic

Molecular Ecology of Saproxylic Beetles in Europe

Lukáš Drag



Great Capricorn beetle
(*Cerambyx cerdo*)



Hermit beetle
(*Osmoderma eremita*)

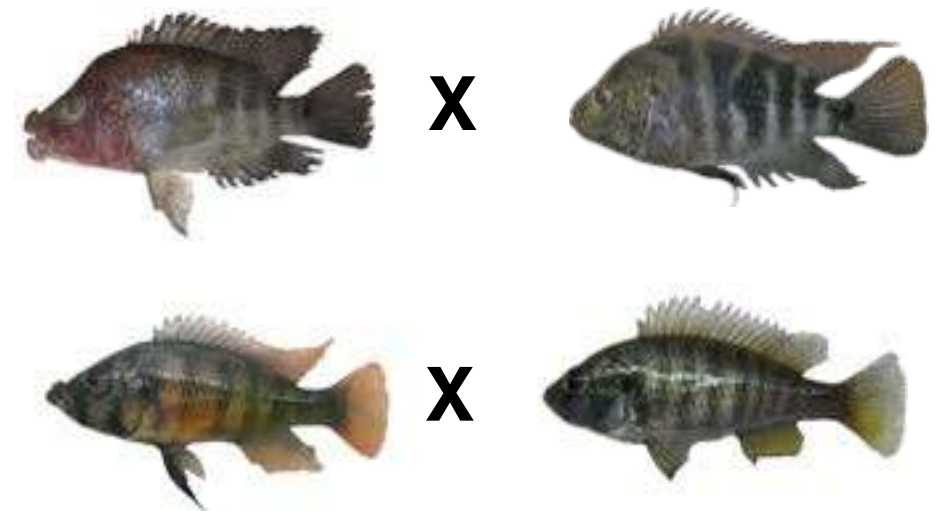


Rosalia Longicorn
(*Rosalia alpina*)

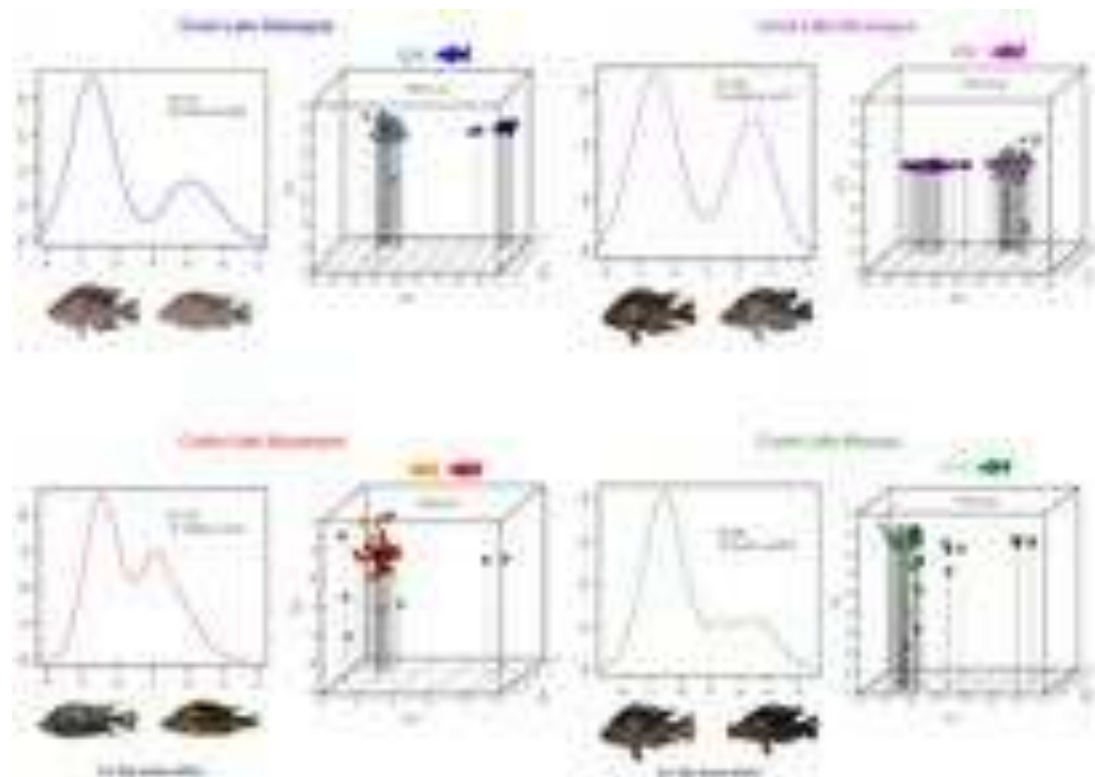
The genetic bases of convergent evolution: hypertrophic lips

Gonzalo Machado-Schiaffino (University of Konstanz, Germany)

QTL mapping in Neotropical and African cichlids (RADseq)



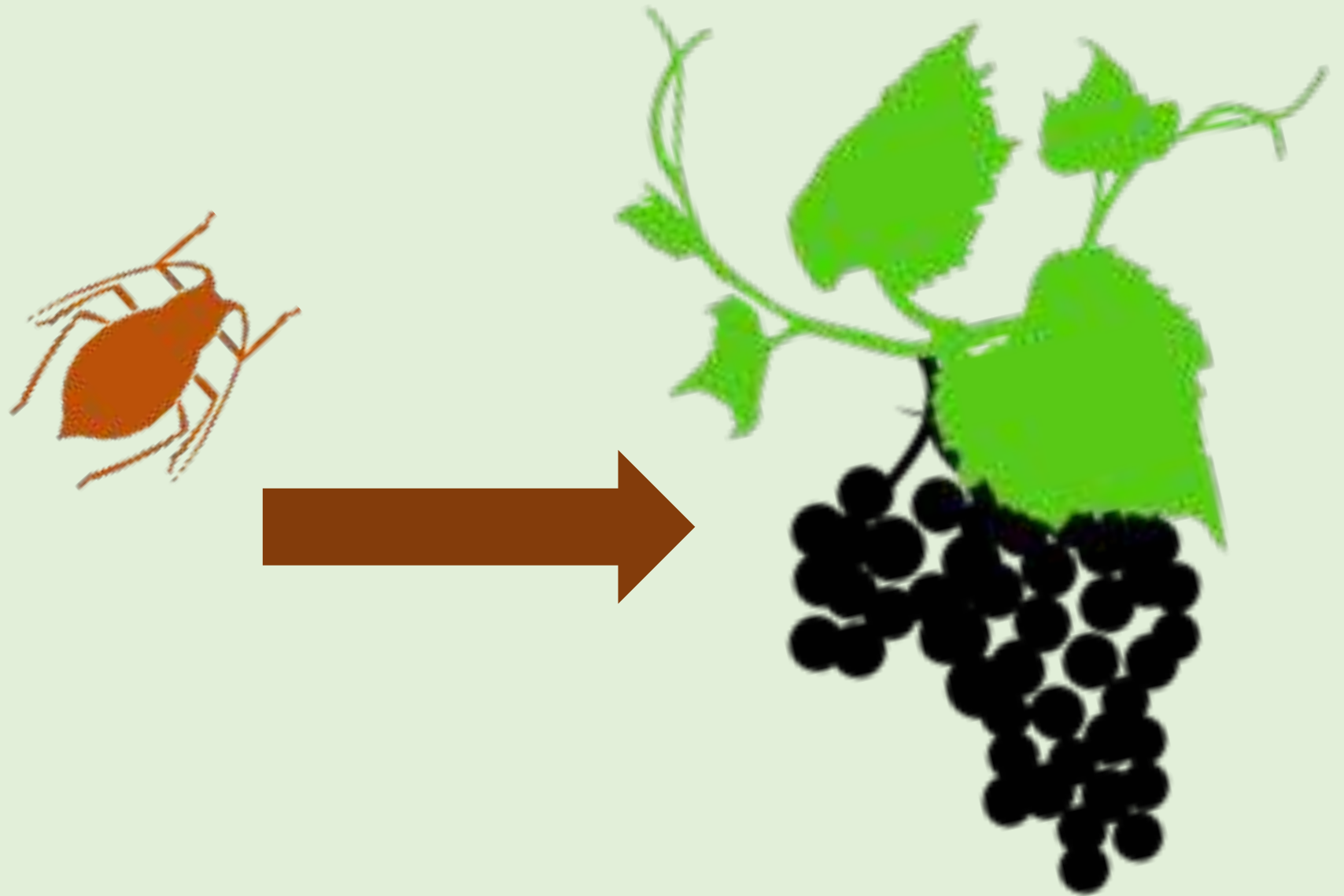
Incipient speciation driven by hypertrophied lips in Midas cichlids fish?



Genetic and morphological differentiation (+ demography + lip function + assortative mating)

Phylloxera

Grafting



劉 筱 蕾

Hsiao-Lei Liu

PhD Student

University of Warwick

E-mail: H.Liu.6@warwick.ac.uk

lei.oct.1985@gmail.com

Matteo Fumagalli

PhD in Bioengineering
Polytechnic University of Milan, Italy



Postdoc (EMBO fellow)
Dept. Integrative Biology
Univ. of California, Berkeley, USA
Nielsen Group

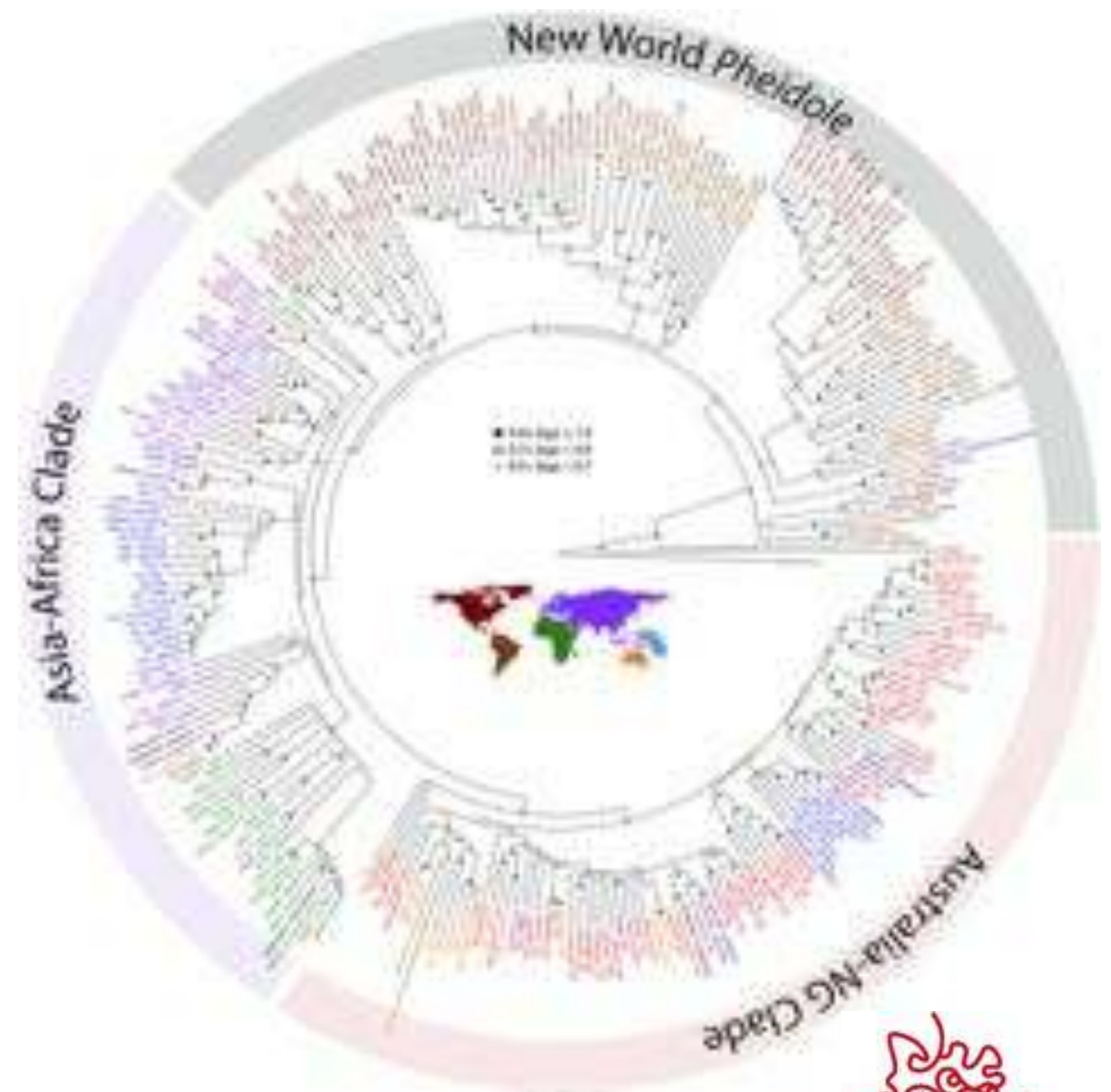
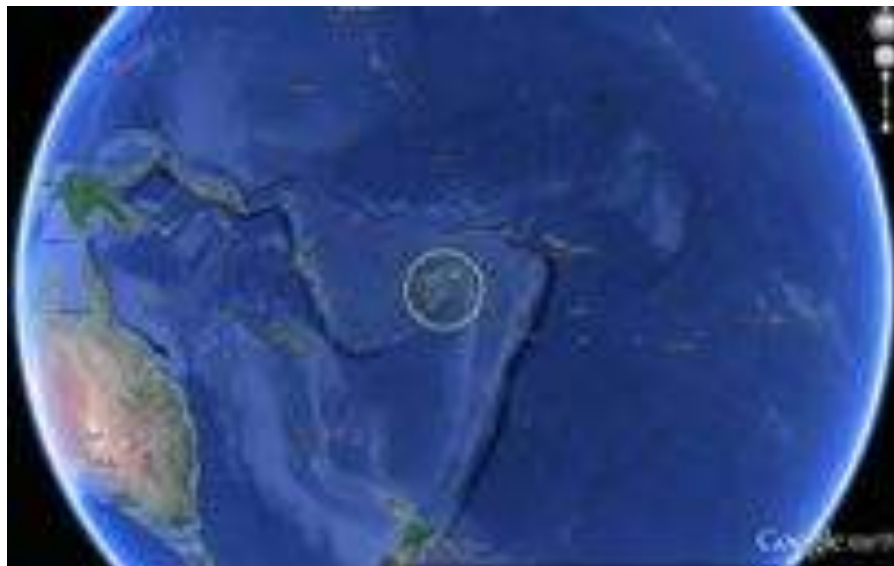


Postdoc (HFSP fellow)
UCL Genetics Institute
University College London, UK
Balloux Group



Ants of Fiji

- Archipelago 2-25 Ma.
- 43 genera; 187 species; 70% endemism
- Adaptive radiations
- Multiple speciation events
- Demographic histories
- Taxon cycle
- Ancient DNA (museum collections) - RADseq



Clive T. Darwell, Economo Unit, Okinawa
Institute of Science and Technology, Japan





