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An increasing number of bee species are commercially reared to ensure pollination services. However, release of reared bees may lead to genetic admixture with wild conspecifics, thereby disrupting local adaptations. While such genetic pollution has been shown for bumble bees, respective data for solitary bees *Osmia* spp. are currently lacking. Here, we use population genetics to investigate whether the release of reared *Osmia* spp. has an effect on genetic diversity and structure of wild *Osmia* spp. populations. In 2022-2023, *Osmia bicornis* and *Osmia cornuta* cocoons were obtained from two commercial breeders and sampled in semi-natural, urban and rural areas of Switzerland with differences in released *Osmia* spp. numbers. Museum specimens of *O. bicornis* sampled in the same areas before *Osmia* spp. commercial rearing started (i.e., in the 1990s) were used as negative controls. Genetic diversity and population structure of each species across sampling areas and time periods were assessed using mitochondrial and nuclear DNA microsatellite markers to assess whether the breeding and commercialization of *Osmia* spp. affected the gene pools of wild populations. Microsatellites analyses revealed high levels of migration between sampling areas in both time periods. In *O. cornuta* no significant differences in genetic diversity levels or in the genetic structure between sampling areas were found. In *O. bicornis*, the same patterns were observed, but when comparing time periods observed heterozygosity declines and significant changes of genetic structure were detected. In the contemporary samples, new alleles were found in all the three sampling areas but an overall decrease of private allelic richness was found. High admixture between sampling sites suggests higher flight distances than previously expected for *Osmia* spp., which are considered philopatric species. Pre- and post-management comparisons indicate changes in population structure and introduction of novel alleles that may be related to management, while the overall decrease of observed heterozygosity and private alleles suggest an ongoing erosion of genetic diversity caused by other stressors. To confirm these results, ongoing mitochondrial DNA analyses will allow better tracking of management effects through the detection of non-local haplotypes into wild populations.

Spatio-temporal population genetics of solitary bees to investigate the impact of *Osmia* spp. management

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Managed solitary bees

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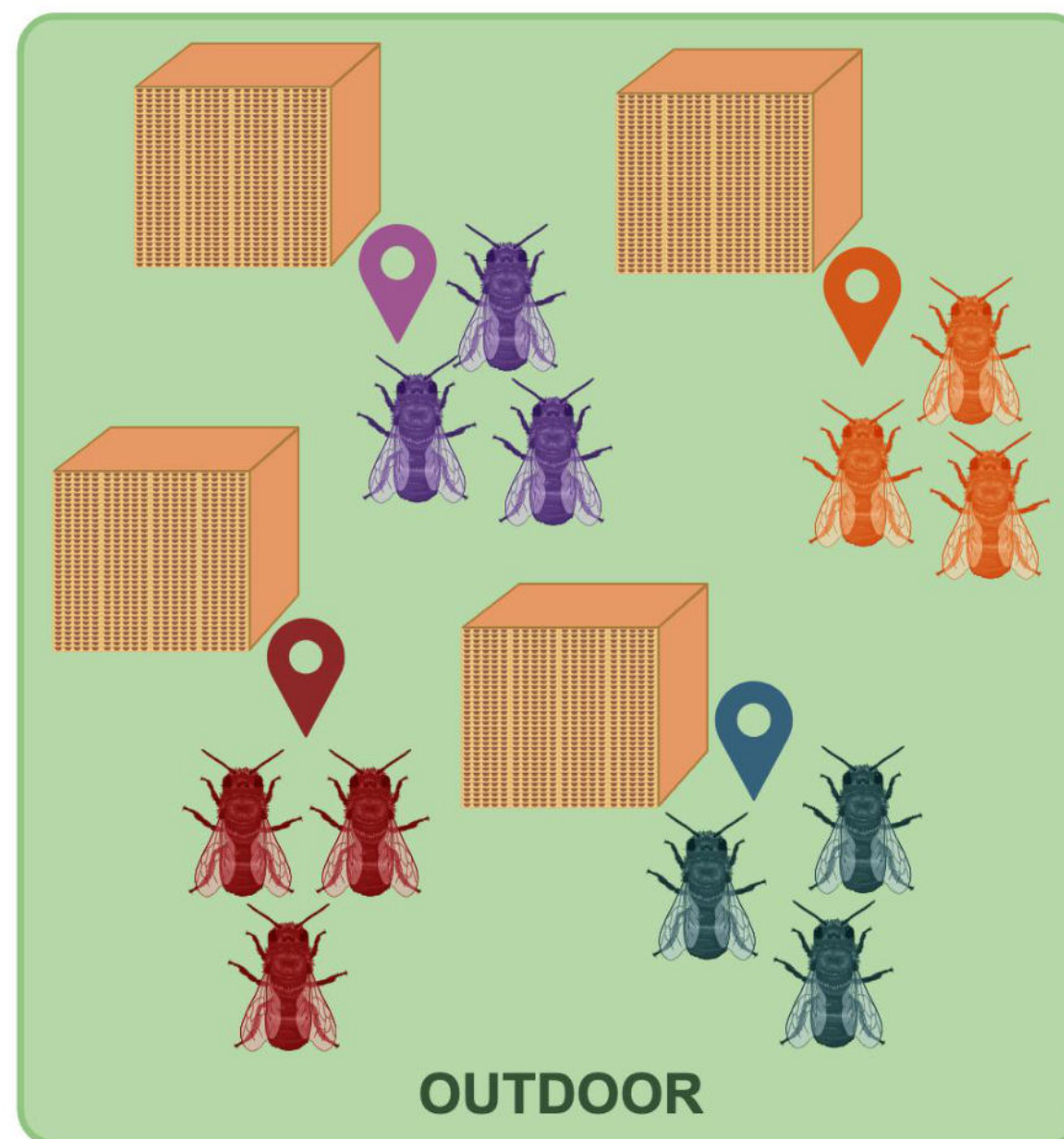
In Europe *Osmia bicornis* is one of the most commonly managed solitary bee species.



