



Society for Conservation Biology



Joint Introduction

Conservation Genomics

An Overview and Hands-on Training with
Genomic Analyses for Biodiversity Conservation (ID: 9)

&

Training to Improve Applications of Genetics and Genomics
for Biodiversity Conservation (ID:33)

Gordon Luikart
William Hemstrom
Jared Grummer



UNIVERSITY OF
COPENHAGEN



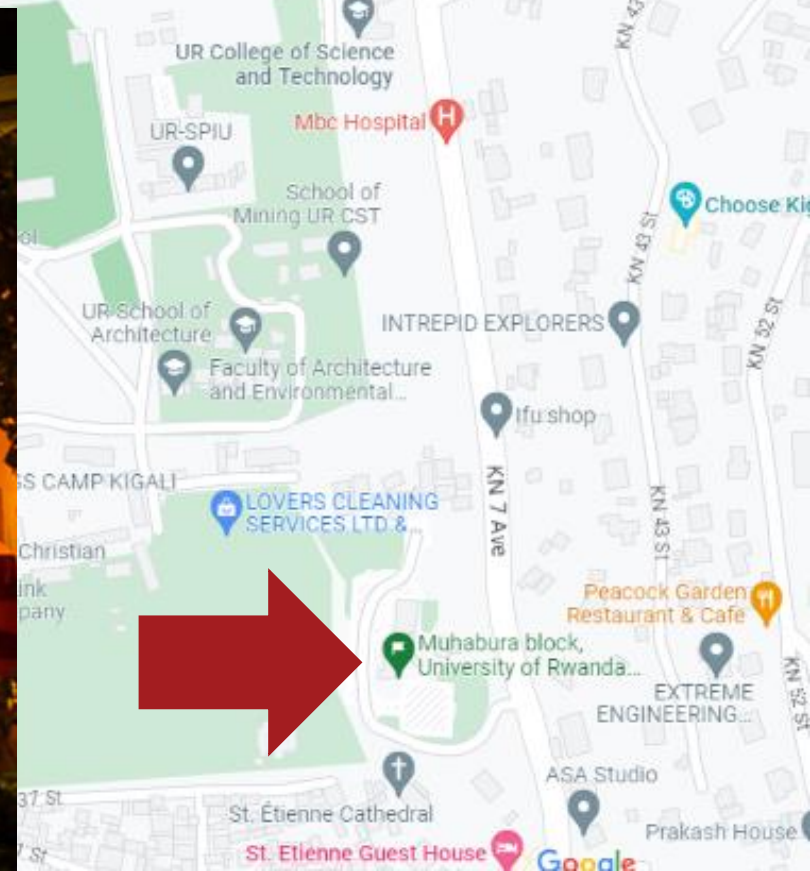
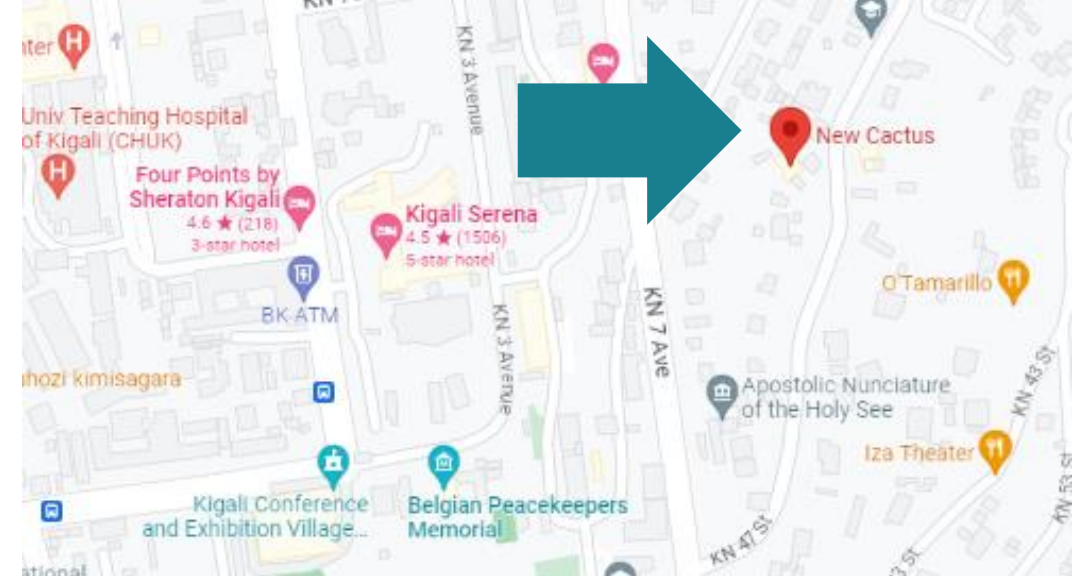
Laura Bertola
Isaac Overcast
Josiah Kuja
Anubhab Khan

Ice breaker: Join us!

New Cactus (KN 47 St)

~15 minutes walking

Pizza is on us!



The importance of genetic diversity

Laura Bertola



KØBENHAVNS
UNIVERSITET

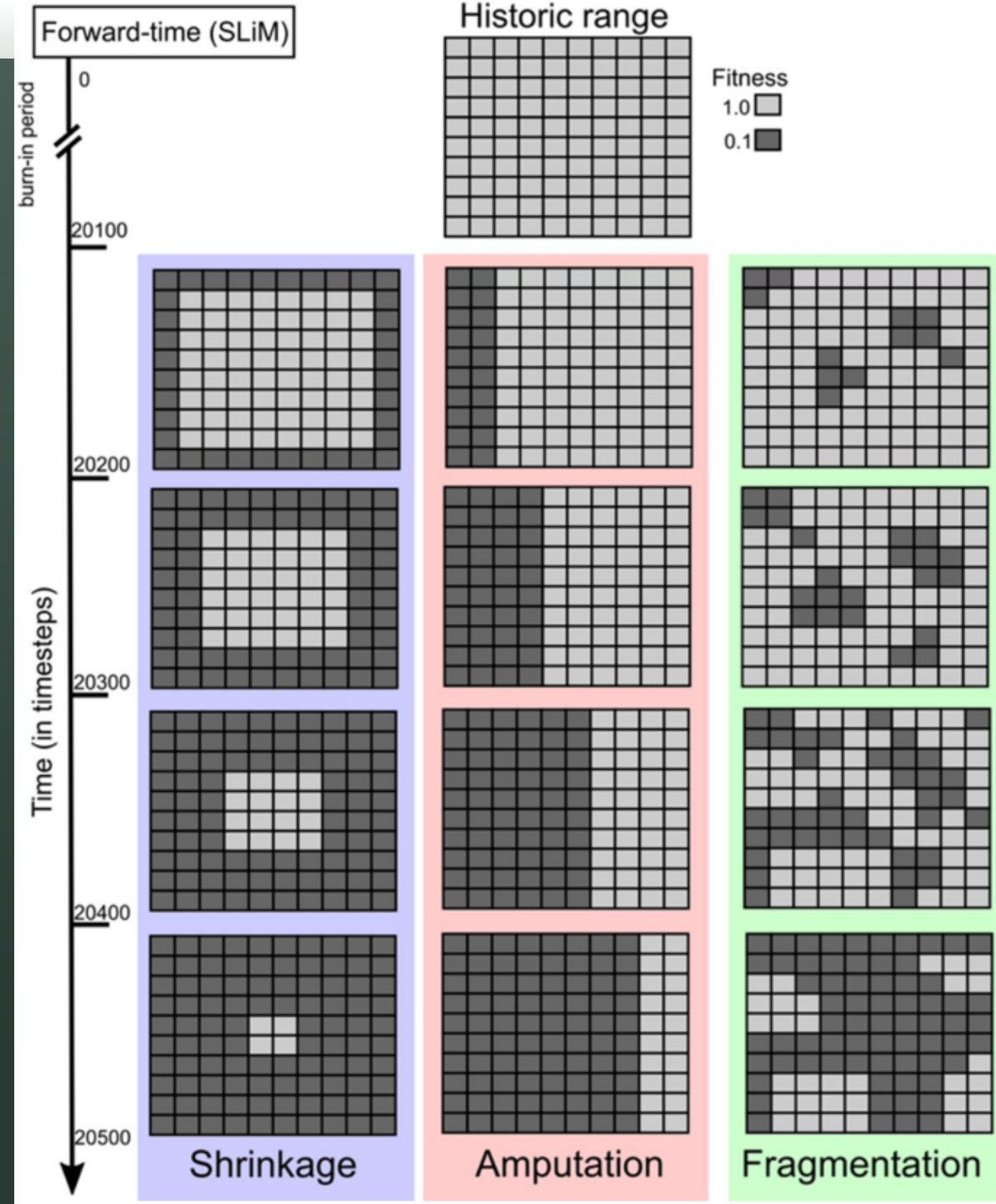


laura.bertola@gmail.com

 [@LauraDBertola](https://twitter.com/LauraDBertola)

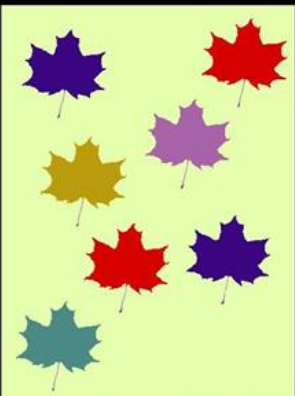
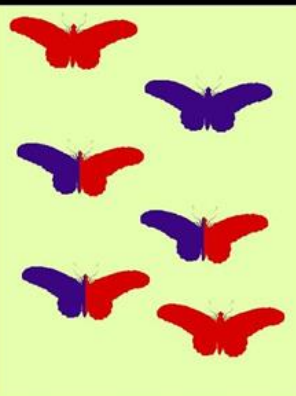
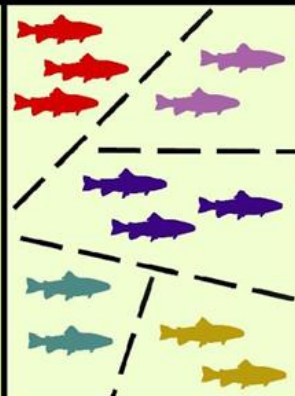
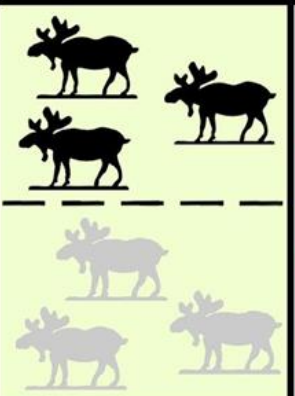
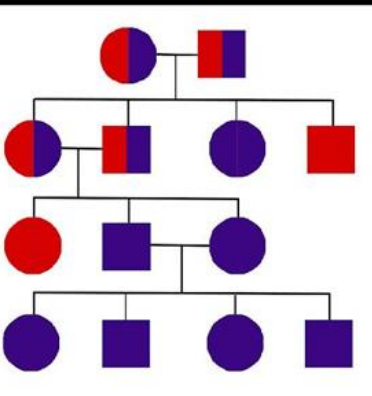
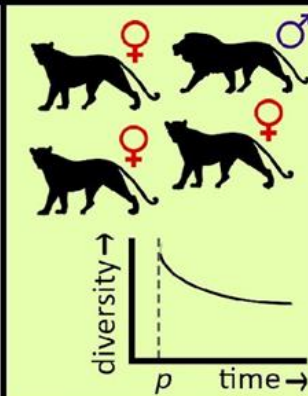
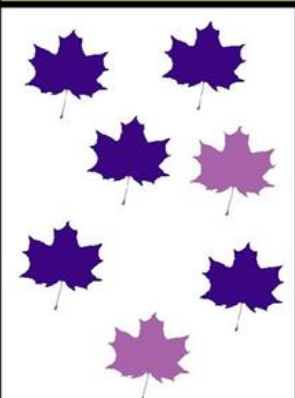
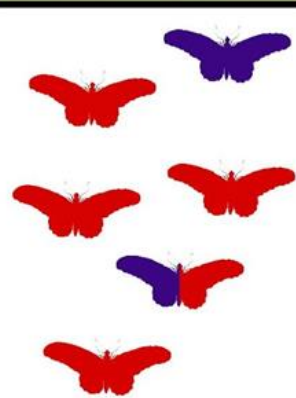
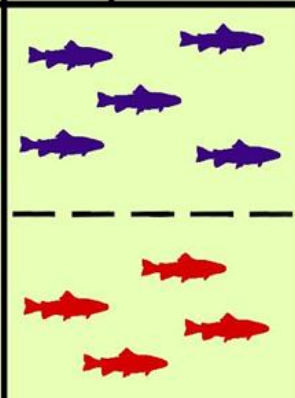
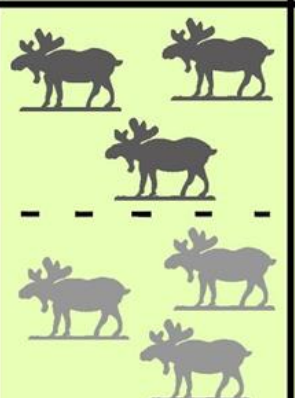
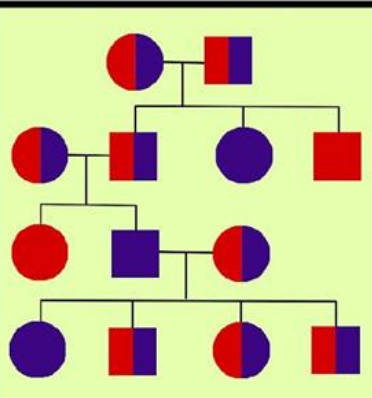
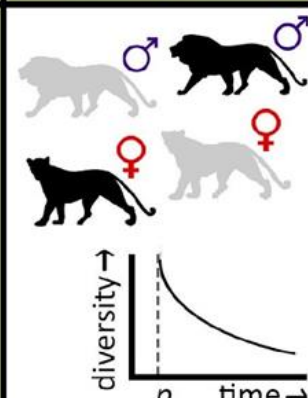
Loss of Biodiversity

- Primarily through loss of populations:
mammals: loss of min. 30% (1900-2015)
almost half: loss of >80%
(Ceballos *et al.*, 2017)
- Not all range loss is equal
(Rogan *et al.*, 2023)



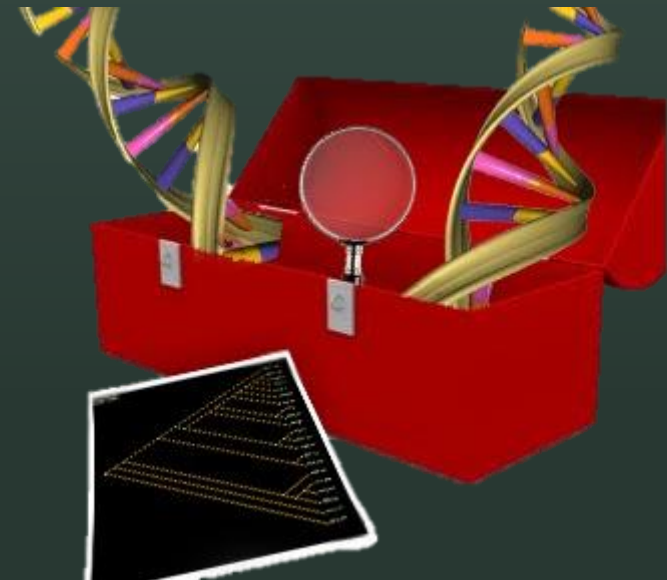
Rogan *et al.*,
2023

Genetic Composition EBVs

	Genetic Diversity		Genetic Differentiation		Inbreeding	Effective Population Size (Ne)
	Richness	Heterozygosity	Number of Genetic Units	Distance Genetic Units		
High						
Low						

Genetic data

- Diversity and connectivity
- Pedigrees, parentage
- Identify individuals (population estimates, individual home ranges)
- Hybridization
- Population history and future trajectory
- Prioritization, e.g. based on uniqueness or adaptive traits



The Expanding Role of Genetics & Genomics in Conservation

**Gordon Luikart,
University of Montana, USA**



Unprecedented Extinctions (2022)

Why be a conservation geneticist?



Approximately 10-30% of all vertebrate and plant species are threatened with extinction over the next few decades.

IUCN (1996, 2008, 2016)



*It will take millions of years to correct the ongoing **loss of genetic** and species **diversity**. This is the folly our descendants are least likely to forgive us.*

Edward O. Wilson (1984)



<https://www.facebook.com/watch/?v=1561429063954907>

<https://earthsky.org/earth/extinct-bird-songs-woodpecker-warbler-kauai-oo/>

LG1
LG2 **Extinctions in 2021**

Genetics has enormous untapped potential to help curb the extinction crisis!

This enormous potential of genetics results from...



Smooth handfish



Slide 3

LG1 Luikart, Gordon, 7/22/2023

LG2 smoot
Luikart, Gordon, 7/22/2023

A combination of advances in three areas

DNA sampling

Noninvasive field
sampling, eDNA
museum sampling

(Beja-Pereira et al. 2009)

Genotyping

Unlimited,
informative
DNA markers
(IcWG-seq)

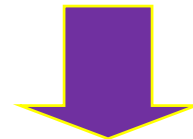
Data analysis

Statistical
methods,
models, &
approaches

(Hemstrom et al. in review)



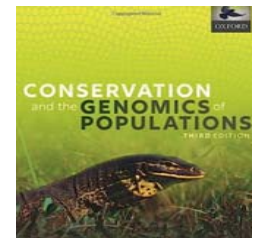
= Information explosion!



Improved conservation and management

**Communication with managers, public,
and policy makers is crucial!**

(Chap 24 in Allendorf et al. 2022)



You & genetics can contribute in many ways!