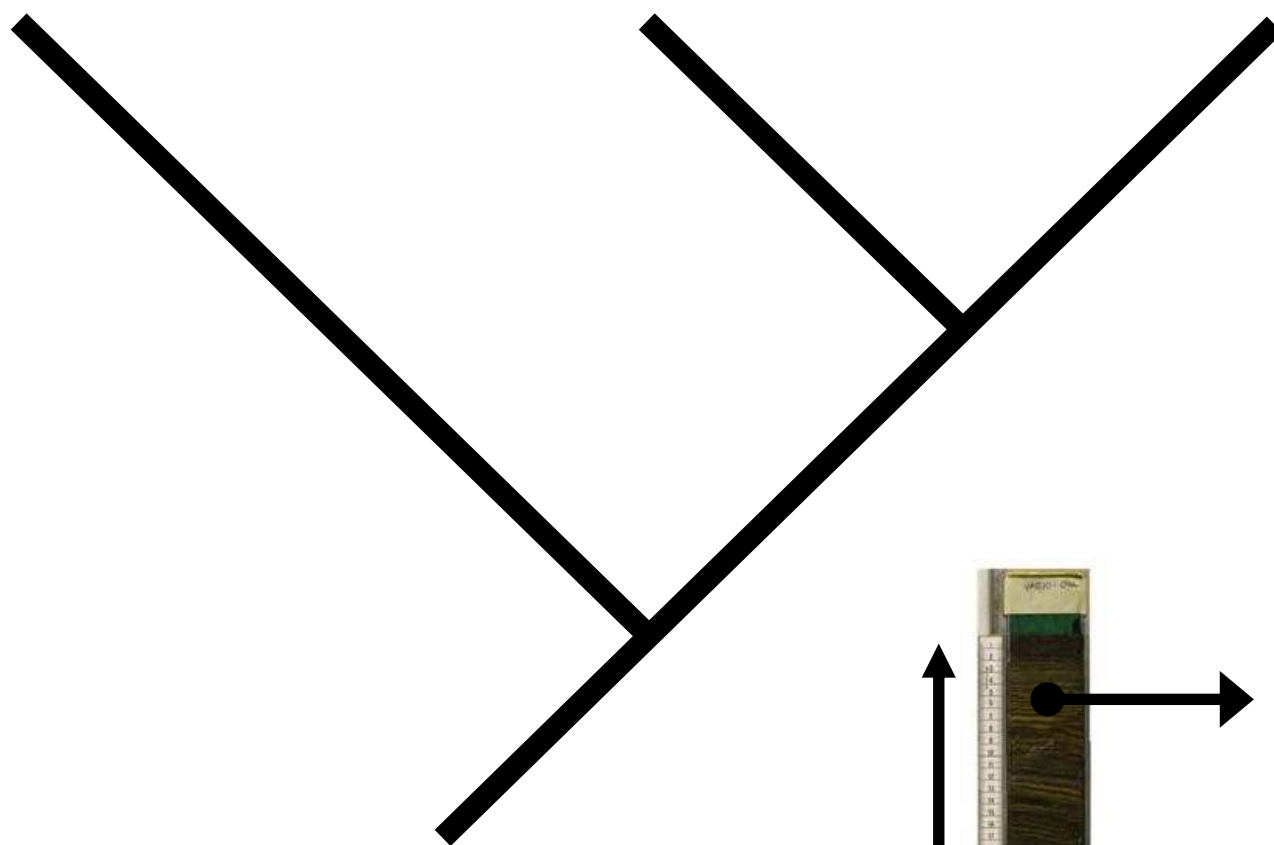
H. elevatus



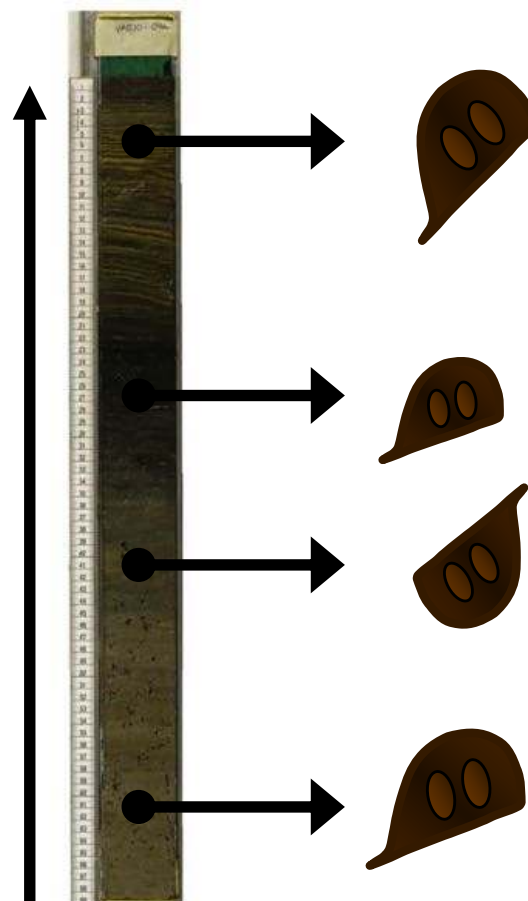
H. timareta



H. melpomene



time



MARKUS MÖST
FWF E. SCHRÖDINGER FELLOW
DEPT. OF ZOOLOGY
UNIVERSITY OF CAMBRIDGE
mm2083@cam.ac.uk

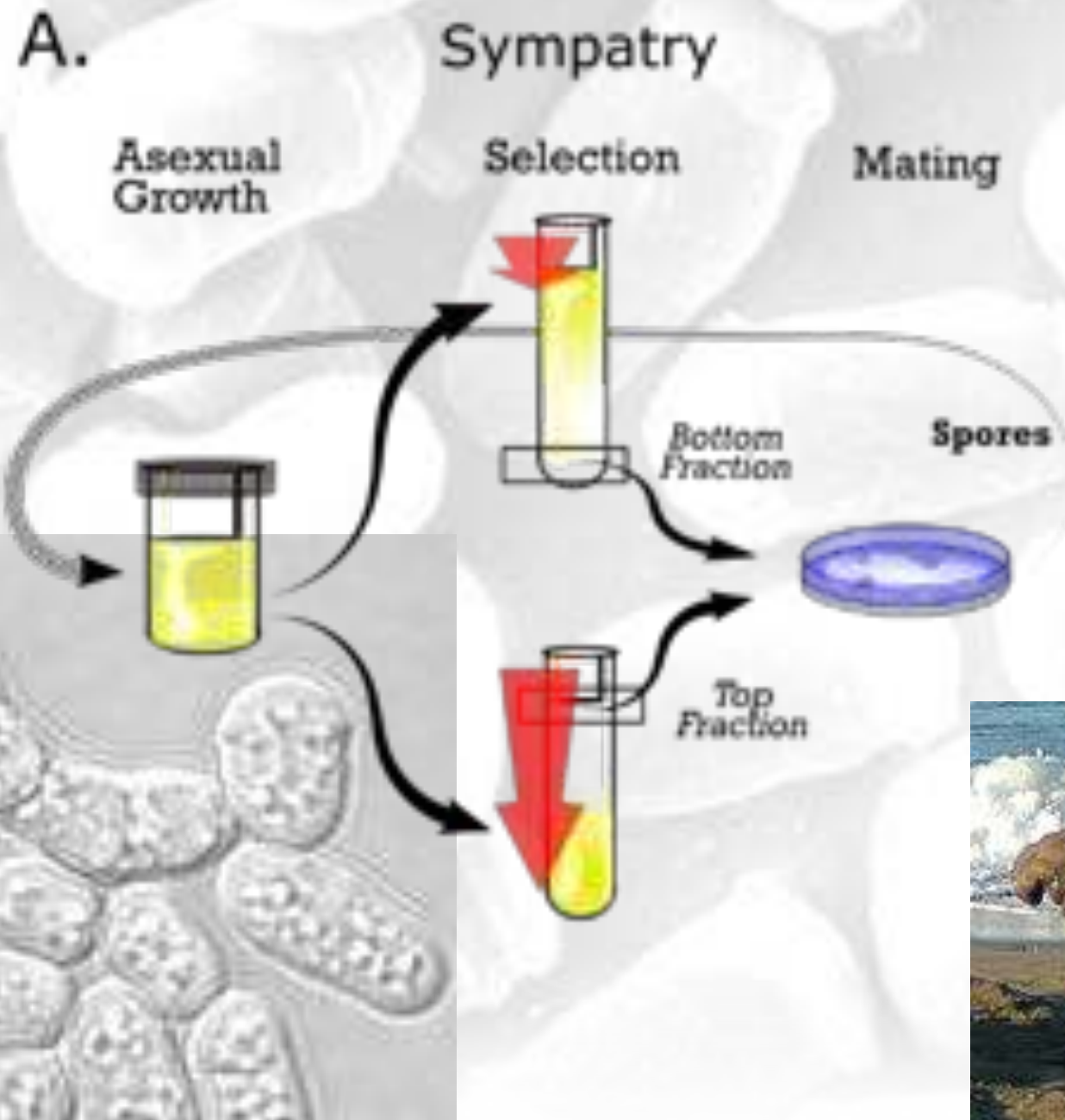
Sergio Tusso

PhD student

Speciation Genomics

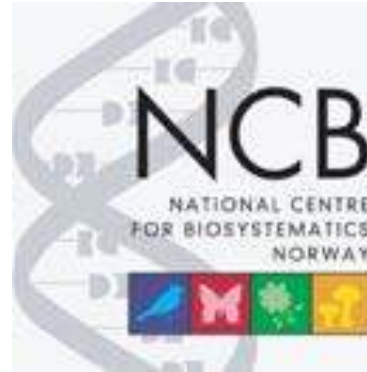


UPPSALA
UNIVERSITET



Origin and genomic history of the Greenlandic sledge dogs and wolves

Mikkel Sinding



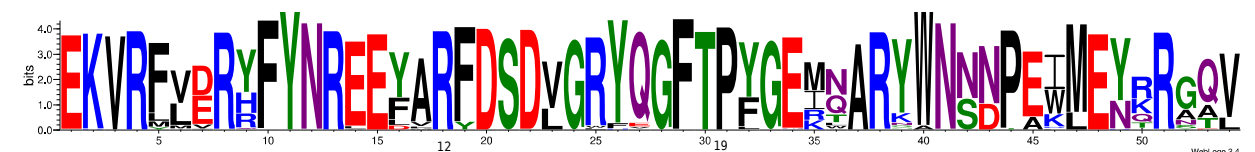
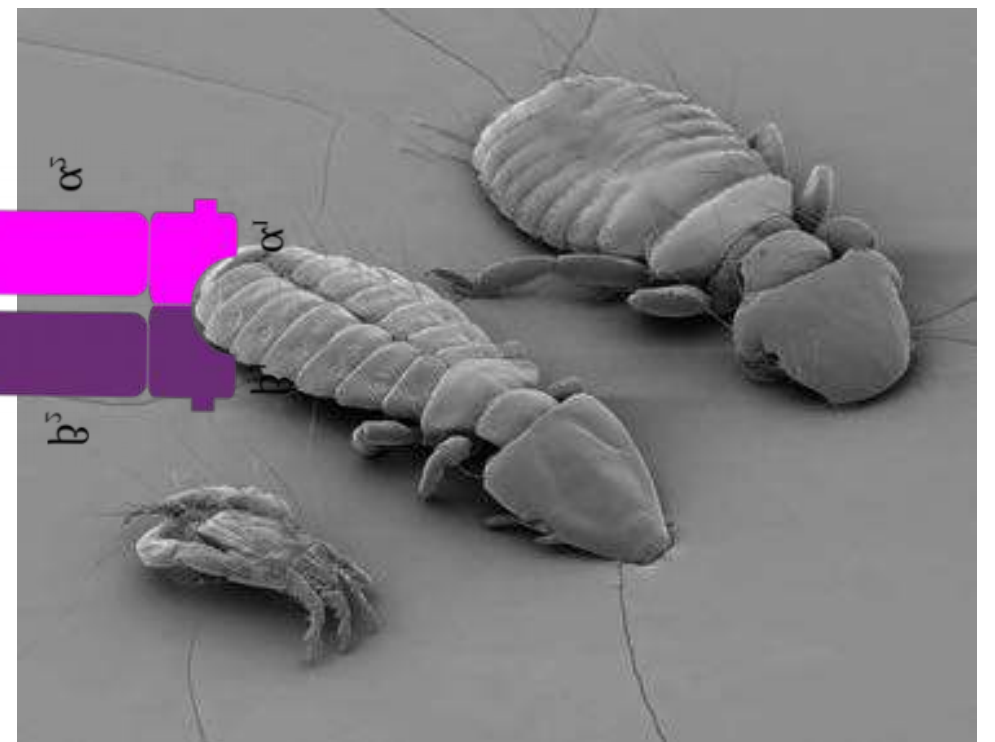
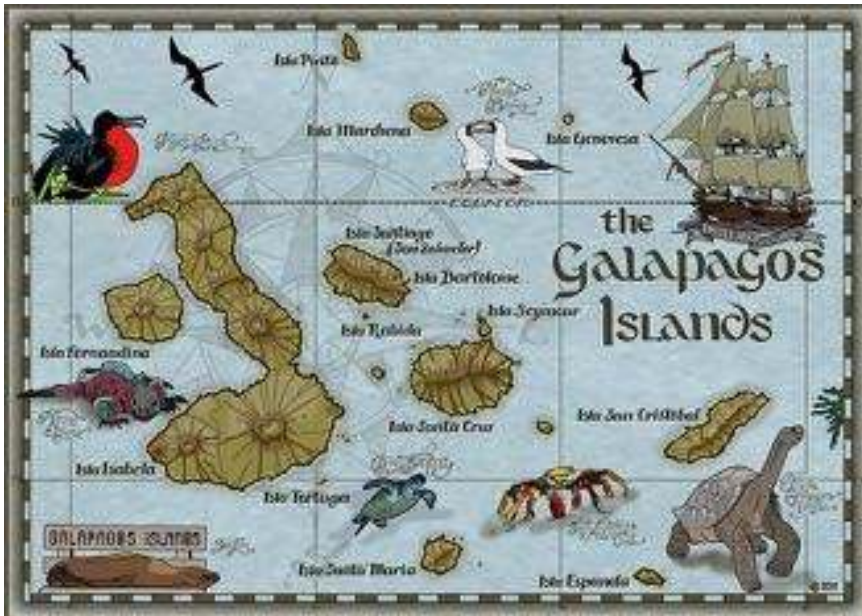
Jakub Vlček



Přírodovědecká
fakulta
Faculty
of Science

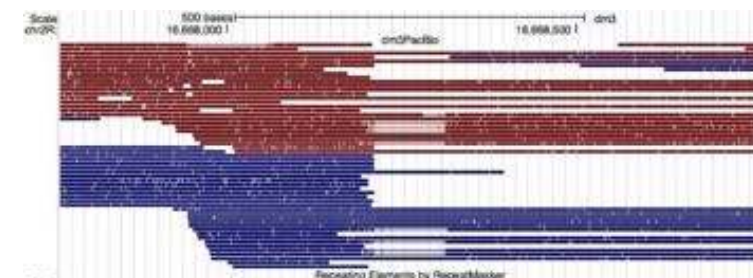
Jihočeská univerzita
v Českých Budějovicích
University of South Bohemia
in České Budějovice

- Wildlife immunogenetics
- Major Histocomp. Complex
- Toll-like receptors





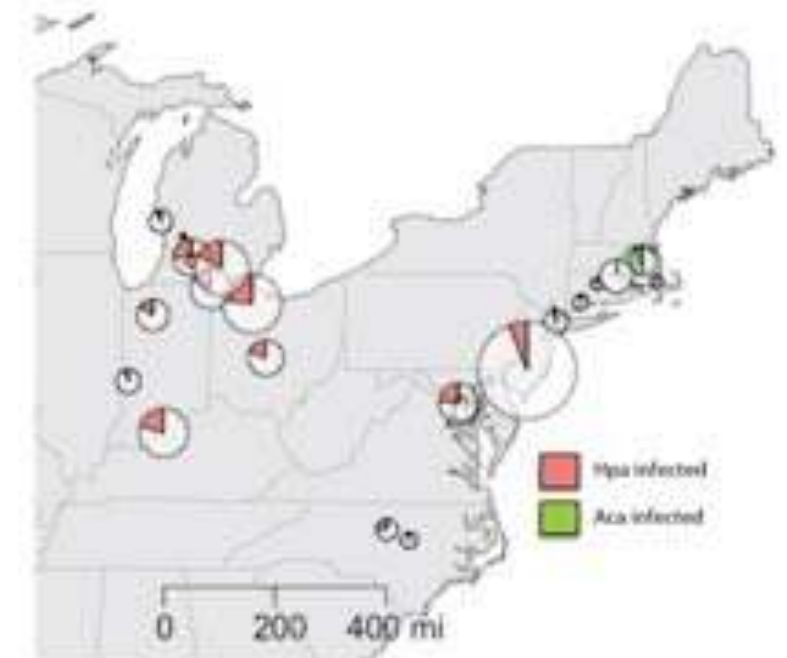
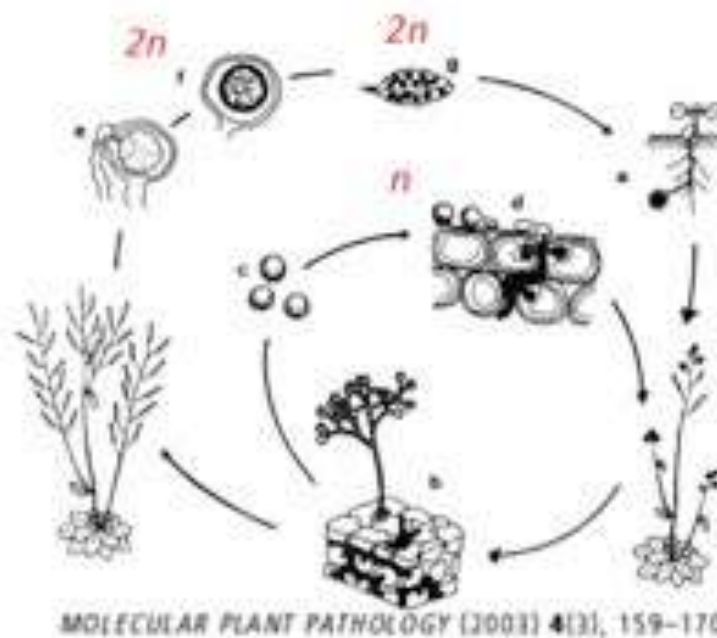
Hypothesis:
Genetic markers of dietary shift phenotypes will be present within the transcriptomes of the insect's mid-gut, where food digestion occurs



Supervisors

- Oliver Niehuis
- Bernhard Misof

Co-evolutionary Tales: *A. thaliana* vs. *H. arabidopsidis*



Research Questions

- How predominant ATH lineage sustains the pathogen pressure?
- Whether genetic structure and virulence spectra of HPA translates into local adaptation
- Are host-pathogen undergoing co-evolution?

Methods

- Combination of RAD-Seq and whole-genome resequencing with both host accessions and pathogen strains
- Laboratory and field based disease and fitness phenotyping

Problem: How to deal with admixture?