How does the solitary bees' management work?

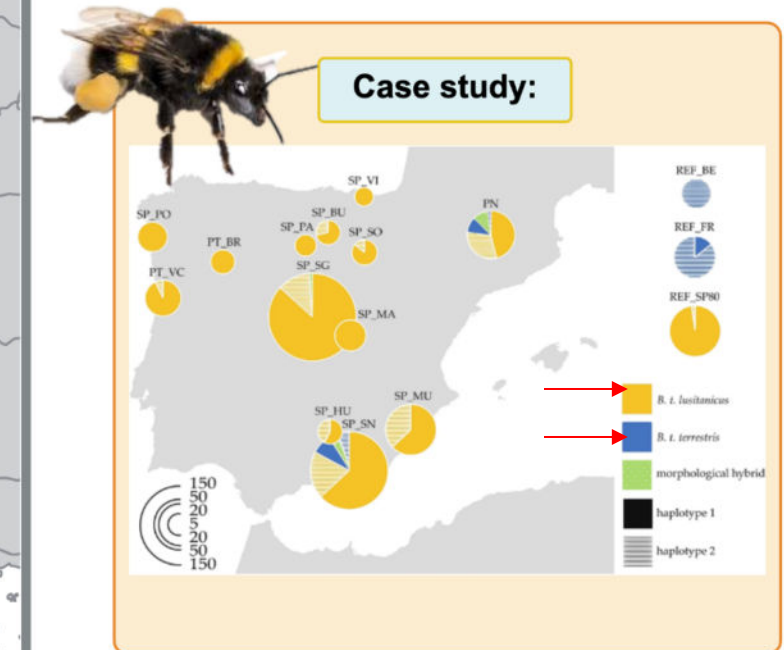
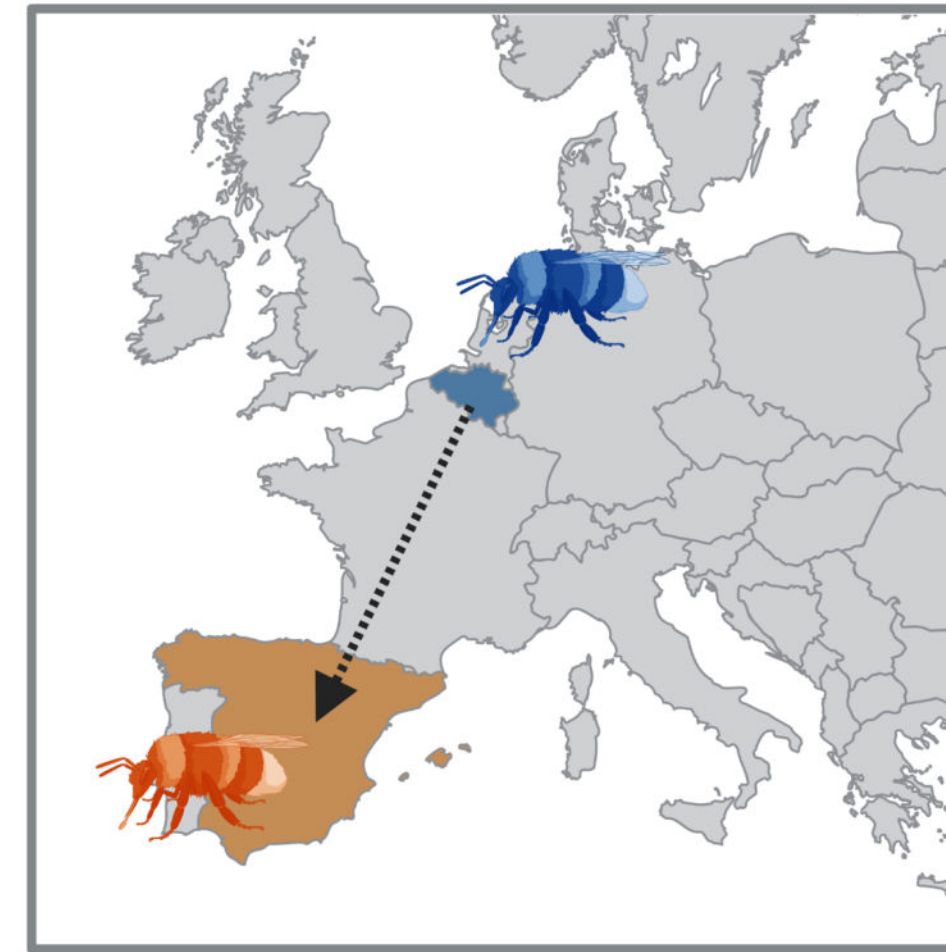