- 1) Genetic diversity, inbreeding, & genetic rescue
- 2) Census & effective population size (past & present)
- 3) Population structure, units (CUs/MUs/ESUs)
- 4) Connectivity: geneflow & dispersal (past & present)
- 5) Local adaptation & selection
- 6) Phylogenetics, hybridization, outbreeding depression
- 7) Forensics, genetic identification, & law enforcement
- 8) Disease ecology & transmission
- 9) Community genomics (interactions improve cons)

*Uses for **ecology & demography** versus **gene diversity** *per se*

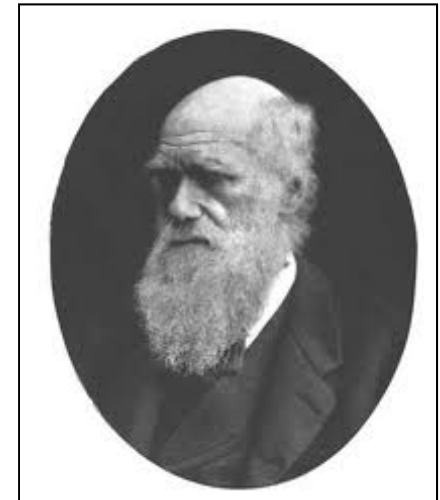
Genes

Ecosystems



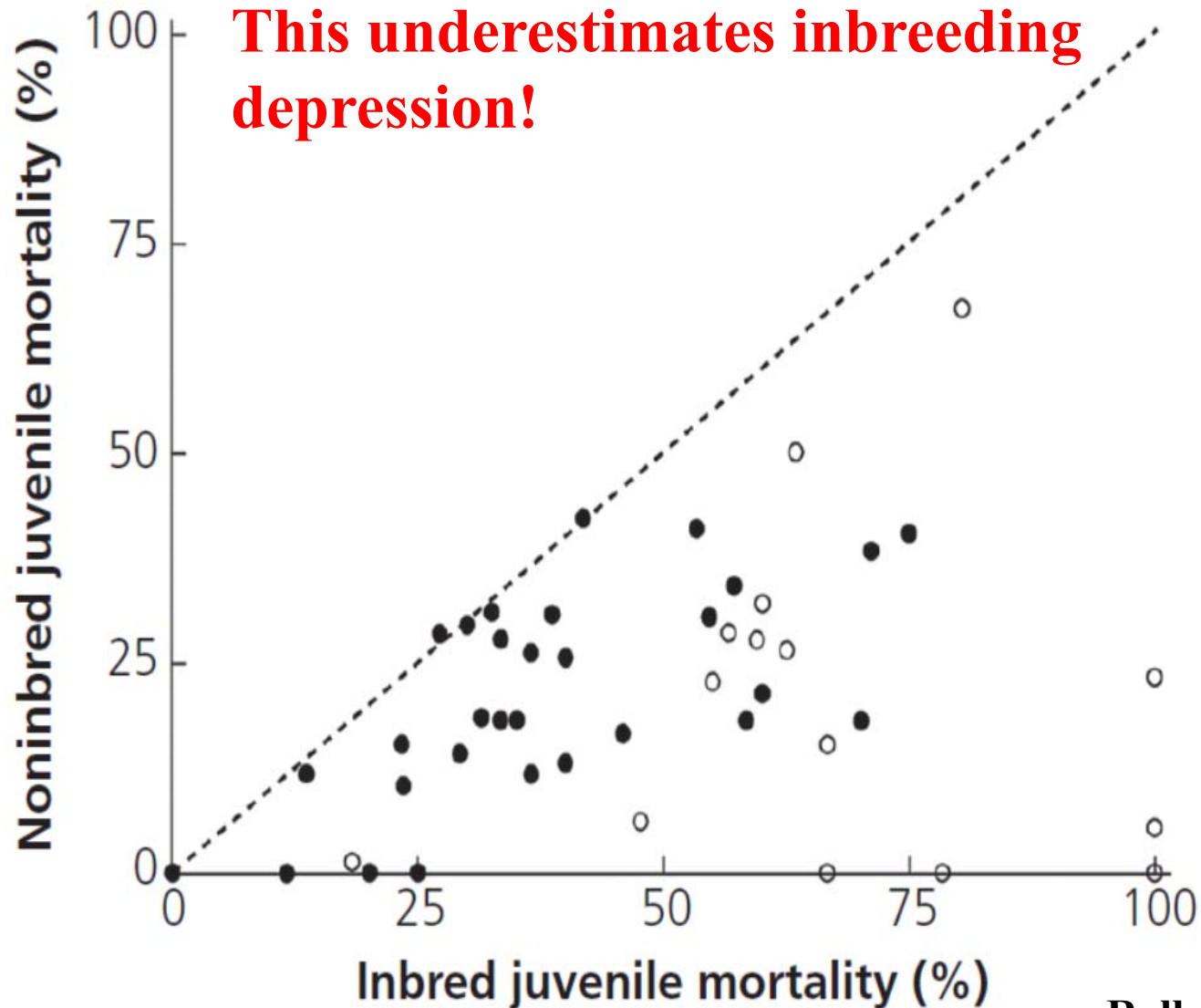
Conservation genetics and inbreeding avoidance has been practiced for >100 years!

As some of our British parks are ancient, it occurred to me that there must have been long-continued close interbreeding with the fallow-deer (*Cervus dama*) kept in them; but on inquiry I find that it is a common practice to infuse new blood by procuring bucks from other parks.



Married his cousin!

Inbreeding reduces individual fitness!

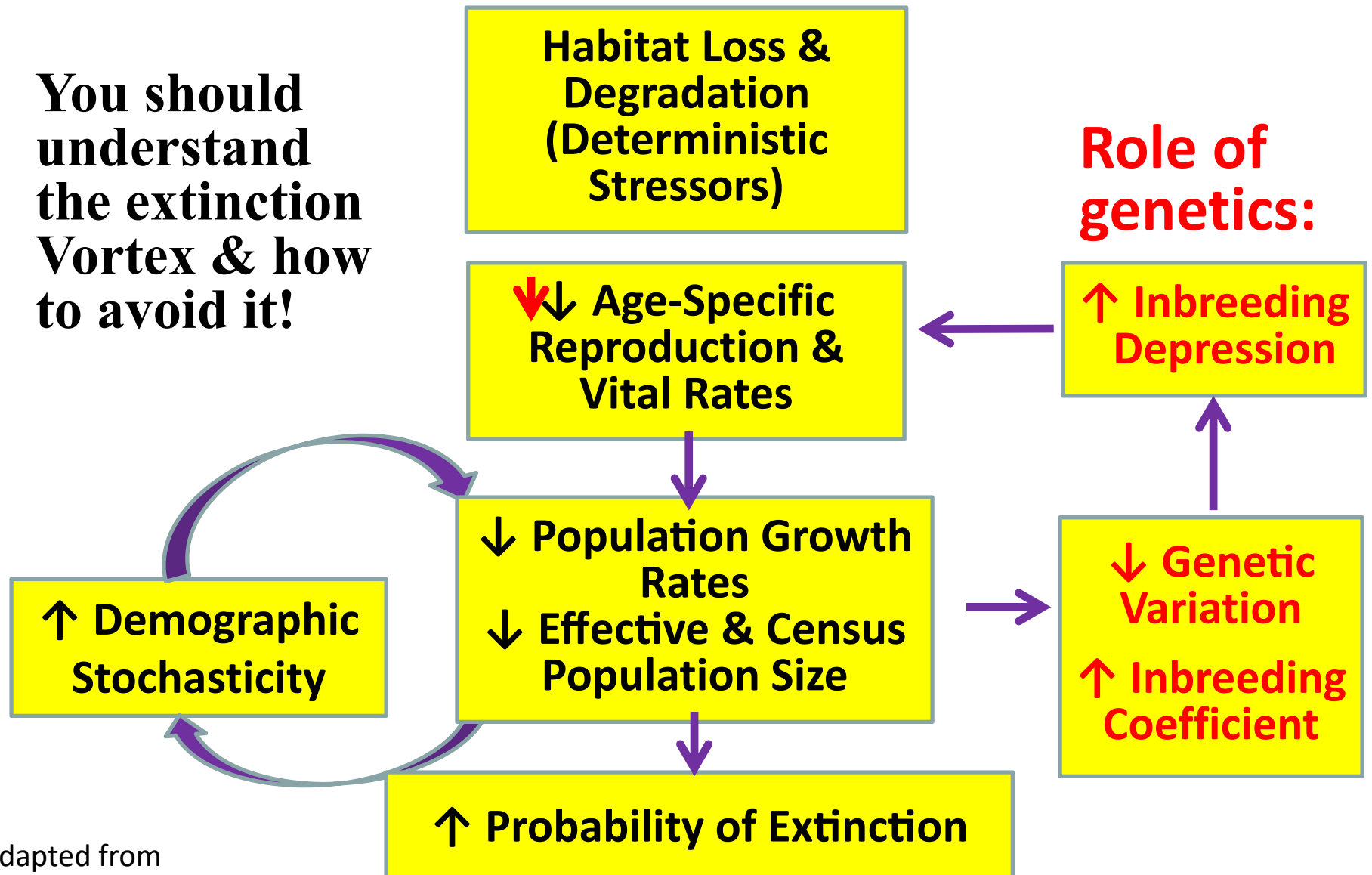


Each circle is one of 44 captive populations of mammals (16 ungulates, 16 primates, and 12 small mammals).

The line shows equal mortality in inbred and non-inbred progeny.

Loss of variation reduces population persistence

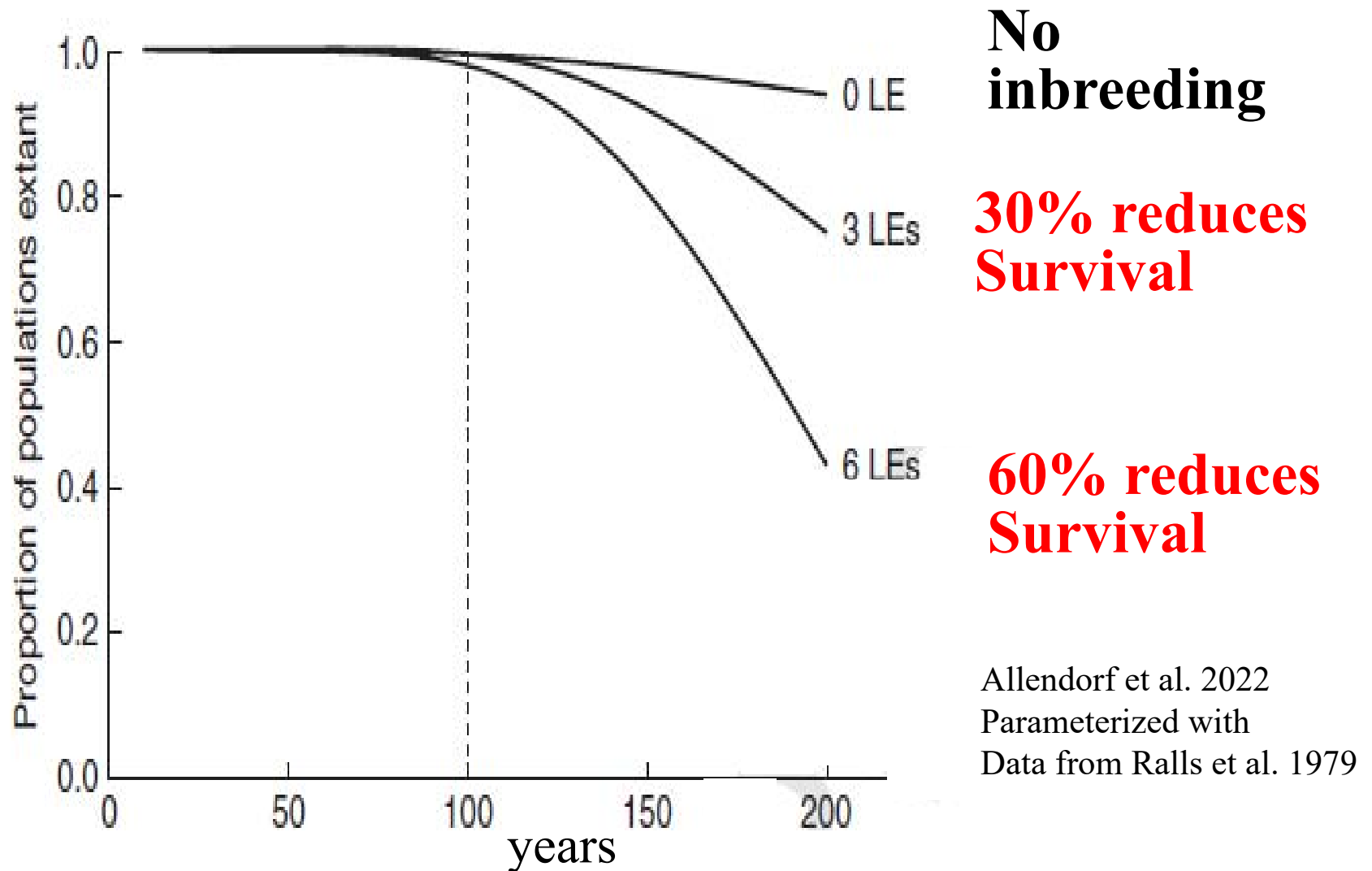
You should understand the extinction Vortex & how to avoid it!



Adapted from
Mills & Soule 1998, *Science*

PVA Simulations (**with genetics!**)





Inbreeding depression can reduce population persistence



Vortex sims of Yellowstone Grizzly population. Inbreeding reduced Juvie survival

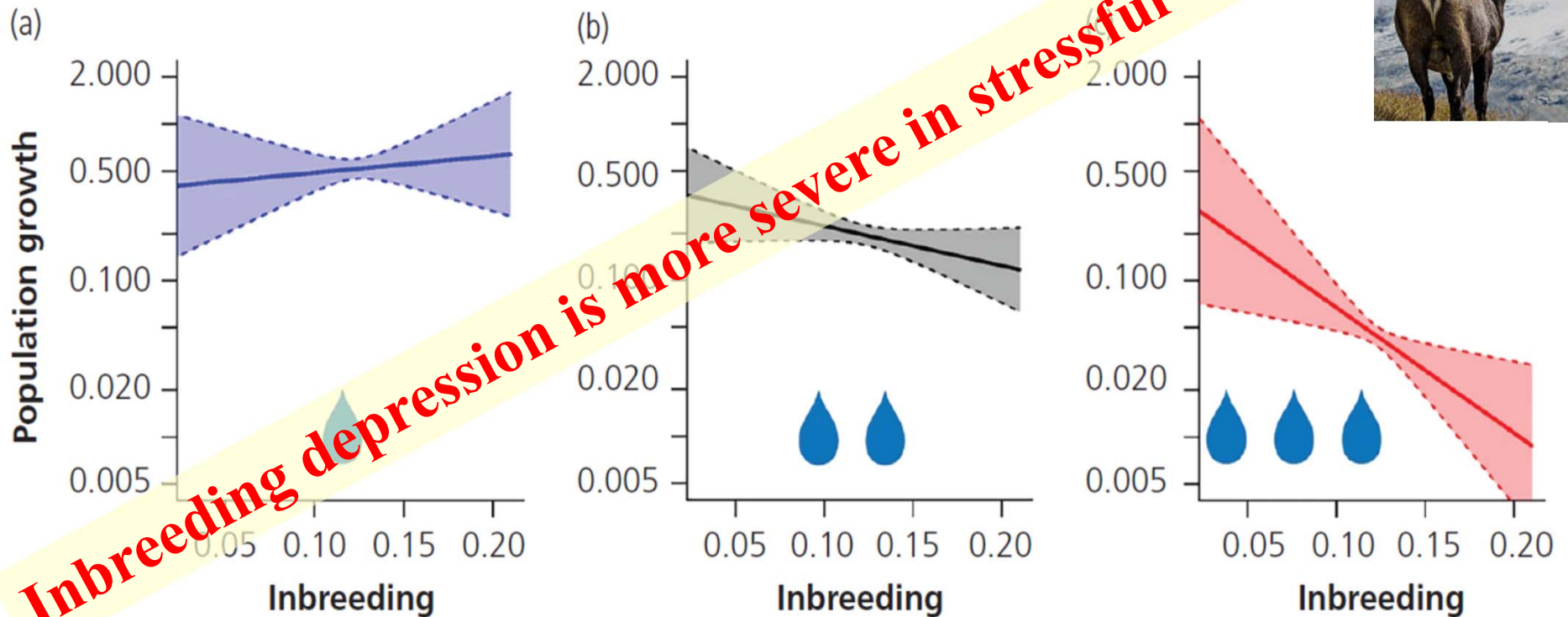
Empirical study 2019

Inbreeding reduces long-term growth of Alpine ibex populations

Claudio Bozzuto ^{1,5,6}, Iris Biebach ^{1,6}, Stefanie Muff ^{1,2}, Anthony R. Ives ^{3*} and Lukas F. Keller ^{1,4*}

Many studies document negative inbreeding effects on individuals, and conservation efforts to preserve rare species routinely employ strategies to reduce inbreeding. Despite this, there are few clear examples in nature of inbreeding decreasing the growth rates of populations, and the extent of population-level effects of inbreeding in the wild remains controversial. Here, we take advantage of a long-term dataset of 26 reintroduced Alpine ibex (*Capra ibex ibex*) populations spanning nearly 100 years to show that inbreeding substantially reduced per capita population growth rates, particularly for populations in harsher environments. Populations with high average inbreeding ($F \approx 0.2$) had population growth rates reduced by 71% compared with populations with no inbreeding. Our results show that inbreeding can have long-term demographic consequences even when environmental variation is large and deleterious alleles may have been purged during bottlenecks. Thus, efforts to

Inbreeding depression reduces population growth rates in alpine ibex




Best-fitting statistical model relating population growth to average inbreeding in interaction with summer precipitation. From 26 reintroduced populations. Population-specific F (inbreeding) computed from microsatellites.

Cautionary note:

 PERSPECTIVE PNAS 2021

The inflated significance of neutral genetic diversity in conservation genetics

João C. Teixeira^{a,b,1}  and Christian D. Huber^{a,1} 

“We argue against the perceived importance of neutral genetic diversity of the conservation of wild populations and species”

The crucial role of genome-wide genetic variation in conservation

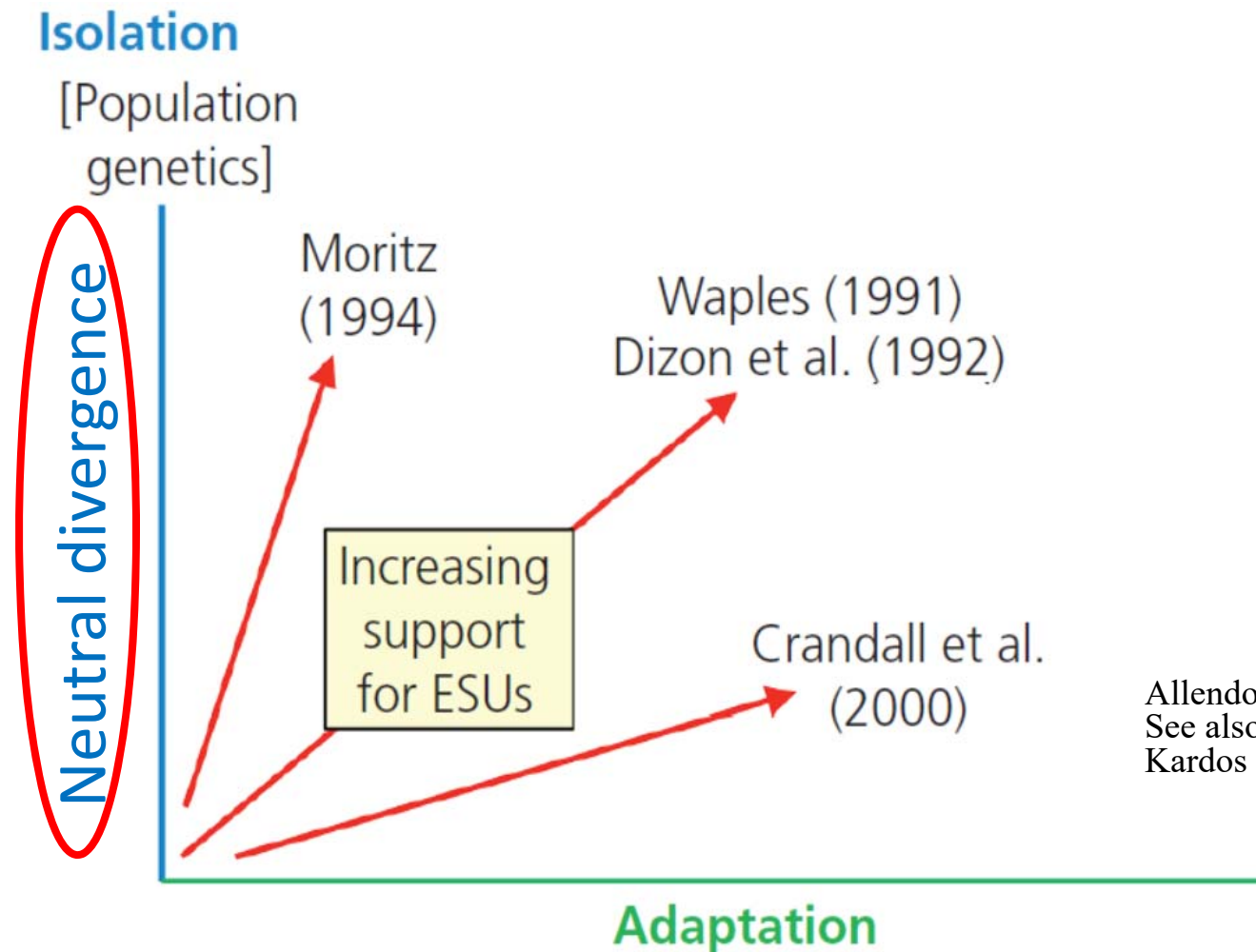
PNAS 2021

Marty Kardos^{a,1} , Ellie E. Armstrong^b , Sarah W. Fitzpatrick^{c,d,e} , Samantha Hauser^f, Philip W. Hedrick^g, Joshua M. Miller^{h,i,j} , David A. Tallmon^k, and W. Chris Funk^l 

The unprecedented rate of extinction calls for efficient use of genetics to help conserve biodiversity. Several recent genomic and simulation-based studies have argued that the field of conservation biology has placed too much focus on conserving genome-wide genetic variation, and that the field should instead focus on managing the subset of functional genetic variation that is thought to affect fitness. Here, we critically evaluate the feasibility and likely benefits of this approach in conservation. We find that population genetics theory and empirical results show that conserving genome-wide genetic variation is generally the best approach to prevent inbreeding depression and loss of adaptive potential from driving populations toward extinction. Focusing conservation efforts on presumably functional genetic variation will only be feasible occasionally, often misleading, and counterproductive when prioritized over genome-wide genetic variation. Given the increasing rate of habitat loss and other environmental changes, failure to recognize

Why conserve genome-wide neutral diversity first, then consider adaptive variation?