Gautam Shirsekar gshirsekar@tuebingen.mpg.de

www.weigelworld.org

Max Planck Institute for Developmental Biology, Tuebingen, Germany

 @gaushi

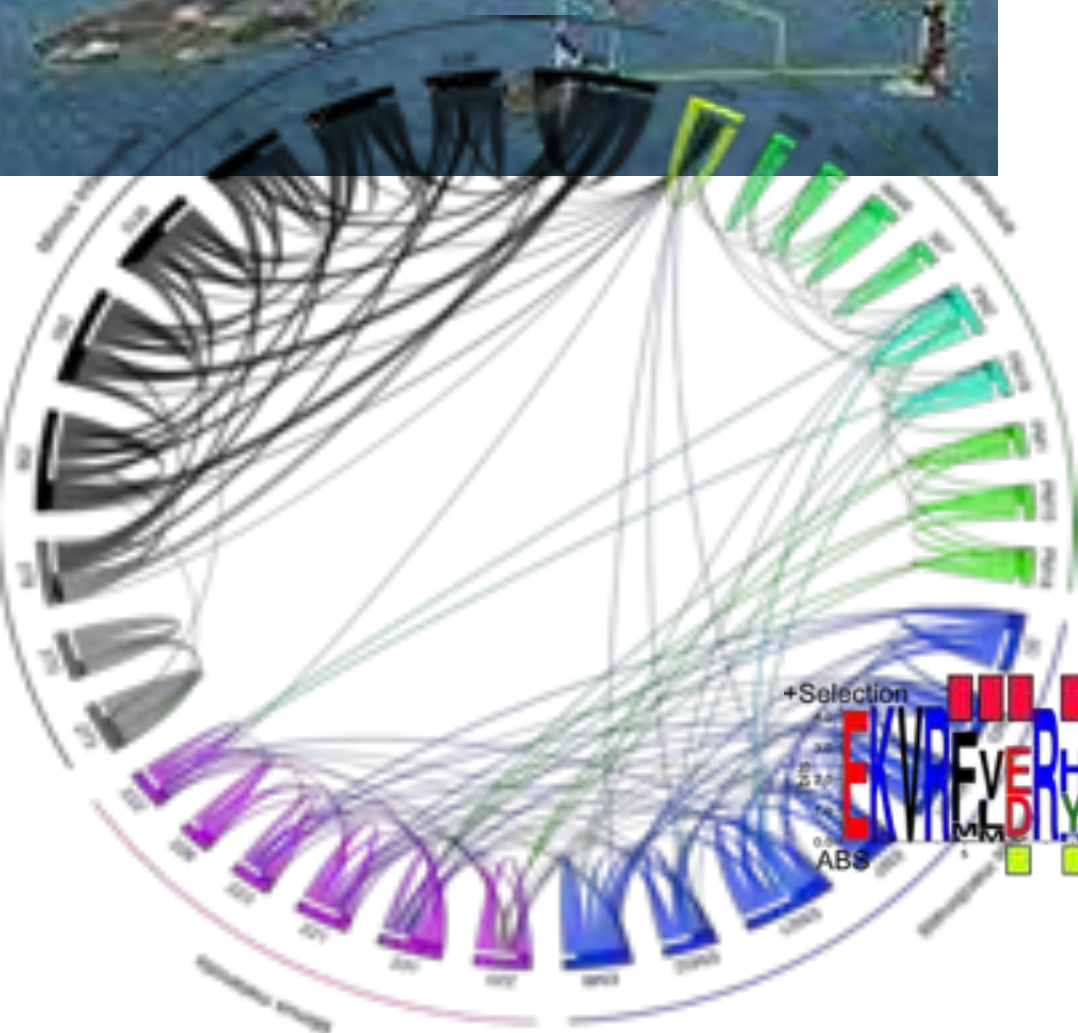
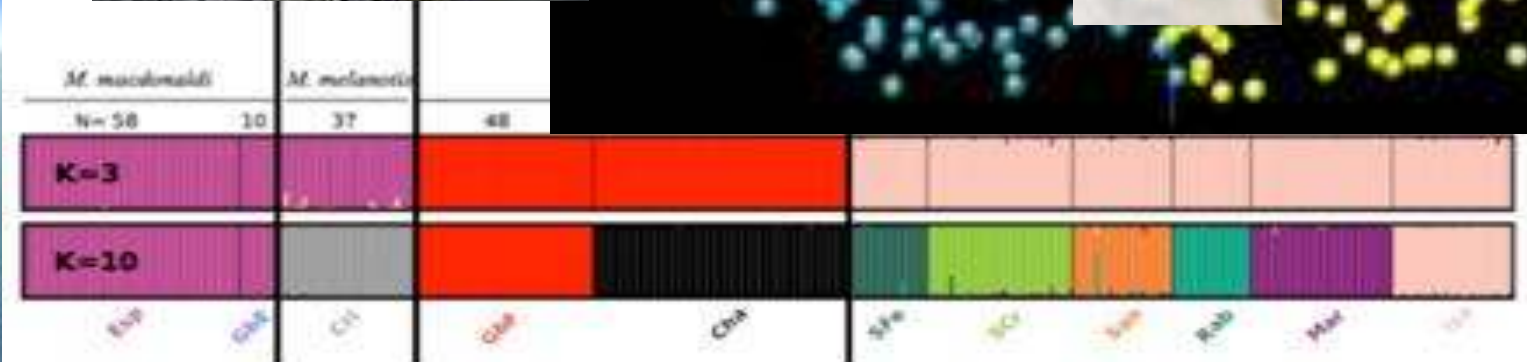
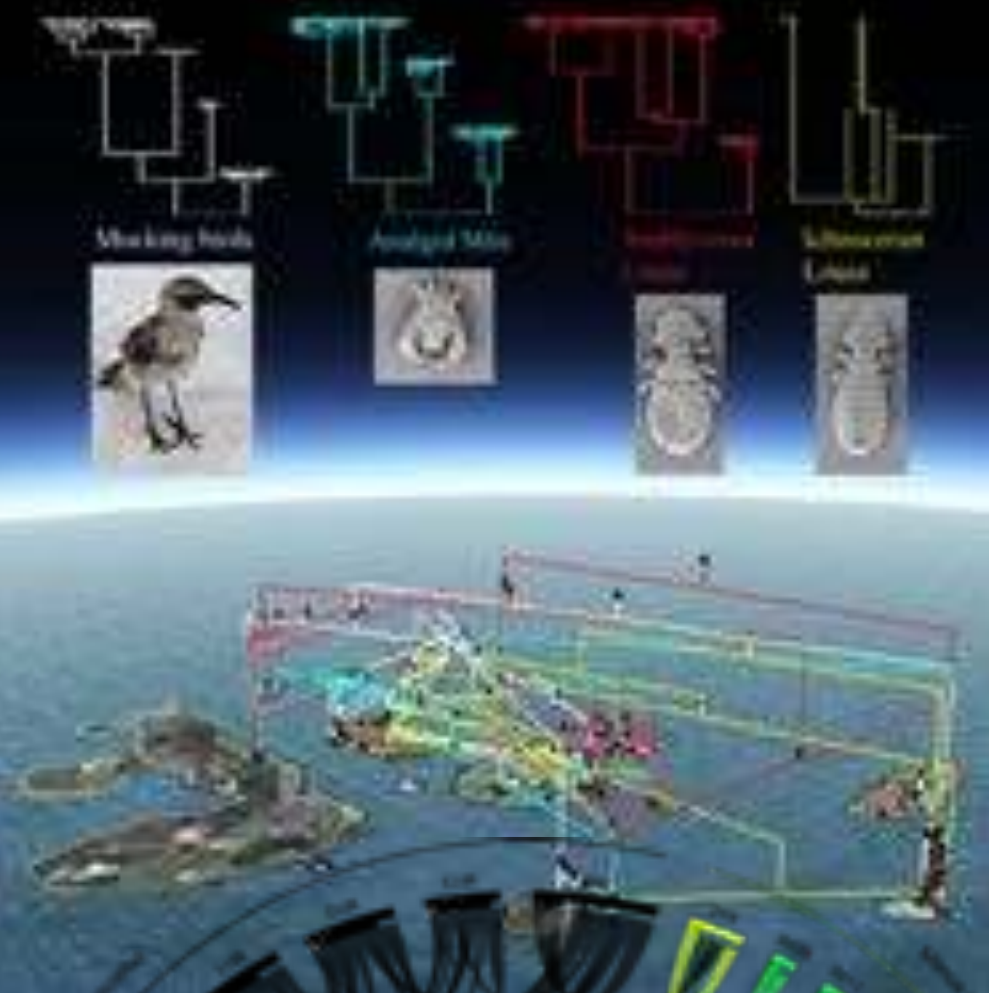
Bastiaan Star

Centre for Ecological and Evolutionary Synthesis (CEES)

University of Oslo, Norway



25.01.2016



Jan Štefka
Biology Centre CAS & Univ. S. Bohemia, České Budějovice, CZ

Migration Patterns, Connectivity, and Population Sizes in Marine Keystone Organisms and their Implications in a Current Conservation Context



Katharina Fietz (PhD candidate)

** Centre for GeoGenetics, Natural History Museum of Denmark*

** Marine Evolution and Conservation Group, University of Groningen*

Presentation slide

Federico Sanchez Quinto, Ph.D.

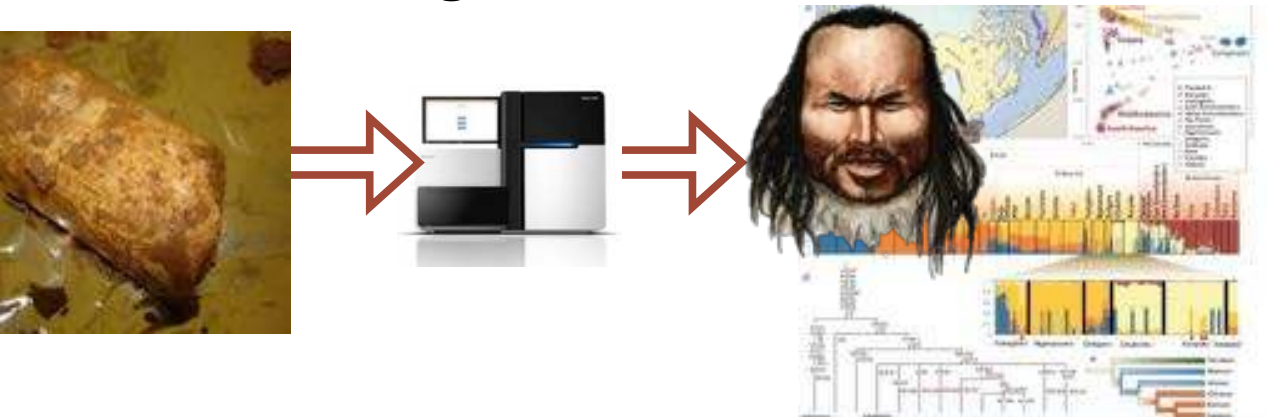
Postdoc at the Jakobsson group

Evolutionsbiologiskt centrum (EBC)

federico.sanchez@ebc.uu.se

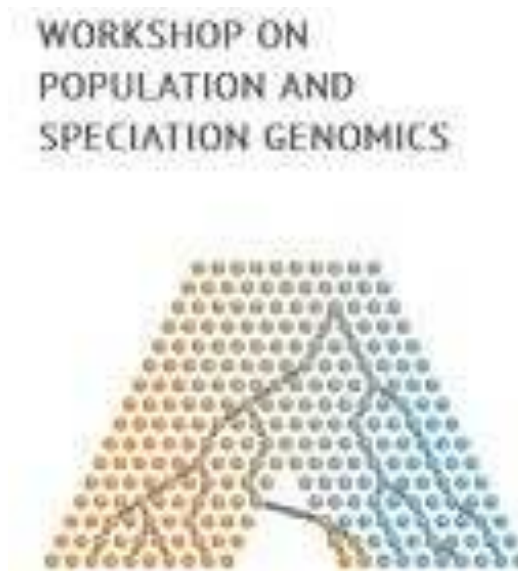
What I do

Paleogenomics



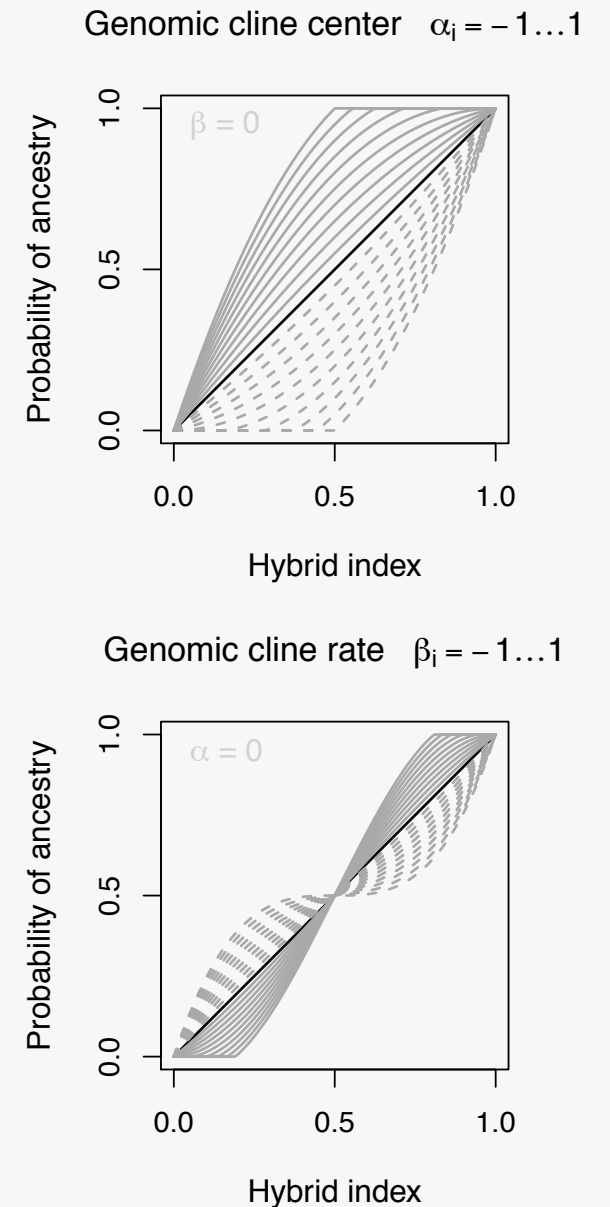
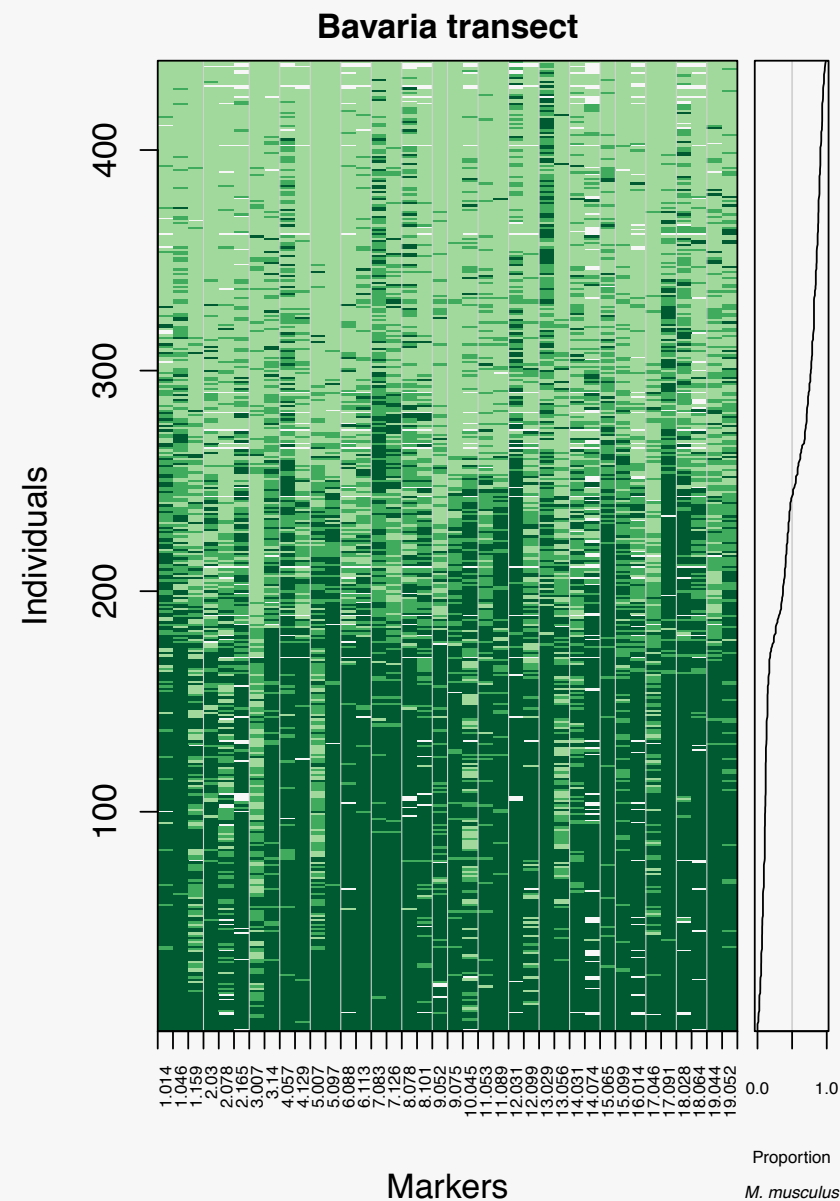
Research interests

Human evolutionary biology



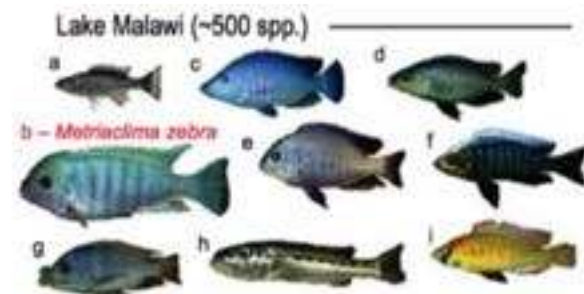
(Statistical) models for hybridization and speciation