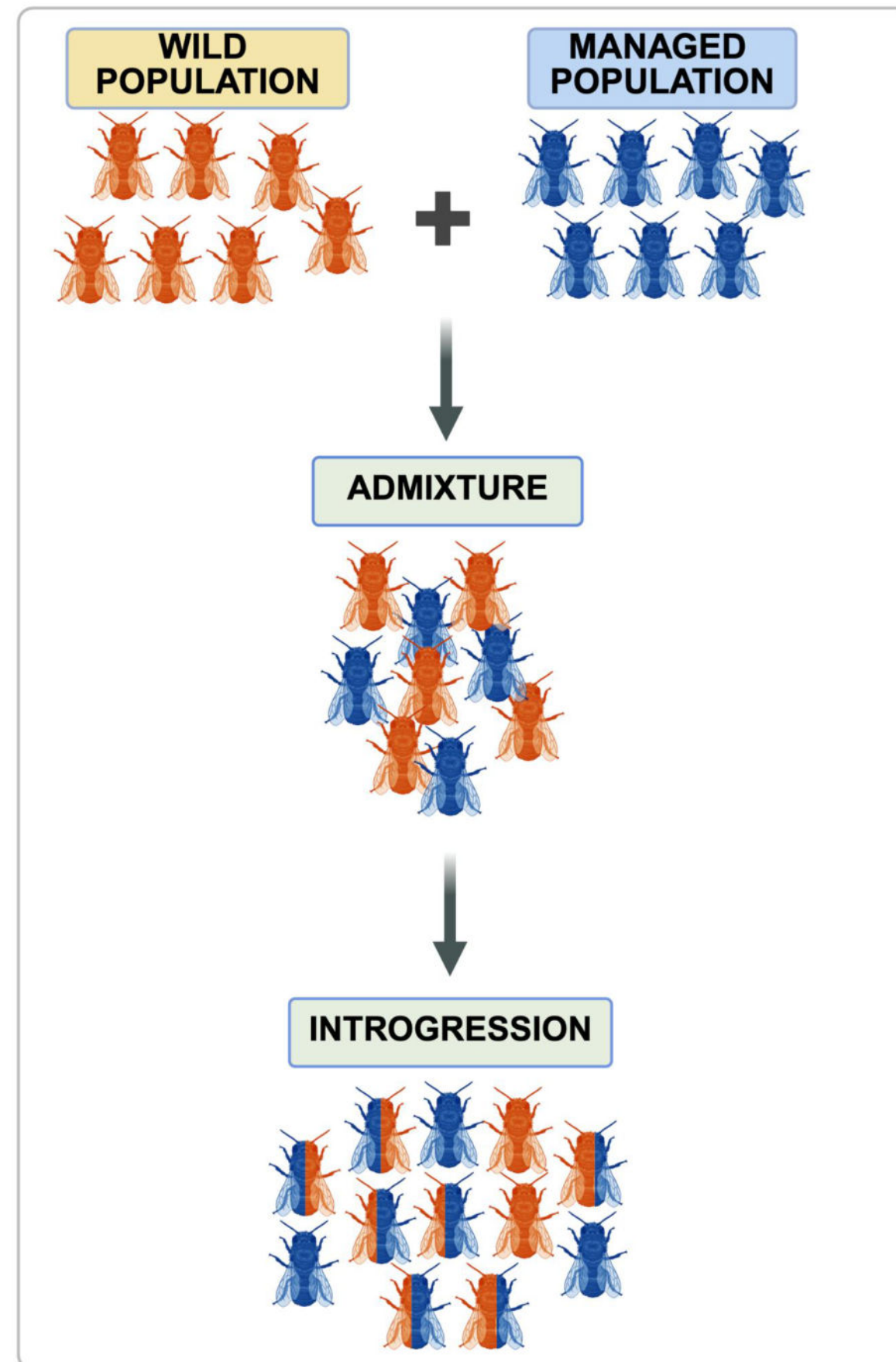
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MATING AND NESTING PHASE



What could be the consequences?