ESU or Distinct Population ID has 2 main requirements/axes



Allendorf et al. 2022;
See also Hoffman et al. 2016
Kardos et al. 2021

Big picture

Why learn population genetics?

It's one of 3 key disciplines in Conservn. Biology

Evolution (= population genetics)

Ecology

Human dimensions

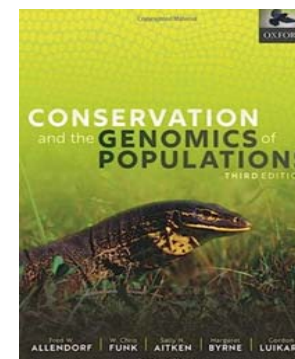
Groom, Meffe, Carroll 2007. Book

Why learn population genetics?

24.4.1 What is a conservation geneticist?

First and foremost, a good conservation geneticist is a population geneticist. To be effective in conservation genetics requires numerous other skills, but underlying all of those has to be a firm knowledge and understanding of genetic theory. This is non-negotiable and means that if you have an interest in applying genetics to conservation, it would be helpful to seek out a graduate training program featuring modules in population genetics. As a graduate student, you need at least one supervisor/advisor who specializes in the subject. Graduate students

Helen Taylor, Chapter 24 in Allendorf et al. (2022) book



Why learn population genetics theory?

American Genetic Association

Testing for Hardy–Weinberg Proportions: Have We Lost the Plot?

ROBIN S. WAPLES 2015

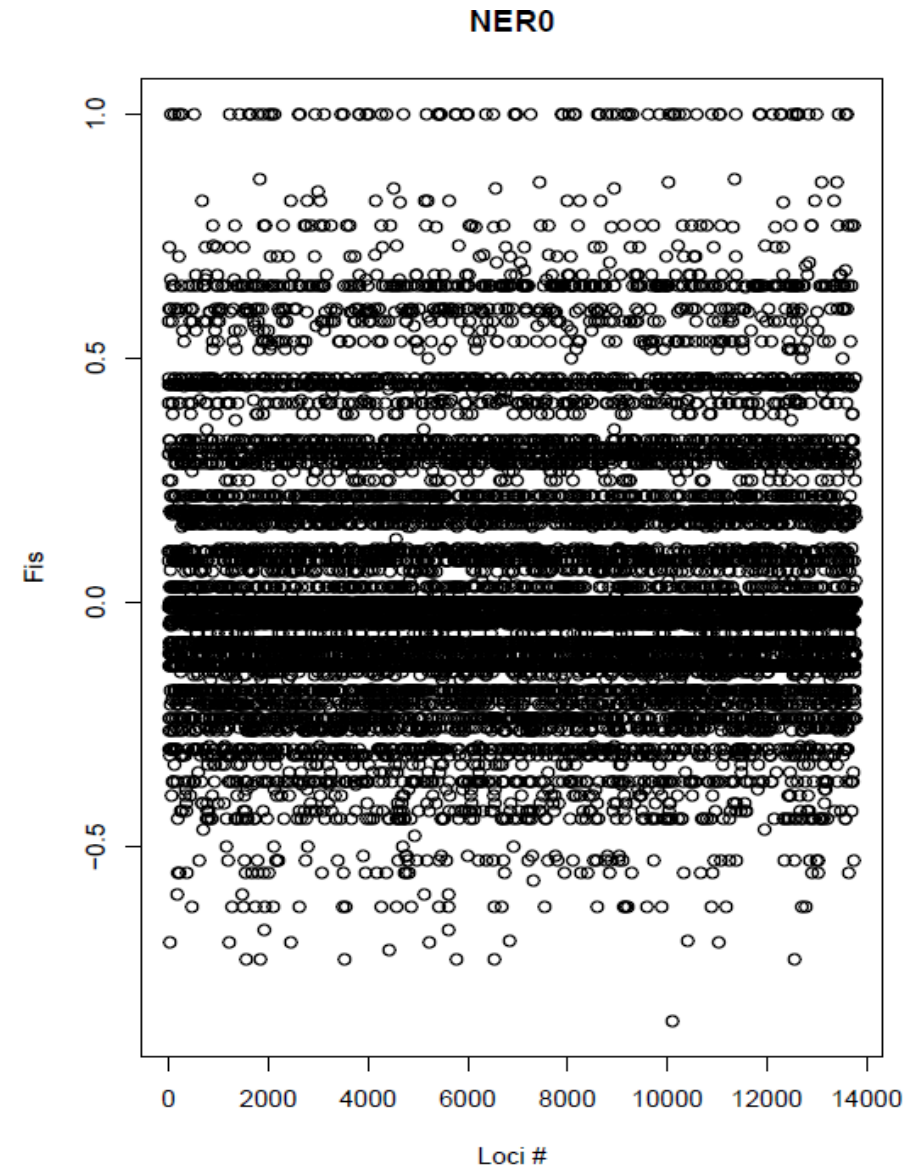
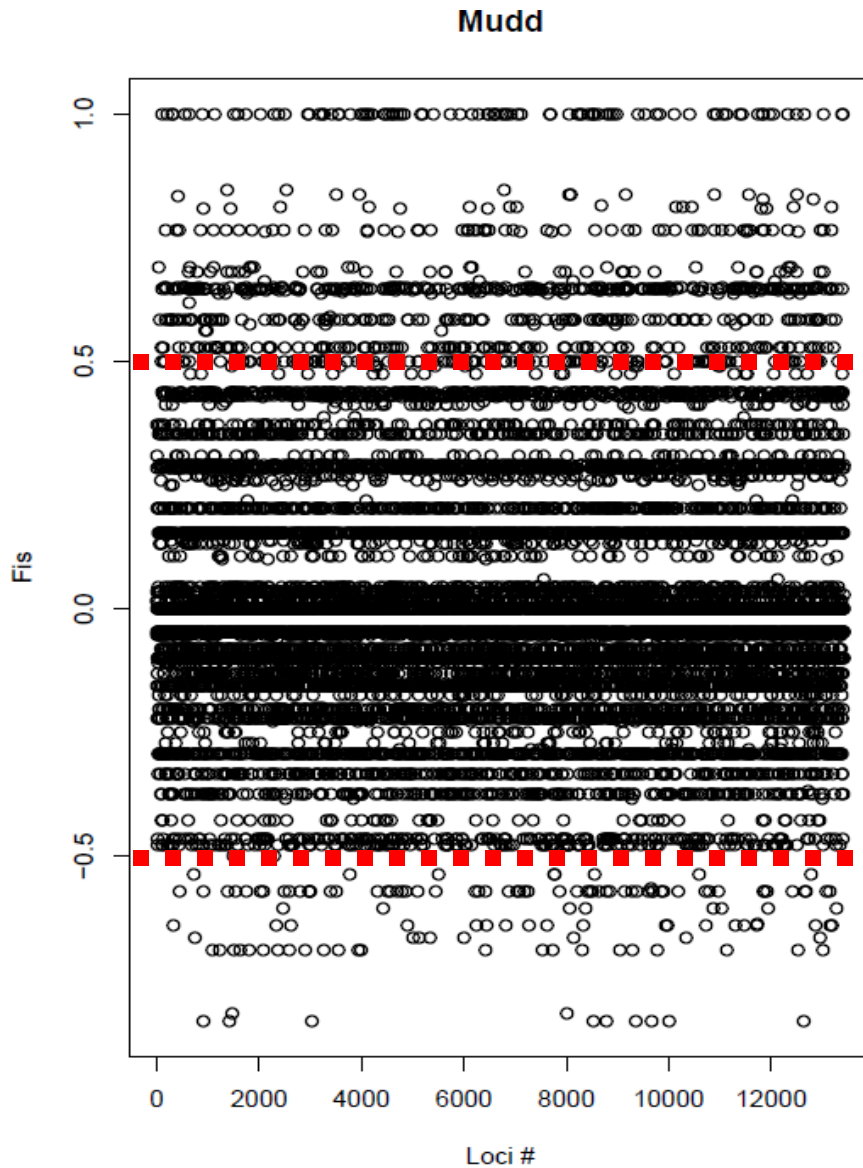
From the Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric

I am constantly appalled in reviewing manuscripts and even published papers to see people go through the motions of performing all the HW and LD tests, reporting the results, and then completely ignoring them, even when significant deviations are found. **Few people know how to properly interpret multiple testing results, and most seem to have lost track of why it is essential to do these tests before using the data for other analyses.**

See Sethuraman et al. 2019, Mol. Ecol. Res.

Why learn coding, line commands, & R?

To *analyze* NGS data (F_{IS} at 14,000 RAD SNPs in elk!)



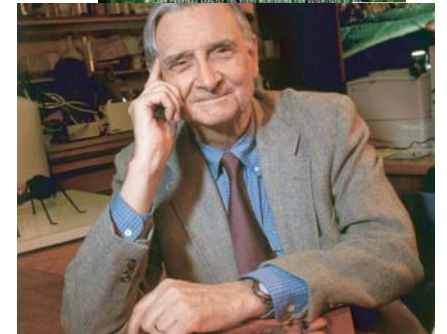
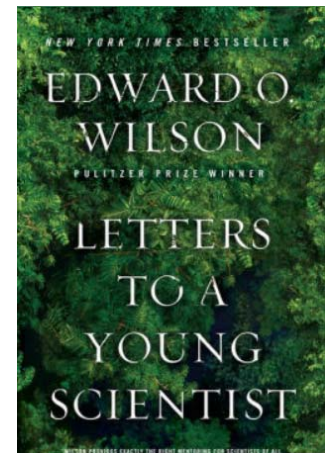
Do not be intimidated by math or coding

“Most successful scientists are only moderately literate in math.” ...Especially those who are most creative, visionary, who **advance their field.**

(Chapter 2 “Mathematics” in Wilson 2002)

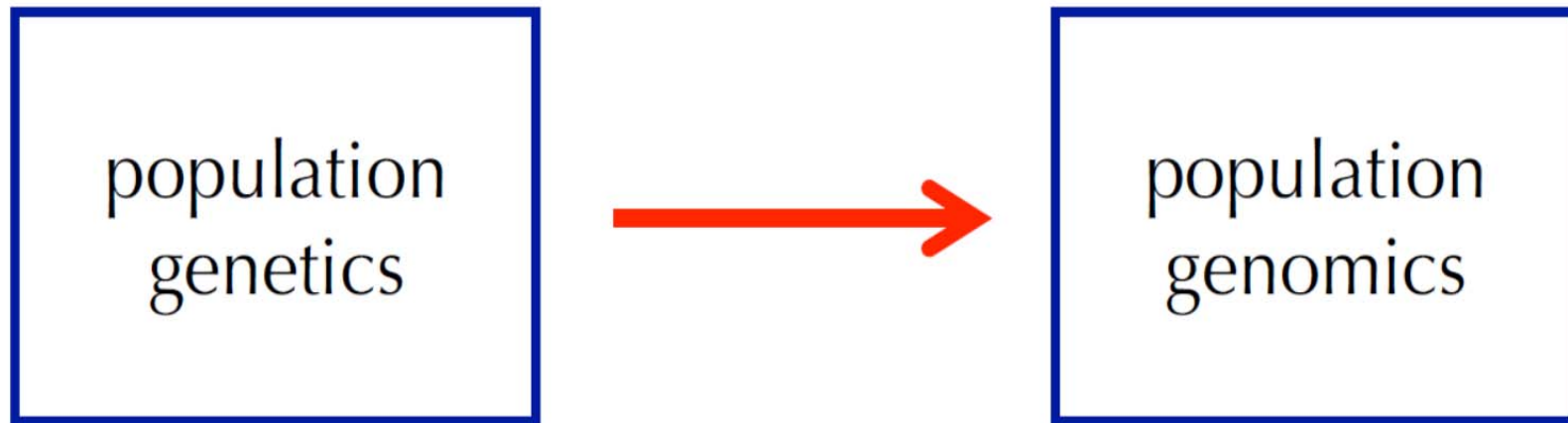
“Work ethic, passion, and collaboration are as important or more important...”

(Chapter 6 “What it takes”; Wilson 2002)



What is conservation genomics?

Application of genomic techniques in conservation



What is conservation genomics?

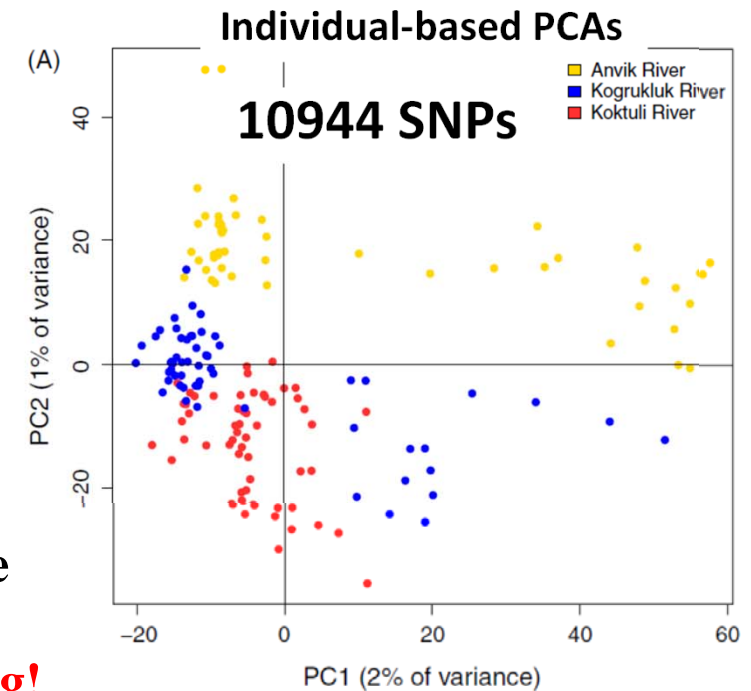
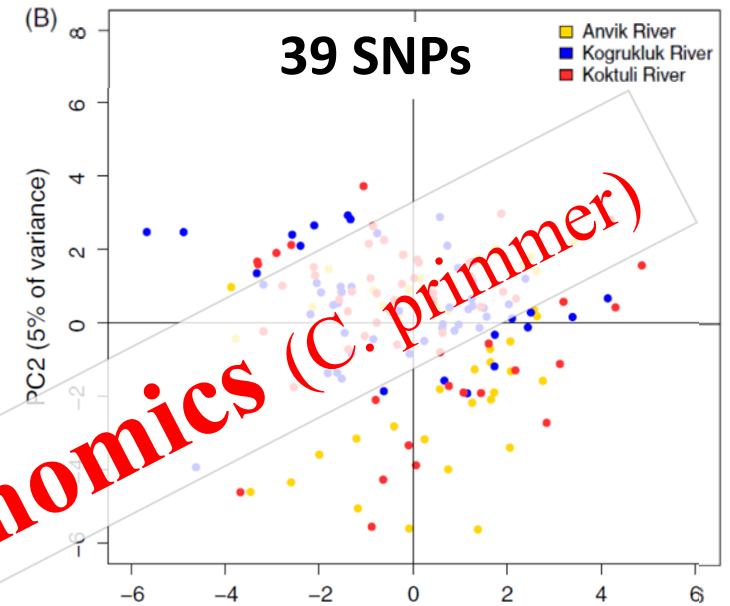
‘Better’ definition (“narrow-sense genomics”)

- address questions impossible with genetics alone
- functionally important loci
 - adaptive or deleterious vs neutral
 - associated with phenotypes (GWAS etc.)

Garner et al (2016) *TREE* 31: 81

Hohenlohe et al (2018) *Population Genomics* (Rajora OP, ed)

More loci improve substructure resolution (often impossible w/o genomics)



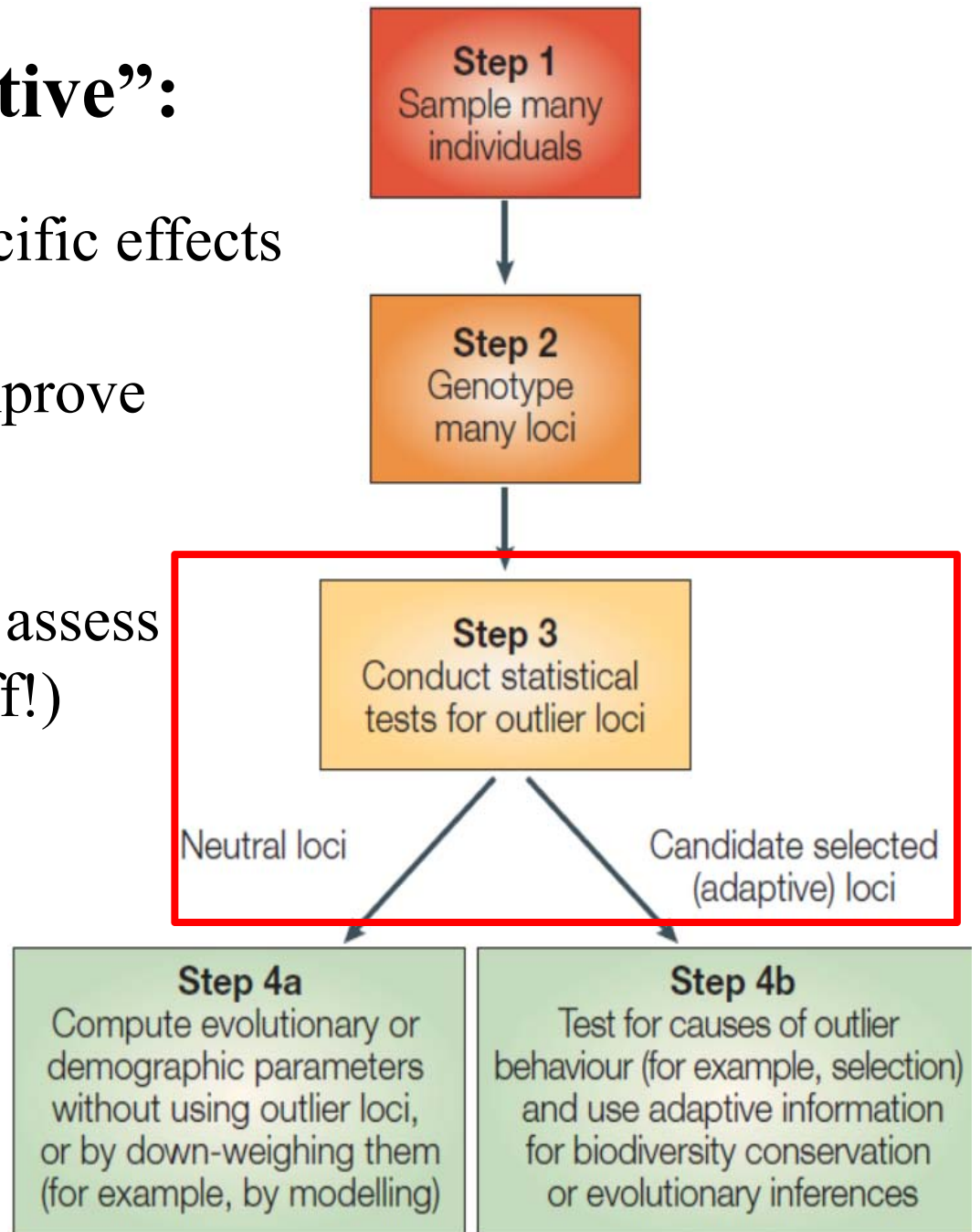
Using only 100 “informative” loci can also improve resolution!