Alex Buerkle – University of Wyoming, USA

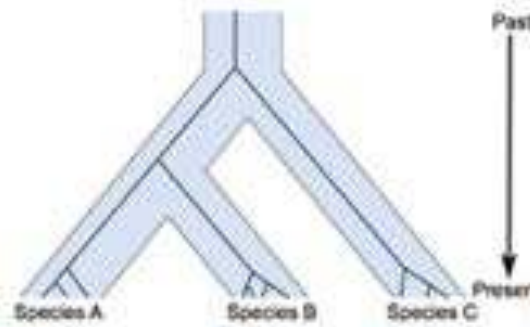


Milan Malinsky

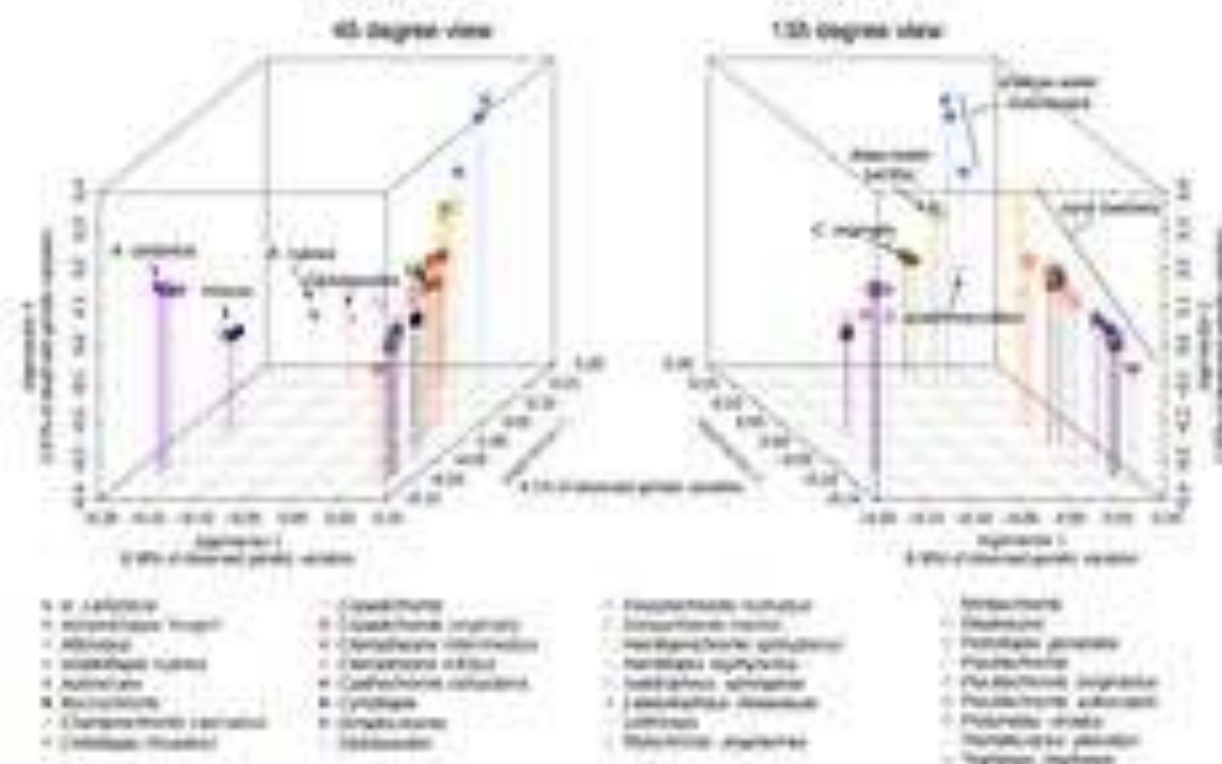
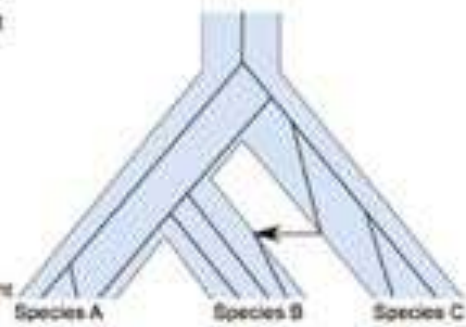
1. Genetic diversity in Lake Malawi cichlids



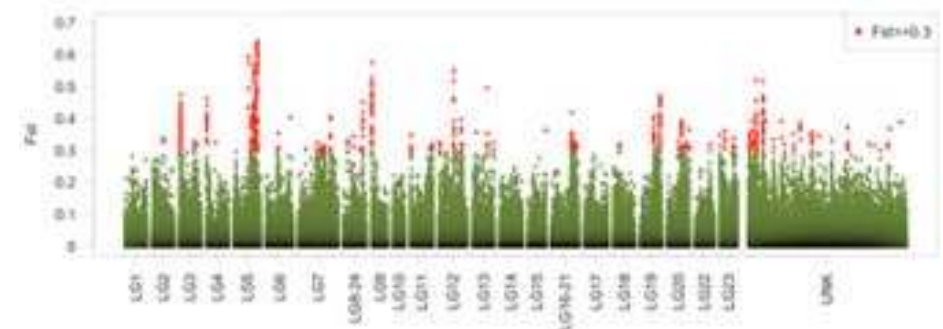
A Classical isolation model with long interspecific branches



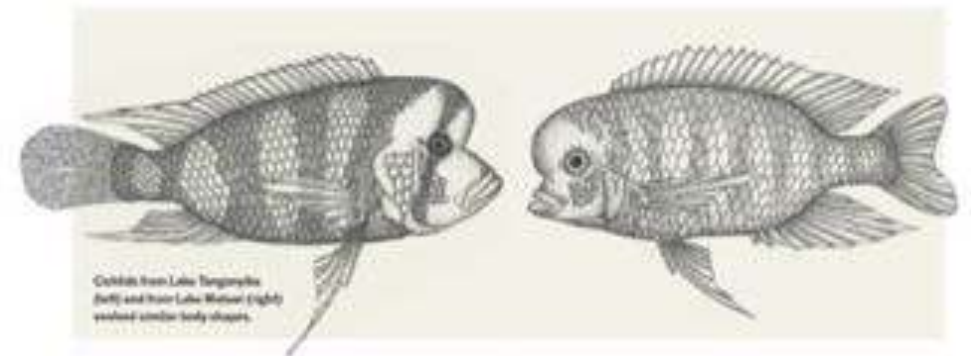
B A genealogy with severe violations of the classical model



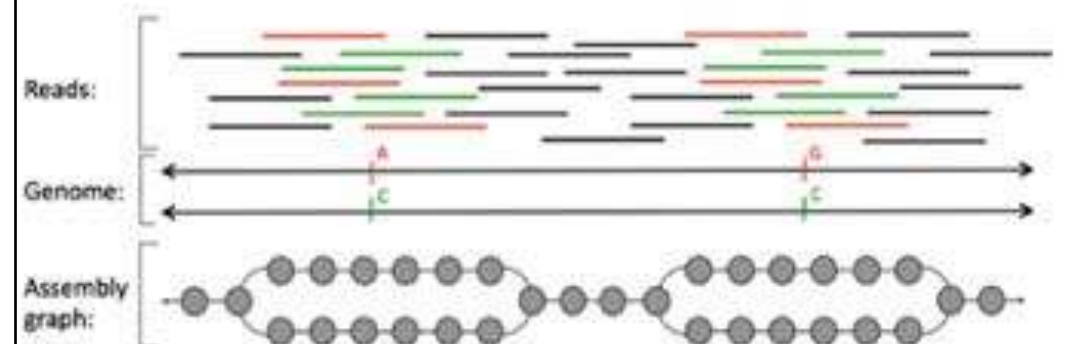
2. Genomics of speciation



3. Parallel/convergent evolution



4. *De novo* genome assembly



+ Y. Franchesco Molina-Henao

PhD Student
Bomblies and Hopkins Labs
Organismic and Evolutionary Biology
The Arnold Arboretum
Harvard University

molinahenao@fas.harvard.edu



Thermal
Adaptation and
Ecological
Speciation

Evolutionary
consequences of
polyploidy

Adaptive
evolution of
meiosis

My main interest is to understand the processes of adaptation and speciation, from molecular mechanisms to ecological interactions. I use diverse tools from ecology, genetics, genomics, molecular, and cell biology to address fundamental questions in evolution.



HARVARD
UNIVERSITY



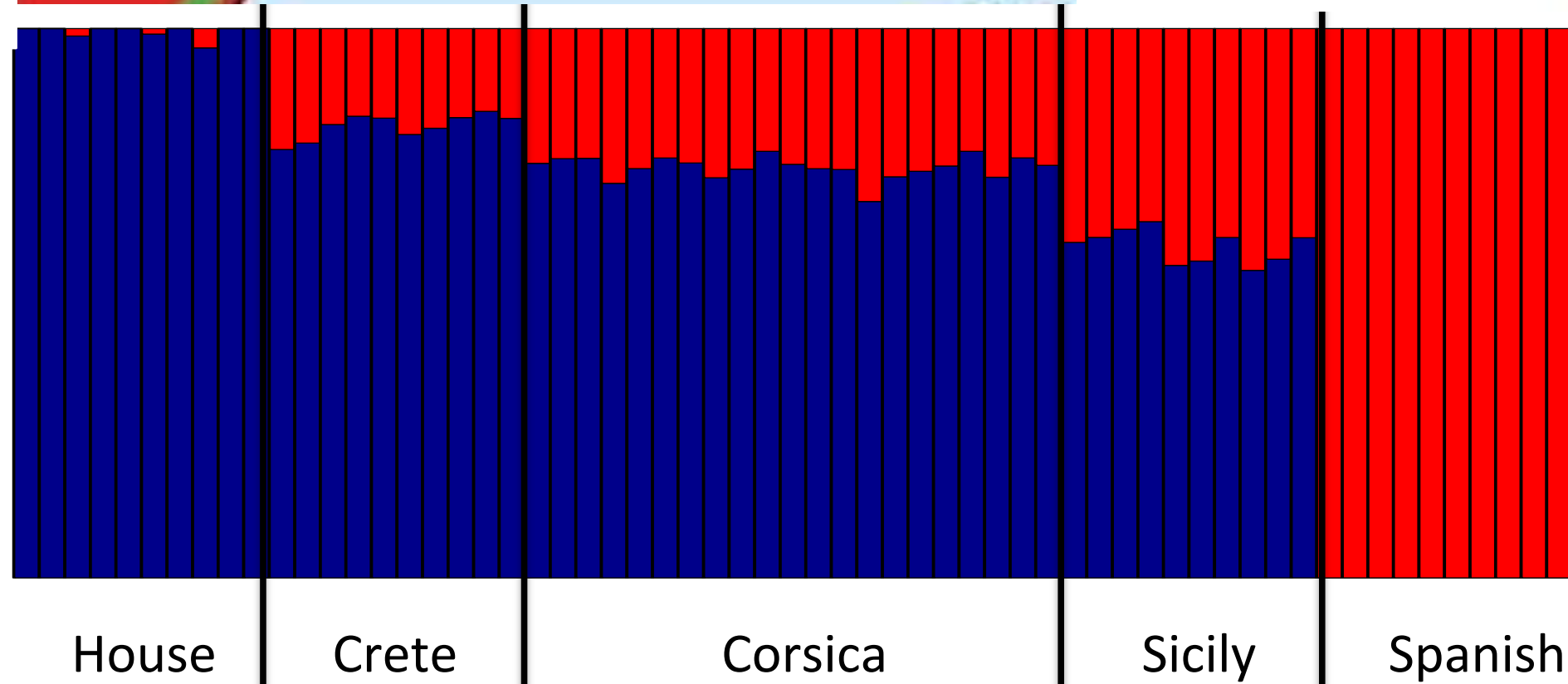
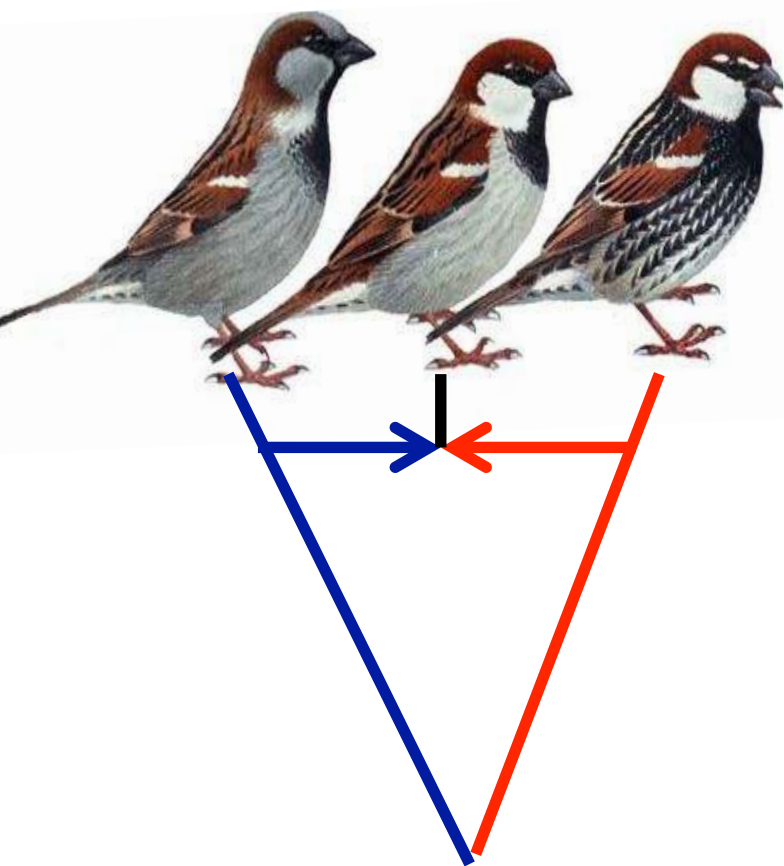
THE ARNOLD
ARBORETUM
of HARVARD UNIVERSITY

FULBRIGHT
COLOMBIA



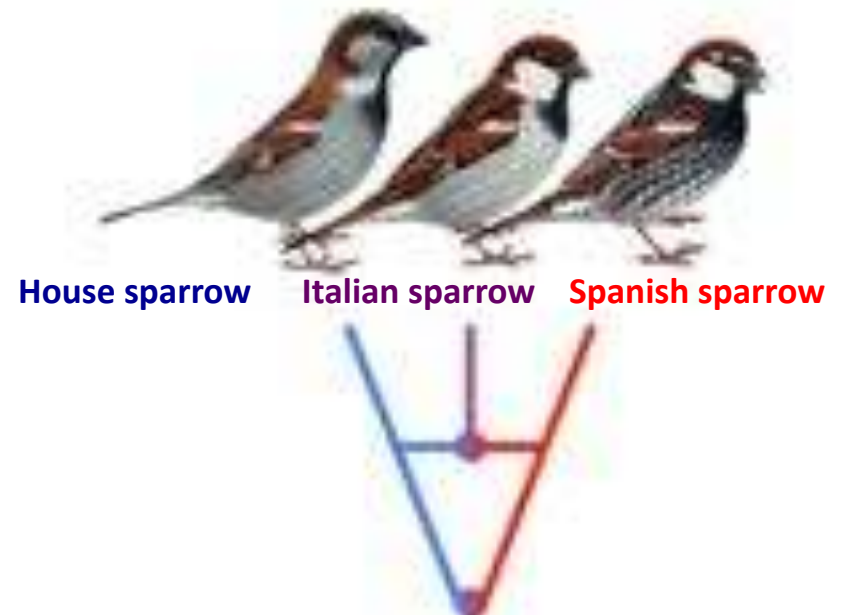
The repeatability of genomic architecture in a homoploid hybrid species

Italian sparrows inherit different proportions of their genomes from the parent species on Crete, Sicily, Corsica and Malta



Linkage, genomic conflict and TE-release in hybrid populations with different genomic architectures

1. Patterns of linkage disequilibrium (LD) in different populations of a hybrid species
2. Genomic conflict resolution and genetic ancestry
3. The role of transposable elements (TEs) in molding a hybrid genome



Diede Maas, MSc

PhD: “Elucidating mechanisms of response to climate change scenarios in marine lake populations”