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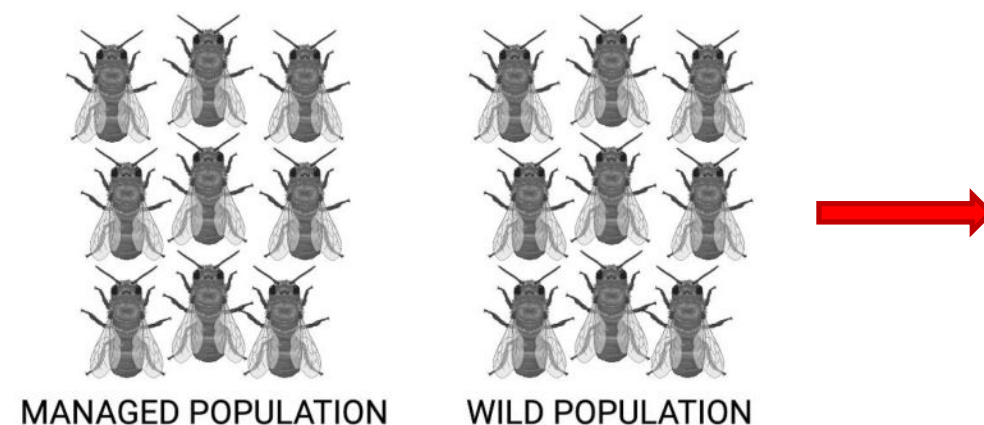
Detrimental effects:

Less capable to survive to the specific conditions of the place where they live (e.g. dry summers).

Why we need population genetics

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Not possible to distinguish wild and managed populations of the same species morphologically

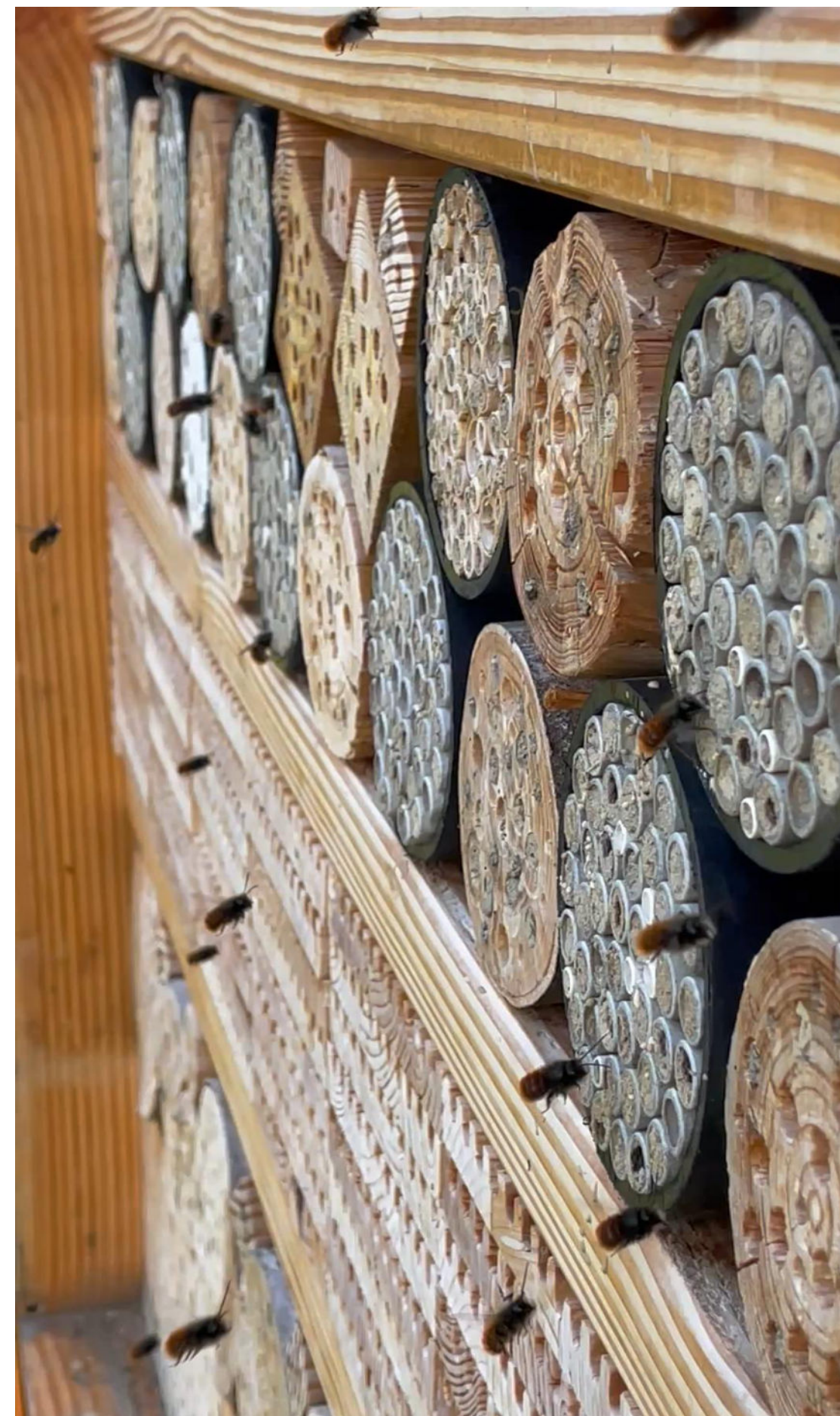


Genetics allow to distinguish between them...