So, won't need genomics for subsequent monitoring!

Larson et al. 2013. Evol Apps.

A “Genomics perspective”:

- Genome-wide vs locus-specific effects
- Remove adaptive loci to improve parameter estimation
- Use outlier/adaptive loci to assess function (the exciting stuff!)



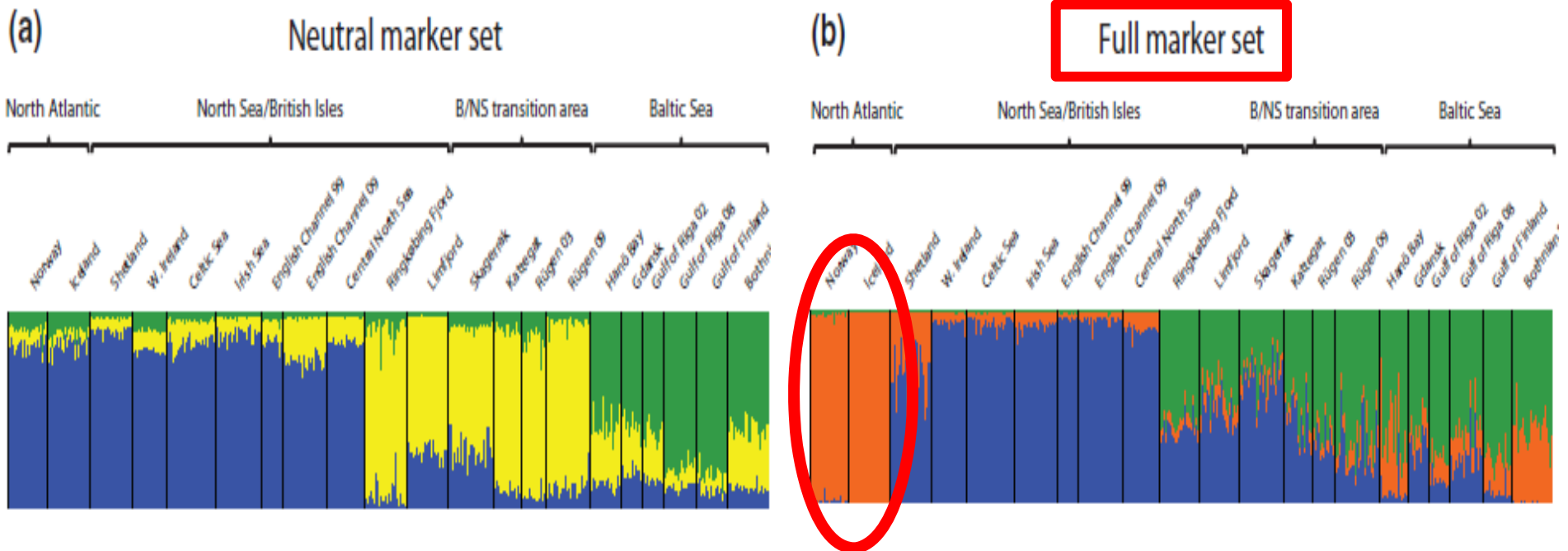
Use of Adaptive loci

MOLECULAR ECOLOGY

Molecular Ecology(2012) 21, 3686–3703

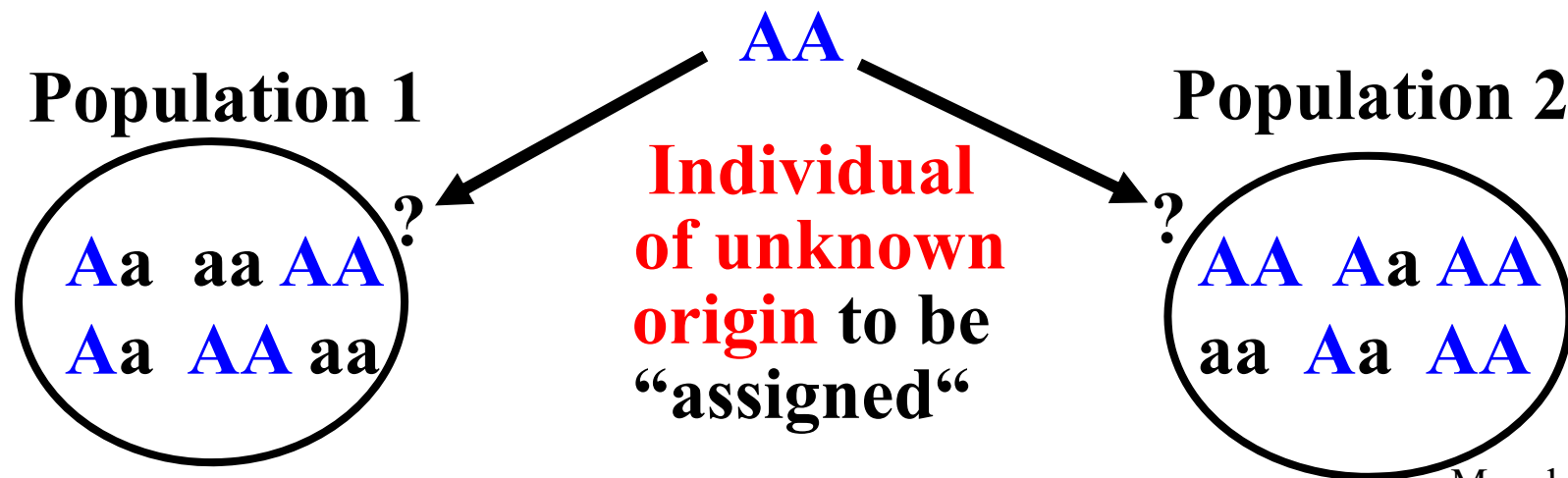
Environmental selection on transcriptome-derived SNPs in a high gene flow marine fish, the Atlantic herring (*Clupea harengus*)

MORTEN T. LIMBORG,*¹ SARAH J. HELYAR,†¹ MARK DE BRUYN,† MARTIN I. TAYLOR,†

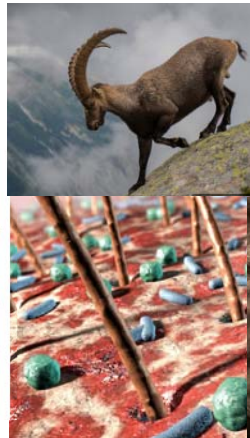


Genomics (adaptive loci) identify a cryptic adaptively-differentiated pop!

Assignment tests (using **informative** loci) help detect wildlife poaching and identify immigrants



Manel et al. 2002



AUTHOREA Pre-print 2023

Low-coverage whole-genome sequencing for highly accurate population assignment: Mapping migratory connectivity in the American redstart (*Setophaga ruticilla*)



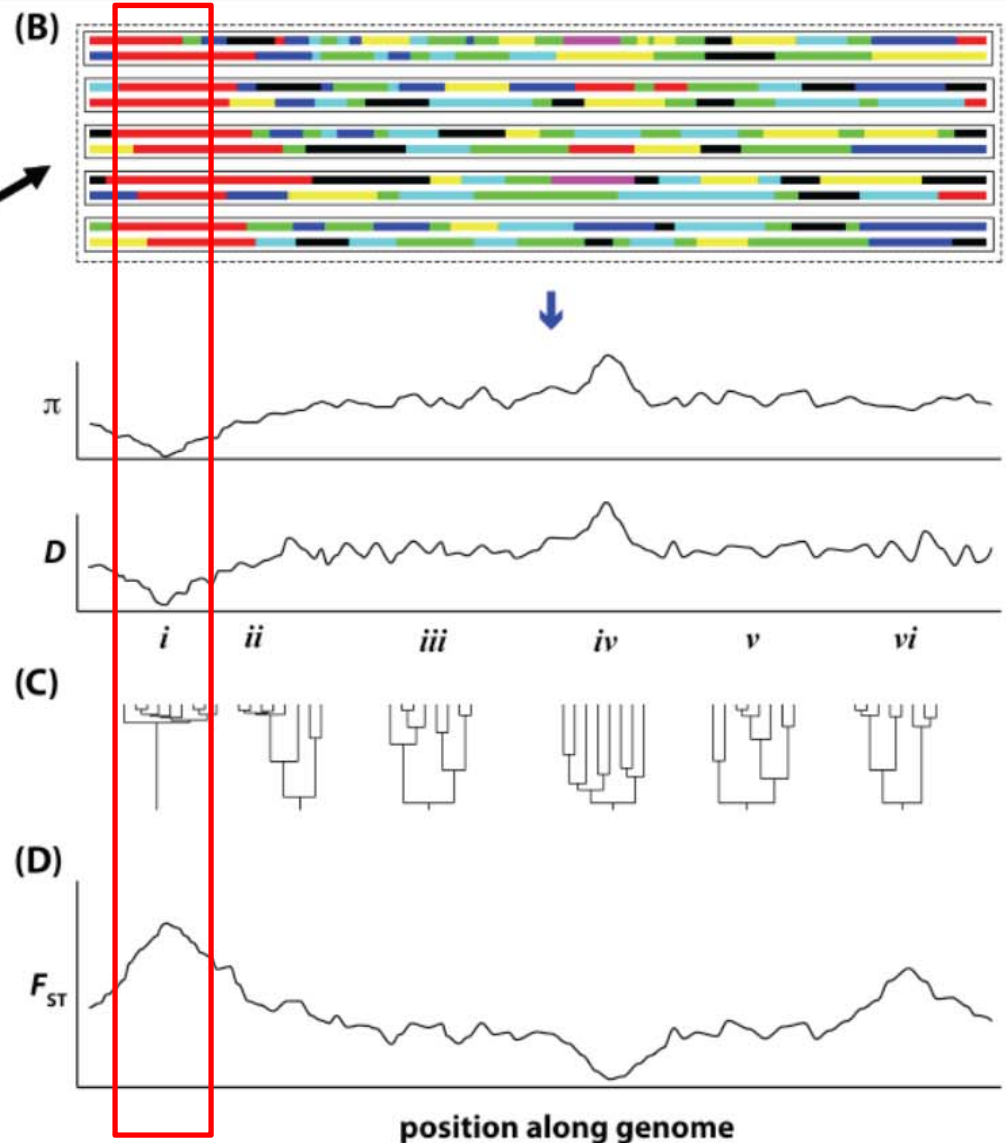
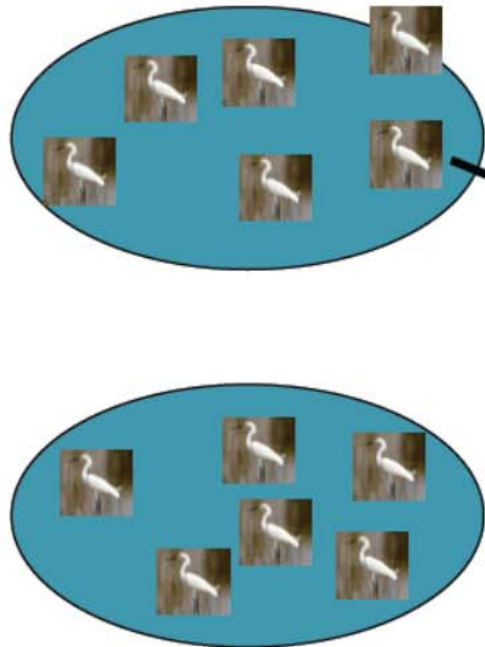
Matthew DeSaix¹, Eric Anderson², Christen Bossu¹, Christine Rayne³, Teia Schweizer Nicholas Bayly⁴, Darshan Narang⁵, Julie Hagelin⁶, H. Lisle Gibbs⁷, James Saracco⁸, Thomas W Sherry⁹, Michael Webster¹⁰, Thomas Smith¹¹, Peter Marra¹², and Kristen Ruegg¹

“We use lcWGS to identify fine-scale population structure of the American Redstart, and accurately assign individuals (>98%) to breeding populations.”

Down-sampling from 1.7x to 0.1x & 0.01x achieved high assignment accuracy!



A genomics perspective: sum stats along the genome



“Population genomics takes data on **haplotypes** within a population and calculates summary statistics as continuous variables along the length of the genome.”

Conclusions & summary

It's an exciting time to be a conservation geneticist!

Use new methods with caution - evaluations are needed!

Know genetics theory & perspectives

Biodiversity conservation needs you!

Thank you! Questions?