Long term

I. Population Genomics

Patterns of evolution in marine lake populations after ~6000 yrs of exposure

II. Gene expression

Adaptive gene expression for range of lakes along environmental gradients

Tool: Genomics

De-novo assembly and annotation draft genome

Short term

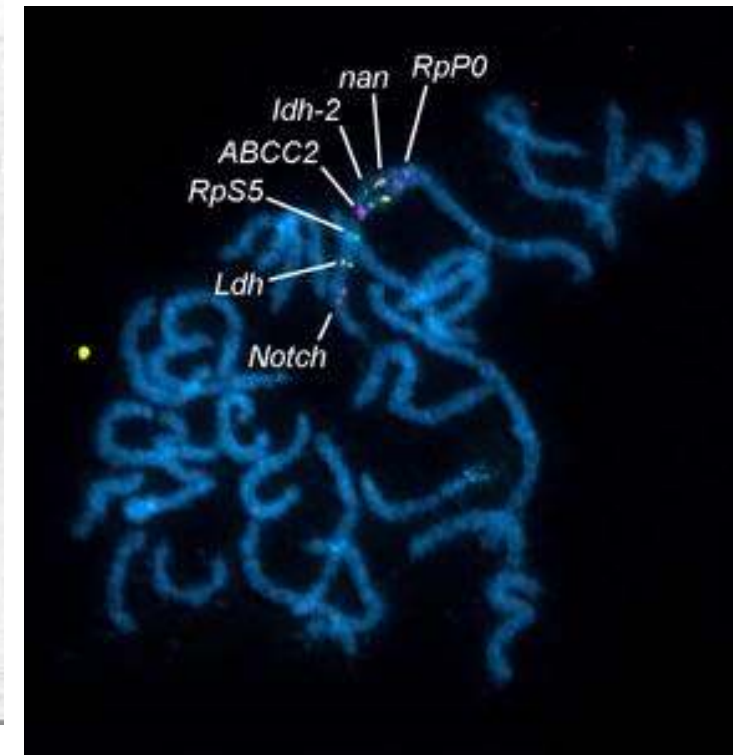
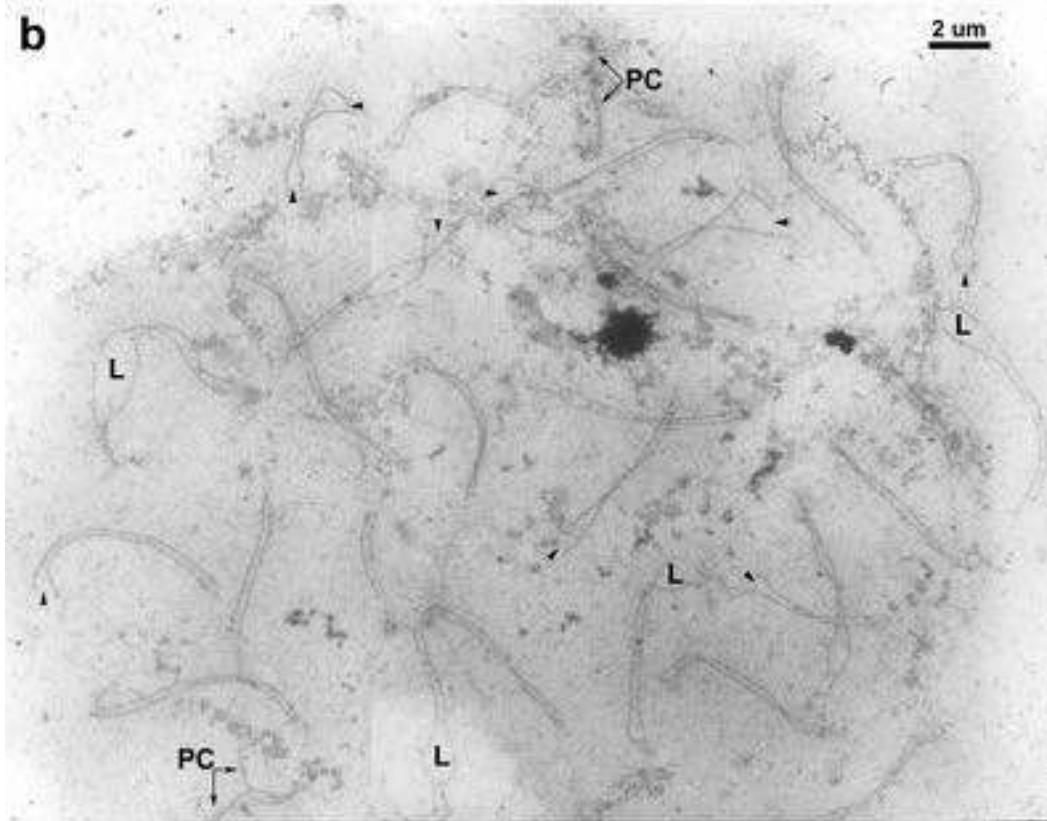
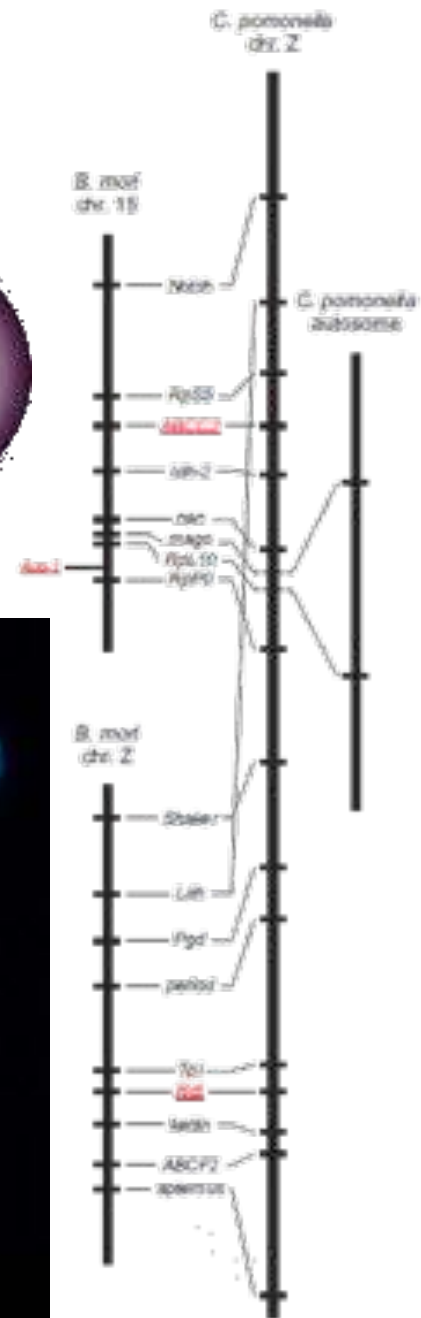
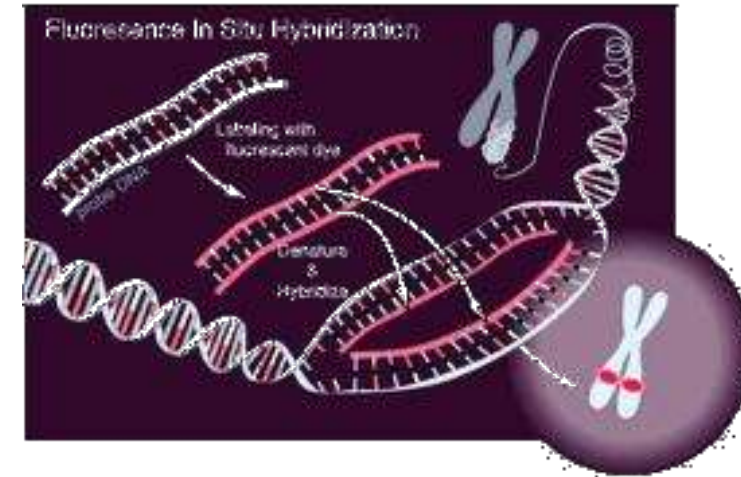
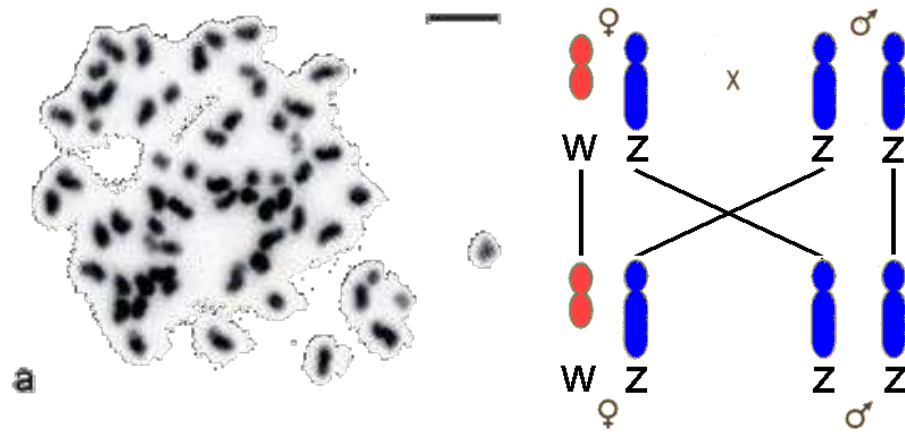
III. Plasticity

Physiology and transcriptomic responses to direct simulation of climate change stressors

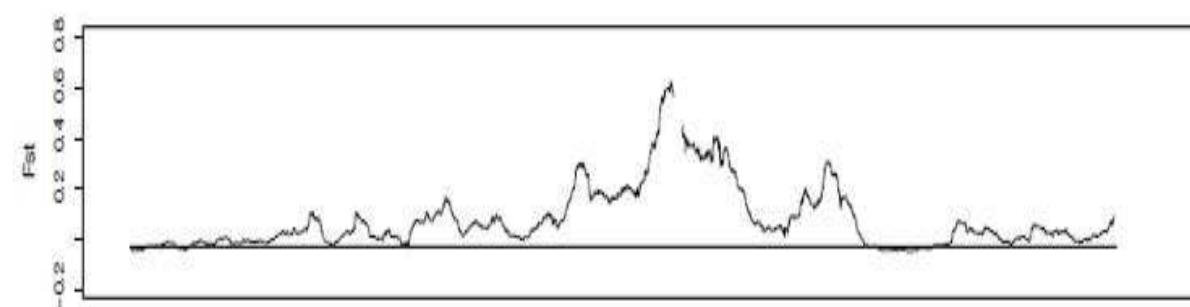
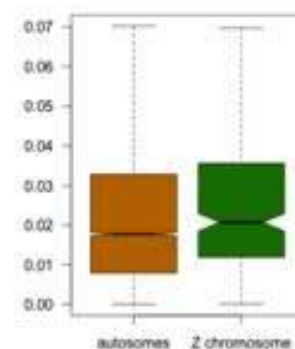
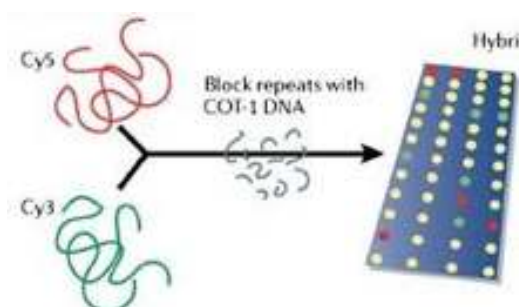
Tool: Mesocosms

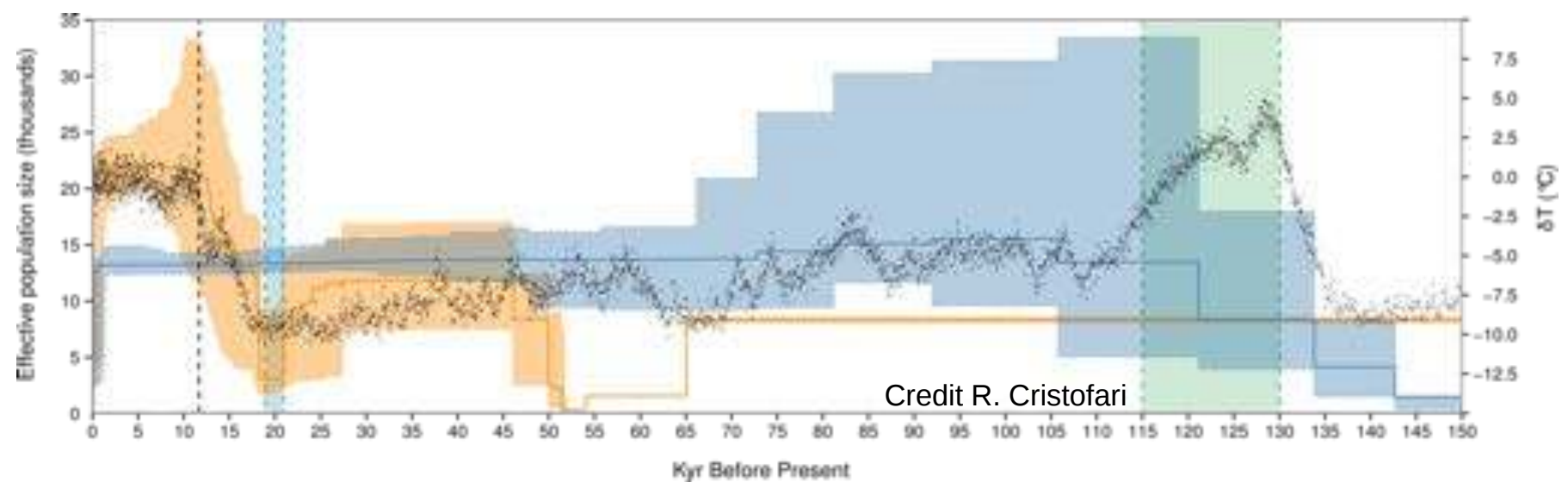
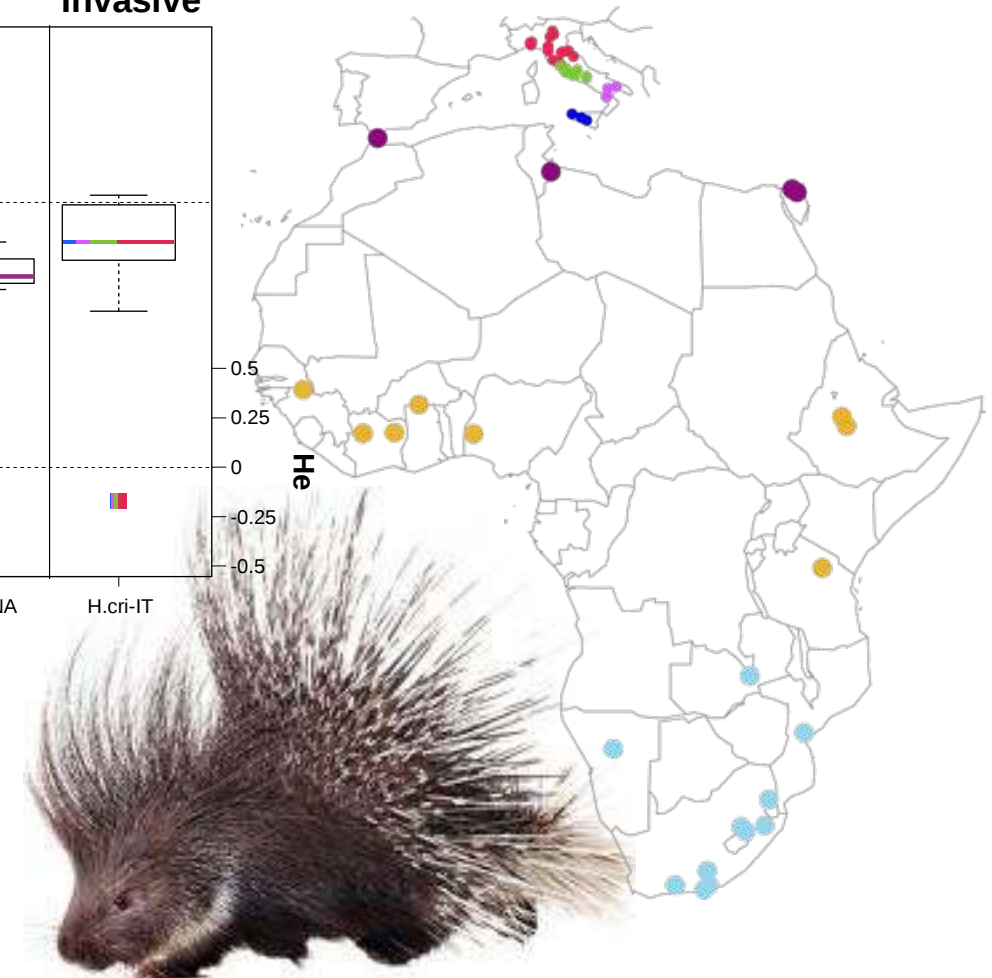
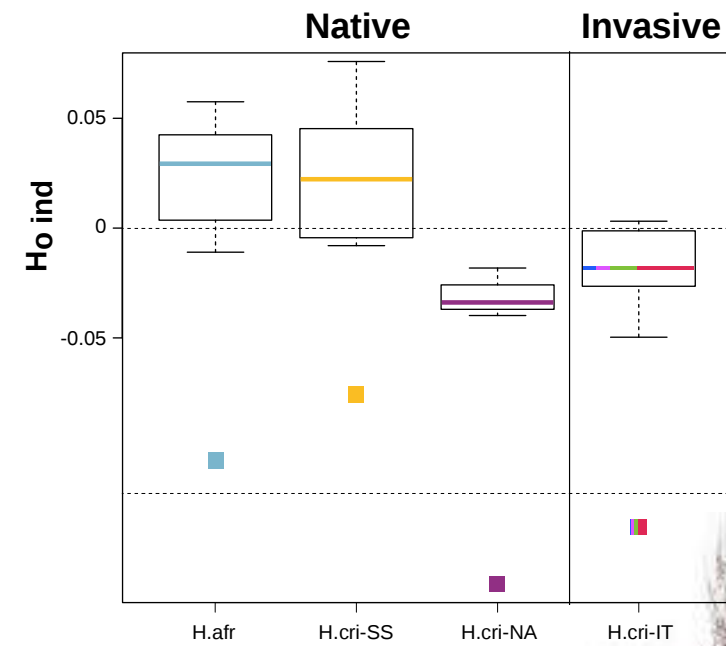
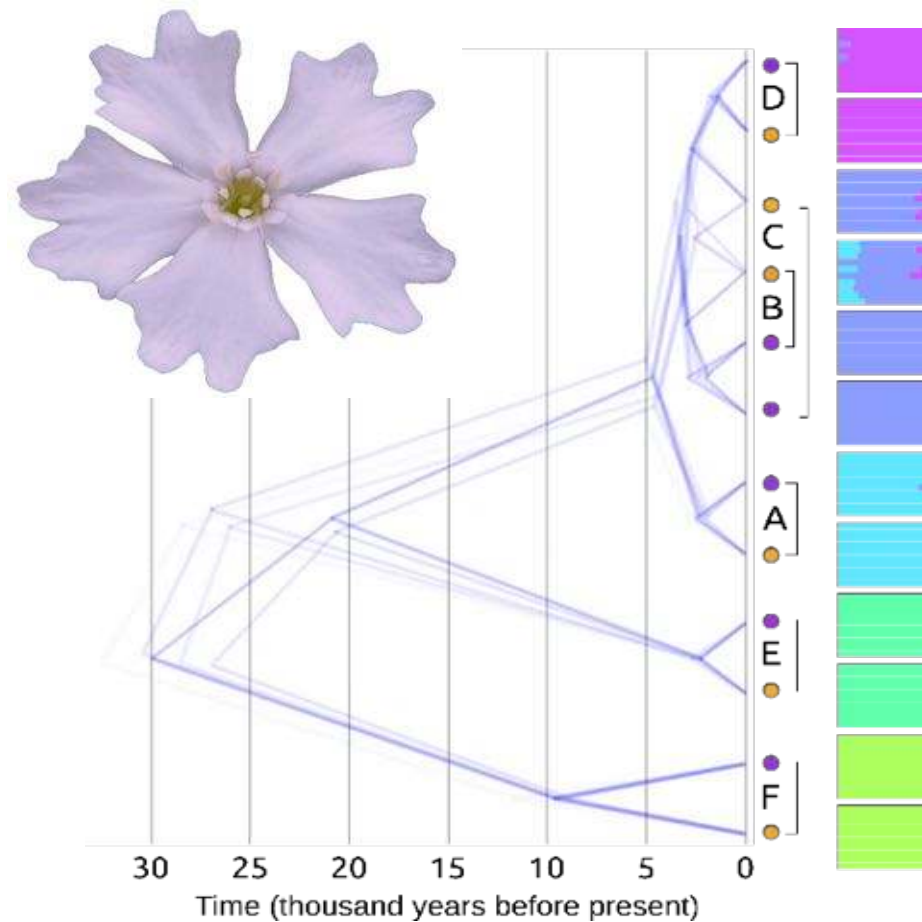