...and to analyse:

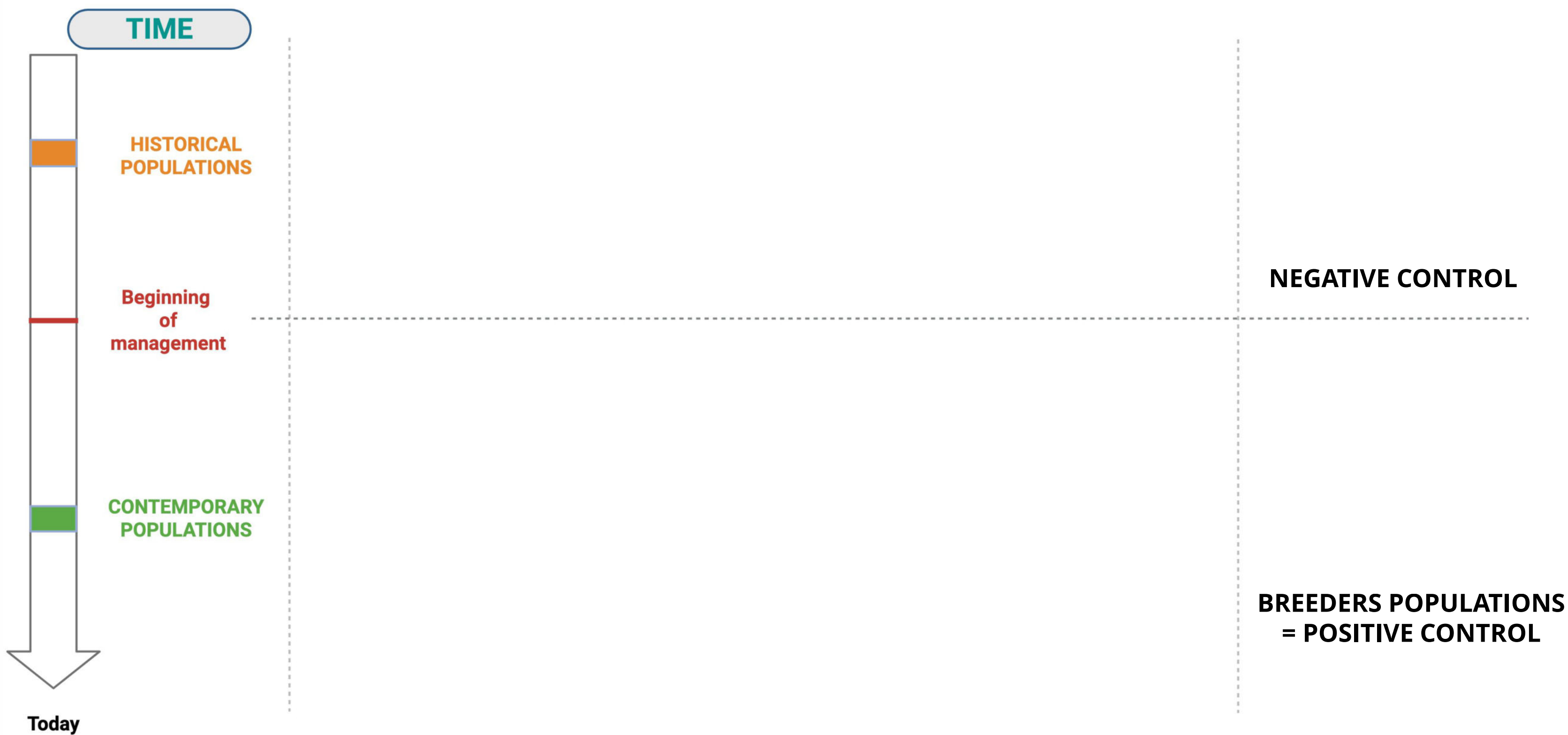


Does management of *Osmia* impact genetics of wild populations?



Goal of the study

Assess whether the management of *Osmia bicornis* can influence the genetics of locally adapted, wild populations through a **spatio-temporal** analysis.



