



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



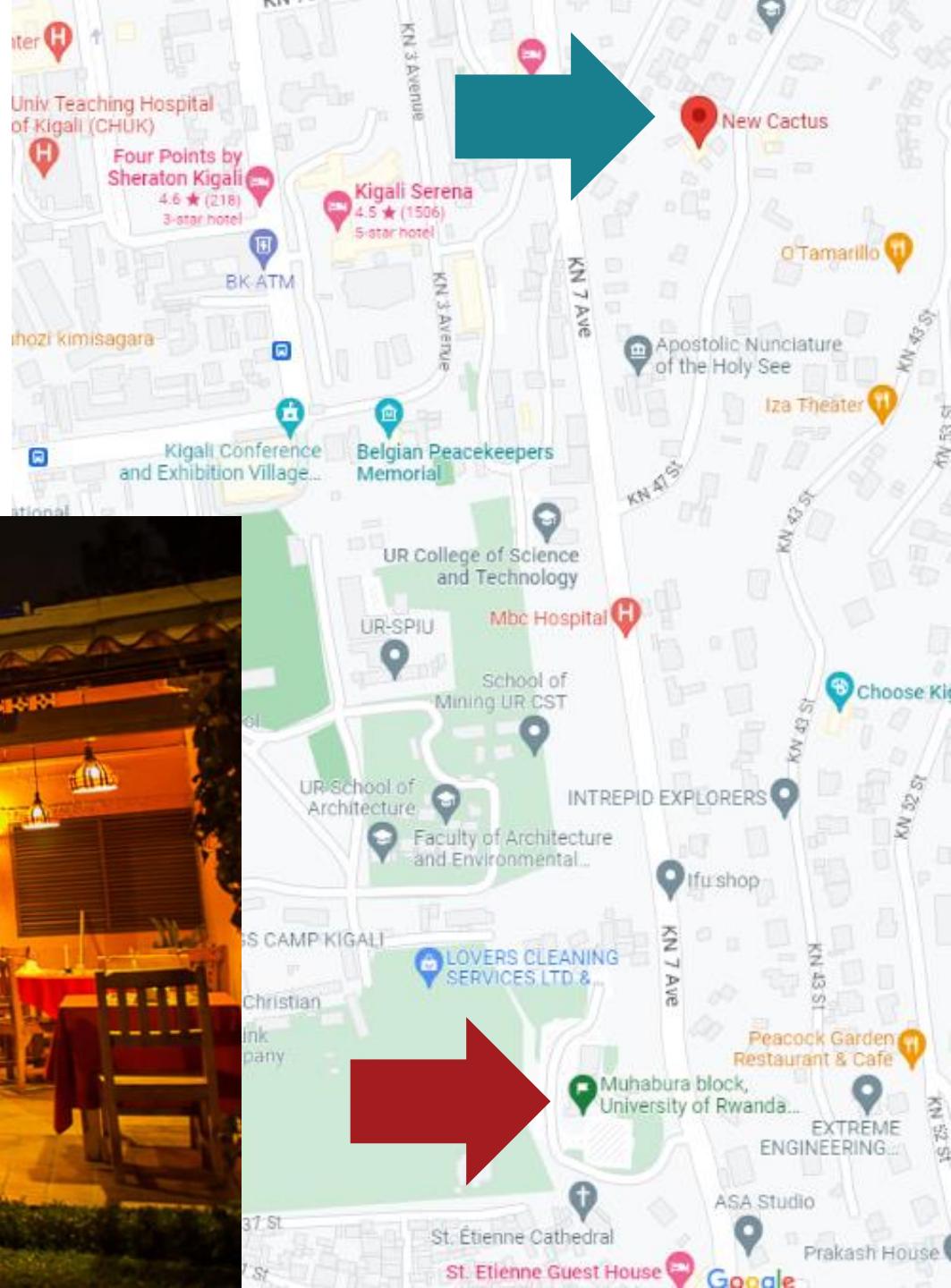
**Laura Bertola**  
**Isaac Overcast**  
**Josiah Kuja**  
**Anubhab Khan**

# Ice breaker: Join us!

New Cactus (KN 47 St)

~15 minutes walking

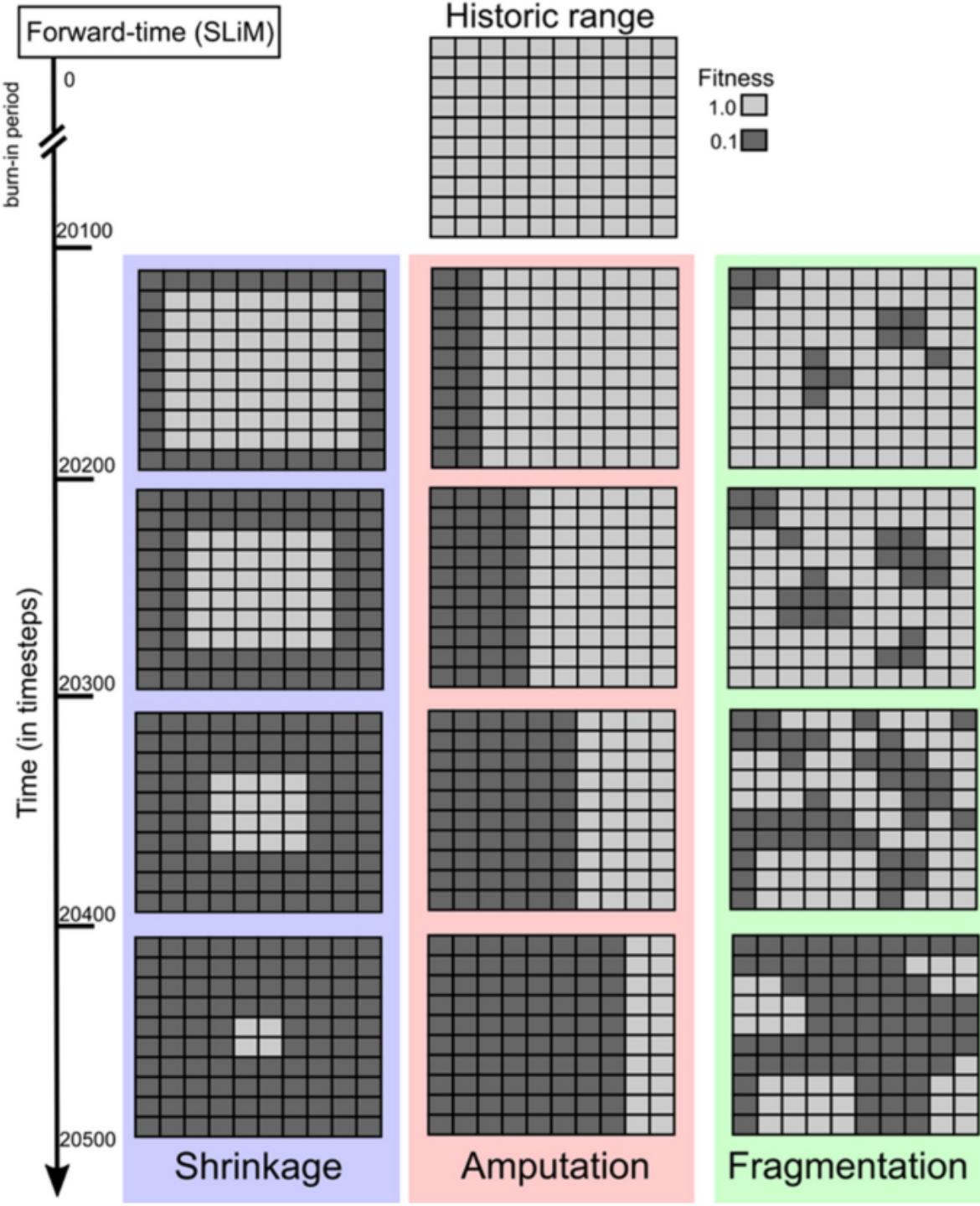
Pizza is on us!