WAGENINGEN **UR**
for quality of life



GGCCCTATCGTGACTGATTACCAGGATCCTAGCG/
TGGTCAGGTTGTTCAACTCGATGACTAGAATATAT
GTAACGTTGCAAATTCAGTCGGTACGTTTCCAGG/
CTGTAGCURLYHAIRGCCCTTGAATCTTGGCAGTC
AACTCATCCAGGAATGGGCCCTACGTACCGTAAC
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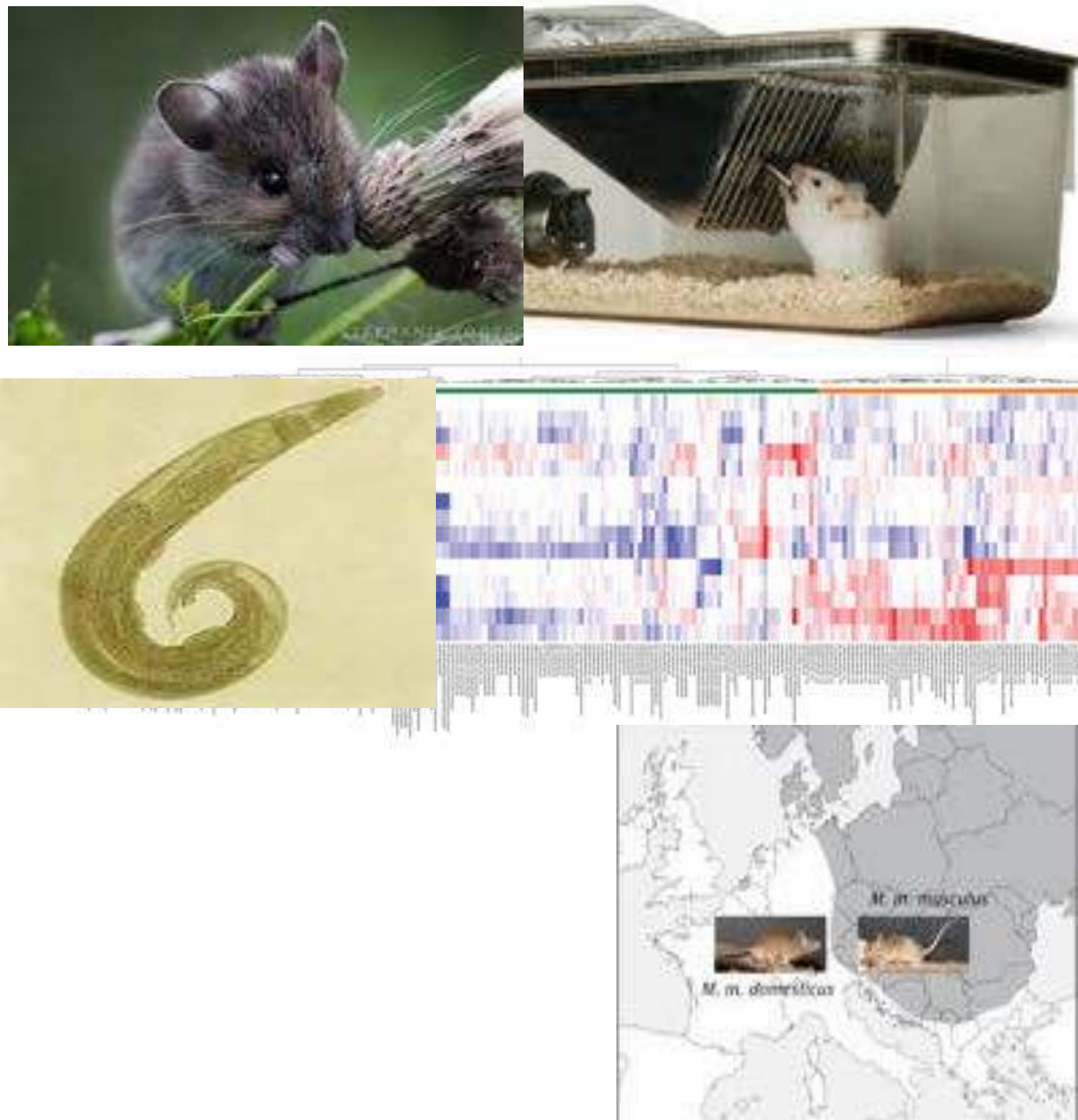
Credit R. Cristofari

Jakub Kreisinger

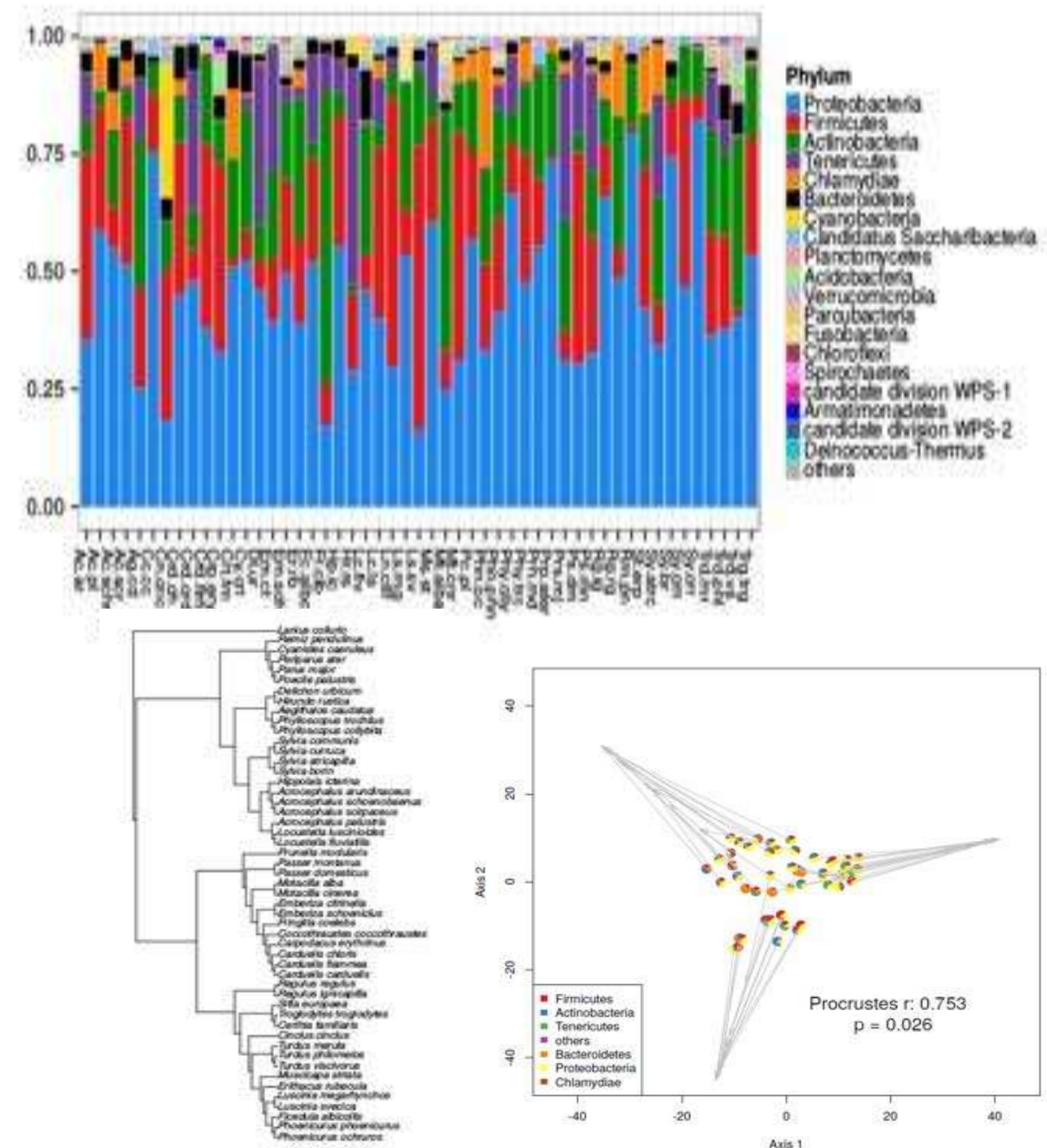
Dept. of Zoology, Charles Univ. in Prague
Inst. of Vertebrate Biol., Czech Academy of Science



Gut microbiota of wild rodents



Gut microbiota of birds



Genetic diversity in Grauer's gorillas

Tom van der Valk



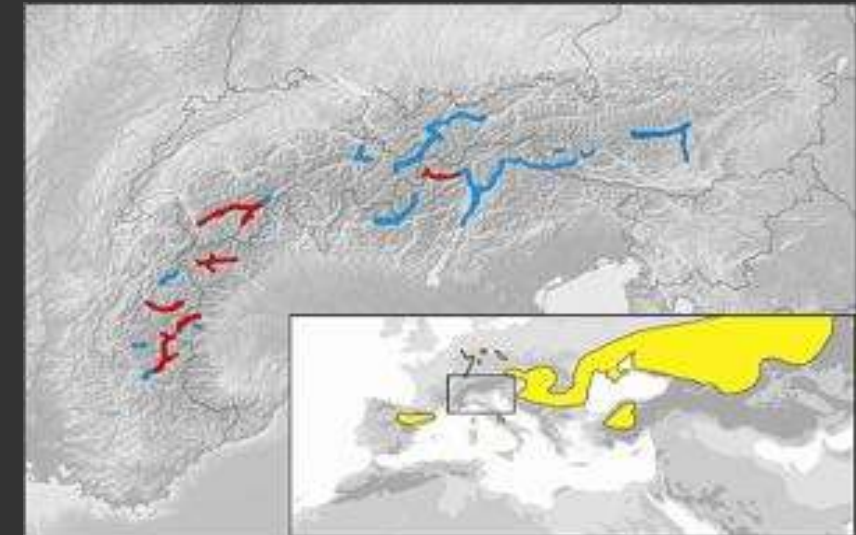
UPPSALA
UNIVERSITET

Philipp Kirschner

PhD-Student at the University of Innsbruck (Austria), Institute of Ecology

Research

- Origin of xerophilic European steppe biota
- Postglacial recolonisation of Alpine dry habitats
- Connectivity among xerothermic habitats in Europe



Studied organisms

- Two grasshoppers
Omocestus petraeus
Stenobothrus nigromaculatus
- One ant
Plagiolepis taurica

Omocestus petraeus



Stenobothrus nigromaculatus



Plagiolepis taurica



Interests

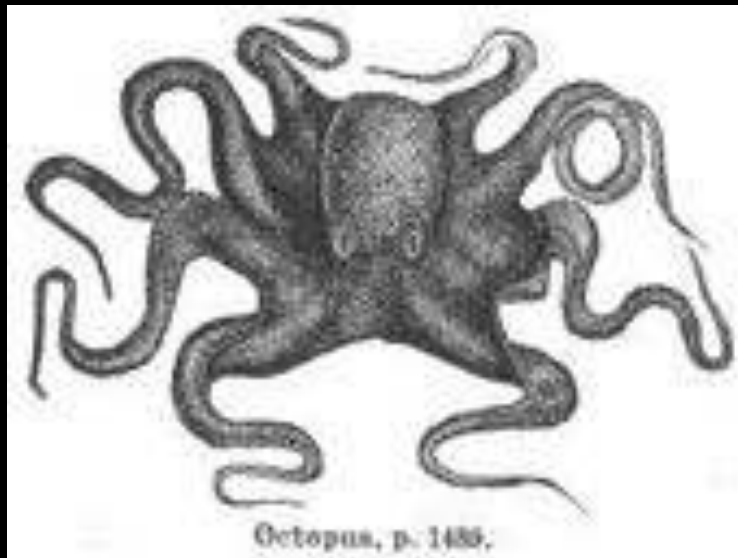
- Processing RAD data
- Admixture models
- Phylogeographic modelling



Marie Krausová

Evolution and Phylogeny of Dicyemids (Mesozoa), parasites of cephalopods

Laboratory of molecular phylogeny and evolution of parasites
third year of PhD, supervisor Jan Štefka



bioinformatics

genomics

population
structure

transcriptomics

linux/bash
scripting

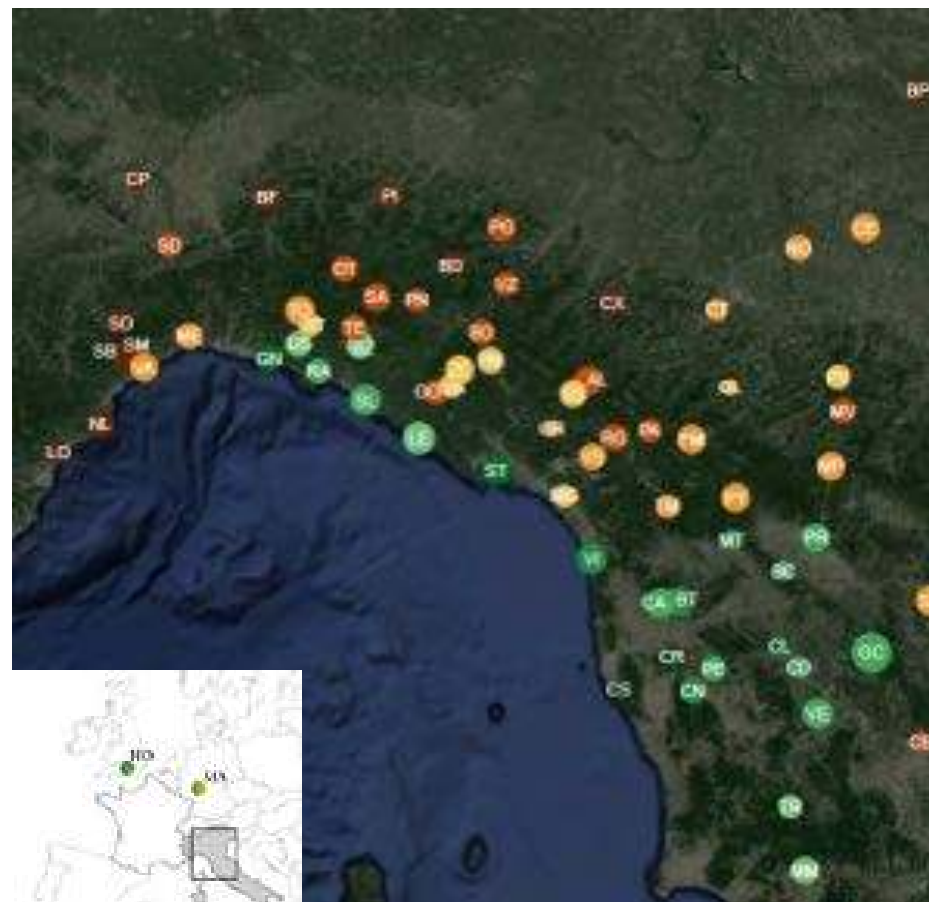
phylogeny

University of South Bohemia Czech Republic

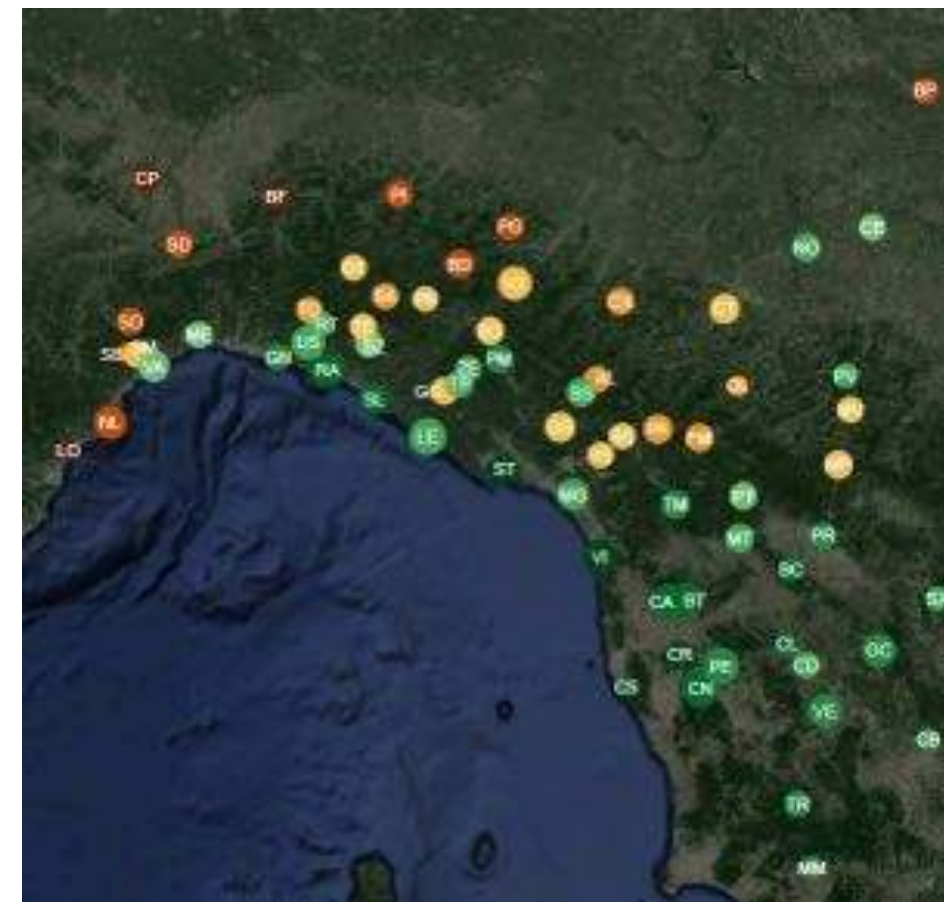
Genomic signature of sexually selected hybridization on common wall lizard