INTRO

METHODS

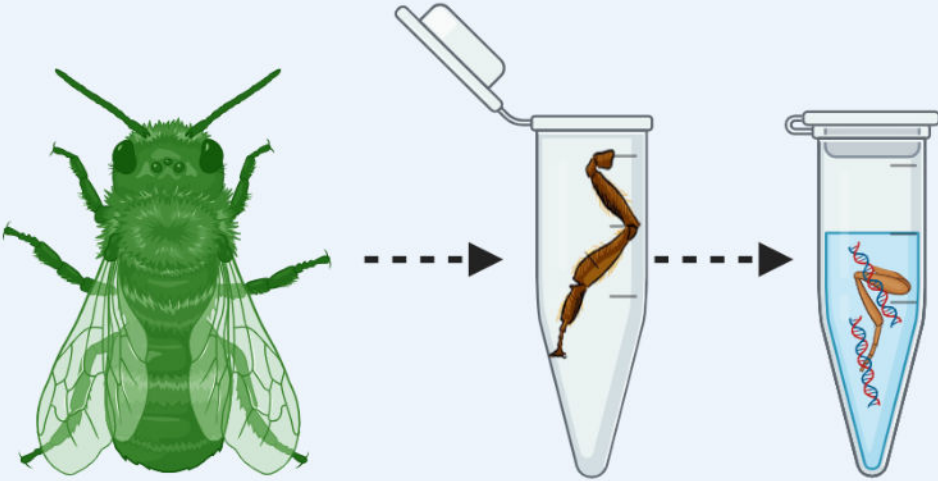
RESULTS

DISCUSSION

Genetic analyses

DNA EXTRACTION

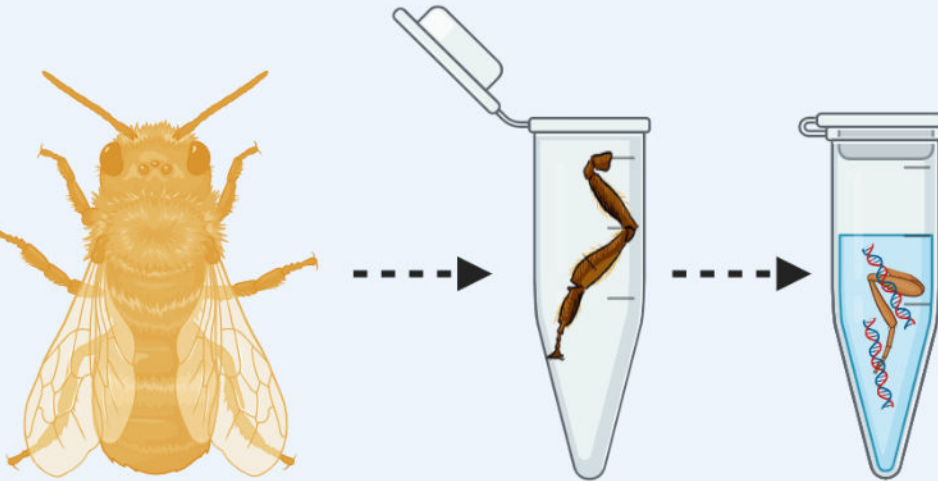
Contemporary samples



(n = 253)

(n = :)

Historical samples



(n = 50)

(n = :)

INTRO

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Hypotheses

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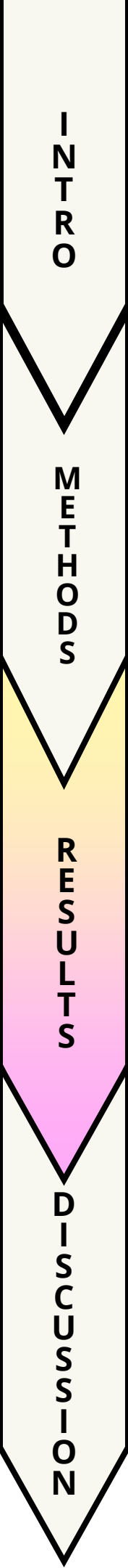
1. ORIGIN

2. DIVERSITY

3. MOVEMENT

Mitochondrial DNA diversity and structure

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Haplotype



- h1 is shared between managed and all contemporary populations;
- **Contemporary populations:**
 - Similar origin,
 - Similar diversity,
 - Movement between populations;