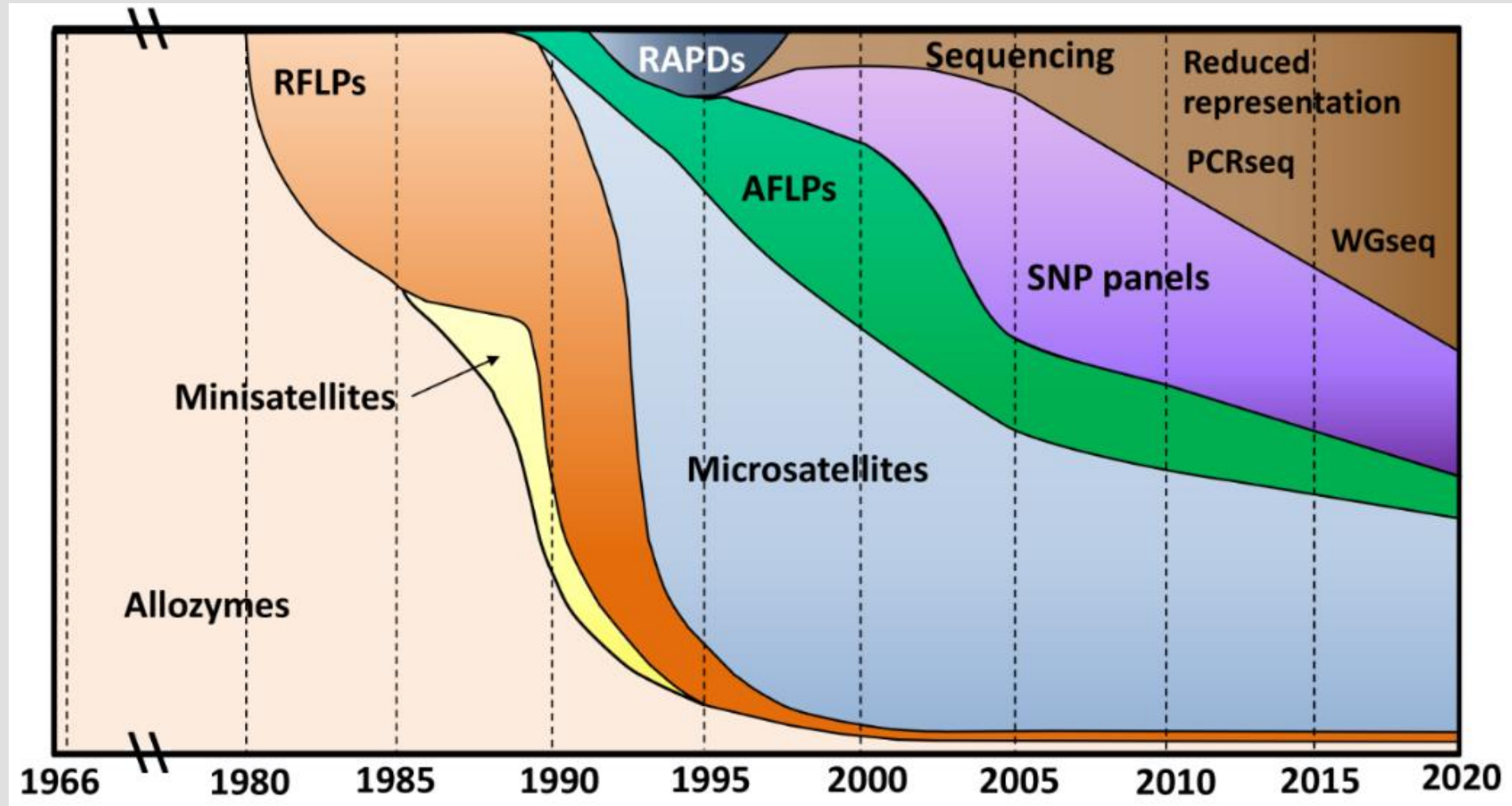


Genetics and Genomics: Data Types

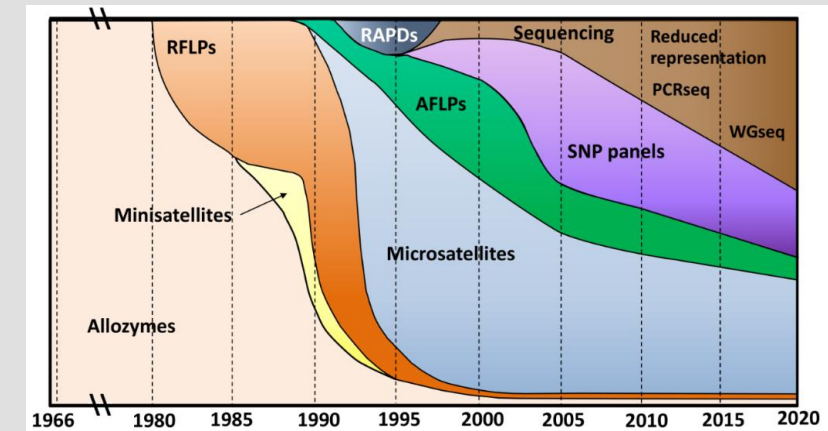
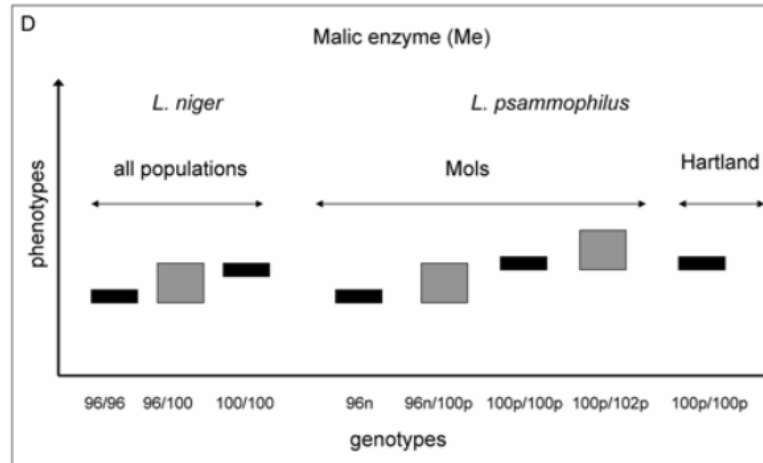
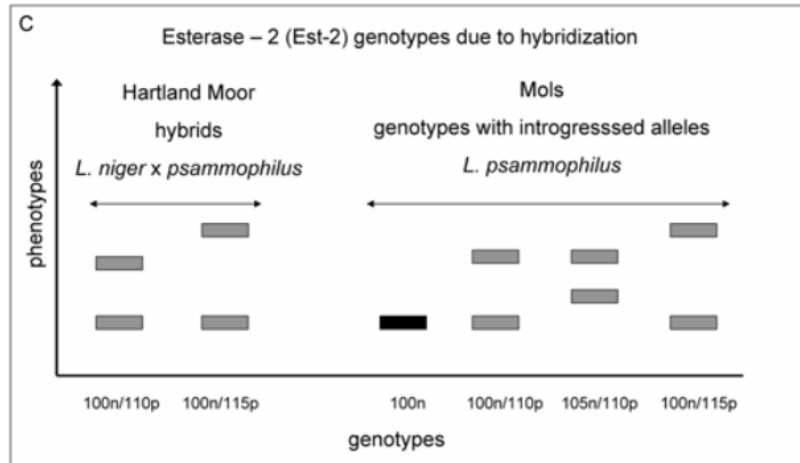
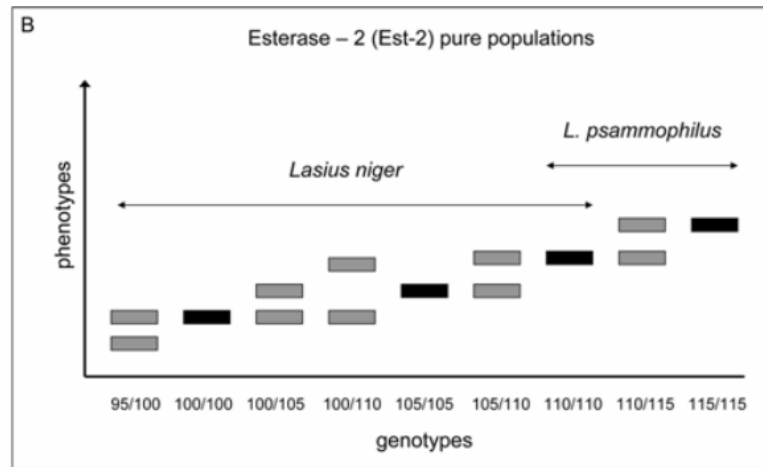
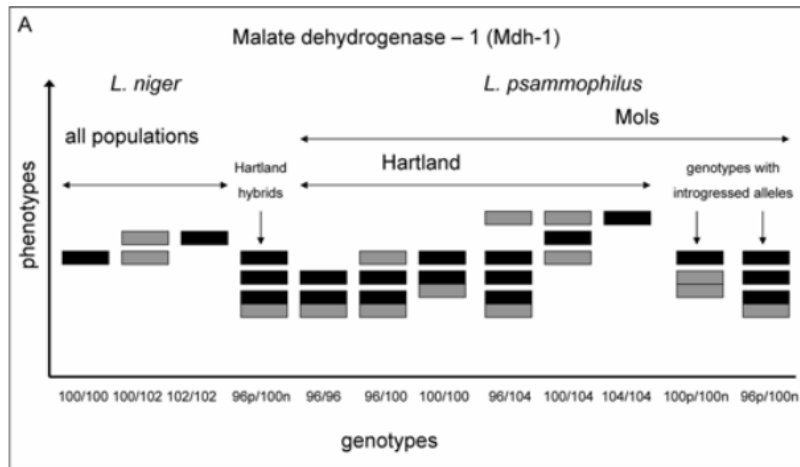
William Hemstrom



Genetics and Genomics: Data Types



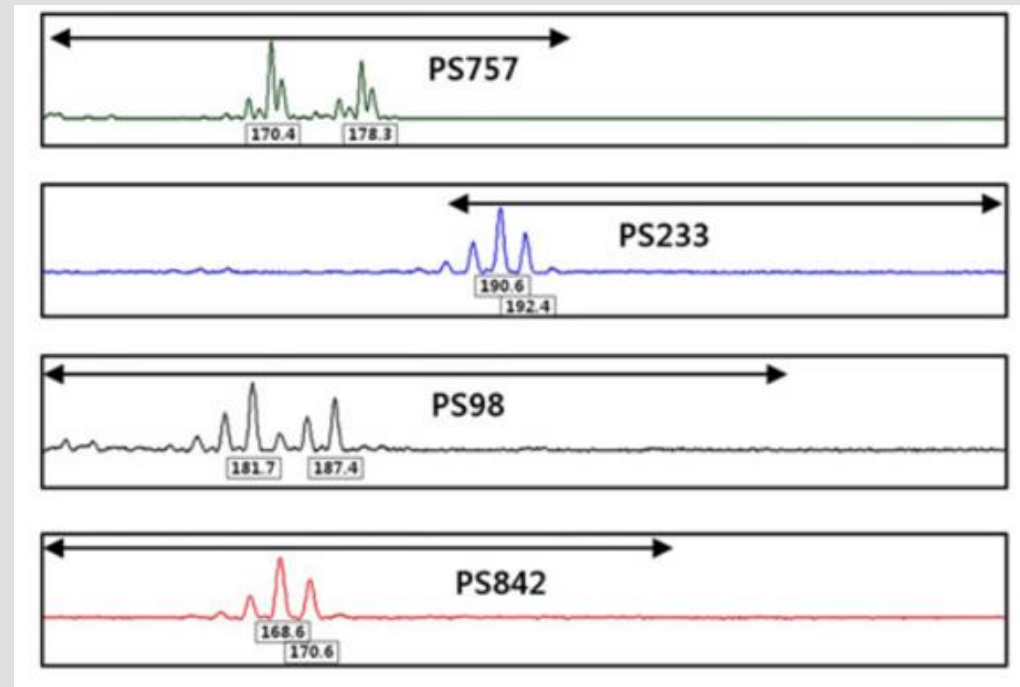
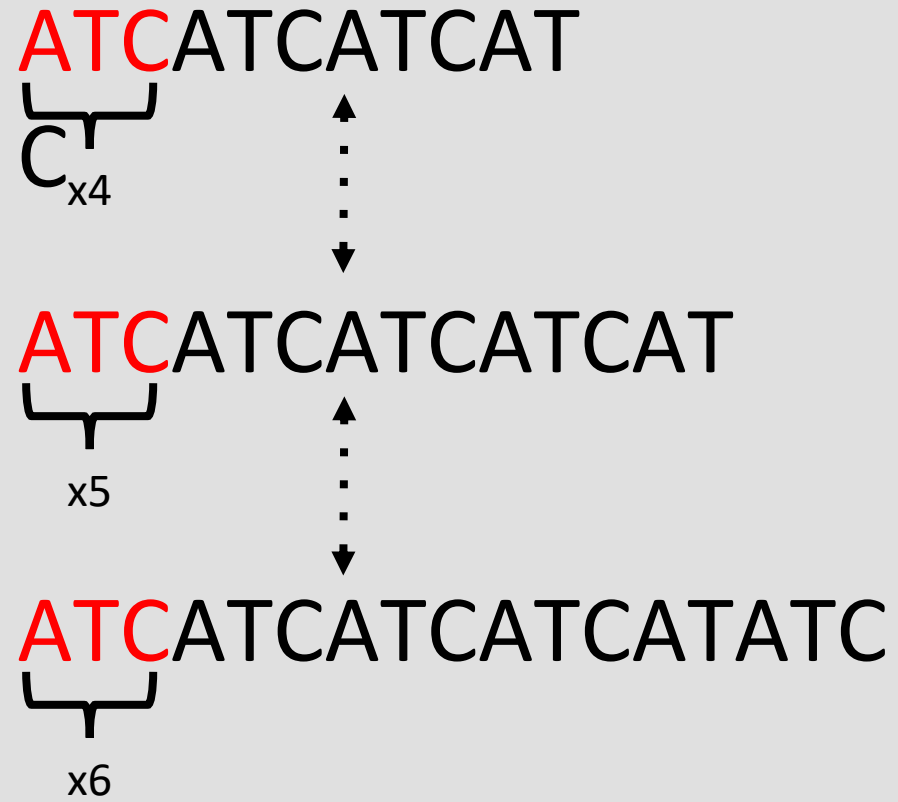
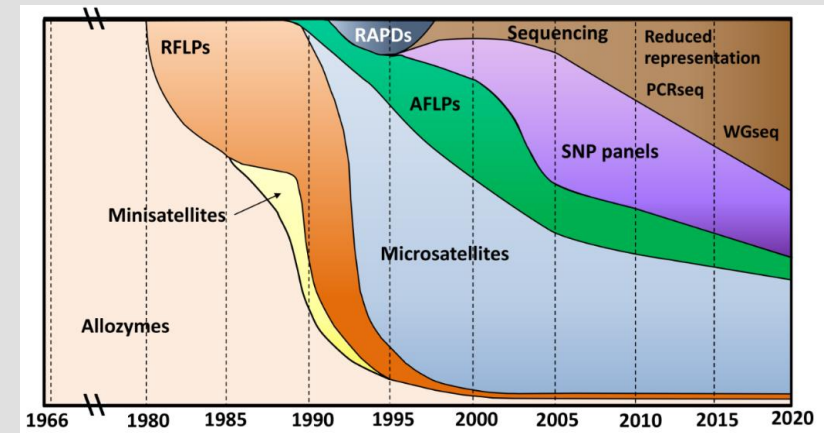
Allozymes and RFLPs



CTGACG
GCAGTC

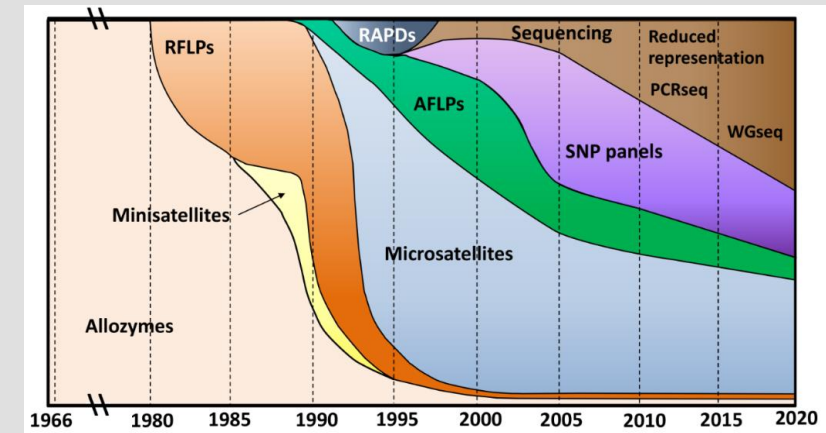
- Enzyme configuration differences (allozymes)
- Restriction fragment length differences (RFLPs)
- Both old, rare today.
- Low power.
- 5-20 loci

Microsatellites



Lee et al 2011

Microsatellites



ATCATCATCAT

C_{x4}



ATCATCATCATCAT

$x5$

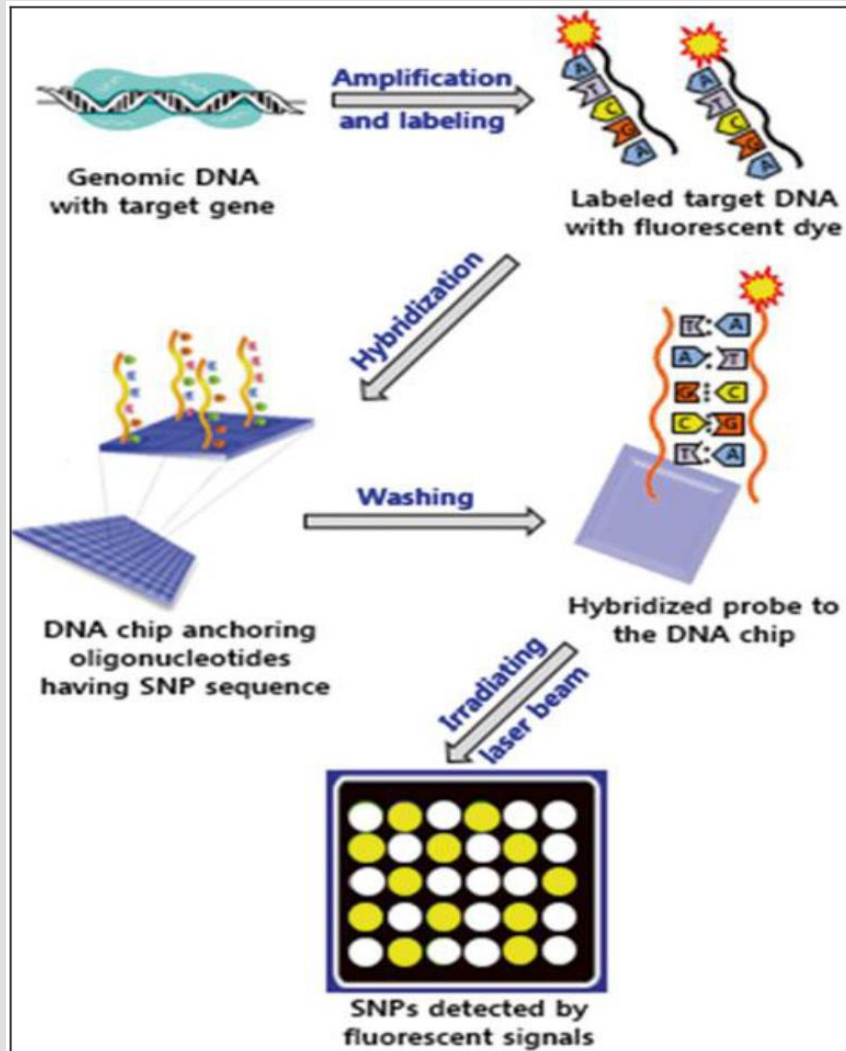


ATCATCATCATCATATC

$x6$

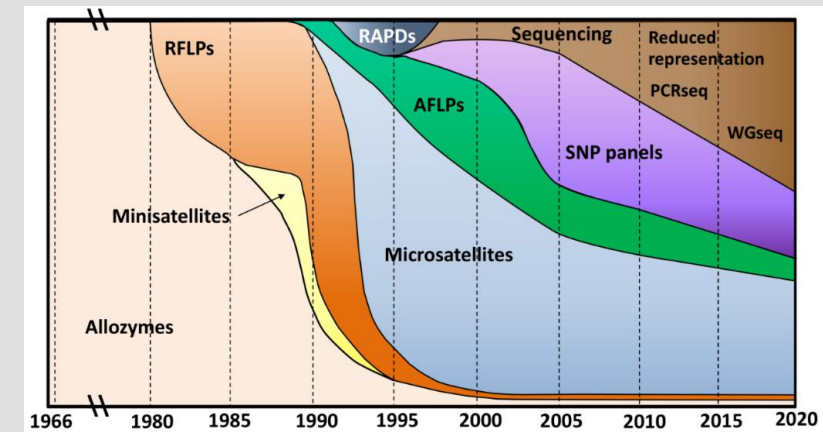
- Variable length repeats
- Highly polyallelic
- Easy
- Cheap
- 5-20 loci
- Still used today!

SNP panels/SNP chips



Mishra et al 2017

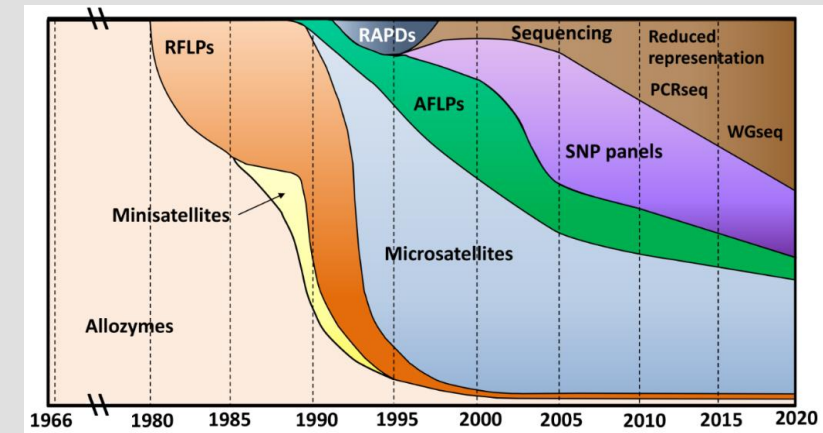
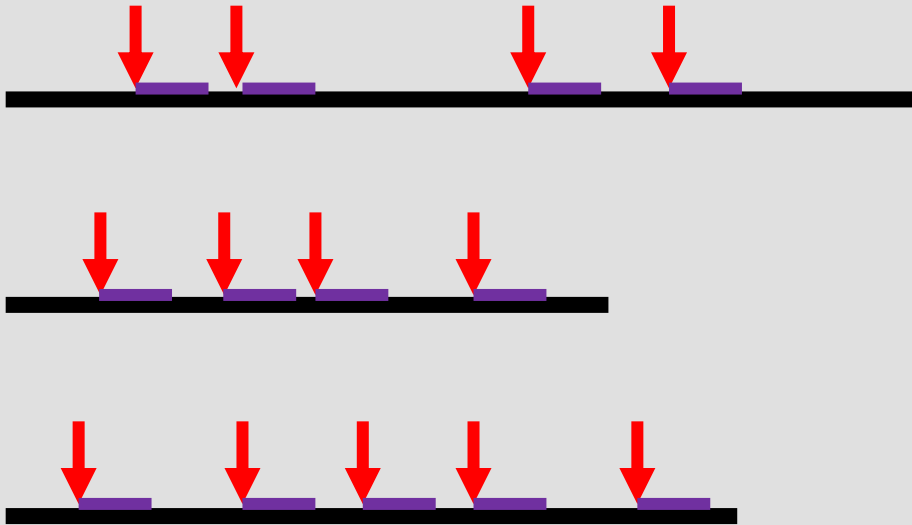
CGGACTACG
CGGAATACG



- Single-nucleotide Polymorphisms (SNPs)
- Only two alleles per locus
- Relatively cheap
- Need to be developed
- Higher level of technical expertise
- 1k – 100k+ loci