# 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)

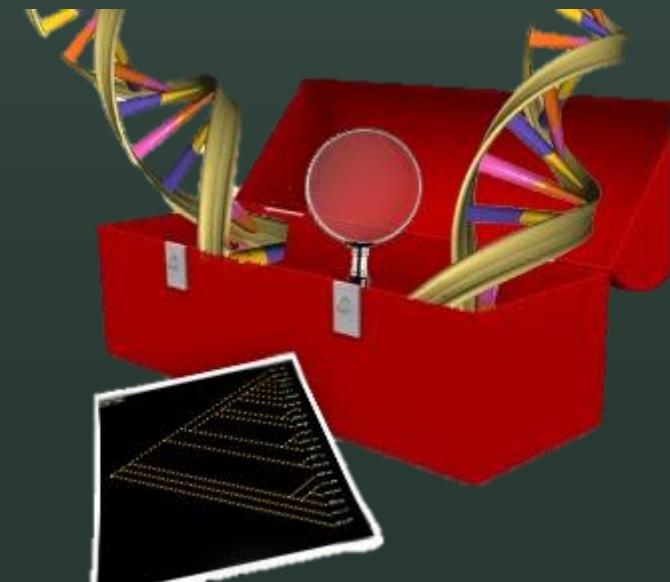
Rogan *et al.*,  
2023



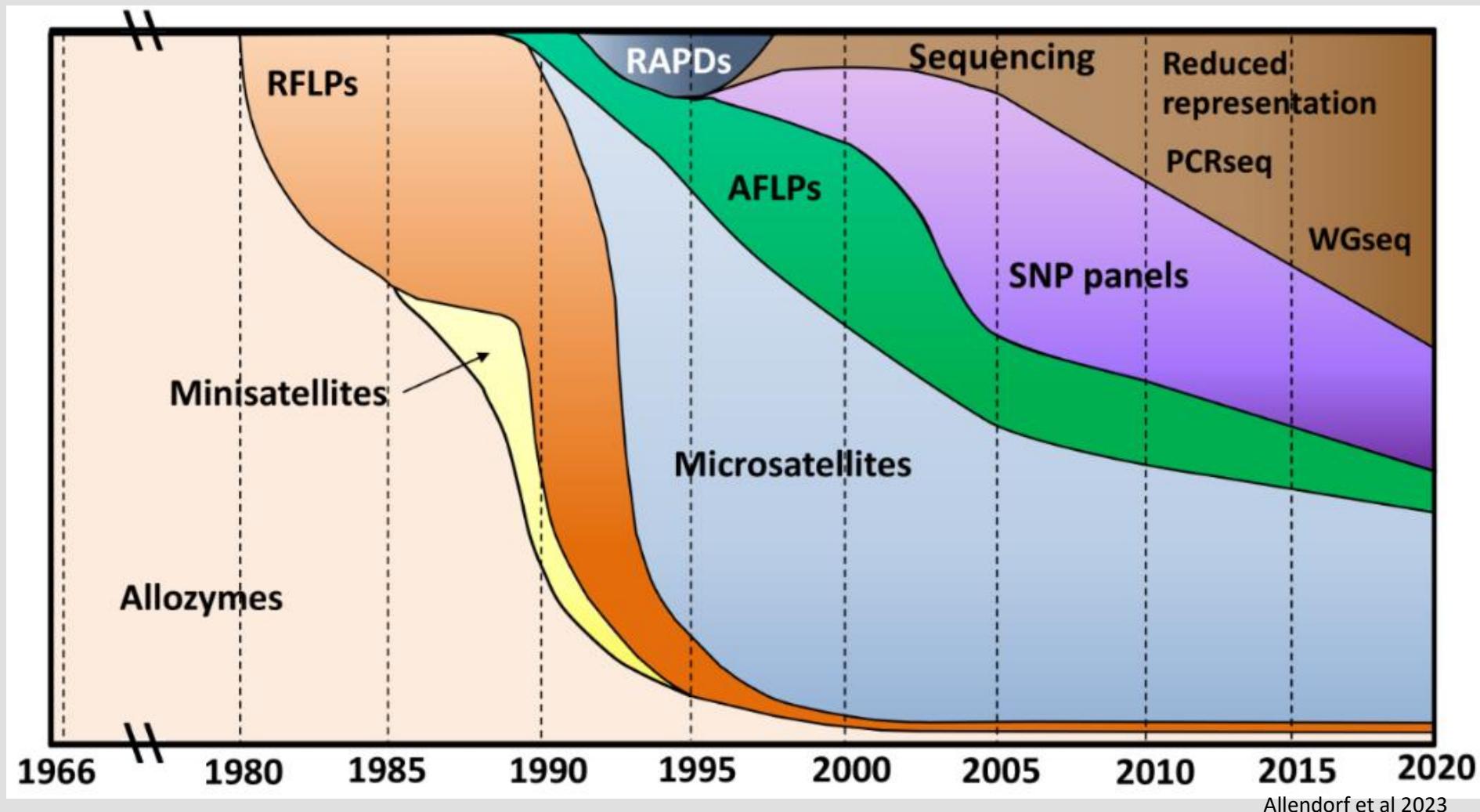
Genetic Composition EBVs						
	Genetic Diversity		Genetic Differentiation		Inbreeding	Effective Population Size (Ne)
	Richness	Heterozygosity	Number of Genetic Units	Distance Genetic Units		
High						 diversity → p time →
Low						 diversity → p time →

# Genetic data

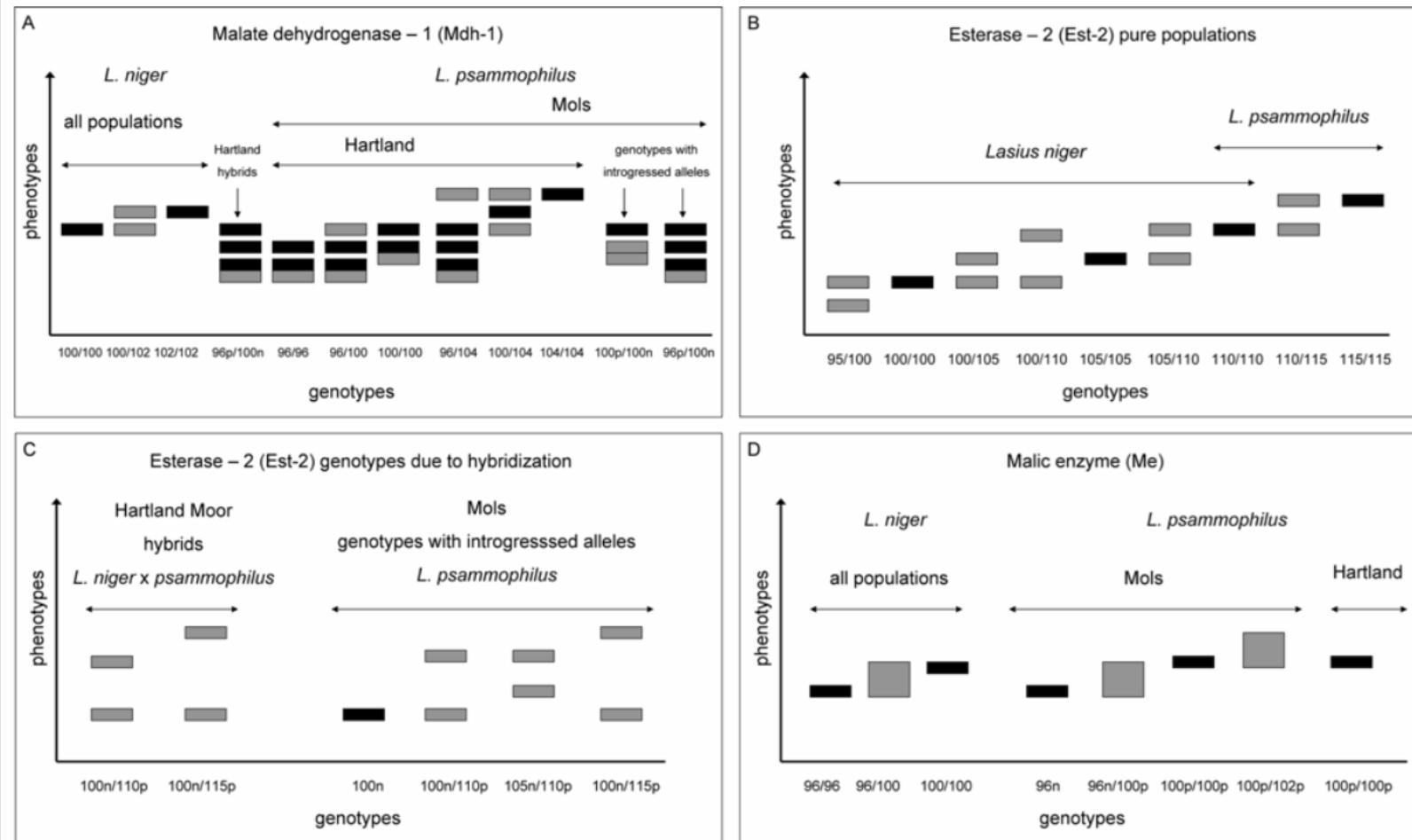
- Diversity and connectivity
- Pedigrees, parentage
- Identify individuals (population estimates, individual home ranges)
- Hybridization
- Population history and future trajectory
- Prioritization, e.g. based on uniqueness or adaptive traits



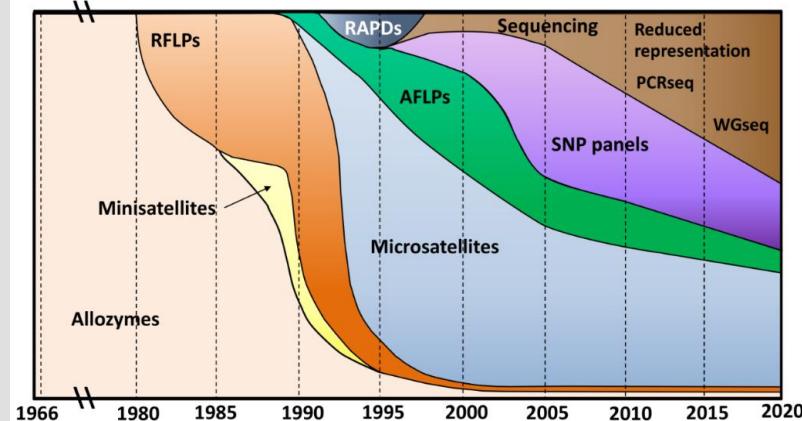
# Genetics and Genomics: Data Types



# Allozymes and RFLPs



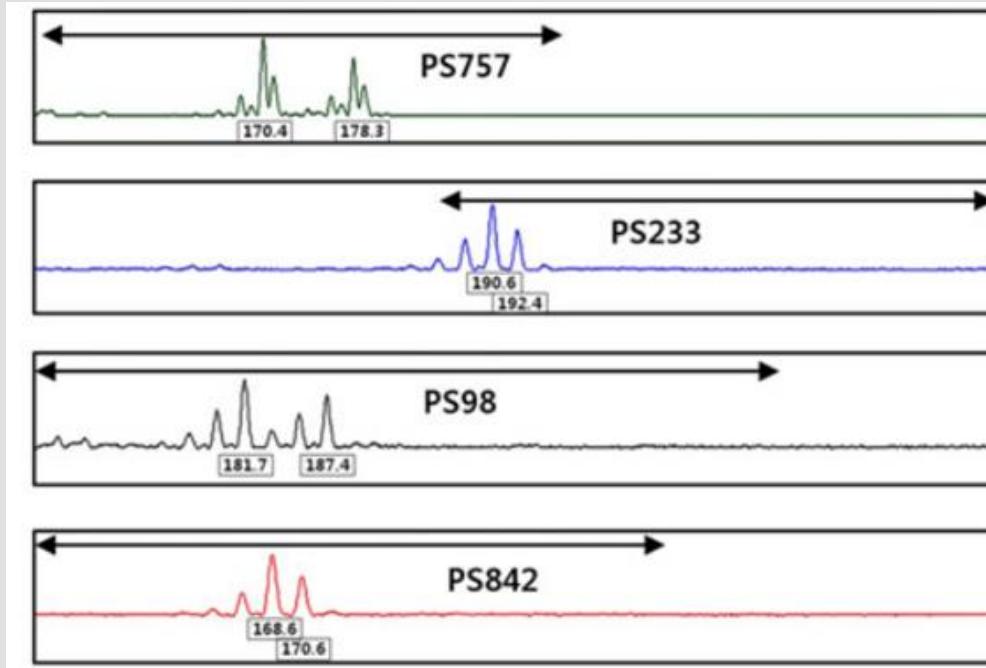
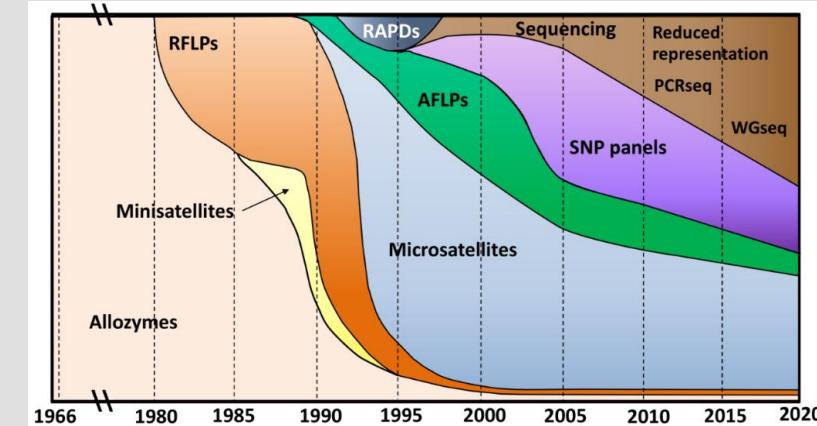
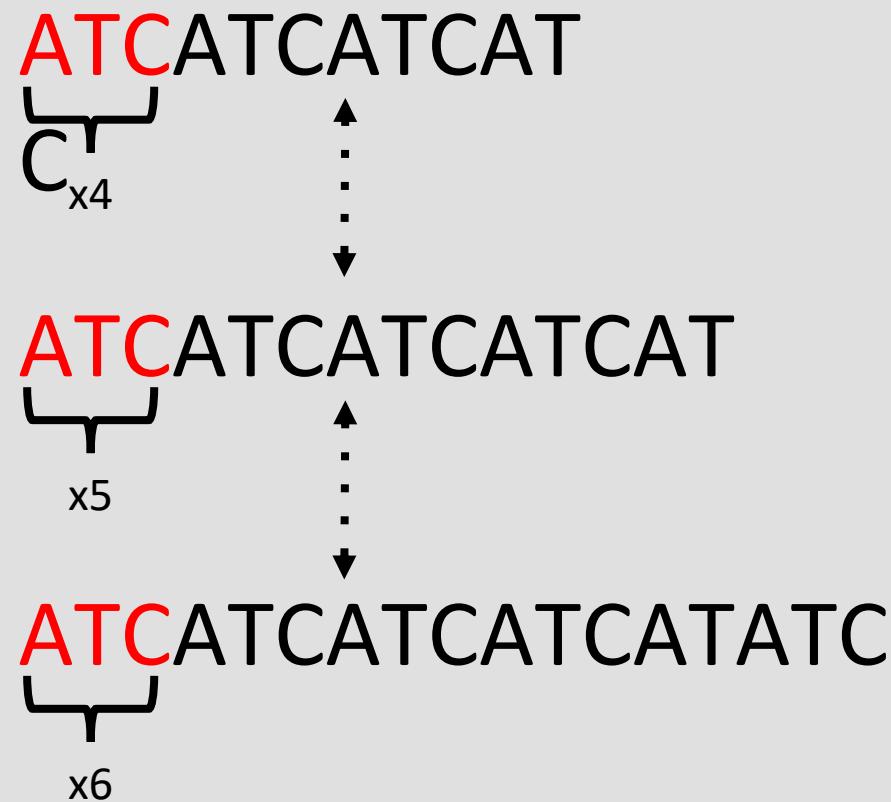
Van der Have et al 2011