Mitochondrial DNA diversity and structure

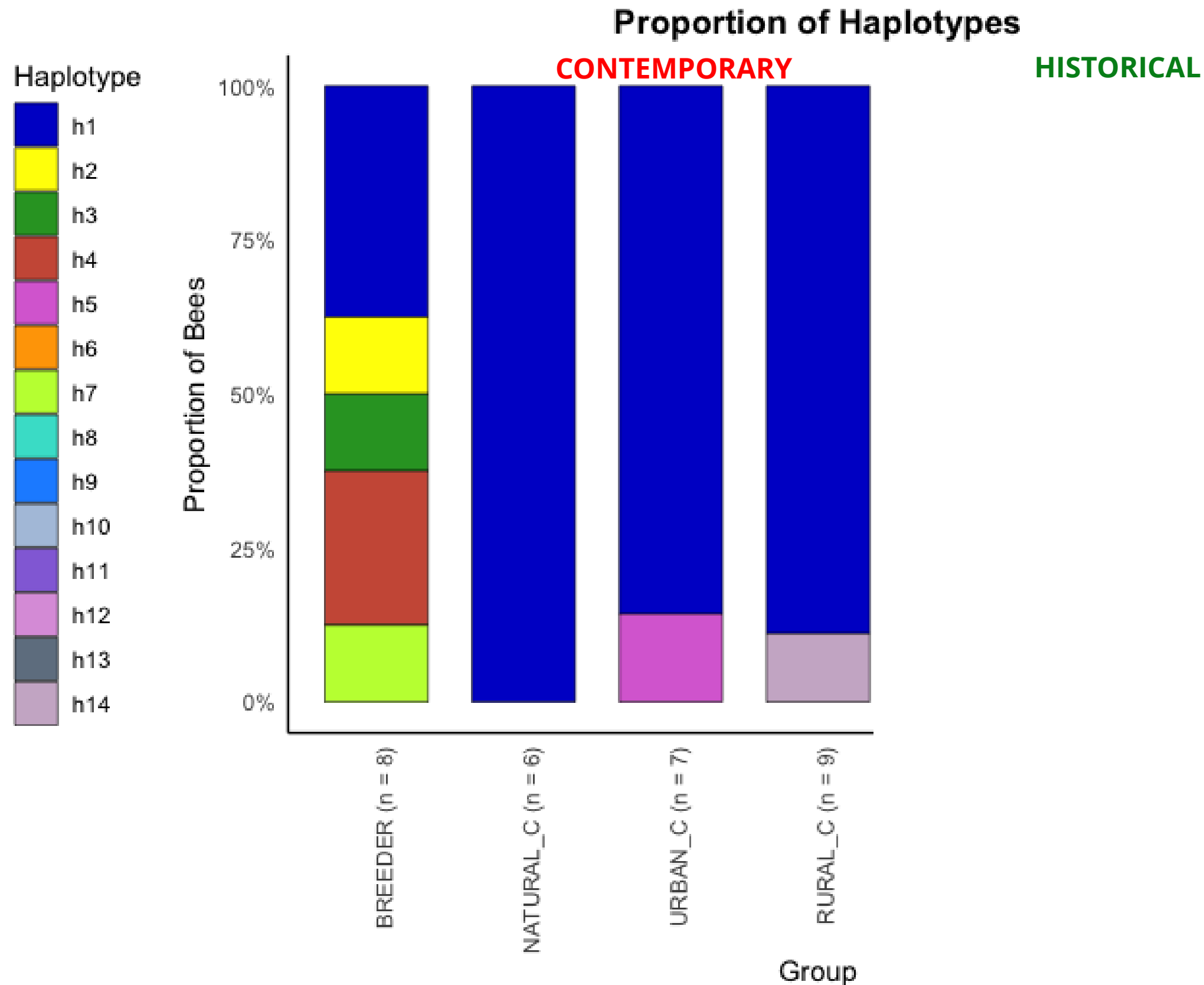
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- h1 is found in all populations;
- **Historical populations:**
 - Similar origin,
 - Higher diversity,
 - Movement between populations;



1) Natural migration over short distances

2) Human-mediated dispersal over long distances

Management effect

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INTRO

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1. ORIGIN

Shared haplotype between
managed and wild
contemporary and historical
populations
=
**no introduction of
“managed” haplotypes**

2. DIVERSITY

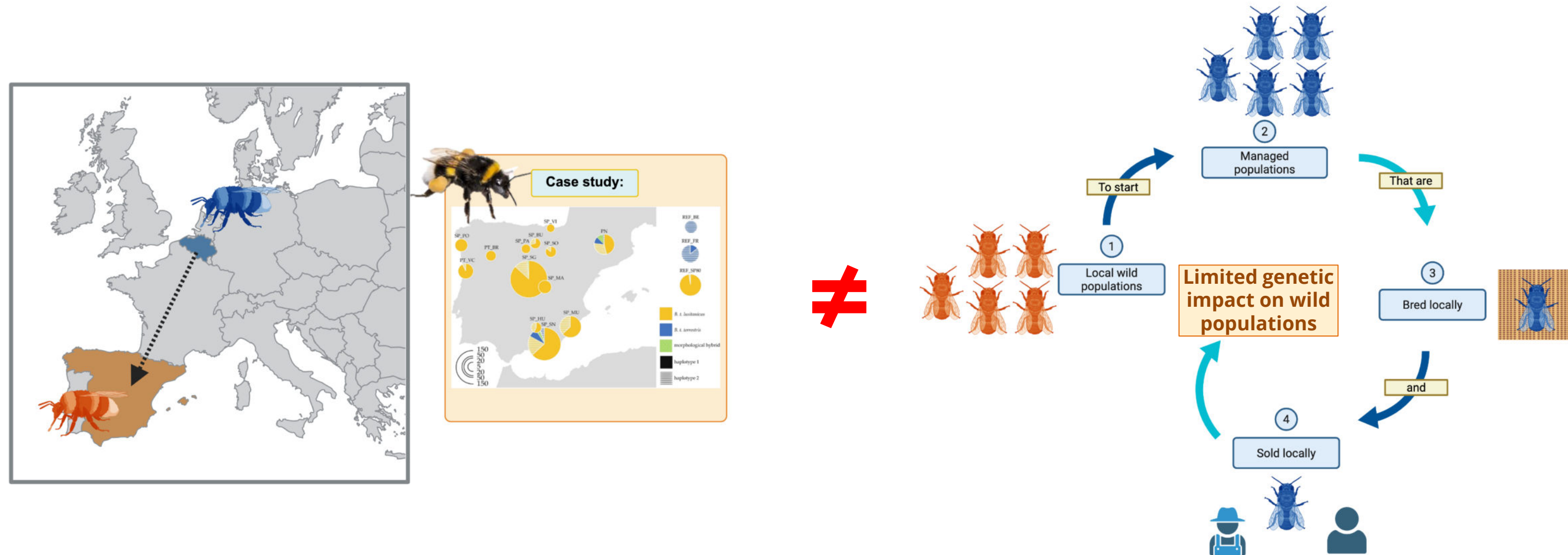
Loss of diversity
=
**External stressors are
eroding genetic diversity**