Weizhao Yang
Lund University
Sweden



Female



Male

Thierry B Hoareau

Dept Genetics, Univ. Pretoria, South Africa



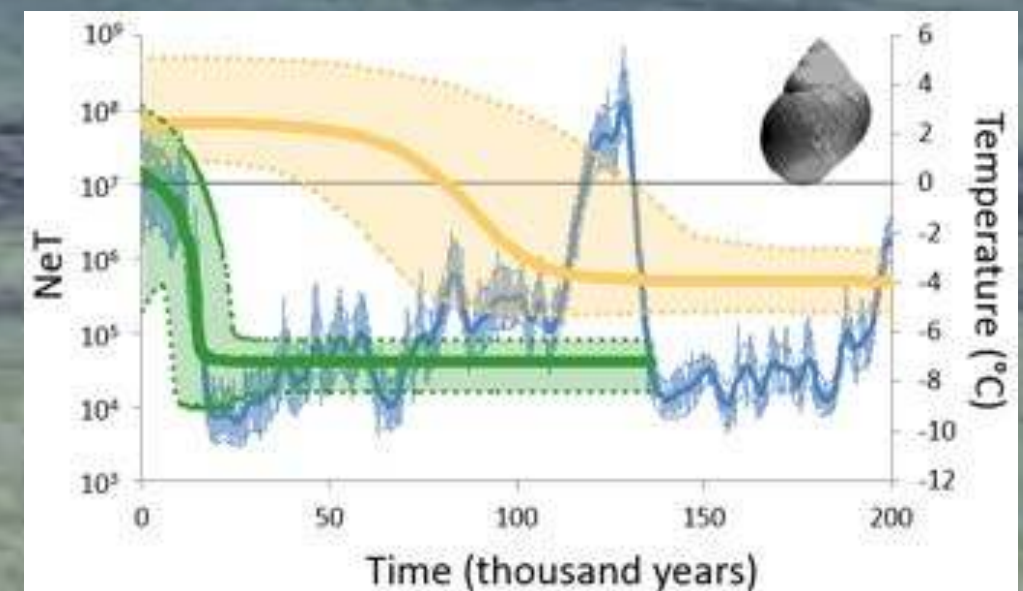
Evolution of marine organisms

Research questions:

LHT
↑
Environmental factors
↑
Evolutionary processes



New method:



Calibration of Demographic Transition = GREEN

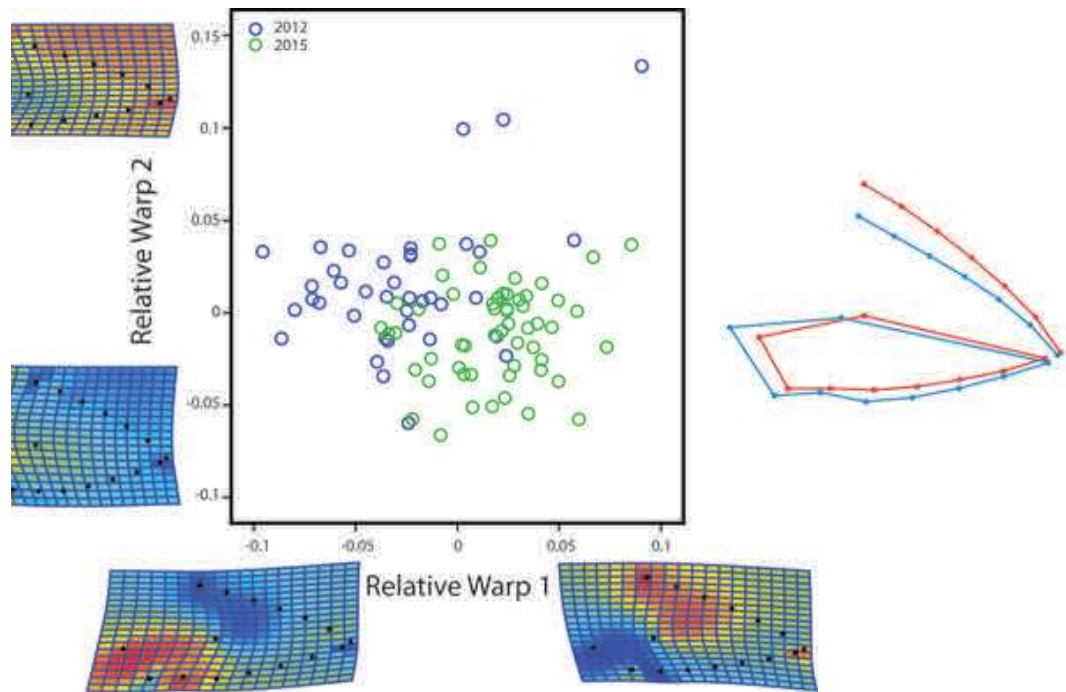
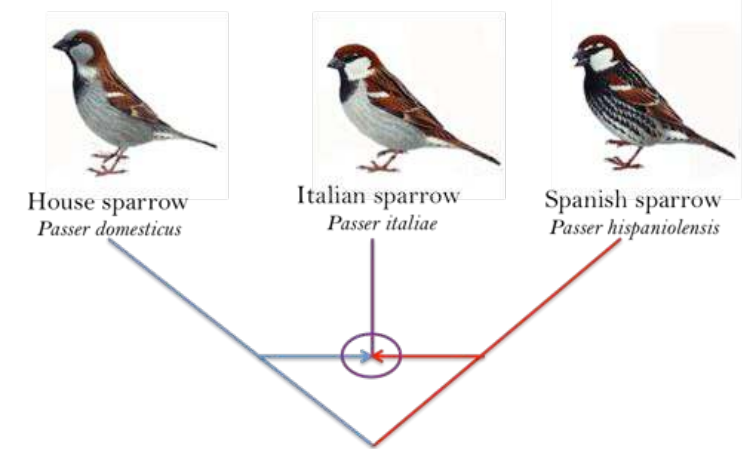
Fossil calibration = ORANGE



MORITZ MUSCHICK

Postdoc, EAWAG, Switzerland
Speciation and diversification in
cichlid fishes and stick insects

The genomic architecture and evolutionary potential of a hybrid species



1. Interspecific variation in genomic regions linked to local adaptation
2. Mapping ecological traits to genomic regions

3. Population structure and isolation by adaptation.
4. Epistatic interactions and Pleiotropy between loci may restrict purging of DMI reducing adaptive potential
5. Species interactions



Angélica Cuevas

PhD research fellow



UiO : Universitetet i Oslo

SCOTT A. HANDLEY

WASHINGTON UNIVERSITY SCHOOL OF MEDICINE
DEPARTMENT OF PATHOLOGY & IMMUNOLOGY

- Metagenomics

- Identification of previously unrecognized pathogens or pathogenic microbiota associated with disease

- AIDS

- Gastrointestinal virome and bacterial microbiome
 - Alterations during AIDS (HIV humans)
 - Alterations following vaccination (SIV macaques)
- Other mucosal surfaces: mouth, lungs, genital tract

- Inflammatory Bowel Disease

- Bacteriophage predation of bacteria instigating pathogenic dysbioitic flora
- Identify candidate viral causes of IBD for vaccine target development



Health / Disease

Who is there?

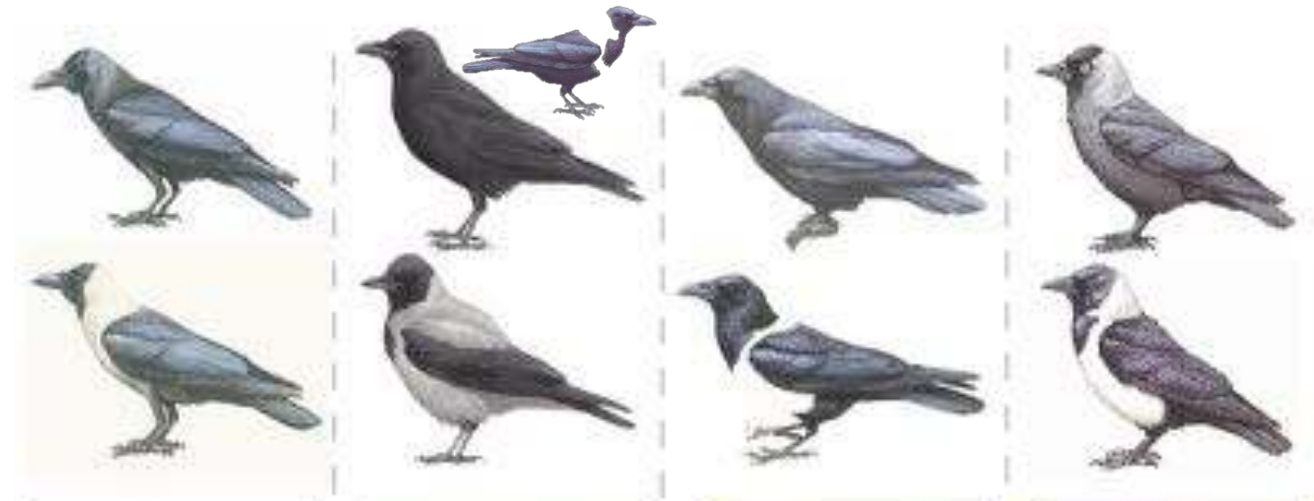
Are they normally there?

Why are they there?



Health / Disease

Matthias Weissensteiner
PhD student
EBC Uppsala
🐦 @crow_speciation



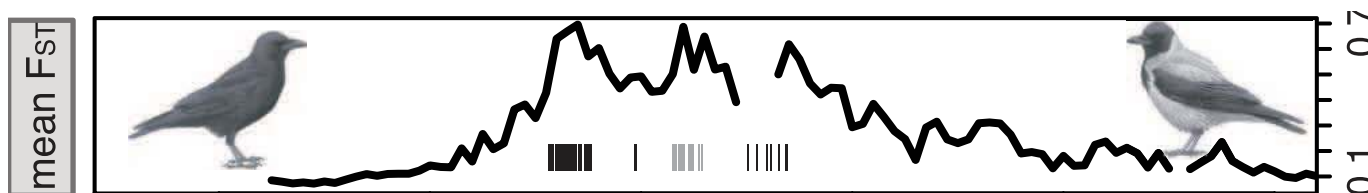
The role of structural variation in phenotype evolution



Long-read seq



Optical Mapping

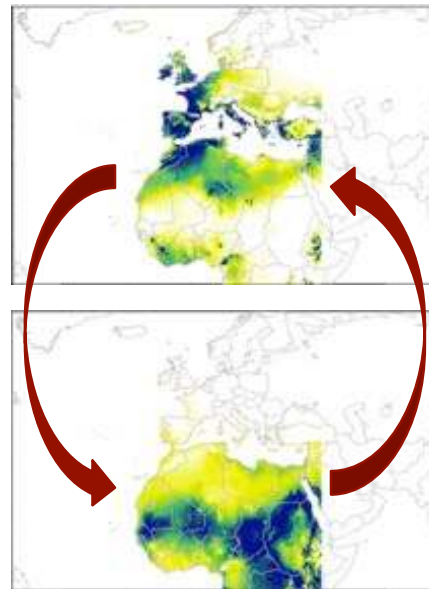


Keywords: Evolution, phylogeography, speciation, genomics, migration, distributions, systematics, biogeography, ecology, insects, butterflies

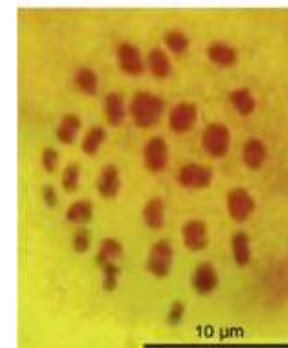
Population genomics of migration



Vanessa cardui



Karyotype-driven speciation



Lysandra coridon

Gerard Talavera
Postdoctoral Associate
Museum of Comparative Zoology
Harvard University



INSTITUT de
BIOLOGIA
EVOLUTIVA

PhD-project: Polyploid Evolution in *Dactylorhiza* (Orchidaceae)



Data

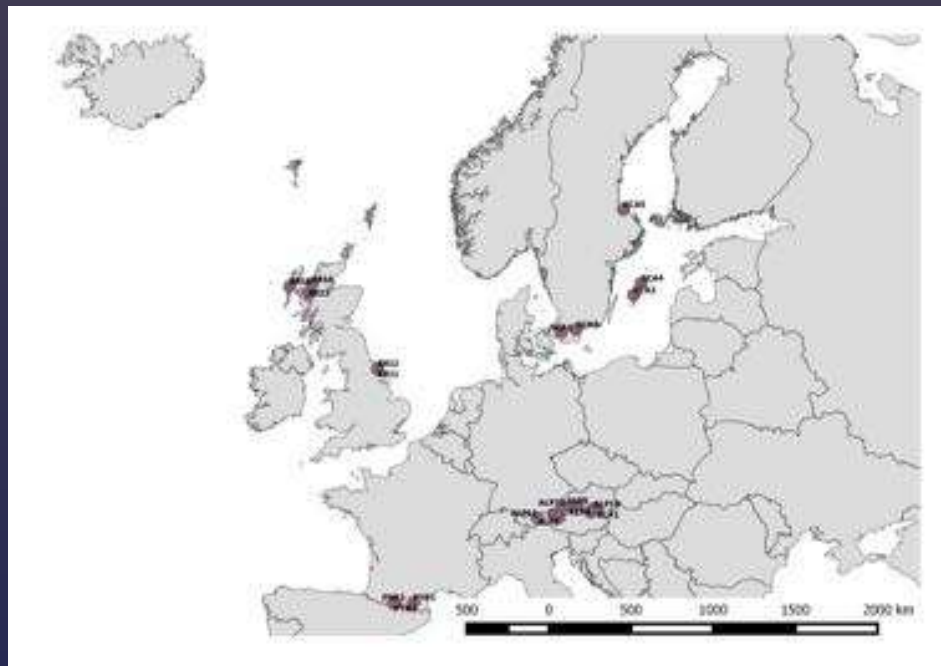
Two sibling allopolyploid species (+ parents)

- *D. traunsteineri* ($2n=80$)
- *D. majalis* ($2n=80$)
- (+*D. purpurella*)



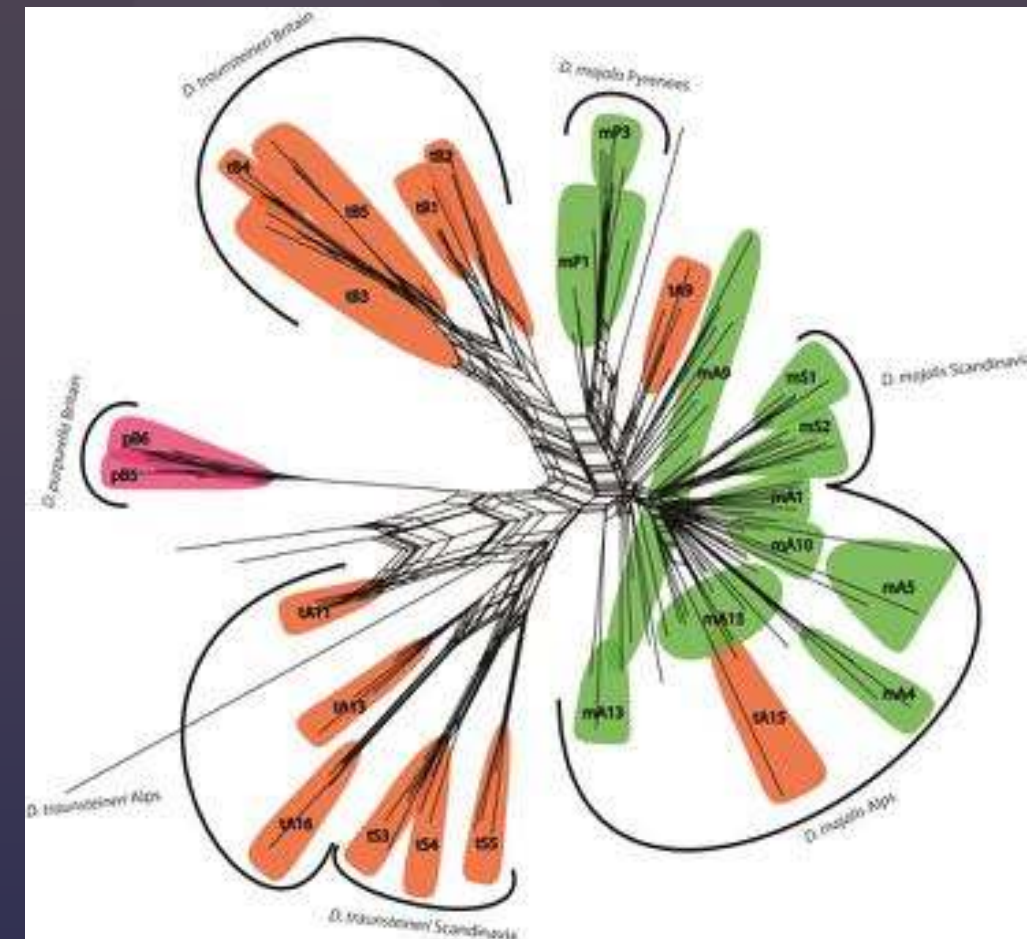
Objective

Investigating genetic structure and polyploid origin
With RAD-seq data (5000+ loci)