CTGACG  
GCAGTC

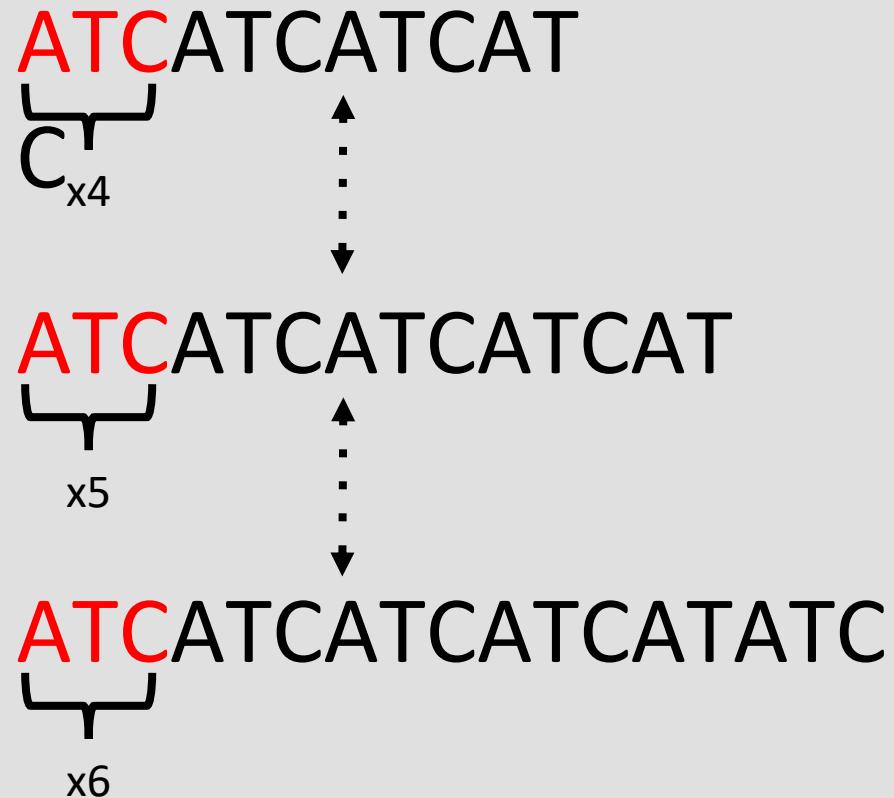
- Enzyme configuration differences (allozymes)
- Restriction fragment length differences (RFLPs)
- Both old, rare today.
- Low power.
- 5-20 loci

# Microsatellites

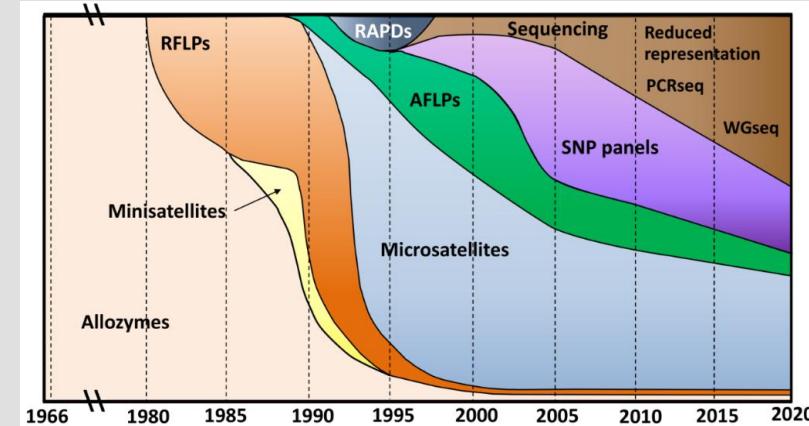


Lee et al 2011

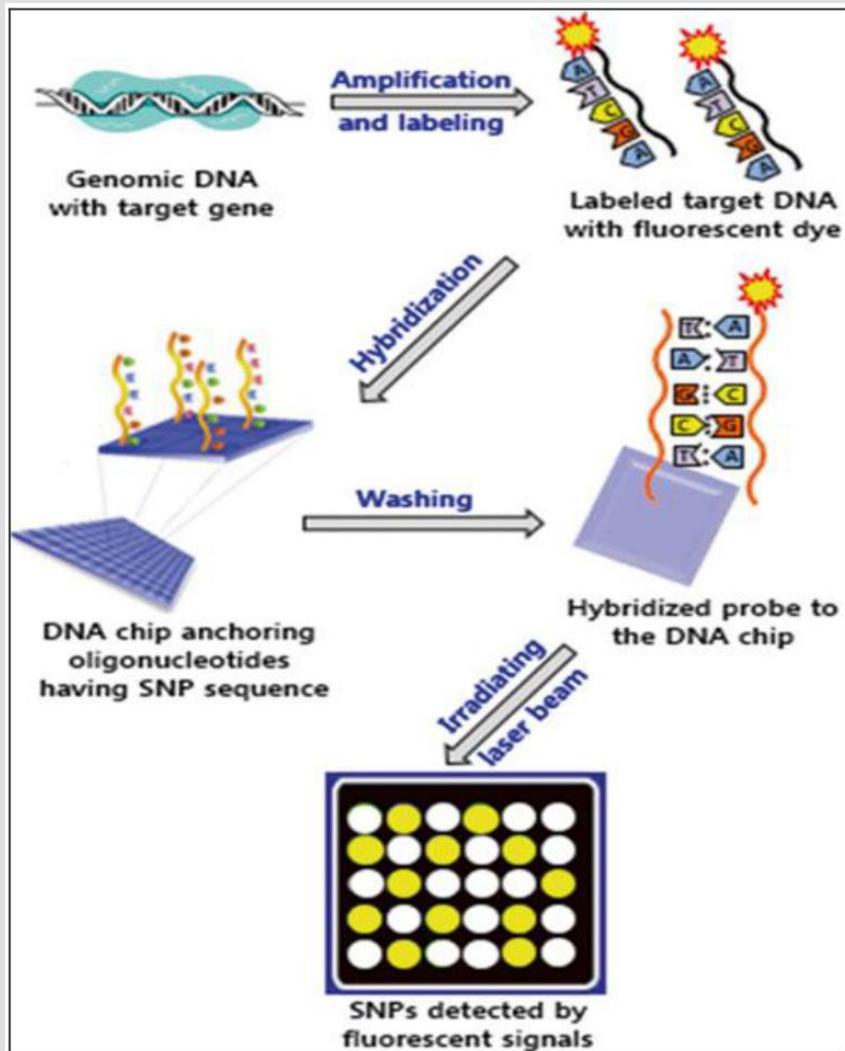
# Microsatellites



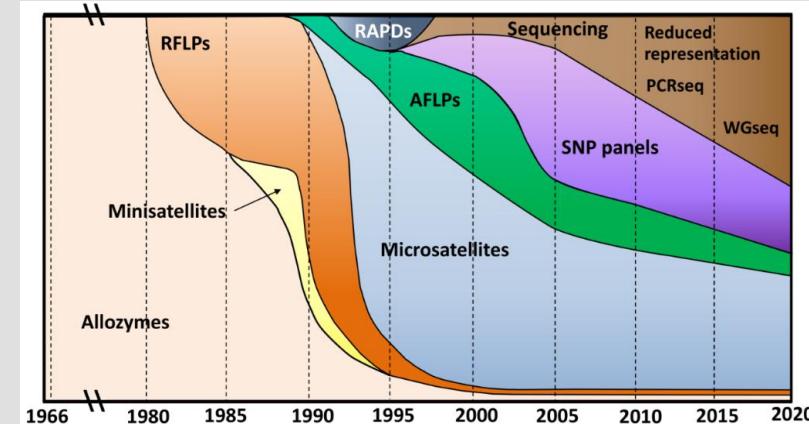
- Variable length repeats
- Highly polyallelic
- Easy
- Cheap
- 5-20 loci
- Still used today!