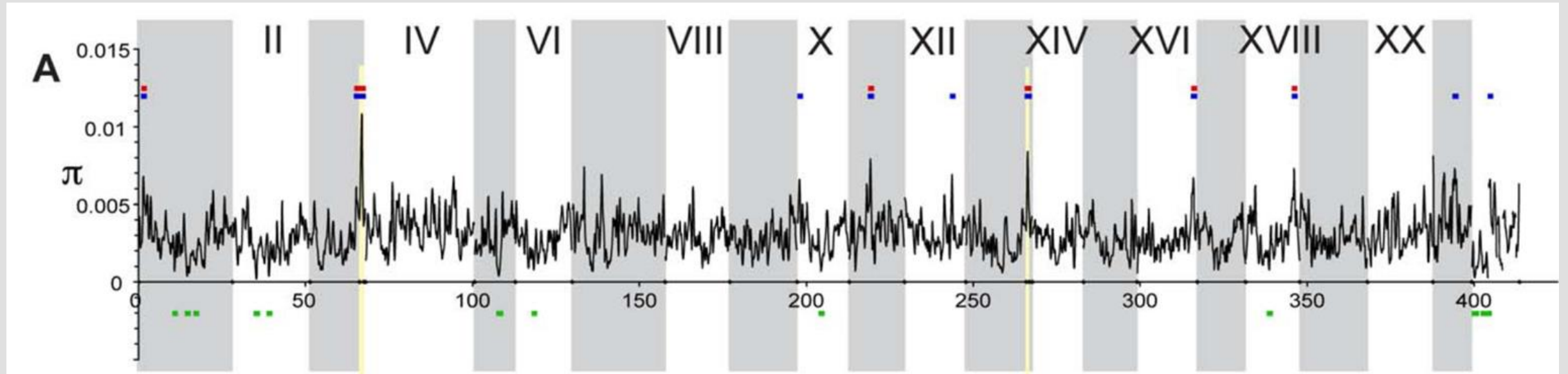
Reduced Representation

CTGACG
G|CAGTC

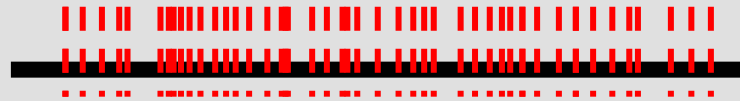
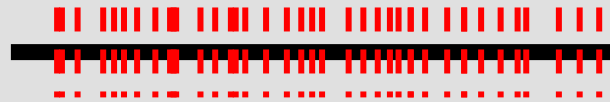
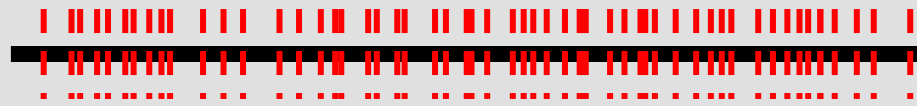
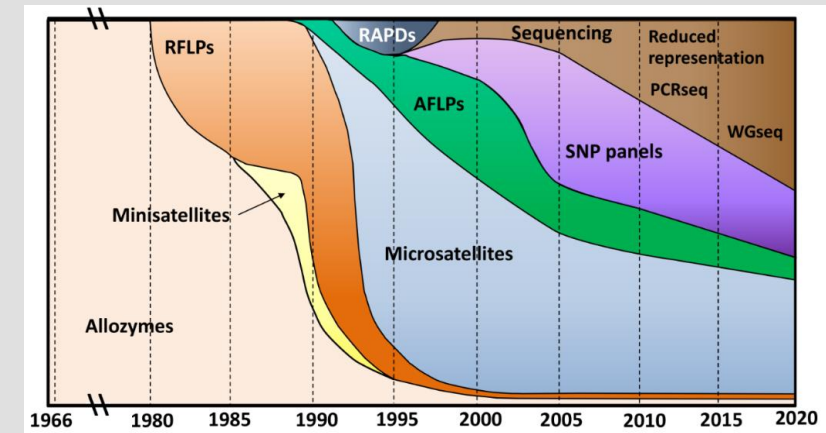


- SNPs/structural variants, etc.
- Can target random areas near cut sites (RAD)
 - Many exciting flavours!
- Can target expressed or specific areas (sequence capture)
- 1k-100k+ loci
- Fairly cheap
- No development needed for some types
 - RAD variants
 - Can benefit from a reference genome
- Great for studying patterns of diversity genome wide in non-model organisms
- Can pool individuals to save money
 - No individual data, just population level

Reduced Representation

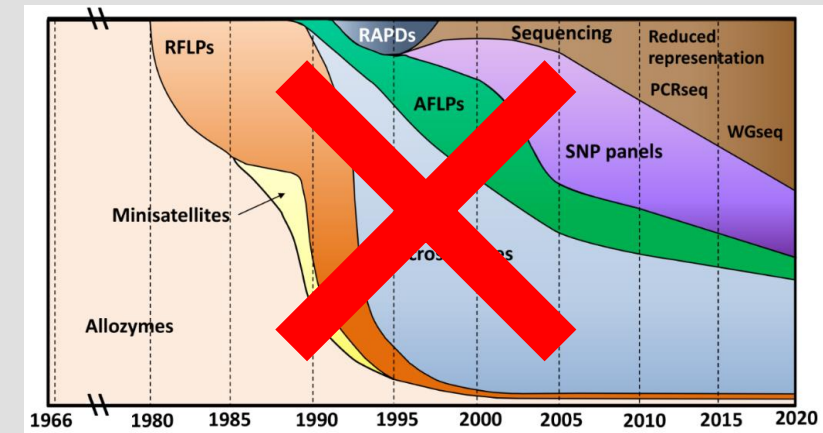


Whole-genome sequencing

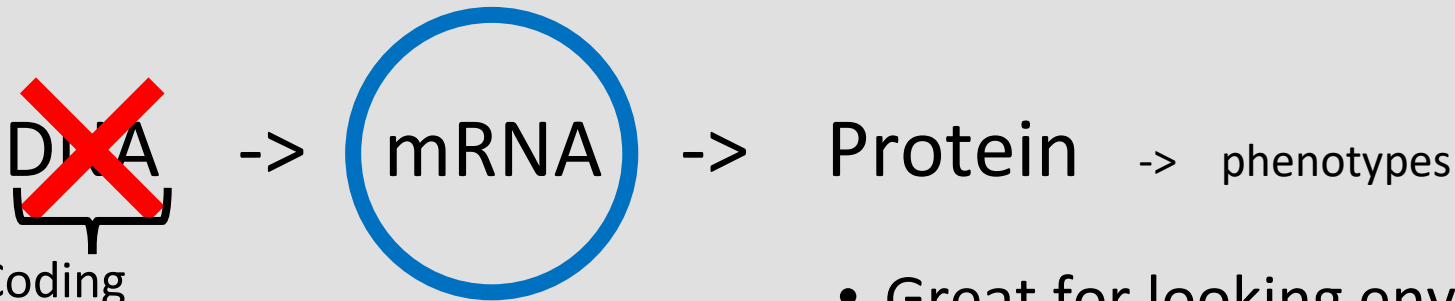


- SNPs/structural variants, etc.
 - Essentially everything barring tough-to-sequence regions
- 100k – 10M+ loci
- Often expensive
 - getting cheaper over time!
- No development needed
 - Greatly benefits from a reference genome.
- Excellent for studying patterns of diversity genome wide
- The gold standard

RNA-seq



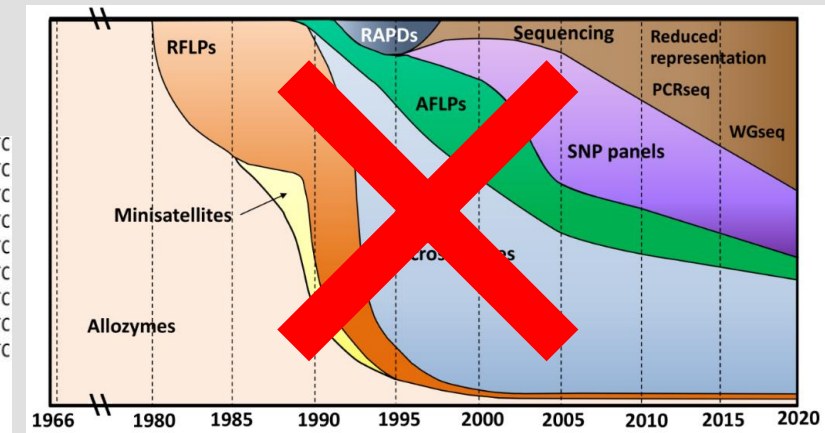
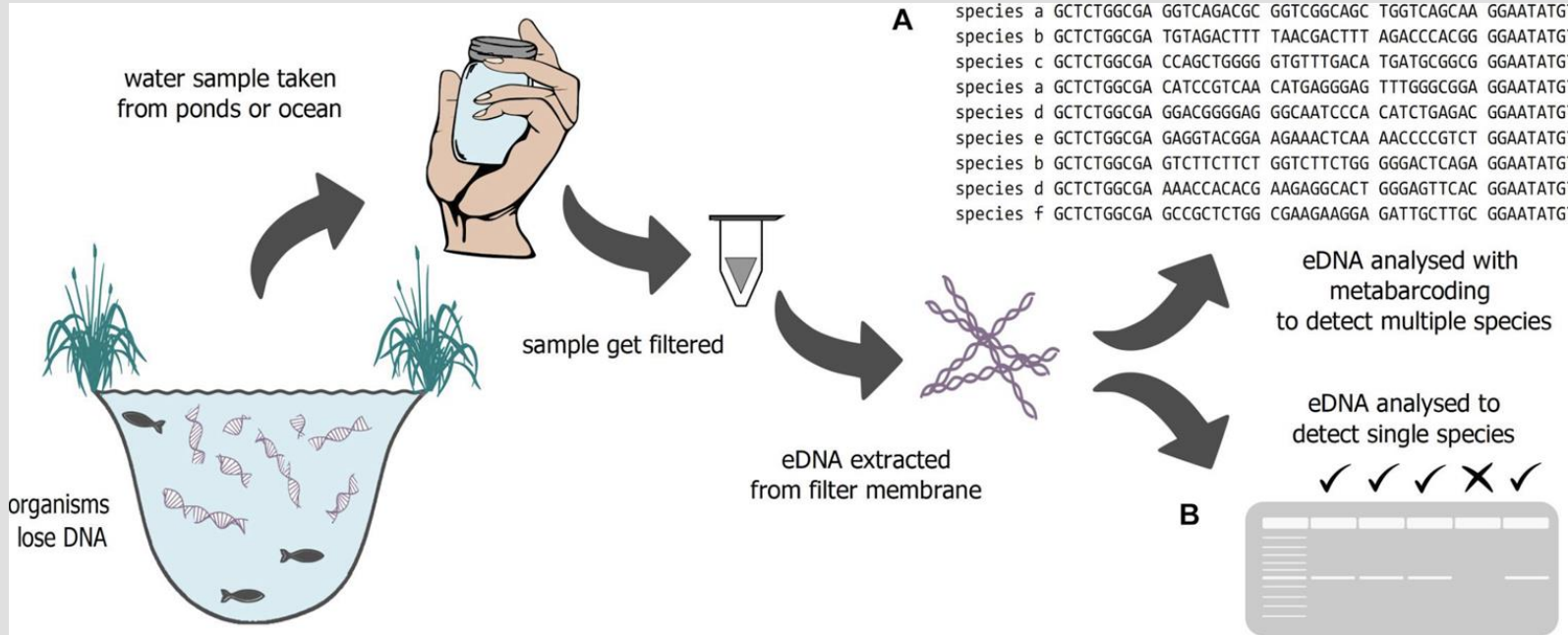
Central Dogma of Molecular Biology:



- Coding
- Regulatory
- Non-coding (“junk”)

- Great for looking environmental effects on expression
- Great for looking for changes only in coding regions
- Can do a great job of population assignment in some cases
- Cannot assume things are neutral
 - Complicates population genetics
- Tricky, somewhat expensive

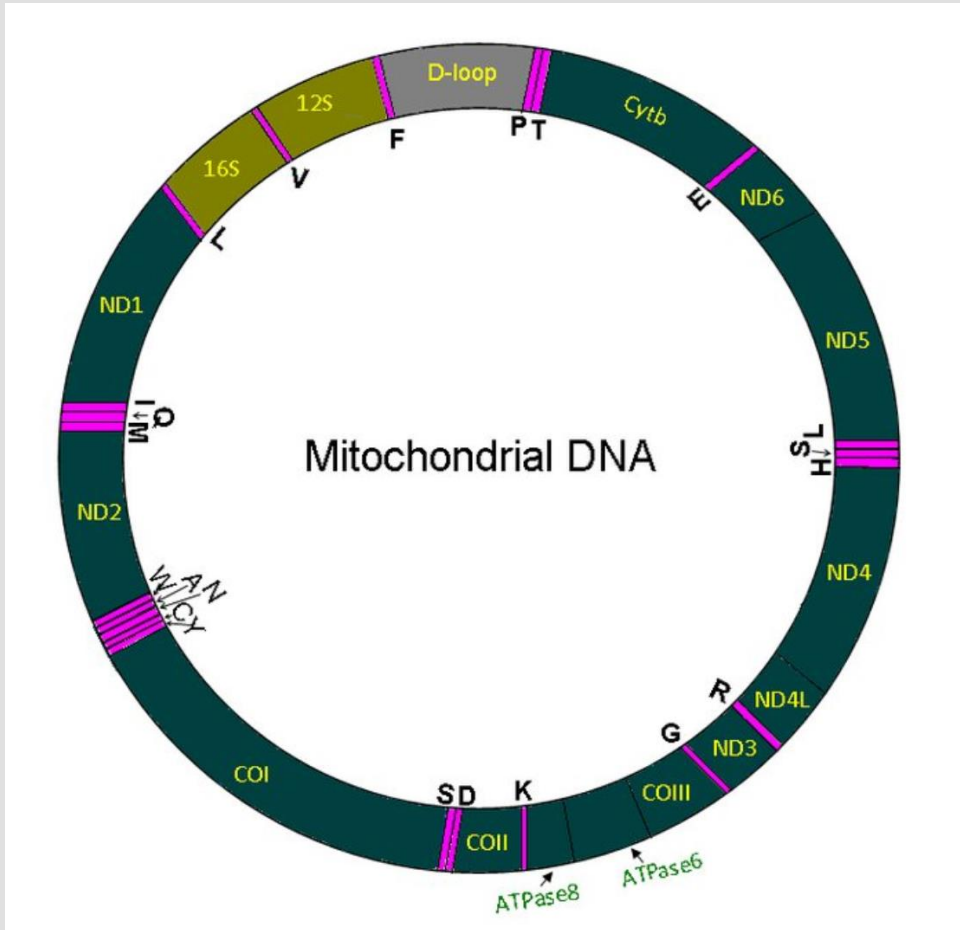
eDNA



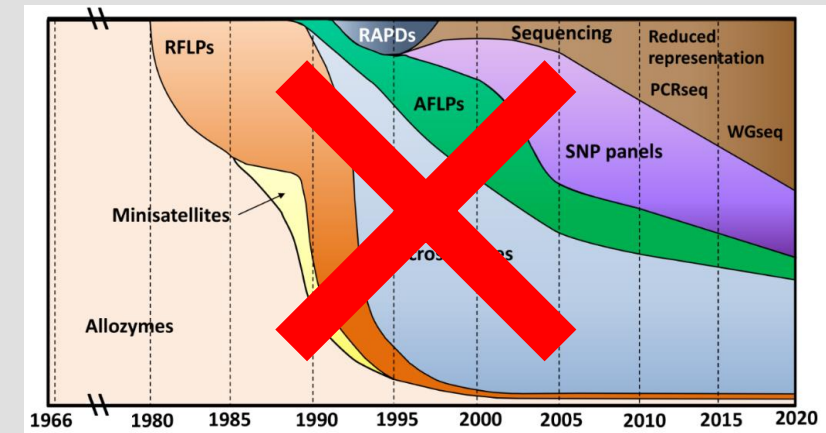
Schadewell and Adams 2021

- Don't need to catch your study species
- Can assess species composition
- Great for species detection
- Hard(er) to do population genetics
 - Depends on types of samples!
- Data quality is often lower

Mitochondrial DNA



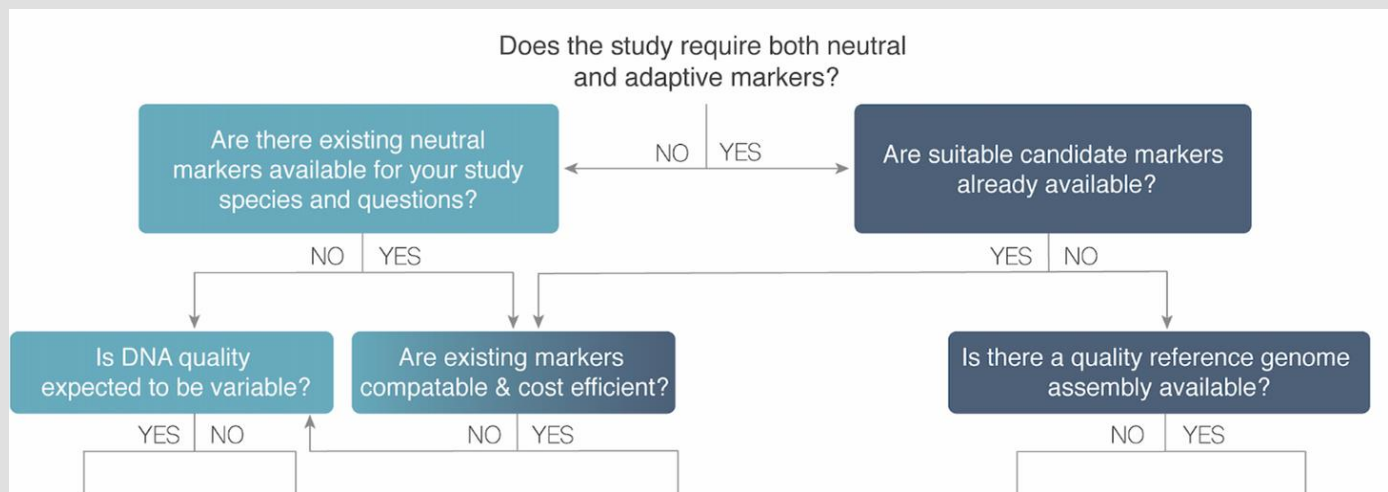
Raju et al 2011



- Cheap and fairly easy
- DNA lasts longer
 - Way more copies!
- Both well conserved regions and some with faster mutation rates.
- Excellent for species identification!

- Limited funding and tech?
 - Consider microsats
- Can't sample your organism directly?
 - Consider eDNA
- Interested in expression?
 - Consider RNAseq
- Need neutral markers only?
 - Consider reduced representation/RAD
- Need neutral and adaptive?
 - Consider RAD (mid resolution) or WGS (high resolution)

Schiebelhut et al *in review: Practical guidance in conservation genomics: from study design to application*



Harnessing genomics for wildlife conservation


Laura Bertola



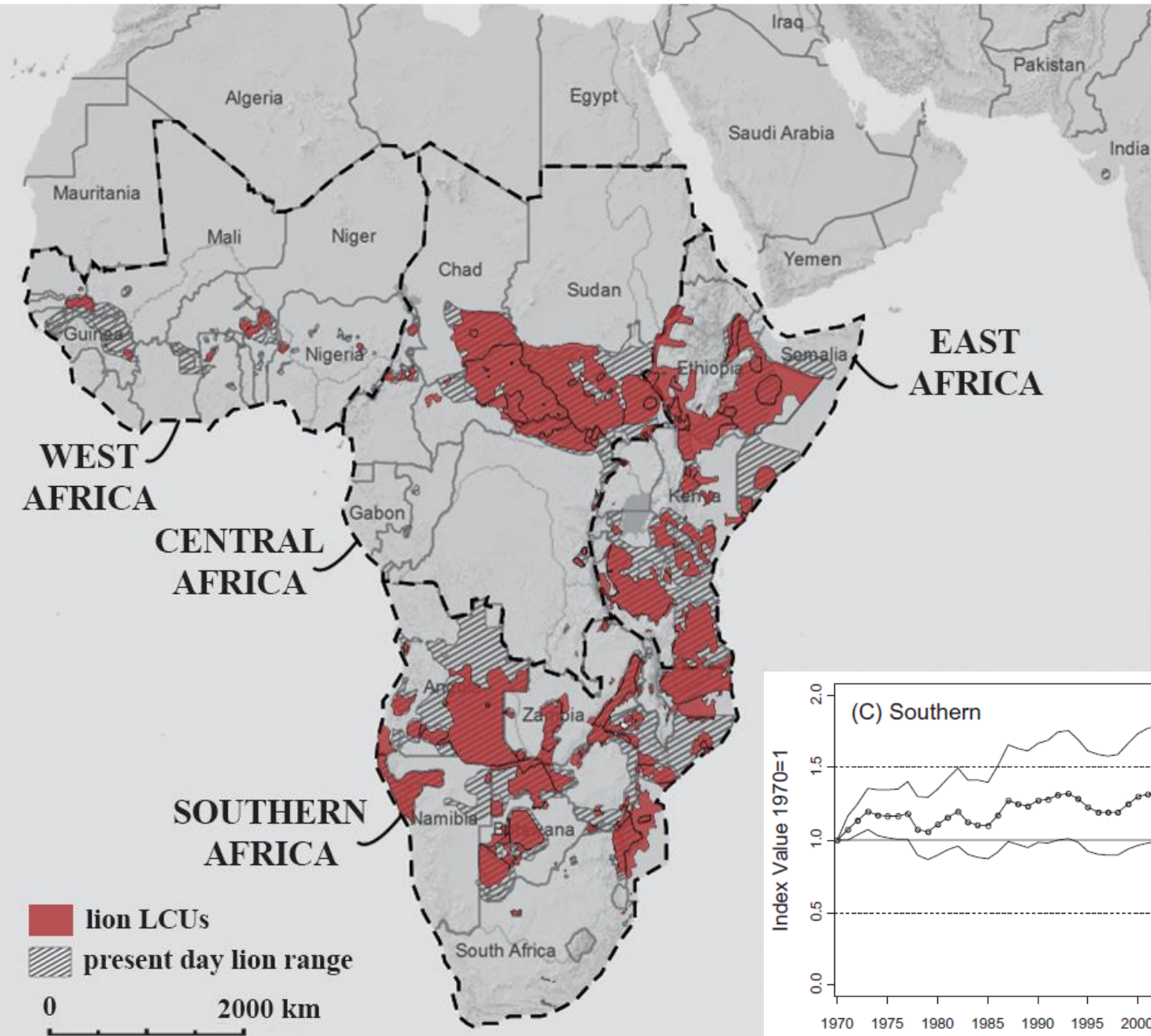
KØBENHAVNS
UNIVERSITET



laura.bertola@gmail.com

 [@LauraDBertola](https://twitter.com/LauraDBertola)