Results

- 5 groups
- Suggest two independent origins of *D. traunsteineri*



Marie Kristine Brandrud

marie.kristine.brandrud@univie.ac.at

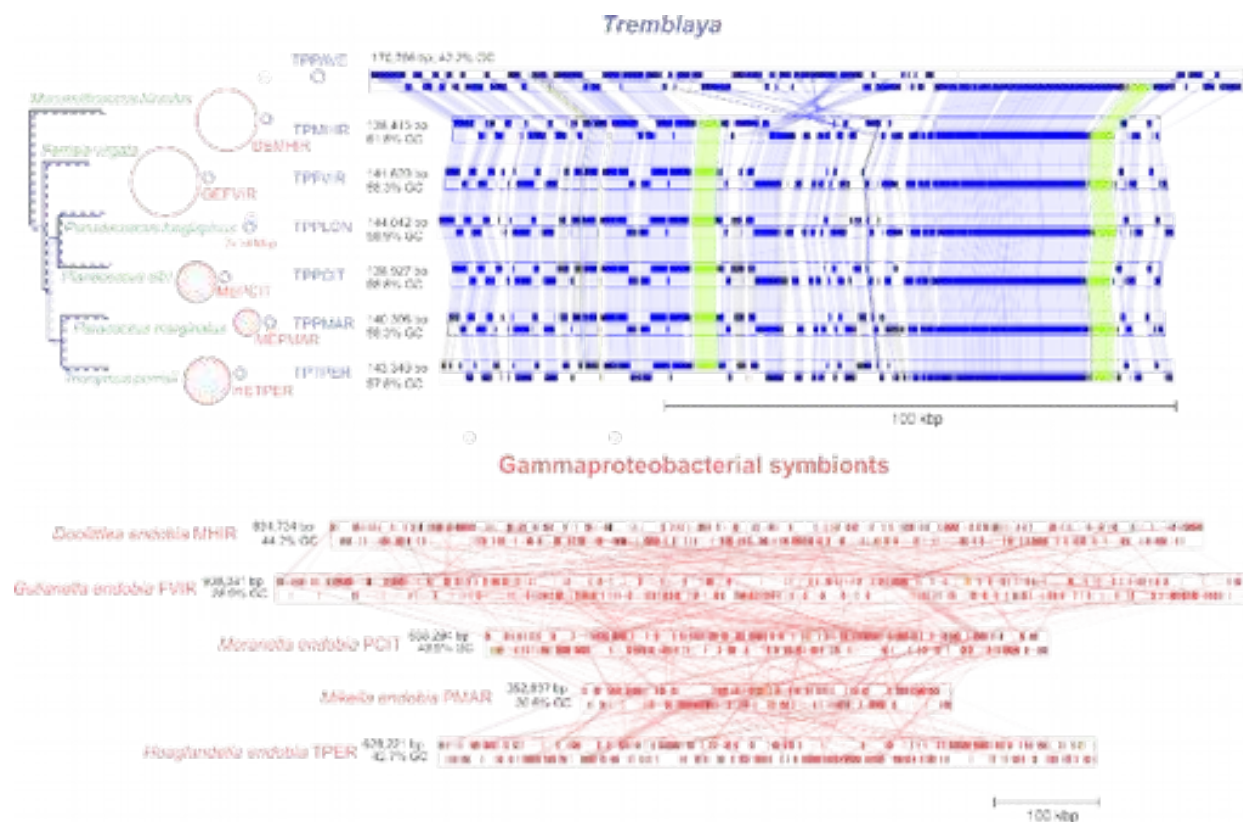
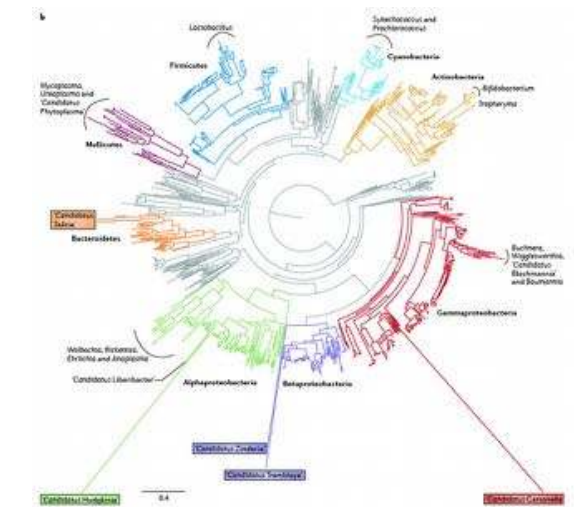
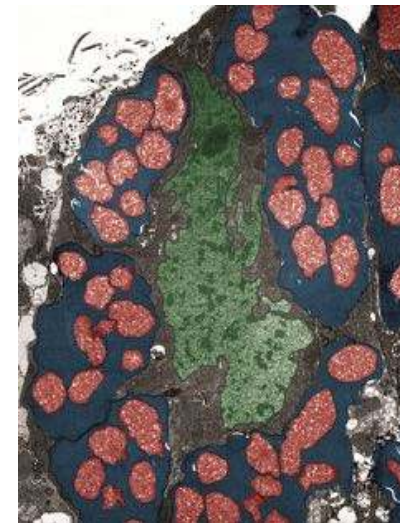
Supervisor:
Ovidiu Paun,
Universität Wien

Genomics of Tripartite Nested Mealybug Symbioses

Filip Husnik

PhD student of Molecular and Cell Biology and Genetics
Institute of Parasitology, Czech Academy of Sciences

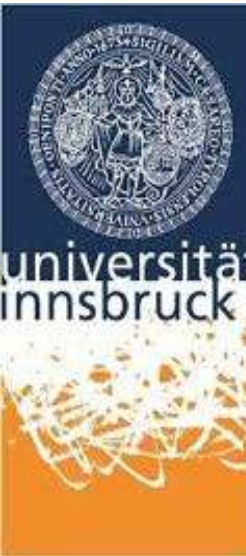
@FilipHusnik 
 filip.husnik@gmail.com



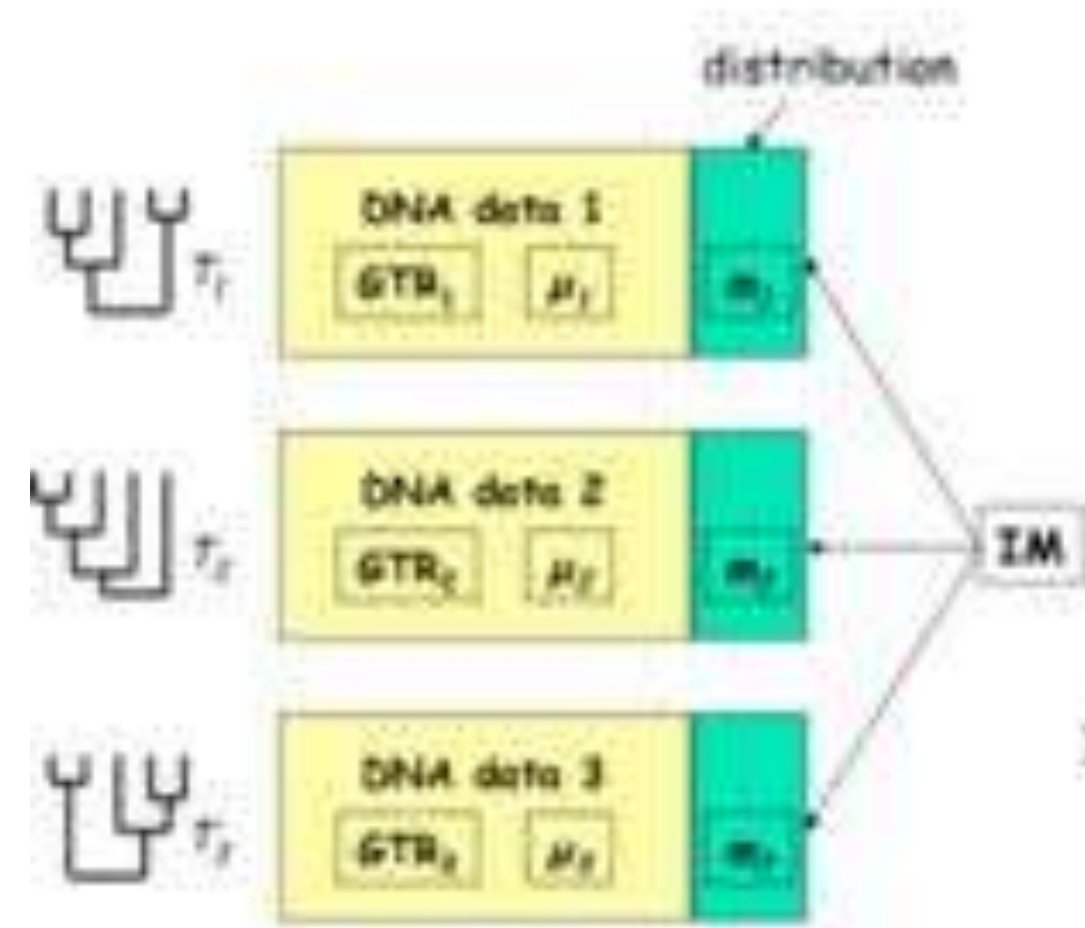
Origin of steppe flora and fauna in inner-Alpine dry valleys

[comparative phylogeography]

Eliska Zaveska
(postdoc)
Inst. of Botany,
Uni. of Innsbruck
Austria



PI. P. Schoenswetter & F. Steiner, **Funded by:** AT science Fund (FWF) no. P25955



Reticulate evolution in *Acropora*



Acropora digitifera



Acropora tenuis



Acropora echinata



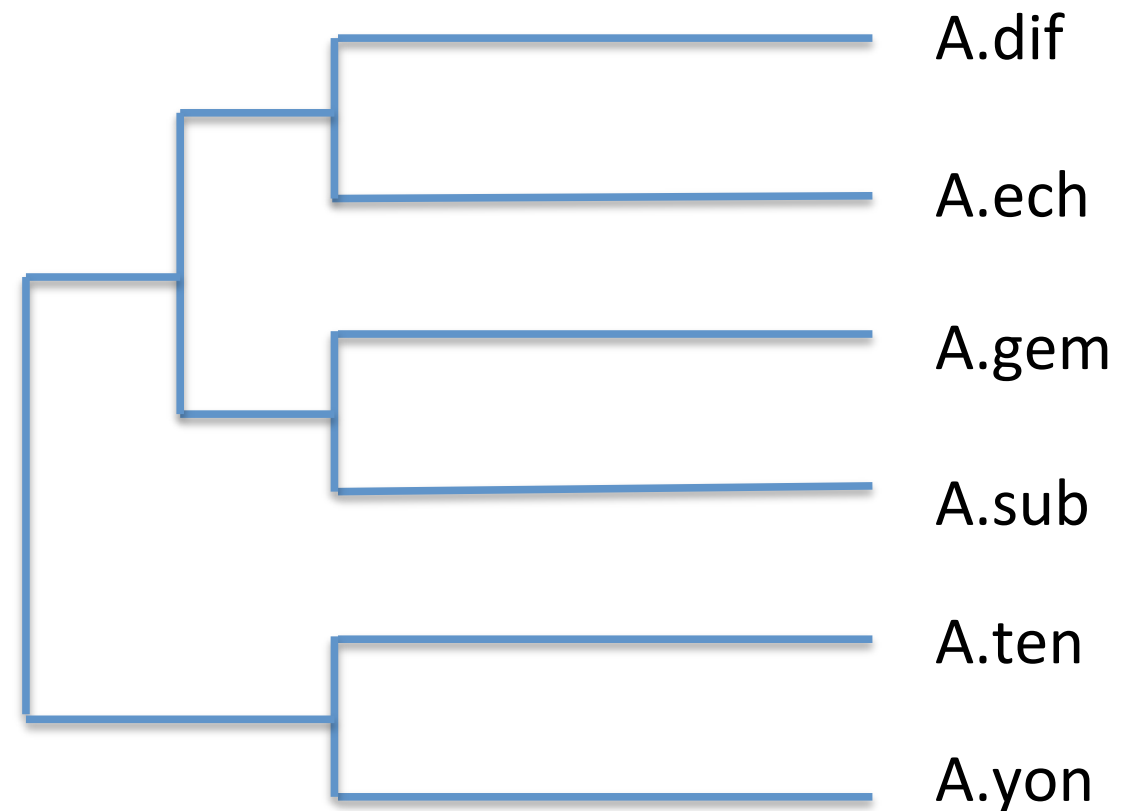
Acropora subglabra



Acropora gemmifera



Acropora yongei



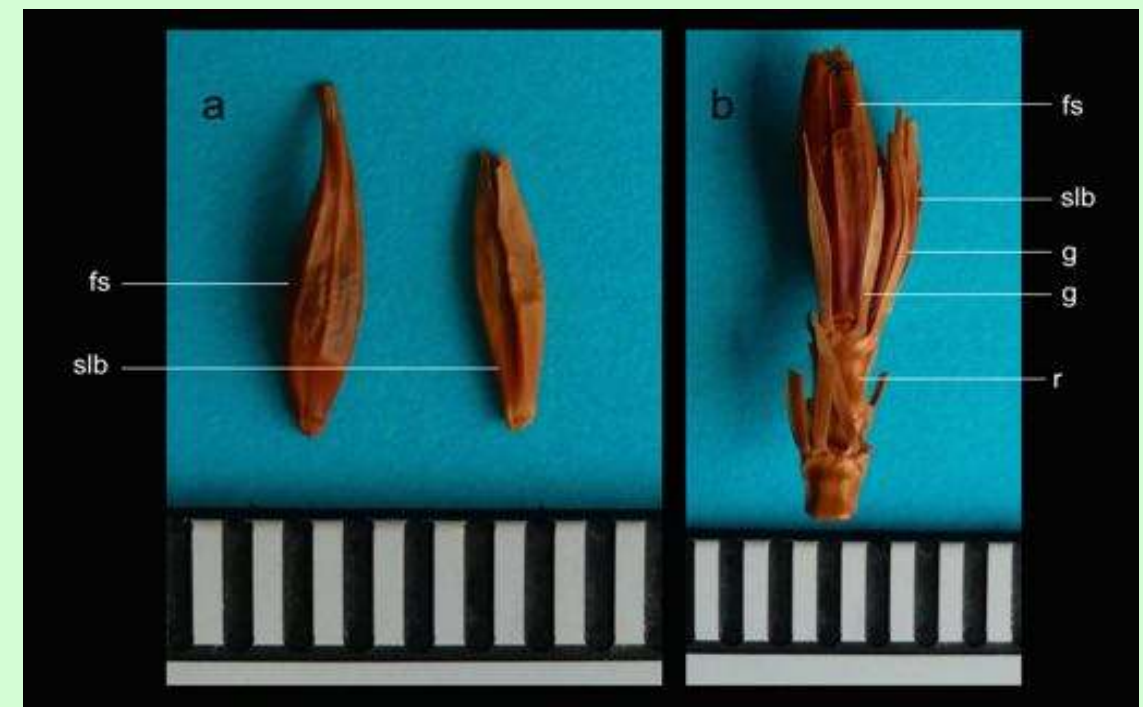
Okinawa Institute of Science and Technology
Graduate University

Yafei Mao
PhD student

William Nicholson

School of Life Sciences, University of Warwick

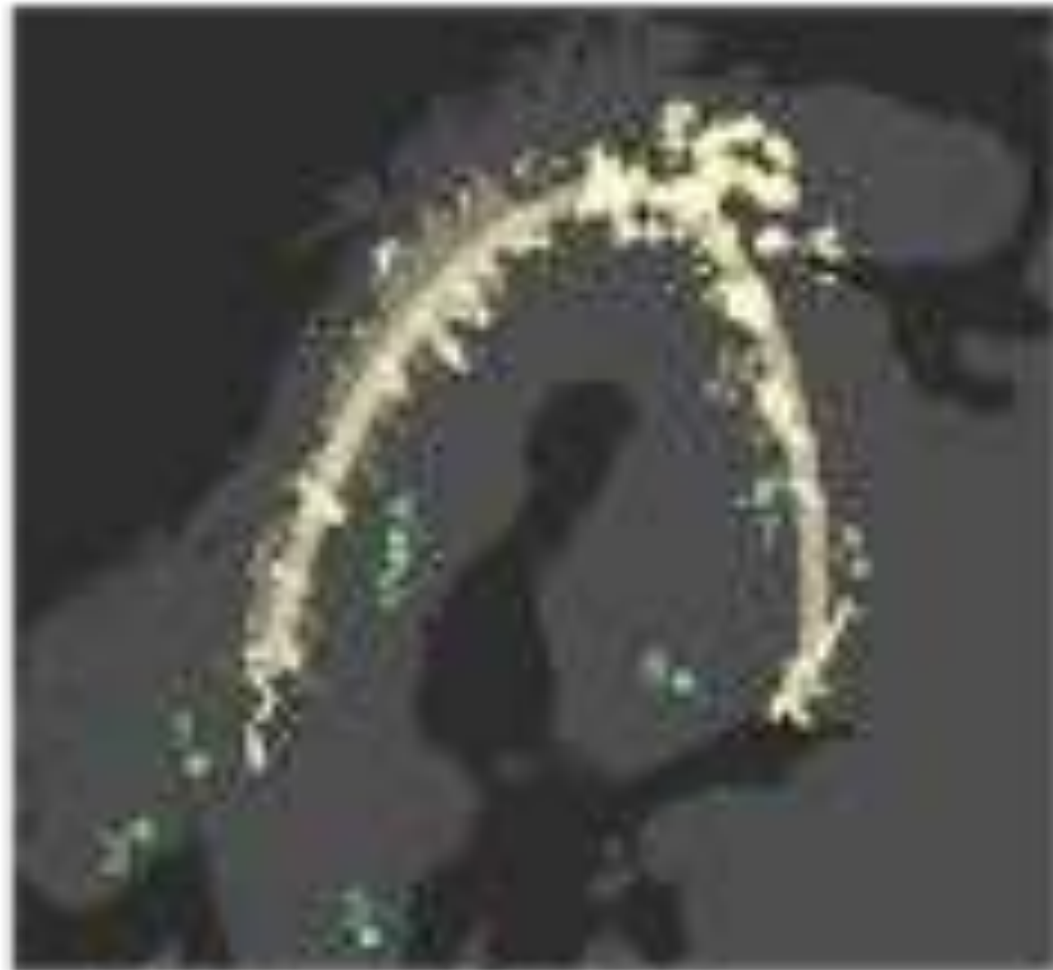
- Project on sorghum – NGS data from about 10 modern and 10 ancient specimens including domestic, wild and feral varieties
 - variant calls made on the data
 - signatures of selection and selective sweeps
 - testing genetic diversity and looking for bottlenecks
 - domestication related loci
 - local adaptation to dry conditions, pest and disease resistance
 - introgression in modern and ancient genomes
- Project on barley
 - NGS data (using DNA capture arrays) from ancient specimens from Qasr Ibrim
 - working on developing software for haplotype phasing





Fungal species traits and dispersal

Sundy Maurice



2. Evaluate the resolution of RAD markers in structuring genetic population at **a finer geographic scale**

4 species * 20 genotypes
*4 localities in Norway

1. Reveal the genomic diversity within species

1 forest 20 individuals * 13 species

3. Northern Eu. Level:

Correlate the population genetic structures of polypore species with a variety of life-history traits

13 species * 20 individuals *
7 localities



Thanks!