# SNP panels/SNP chips

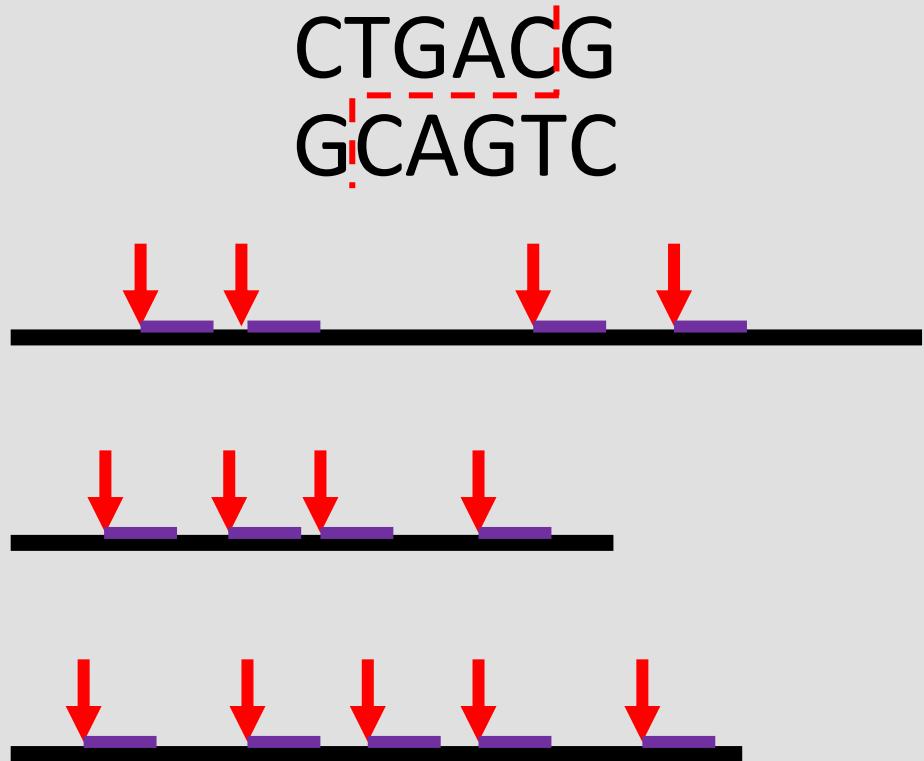


CGGACTACG  
CGGA~~A~~TACG

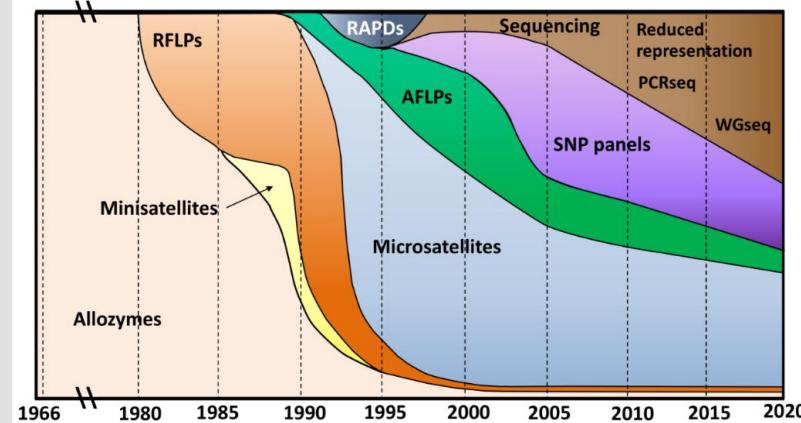


- Single-nucleotide Polymorphisms (SNPs)
- Only two alleles per locus
- Relatively cheap
- Need to be developed
- Higher level of technical expertise
- 1k – 100k+ loci

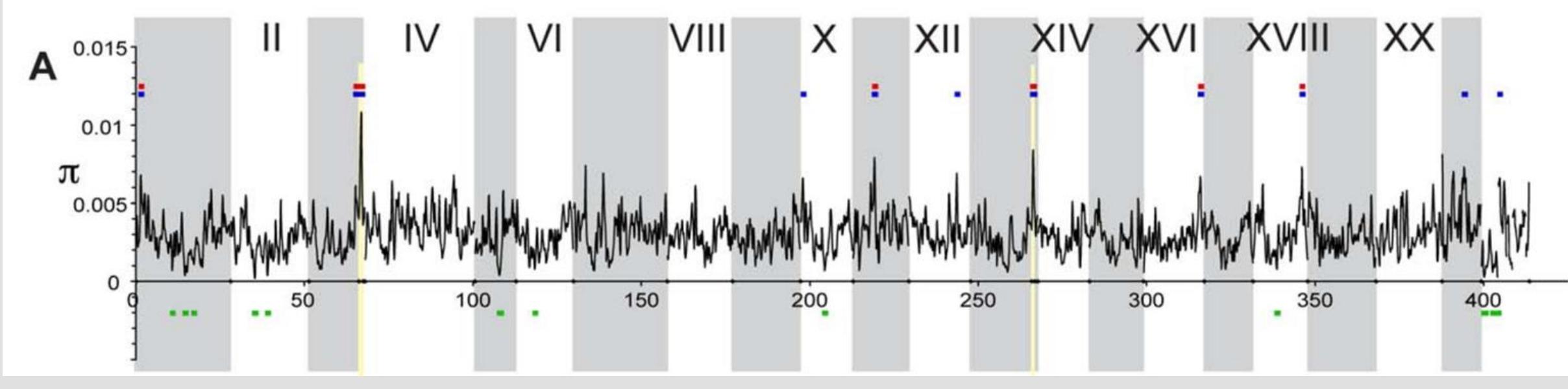
# Reduced Representation



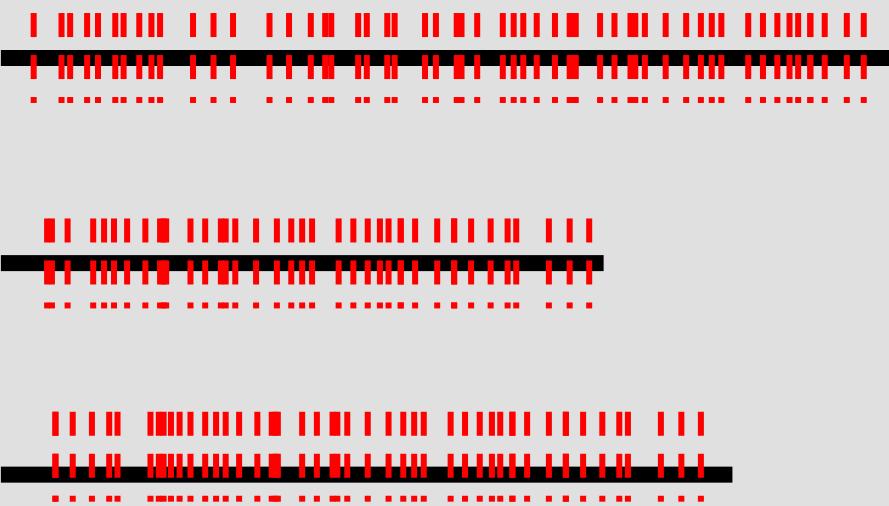
- SNPs/structural variants, etc.
- Can target random areas near cut sites (RAD)
  - Many exciting flavours!
- Can target expressed or specific areas (sequence capture)
- 1k-100k+ loci
- Fairly cheap
- No development needed for some types
  - RAD variants
  - Can benefit from a reference genome
- Great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



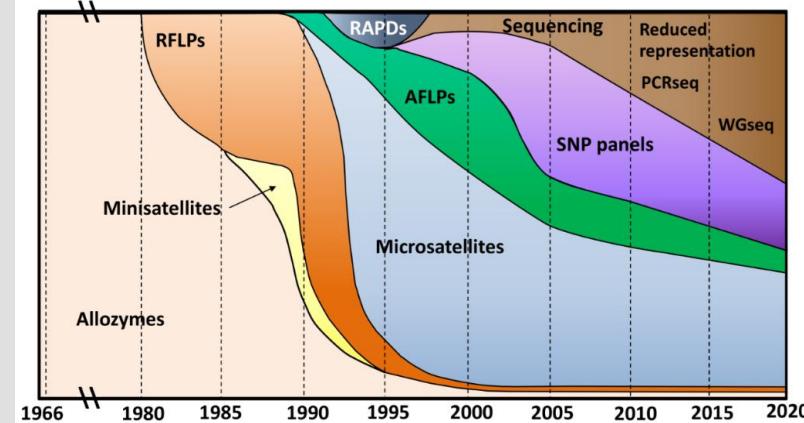
# Reduced Representation



# Whole-genome sequencing

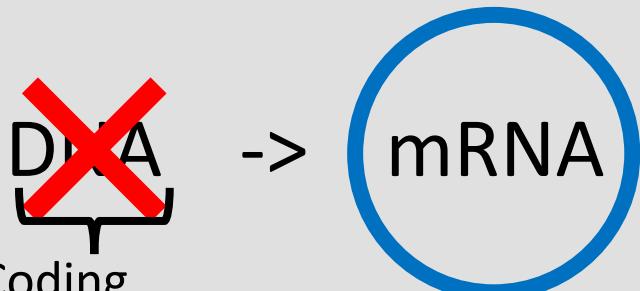


- SNPs/structural variants, etc.
  - Essentially everything barring tough-to-sequence regions
- 100k – 10M+ loci
- Often expensive
  - getting cheaper over time!
- No development needed
  - Greatly benefits from a reference genome.
- Excellent for studying patterns of diversity genome wide
- The gold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



# RNA-seq

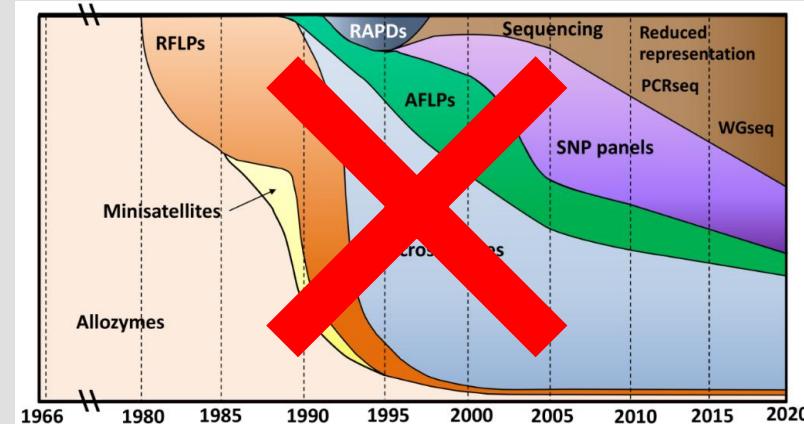
## Central Dogma of Molecular Biology:



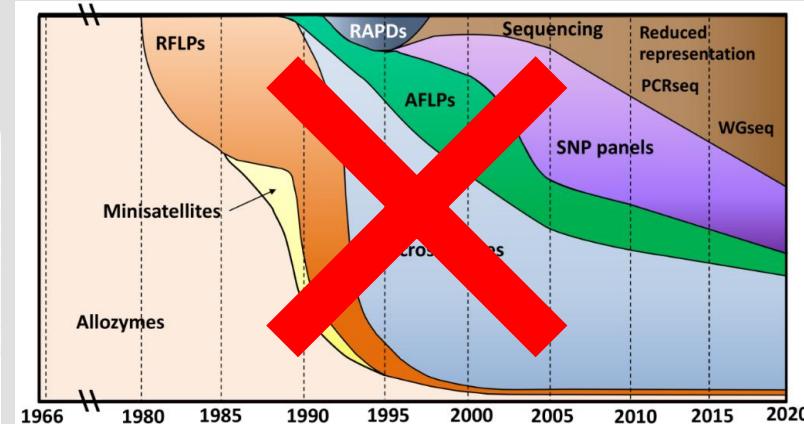
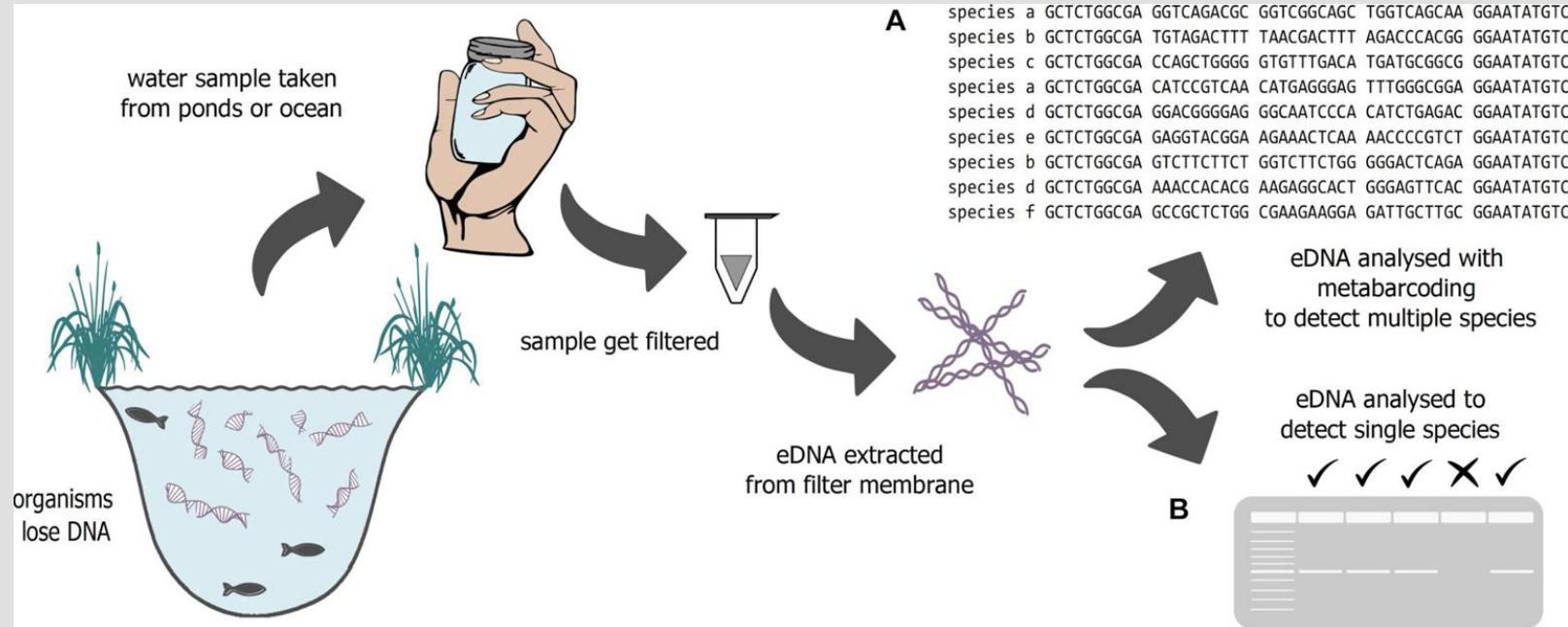
- Coding
- Regulatory
- Non-coding ("junk")