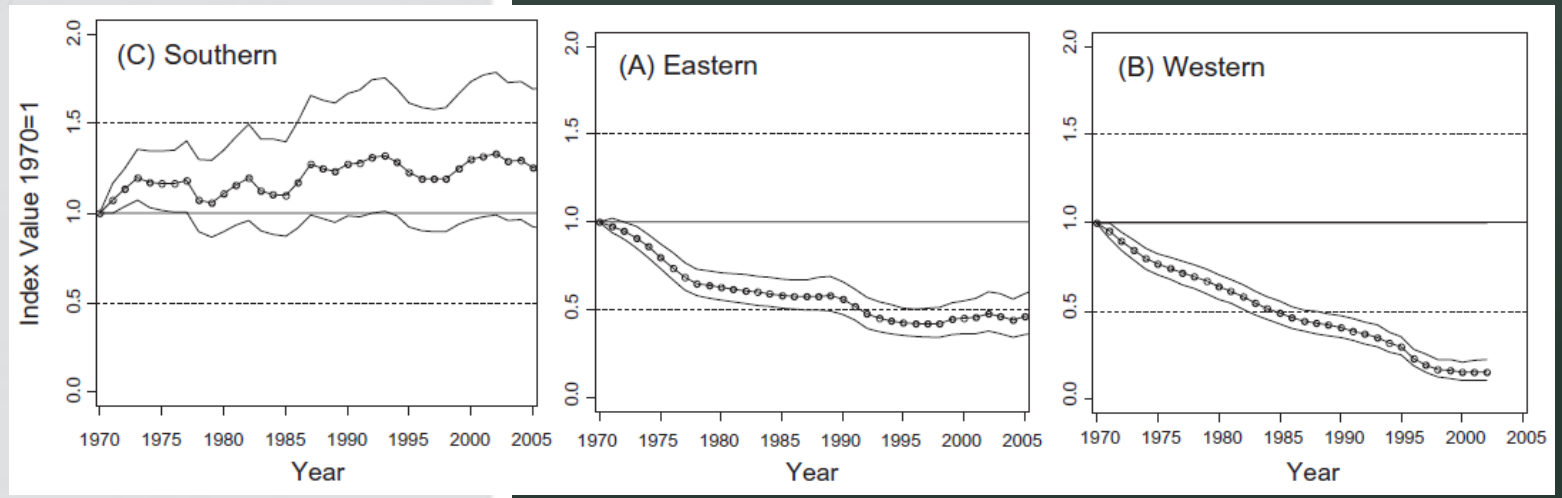


20,000-30,000 lions

~75% decline since 1970

West and Central Africa strongest declines.

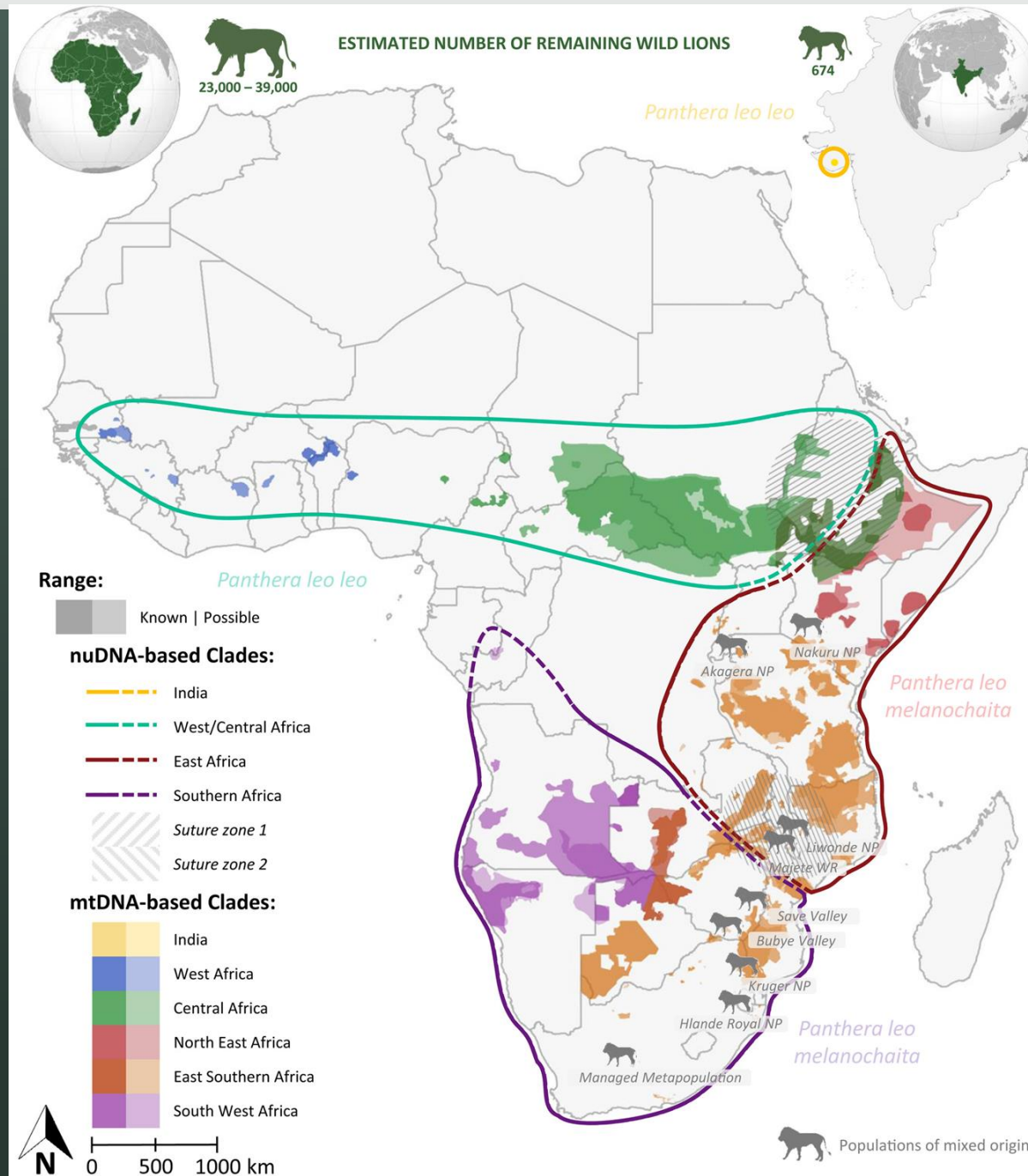
Craigie *et al.*, 2010



Generating genomic resources:



Baseline data



Bertola *et al.*,
Evolutionary Applications
2022

A conservation genomics tool: SNP panels

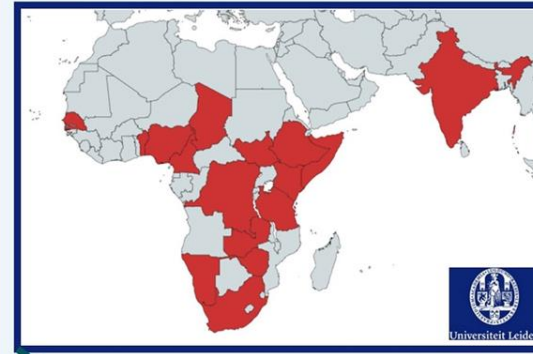
- Leiden University: 335 nuDNA SNPs + 25 mtDNA SNPs
- SLU (Göran Spong): 92 nuDNA SNPs, incl. 3 sex-linked + 4 mtDNA

☐ **combined panel**

Leiden University SNP panel

335 nuDNA SNPs + 25 mtDNA SNPs

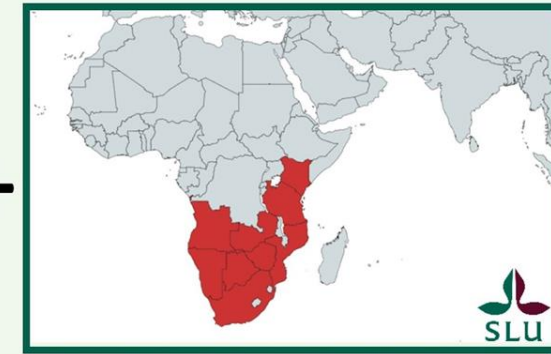
Emphasis on range-wide diversity, including hybridization zone in horn of Africa, and northern subspecies *Panthera leo leo*



SLU SNP panel

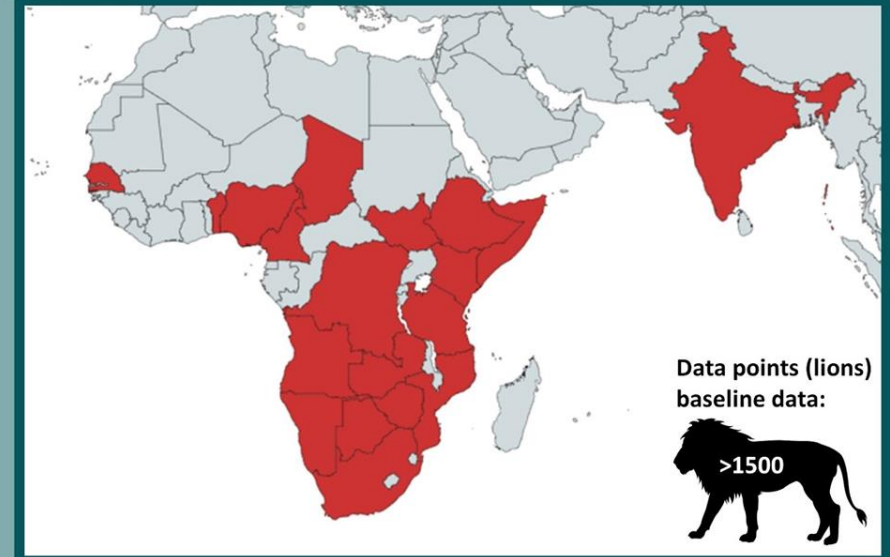
92 nuDNA SNPs, incl. 3 sex-linked + 4 mtDNA

Emphasis on validation of non-invasively collected samples, sex identification, and subspecies *Panthera leo melanochaita*



+

Combined SNP panel

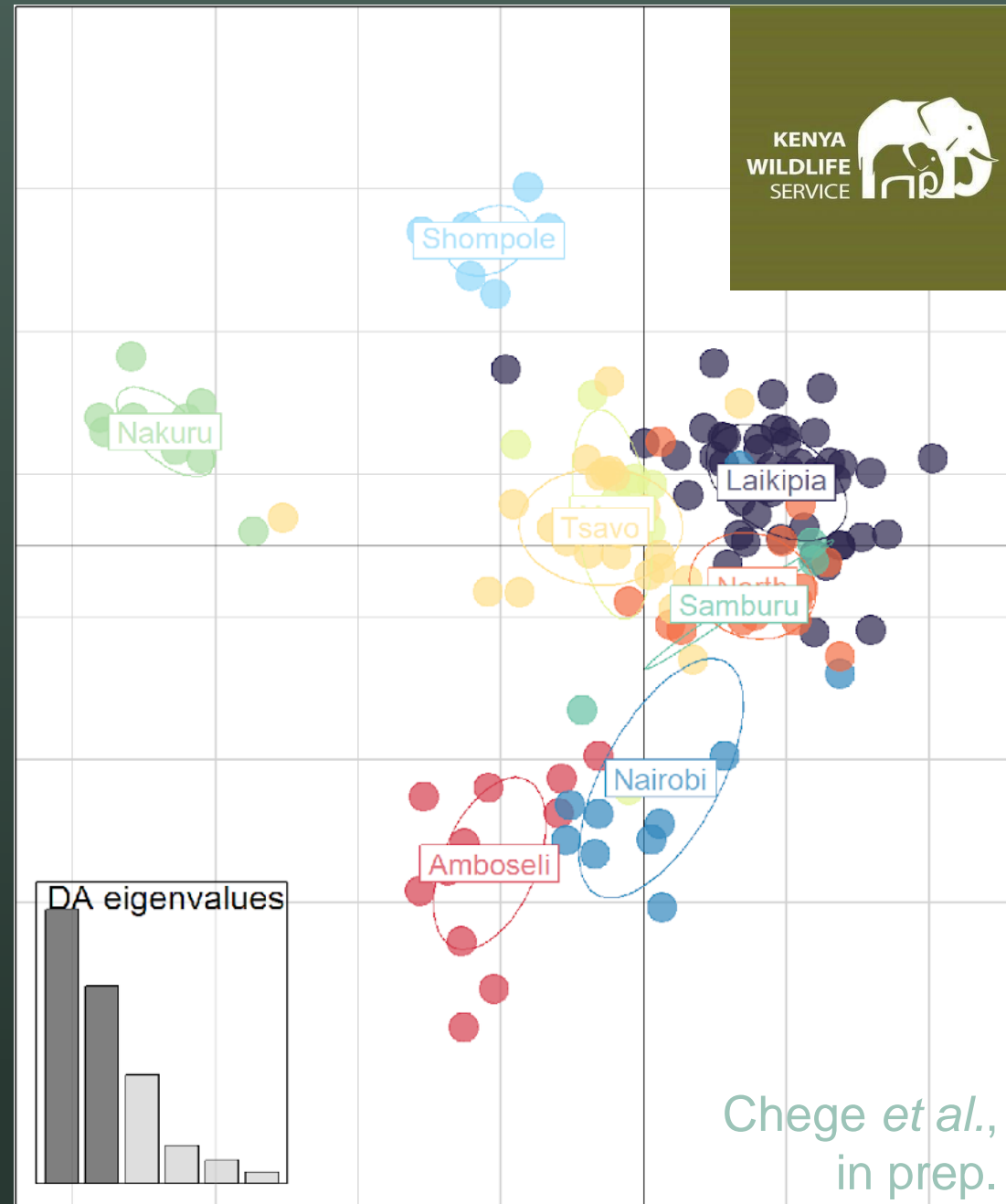
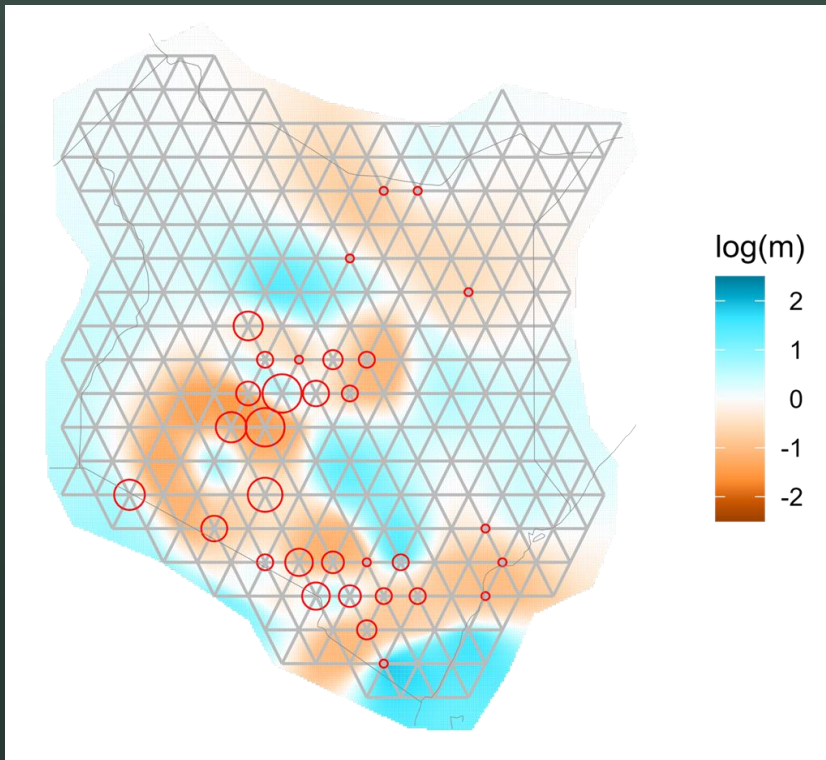


- Improved (combined) geographic coverage
- Connected baseline data (genotypes available for >1500 lions)
- Validation for use with low quality (i.e. non-invasively collected) samples
- Modular format, flexible use depending on specific data requirements
- Improved genome-wide coverage
- Sex-linked information
- Cost-effective (~50 euro/sample)