-> Protein -> phenotypes

- 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



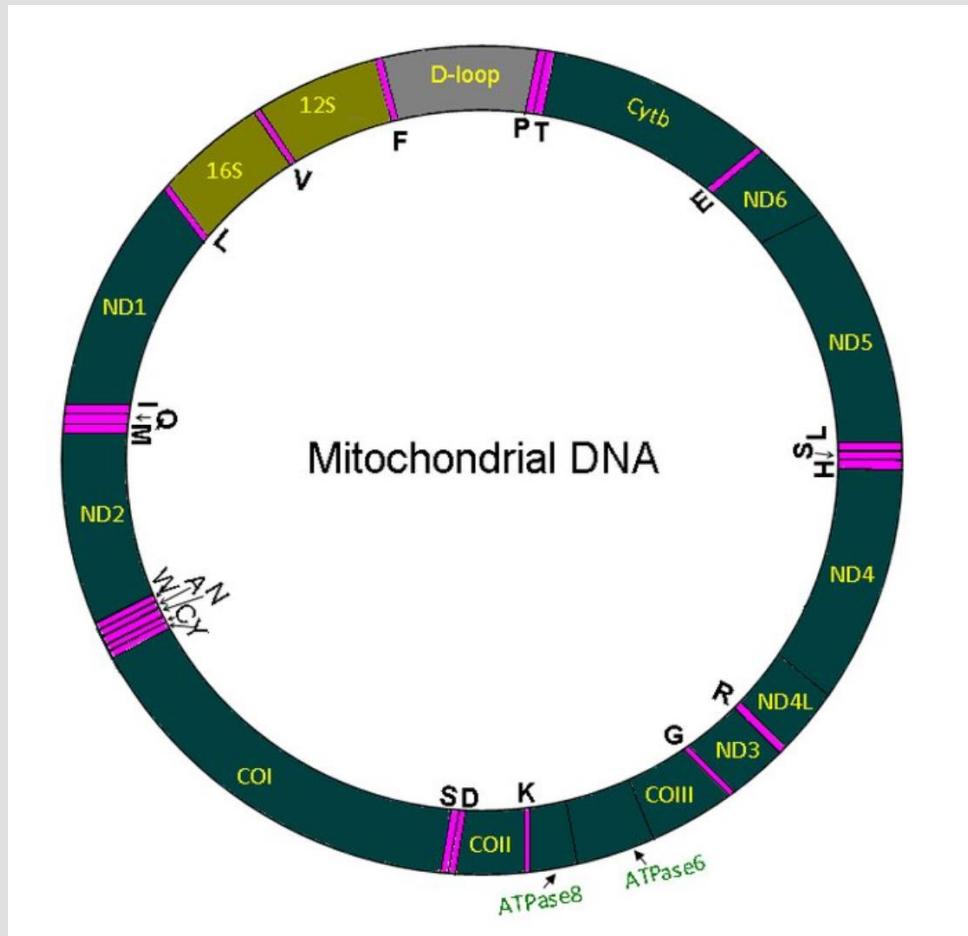
# eDNA



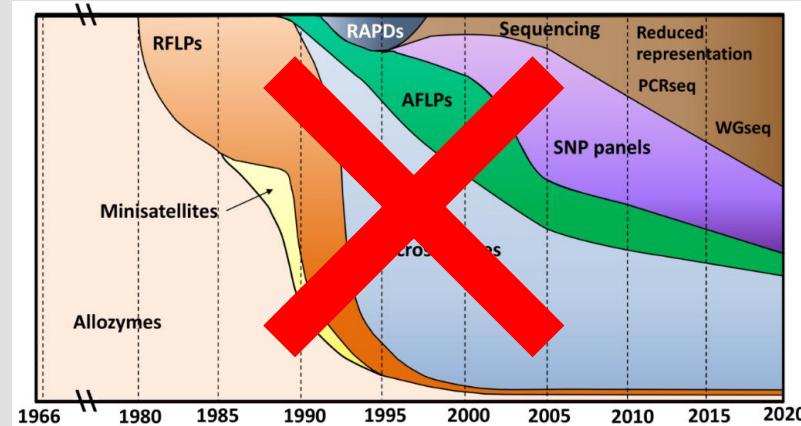
Schadewell and Adams 2021

- 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



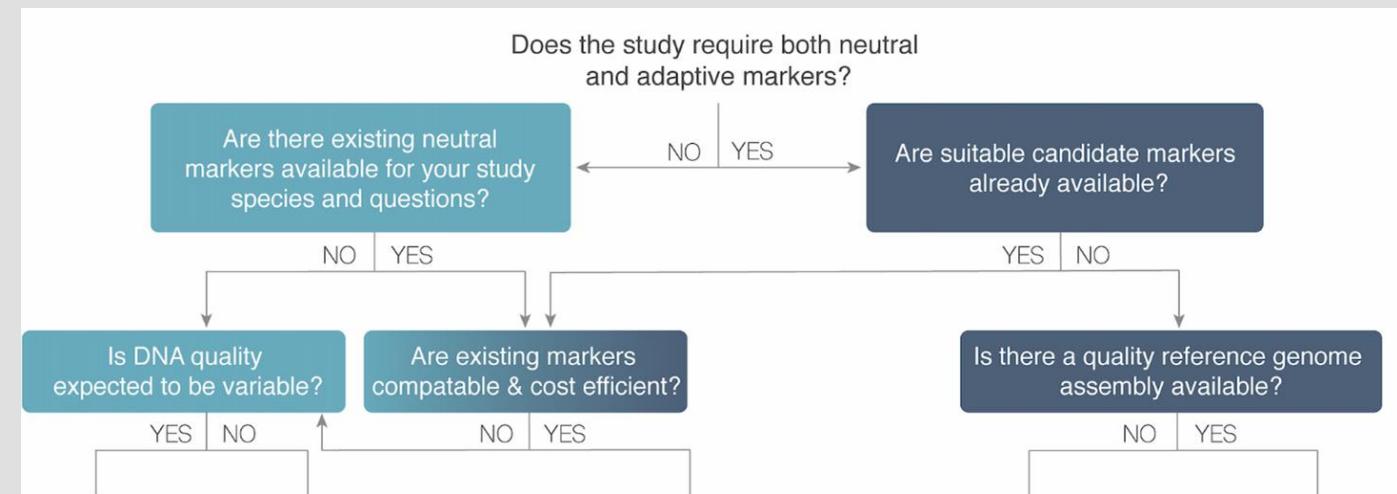
Raju et al 2011



- 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

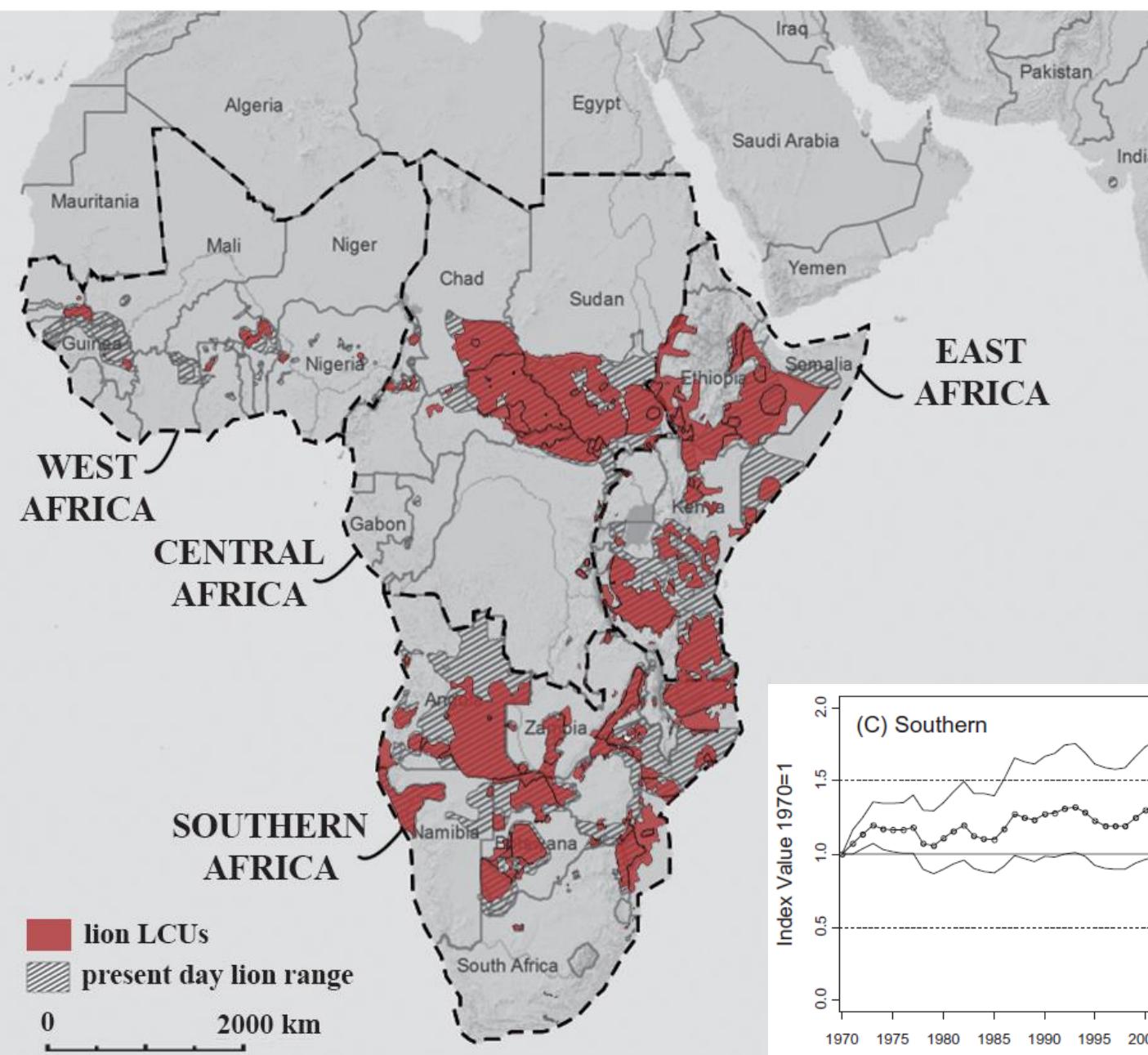


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 @LauraDBertola



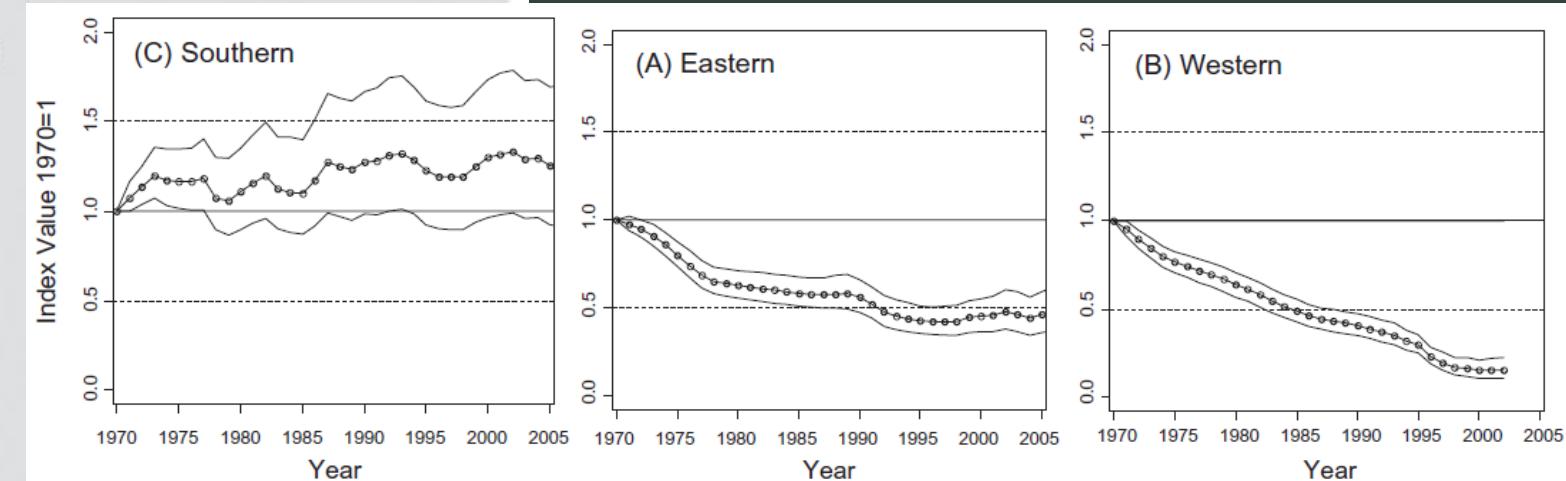


20,000-30,000 lions

~75% decline since 1970

West and Central Africa strongest declines.

Craigie et al., 2010

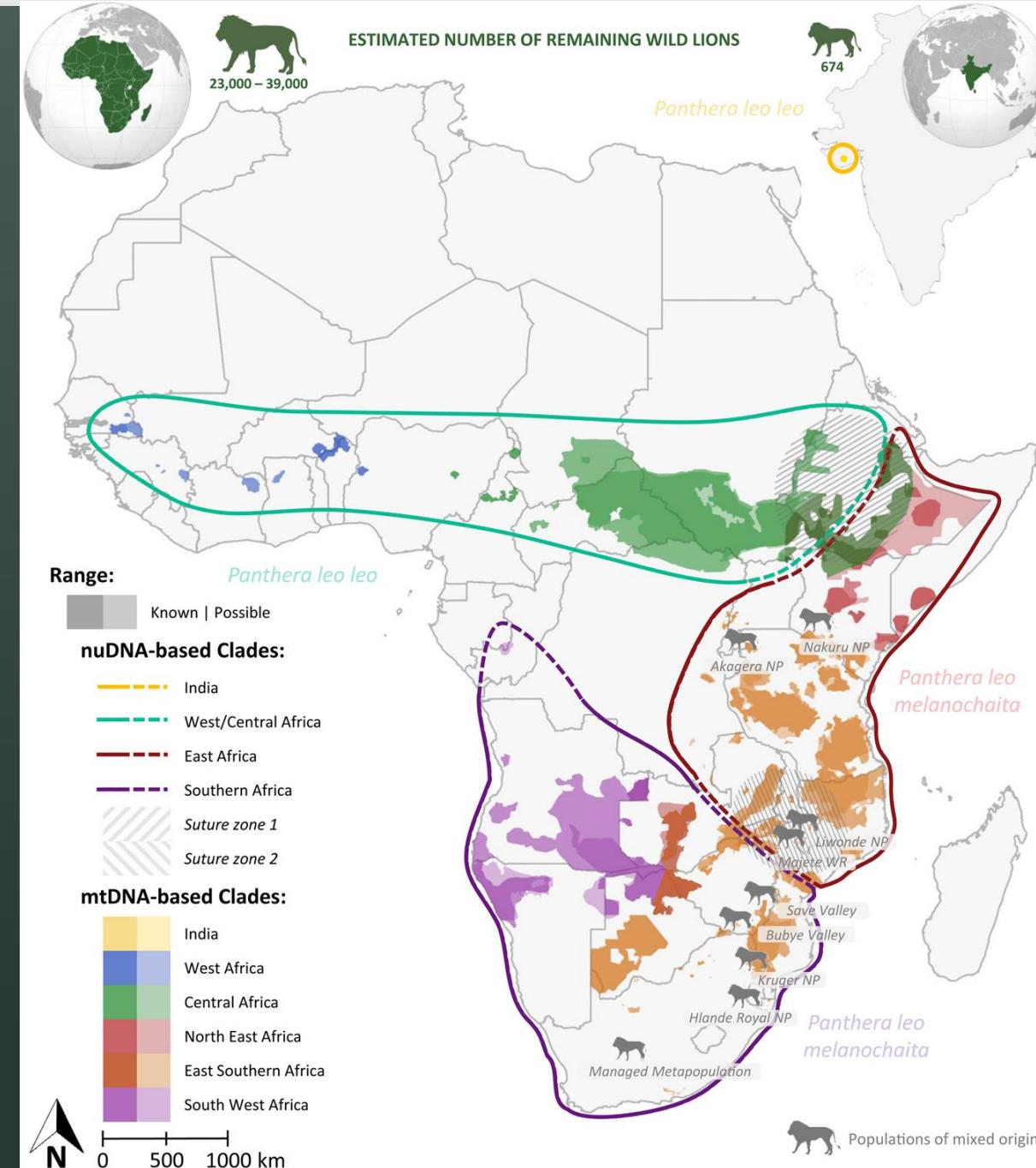


# Generating genomic resources:



# Baseline data

Bertola *et al.*,  
Evolutionary Applications  
2022



# A conservation genomics tool: SNP panels

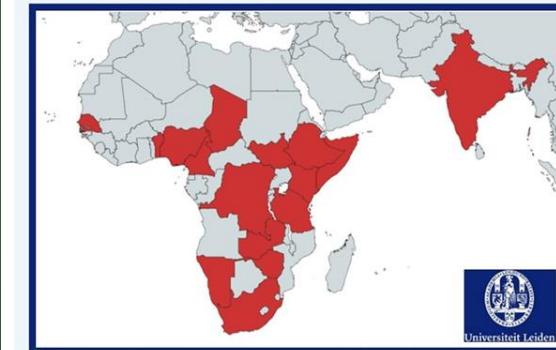
- Leiden University:  
335 nuDNA SNPs + 25 mtDNA SNPs
- SLU (Göran Spong):  
92 nuDNA SNPs, incl. 3 sex-linked +  
4 mtDNA

combined panel

## Leiden University SNP panel

335 nuDNA SNPs + 25 mtDNA SNPs

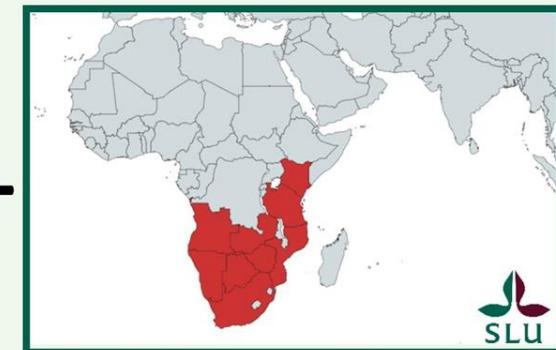
Emphasis on range-wide diversity, including hybridization zone in horn of Africa, and northern subspecies *Panthera leo leo*



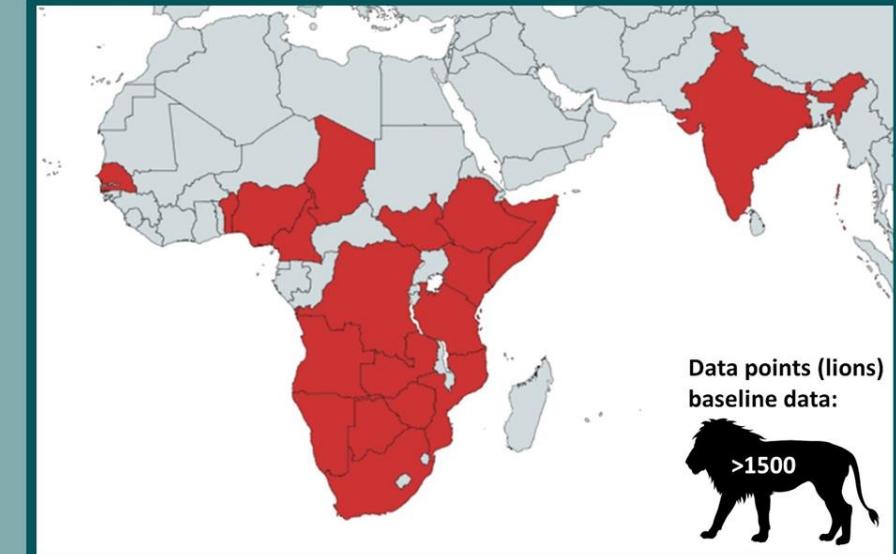
## SLU SNP panel

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

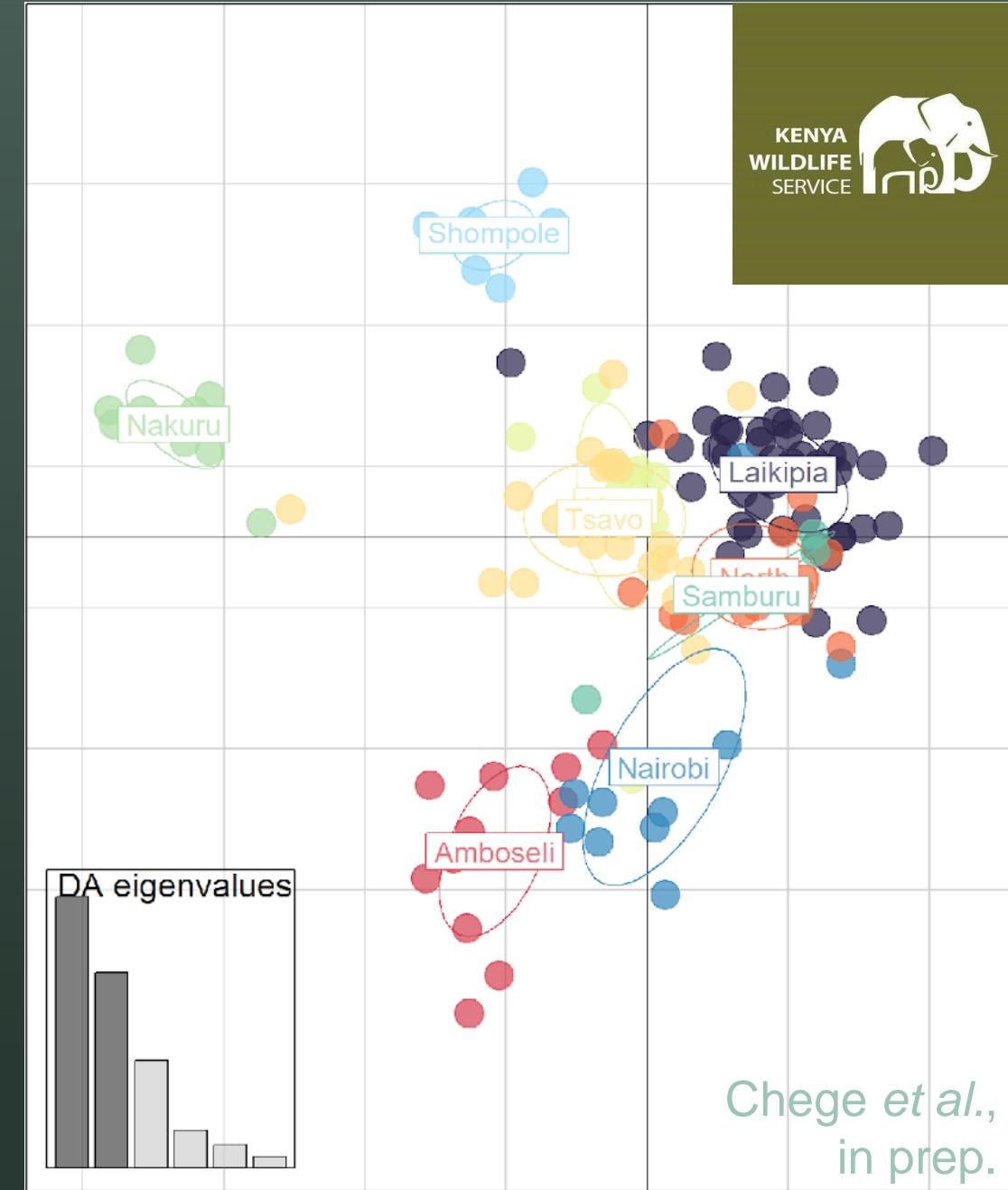
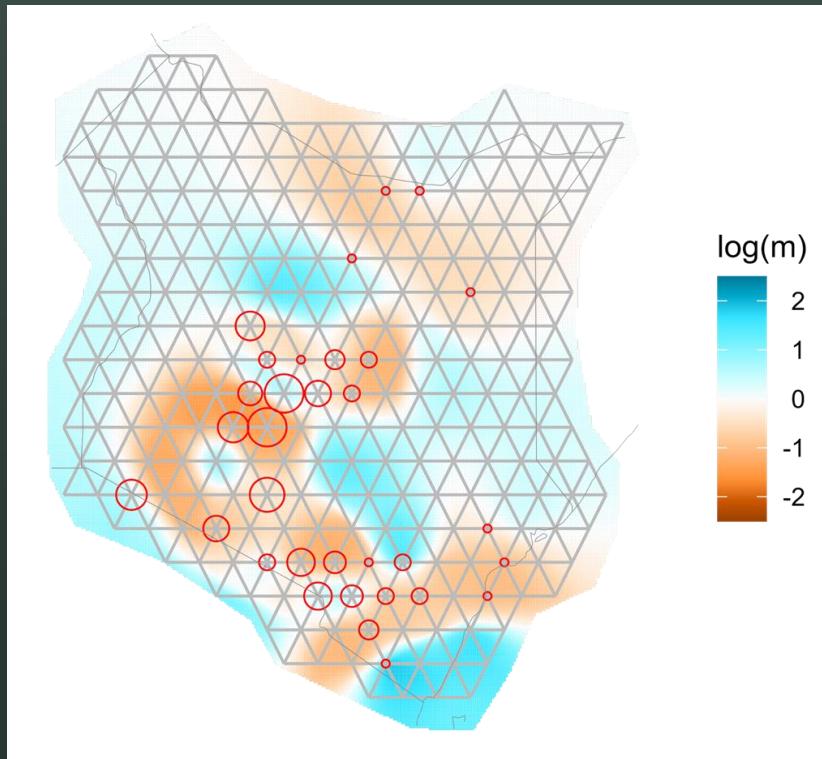


- Improved (combined) geographic coverage
- Connected baseline data (genotypes available for >1500 lions)
- Validation for use with low quality (i.e. non-invasively collected) samples
- Modular format, flexible use depending on specific data requirements
- Improved genome-wide coverage
- Sex-linked information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