1) Local conservation decisions

~150 Kenyan lions genotyped

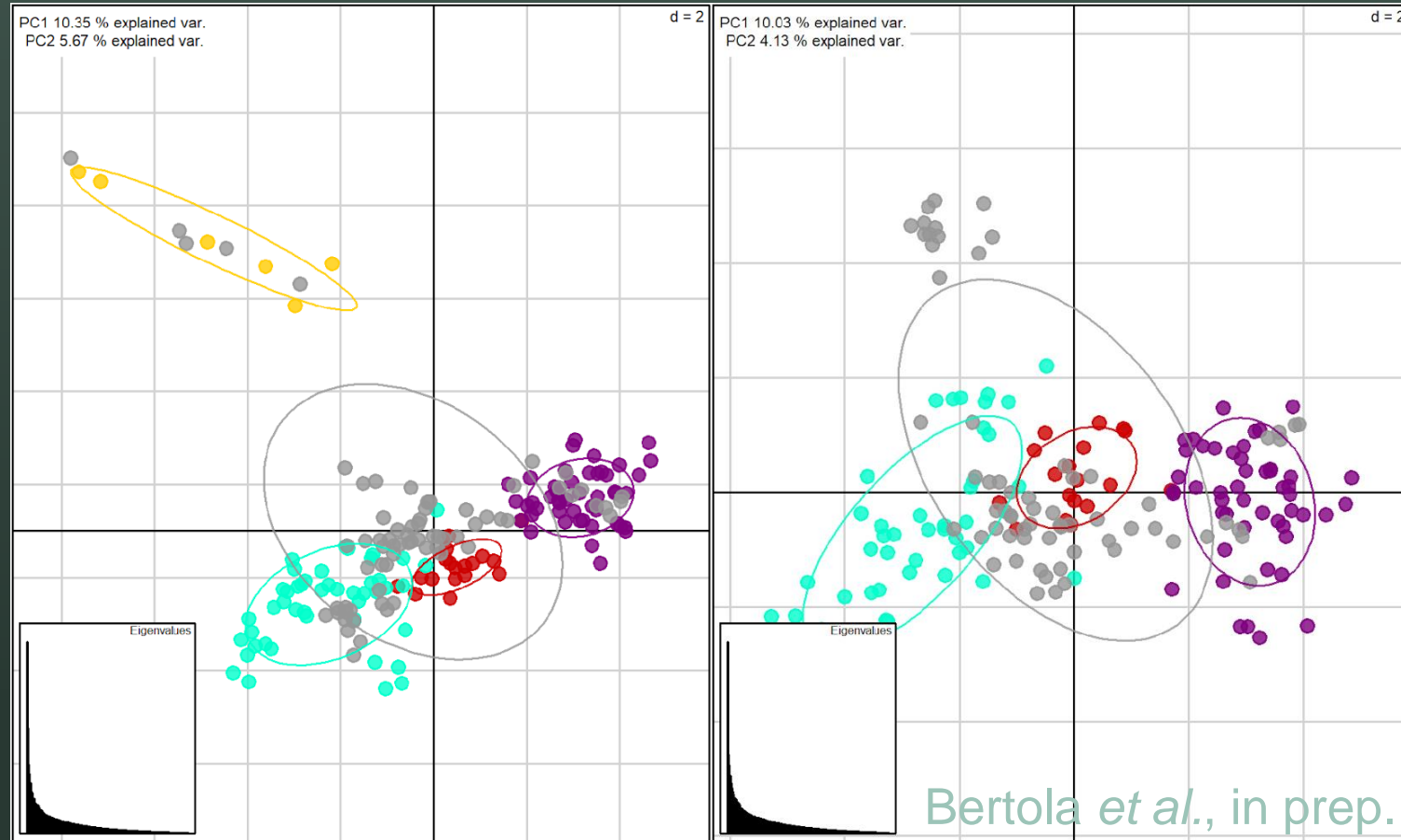
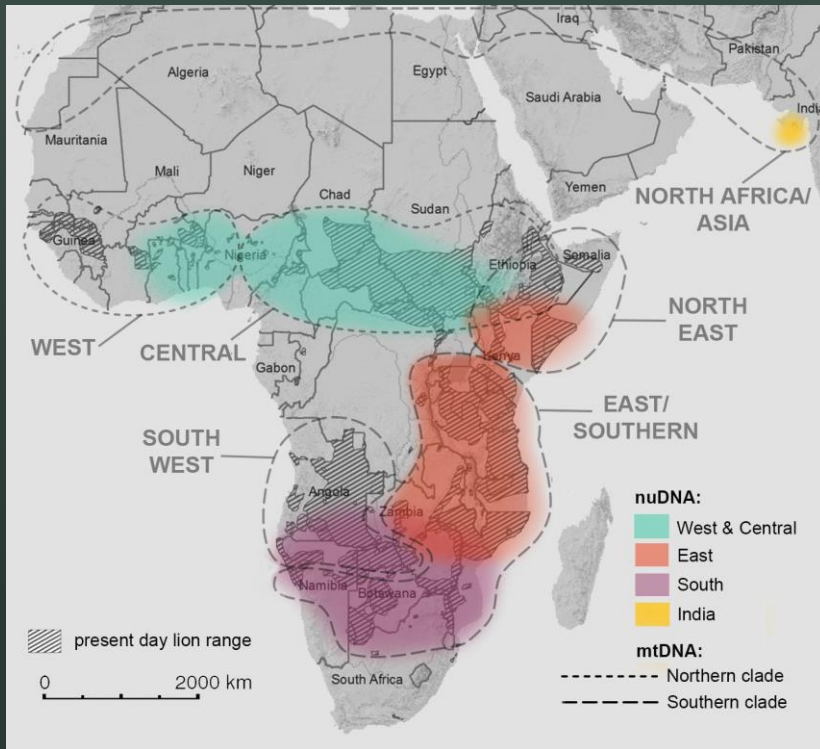
- Population structure
- Population diversity
- Translocation history



2) *Ex situ* population management

~70 zoo lions genotyped (in grey)

- Assignment to genetic cluster
- Level of genetic diversity
- Relatedness



Bertola et al., in prep.

3) Forensics:

Traceability through Lion Localizer:
 Source population, poaching hotspots, trade routes.
 Currently based on mtDNA, SNP panel complimentary.



Lion Localizer

QUERY
INSTRUCTIONS
LABORATORY PROTOCOLS
FAQ
REFERENCES
ADMIN LOGIN

```

CAGCCTTCATAGGATATGCTTACCGTGGGGCCAAATATCCCTTTGAGGTGCAACTGTAATCACATAATCTCCATACGCAATCCCAT
GGCCGACCTAGTAGAGTGGATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCCTGACACGATTCCTTGCCTTCCACTTCATCCTTCC
ATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAAACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAA
TCCATCCACTATAACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACACTCATACTACTCGTCCATTCTCACCAGACCT
AGATCCCGACAACATAACCCCGCCAACTCTAAGCACCCCTCCCATATCAAACCTGAATGGTACTTCTCTATTGTCATATGCAATG
TCTATTTCCCAATAAACTAGGAGGAGTTTTAGCCCTAGTTCTATCCATCTTAATCTTAGCAATTATCCCTGCCCTCCACACTCCAAAC
GATTAATGTTTCGACCACTAAGTCAATGCTTATTCTGATTCCTAGTAGCGGACCTTCTGACCCTGACATGAATTGGTGGCCAACTGT
CCCCCTCATACCATCGGCCAAGCTCCATCTATACTTCTCCATTCTTCTAATCCTAATACCCATCTCAGGCATTATTGAAAAC
CTCAAATGAAGA
                    
```

Locations may be shown or removed as pins on the map by clicking on the box next to each location name. However, this is enabled only for the closest-matching haplotype at each geographic location. Location and closest haplotype information may also be shown by clicking on an icon or pin on the map itself.

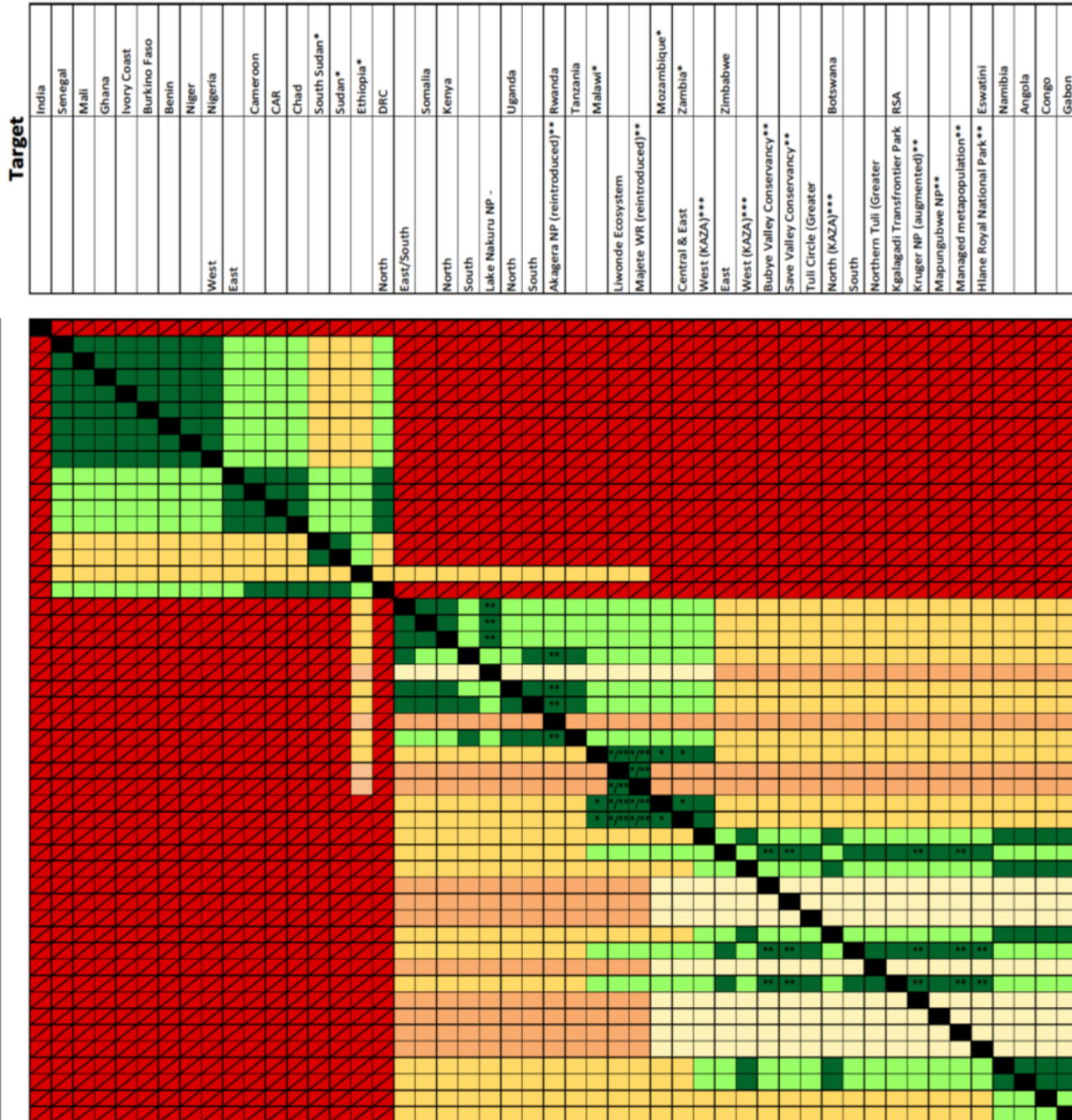
	Haplot...	Mismatches	Match...	Locality	Country
<input checked="" type="checkbox"/>	LEO0002	0	1140	(11.6; -9.3)	Guinea
<input checked="" type="checkbox"/>	LEO0002	0	1140	(11.05; 1.517)	Benin
<input checked="" type="checkbox"/>	LEO0002	0	1140	Kainji NP	Nigeria

4) Translocations

Identifying suitable source-target population pairs.

Bertola *et al.*,
Evolutionary Applications
2022

Country	Lion range/LCU	Source
India		
Senegal		
Mali		
Ghana		
Ivory Coast		
Burkina Faso		
Benin		
Niger		
Nigeria	West	
	East	
Cameroon		
CAR		
Chad		
South Sudan*		
Sudan*		
Ethiopia*		
DRC	North	
	East/South	
Somalia		
Kenya	North	
	South	
	Lake Nakuru NP - Soysambu**	
Uganda	North	
	South	
Rwanda	Akagera NP (reintroduced)**	
Tanzania		
Malawi*		
	Liwonde Ecosystem (reintroduced)**	
	Majete WR (reintroduced)**	
Mozambique*		
Zambia*	Central & East	
	West (KAZA)***	
Zimbabwe	East	
	West (KAZA)***	
	Bubye Valley Conservancy**	
	Save Valley Conservancy**	
	Tuli Circle (Greater Mapungubwe TFCA)**	
Botswana	North (KAZA)***	
	South	
	Northern Tuli (Greater Mapungubwe TFCA)**	
RSA	Kgalagadi Transfrontier Park	
	Kruger NP (augmented)**	
	Mapungubwe NP**	
	Managed metapopulation**	
Eswatini	Hlane Royal National Park**	
Namibia		
Angola		
Congo		
Gabon		



Target

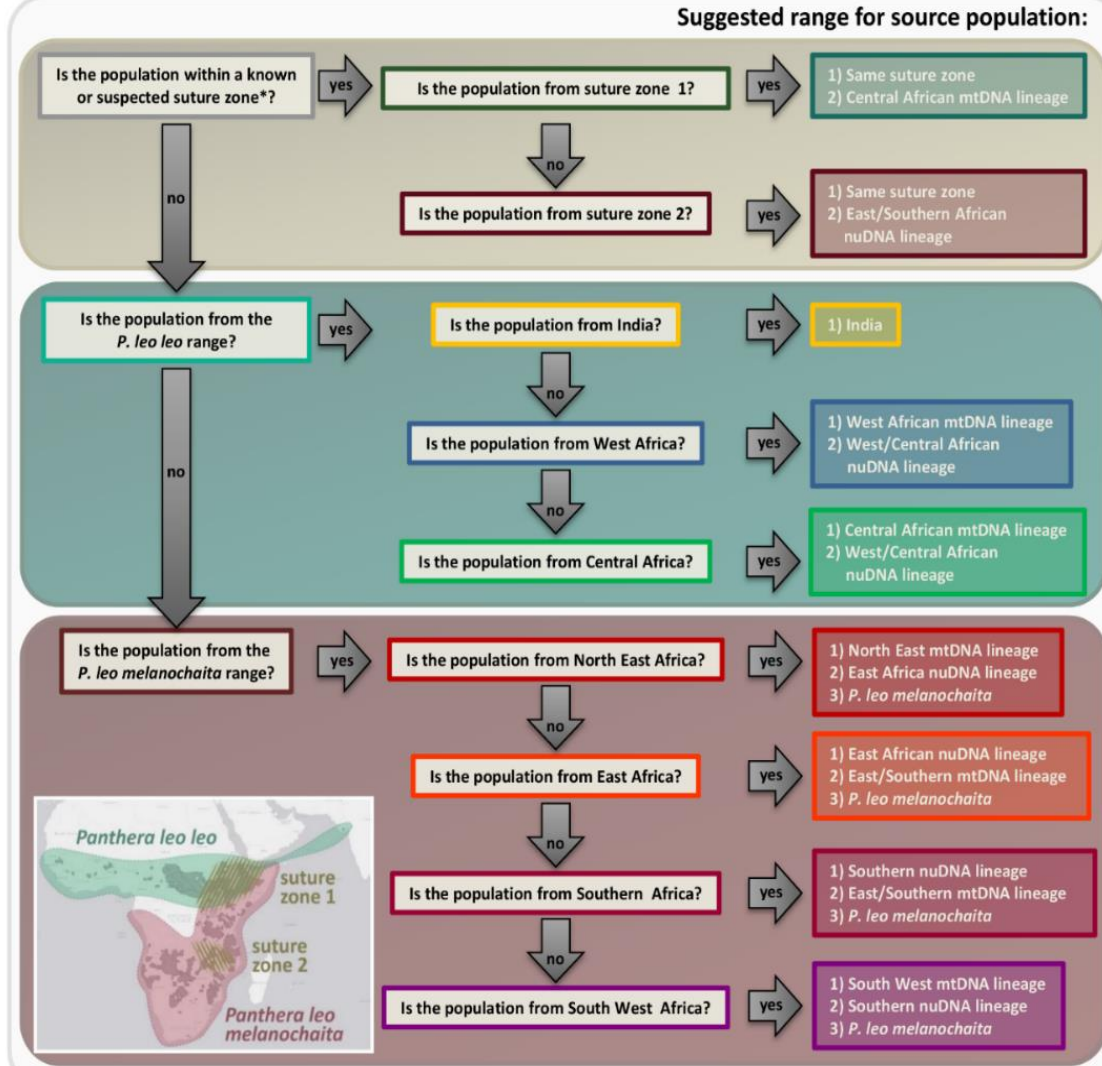
India
Senegal
Mali
Ghana
Ivory Coast
Burkina Faso
Benin
Niger
Nigeria
West
East
Cameroon
CAR
Chad
South Sudan*
Sudan*
Ethiopia*
DRC
North
East/South
Somalia
Kenya
North
South
Lake Nakuru NP -
North
South
Akagera NP (reintroduced)**
Rwanda
Tanzania
Malawi*
Liwonde Ecosystem
Majete WR (reintroduced)**
Mozambique*
Zambia*
Central & East
West (KAZA)***
East
Zimbabwe
West (KAZA)***
Bubye Valley Conservancy**
Save Valley Conservancy**
Tuli Circle (Greater
North (KAZA)***
South
Northern Tuli (Greater
RSA
Kgalagadi Transfrontier Park
Kruger NP (augmented)**
Mapungubwe NP**
Managed metapopulation**
Hlane Royal National Park**
Eswatini
Namibia
Angola
Congo
Gabon

Communicating genomic resources:

Decisions Guide.

Bertola et al.,
Cat News
2022

Questions refer to the target population for a potential lion conservation translocation



Known/inferred suture zones:
 1) Sudan, South Sudan and Ethiopia (suture *P. leo leo* and *P. leo melanochaita*);
 2) Zambia, Malawi, Mozambique (suture East and Southern African nuDNA lineages)

SOM: Bertola et al. (2022) Policy implications from genetic guidelines for the translocations of lions (*Panthera leo*). Cat News.

Para mais informação: Bertola et al. (2022) Genetic guidelines for translocations: Maintaining intraspecific diversity in the lion (*Panthera leo*). Evolutionary Applications, 15(1), 22-39. DOI: 10.1111/evo.13318

Orientações genéticas para a translocação de leões

Sumário executivo

Para a conservação efetiva da biodiversidade, a diversidade genética intraspecifica é crucial. No entanto, a diversidade genética é frequentemente perdida durante as translocações. Este guia fornece orientações para a seleção de populações-fonte para translocações de leões, considerando a diversidade genética e a viabilidade das populações.

SOM: Bertola et al. (2022) Policy implications from genetic guidelines for the translocations of lions (*Panthera leo*). Cat News.

To accompany: Bertola et al. (2022) Genetic guidelines for translocations: Maintaining intraspecific diversity in the lion (*Panthera leo*). Evolutionary Applications, 15(1), 22-39. DOI: 10.1111/evo.13318

Lignes directrices génétiques pour la translocation du lion

Résumé exécutif

La diversité génétique au sein des espèces doit être prise en compte pour la conservation effective de la biodiversité. Cependant, la diversité génétique est souvent perdue lors des translocations. Ce guide fournit des orientations pour la sélection de populations sources pour les translocations de lions, en tenant compte de la diversité génétique et de la viabilité des populations.

SOM: Bertola et al. (2022) Policy implications from genetic guidelines for the translocations of lions (*Panthera leo*). Cat News.

To accompany: Bertola et al. (2022) Genetic guidelines for translocations: Maintaining intraspecific diversity in the lion (*Panthera leo*). Evolutionary Applications, 15(1), 22-39. DOI: 10.1111/evo.13318

Genetic guidelines for the translocations of lions

Executive summary

In order to effectively conserve biodiversity, genetic diversity within species must be taken into account. Management interventions, such as translocations, should incorporate genetics by building on the vast data available in the literature.

Here, we summarize all available information on lion genetics, infer genetic assignments of populations for which data are currently lacking, and translate this into recommendations for translocations.

Background

Data from the CITES Trade Database illustrate that in the past 40 years more than 1000 lions have been translocated into lion range states. Although there has been a variety of sources and purposes for these translocations, we estimate that there often is a risk of affecting local lion genetics. Hereby, the natural distribution of genetic diversity in the lion can be negatively affected. We therefore urge managers to take genetics into account when selecting source/target populations for management interventions.

Genetic markers

Genetic assignments to a particular clade (group) are studied through different genetic markers, each representing a different part of the genome. By combining the information from these different genetic markers, we can obtain a more complete picture of the diversity within species:

- Mitochondrial DNA (mtDNA): widely used, represents maternal lineage, tends to overestimate structure
- Nuclear DNA (nuDNA): less widely used, provides a more complete image of the evolutionary history

Proposed suitability score

We assess all 132 lion populations/Lion Conservation Units for available genetic data, and assign them to specific genetic clades. For populations without data available, we infer their genetic assignment, based on knowledge from neighbouring populations.

Based on data from mtDNA and nuDNA genetic markers, we propose the following suitability for source/target combinations for translocations:

First choice: same nuDNA + same mtDNA clade
 same nuDNA, different mtDNA clade
 different nuDNA clade, same subspecies

No option: different subspecies + Indian population

We provide a decision making tool (next page) and a matrix (Bertola et al. 2022, Evol. Appl.) in which the score for each possible source/target combination for each of the 132 lion populations is shown.

Maio 2022
Guia de Decisões

Maio 2022
Guide de Décisions

May 2022
Decisions Guide