# 1) Local conservation decisions

~150 Kenyan lions genotyped

- Population structure
- Population diversity
- Translocation history

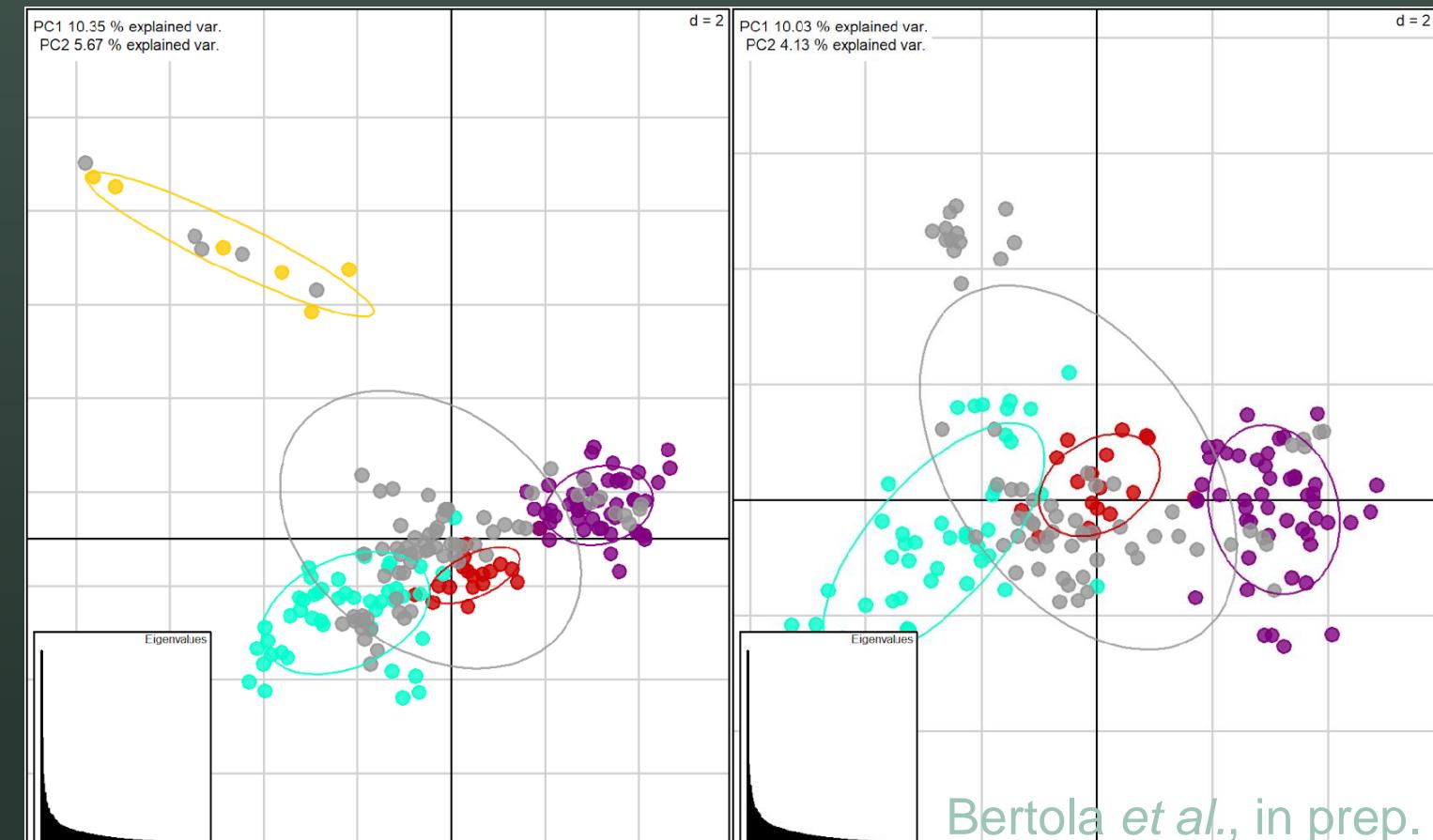
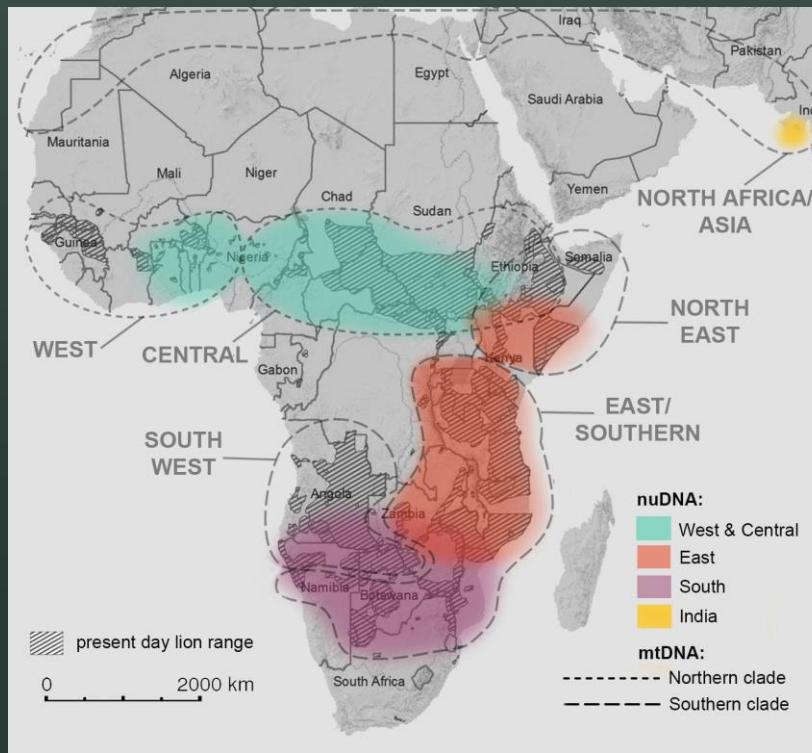


Chege *et al.*,  
in prep.

## 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

**Map**    Satellite



The map displays the African continent with a focus on the distribution of lions. Numerous red pins are placed on the map, indicating specific sampling locations across various countries including Senegal, Gambia, Guinea-Bissau, Sierra Leone, Liberia, Togo, Ghana, Nigeria, Benin, Niger, Chad, Central African Republic, South Sudan, Eritrea, Djibouti, Somalia, Kenya, Uganda, Rwanda, Burundi, Tanzania, DRC, and Cameroon. Major cities like Abidjan, Lagos, Yaoundé, Nairobi, and Dar es Salaam are also labeled.

CAGCCCTTCATAGGATAATGCTTACCGTGGGGCCAAATATCCTTTGAGGTGCAACTGTAATCACTAACTCCATCAGCAATCCCATA  
 GGCGACCTAGTAGAGTGATCTGAGGAGGCTCTAGTAGACAAAGCCACCCCTGACACGATTCTGCCTTCACTTCATCCTTCA  
 ATCTCGCCCTAGCAGCAGTCCACCTCCTGATGAAACAGGATCTAAACCCCTCAGGAATGGTATCTGACTCAGATAAA  
 TCCATCCATACTATACAATCAAAGATATCTAGGCCCTCTAGTACTAATCTAACACTCATACTACTCGTCTTCTACCAGACCT  
 AGATCCGACAACTATACCCCGCCAATCTCTAAGCACCCCTCCCATATCAAACCTGATGGTACTCCTATTGATATGCAATC  
 TCTATTCCAATAAACTAGGAGGAGTTAGCCCTAGTCTATCCATCTTAATCTAGCAATTATCCCTGCCCTCCACACTTCAAAC  
 GATTAATGTTGACCAACTAAGTCAATGCTTATCTGATCTCTAGTAGCGGACCTCTGACCCCTGACATGAATTGGTGGCAACCTG  
 CCCCTCATCACCATGGCCAAGTAGCCTCCATCCTACTTCTCATTCTCTAATCCTAATACCCATCTCAGGCATTATTGAAAAC  
 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.

	Hapl...	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



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Biodiversity for Life



# 4) Translocations

Identifying suitable  
source-target  
population pairs.



# Communicating genomic resources:

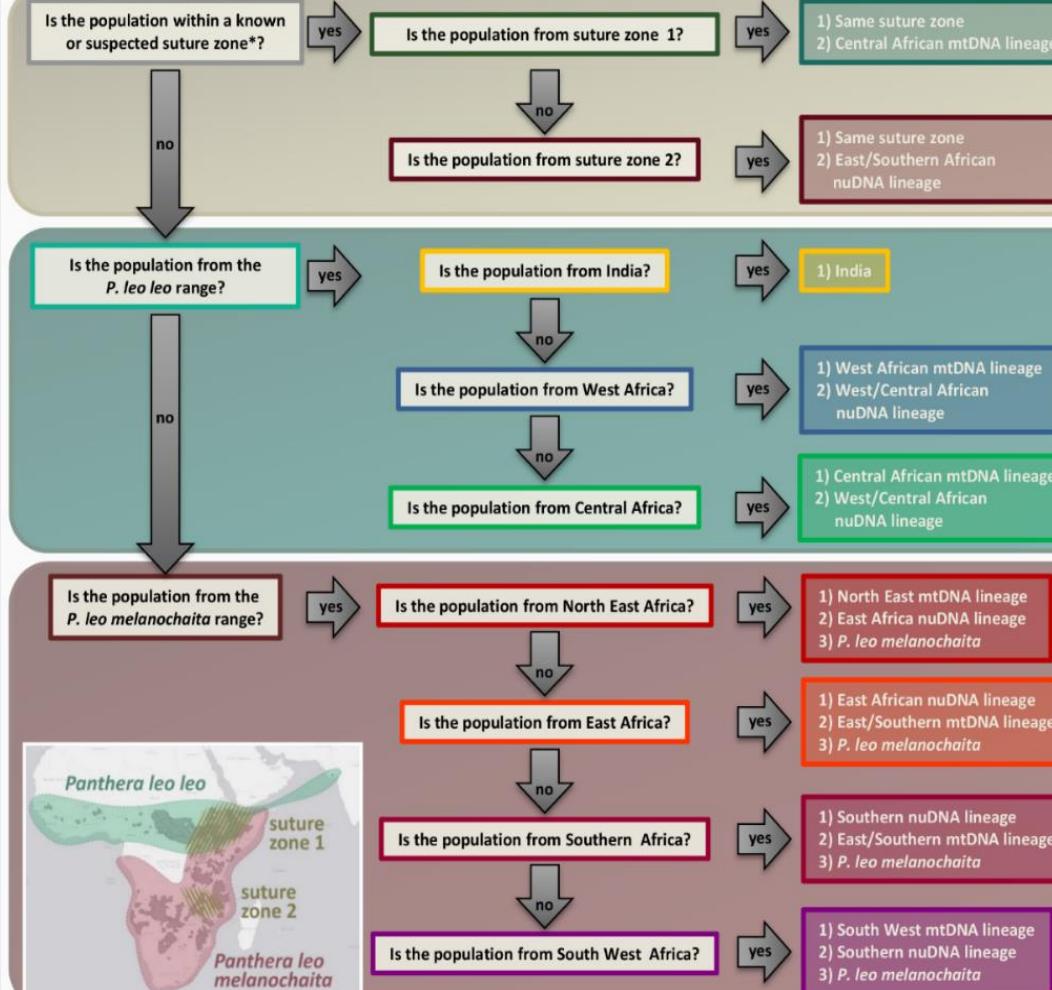
## Decisions Guide.

Bertola et al.,  
Cat News  
2022

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



#### Suggested range for source population:



SOM: Bertola et al. (2022) Policy implications from genetic guidelines for the translocations of lions (*Panthera leo*). Cat News. Para citar: Bertola et al. (2022) Policy implications from genetic guidelines for translocations: Maintaining intraspecific diversity in the lion (*Panthera leo*). Evolutionary Applications, 15(1), 22–39. DOI: 10.1111/eva.13318

Maio 2022  
Guia de Decisões



#### Orientações genéticas para a translocação de leões

Sumário executivo

Para a conservação efetiva da biodiversidade, a diversidade genética intraspecífica deve ser considerada. As diretrizes genéticas para a translocação de leões (*Panthera leo*) foram desenvolvidas para fornecer orientações para os gerentes de conservação que realizam translocações de leões. Elas visam garantir que a diversidade genética seja mantida dentro das populações de leões.

Mai 2022  
Guide de Déisions



#### Lignes directrices génétiques pour la translocation du lion

##### Résumé exécutif

La diversité génétique au sein des espèces doit être prise en compte pour assurer une conservation efficace de la biodiversité. Les directives génétiques pour la translocation des lions (*Panthera leo*) ont été élaborées pour fournir des recommandations aux gestionnaires qui effectuent des translocations de lions. Elles visent à assurer que la diversité génétique soit maintenue à l'intérieur des populations de lions.

Mai 2022  
Decisions Guide



#### Genetic guidelines for the translocations of lions

##### Executive summary

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 indicates that over 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. Hence, we propose to take genetic diversity in the lion 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 providing 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 maternal lineage, provides a less complete image of the evolutionary history.
- 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 both mtDNA and nuDNA genetic markers, we propose the following suitability for source/target combinations for translocations:

**First choice:** same nuDNA + same mtDNA clade  
**Second choice:** different nuDNA clade, same mtDNA clade  
**No choice:** different mtDNA clade, same nuDNA clade  
  
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.