3. MOVEMENT

Increased movement
between populations over
time

Conclusion

1. Management is unlikely to interfere with genetics of wild solitary bees



2. Genetics eroded over time = enhanced need for conservation of solitary bees

Many thanks for your attention



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LUZERN Natur
Geschichte
Gesellschaft

ETH zürich
Entomological Collection

NATUR
HISTORI
SCHES
MUSEUM
BERN

 UNESCO Biosphäre
Entlebuch
LUZERN SCHWEIZ

 URSULA WIRZ-STIFTUNG

 Schweizerische Eidgenossenschaft
Confédération suisse
Confederazione Svizzera
Confederaziun svizra

Eidgenössische Departement für
Wirtschaft, Bildung und Forschung WBF
Département fédéral de l'économie
de la formation et de la recherche DEFR
Agroscope

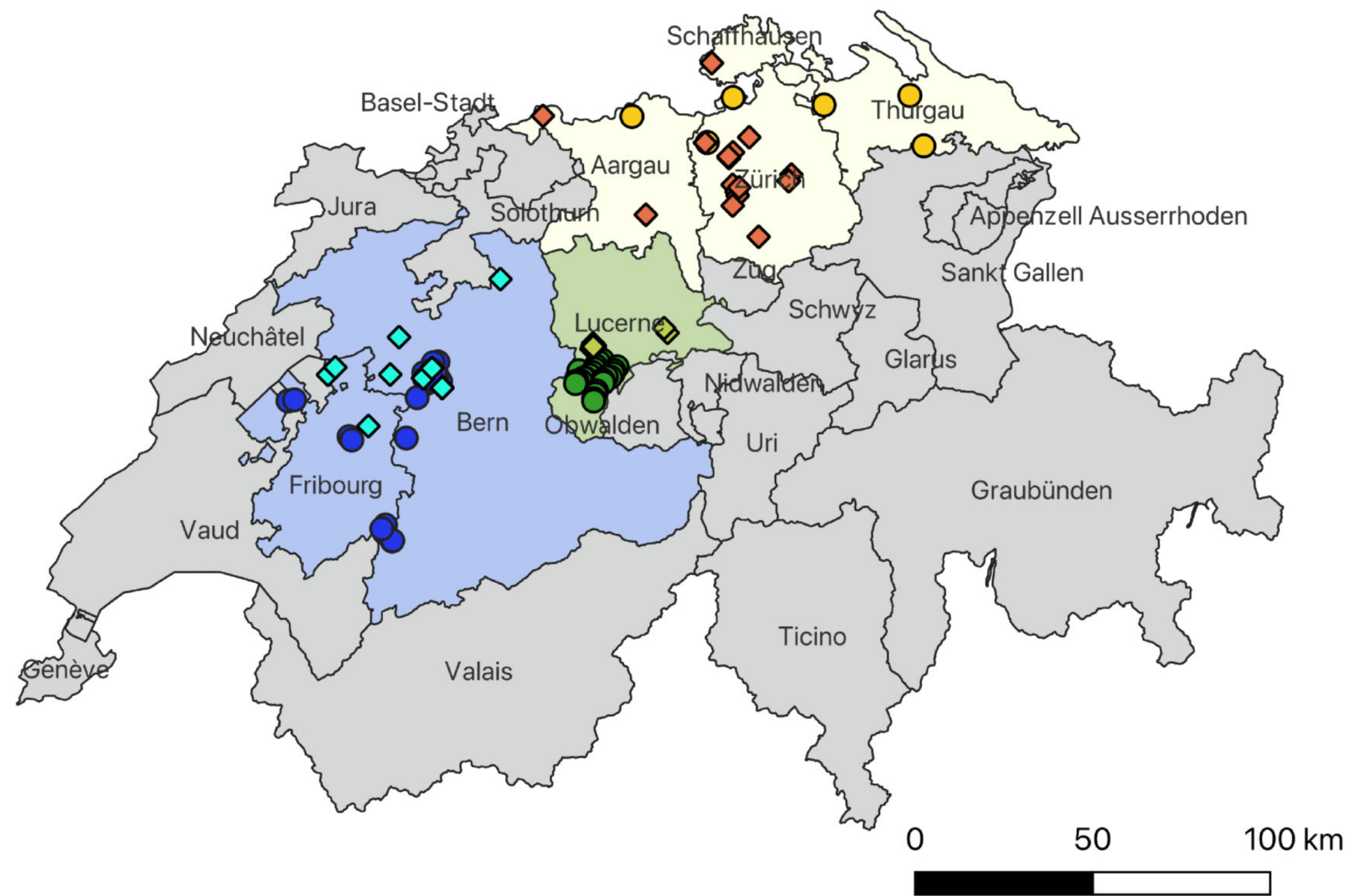
Sampling areas

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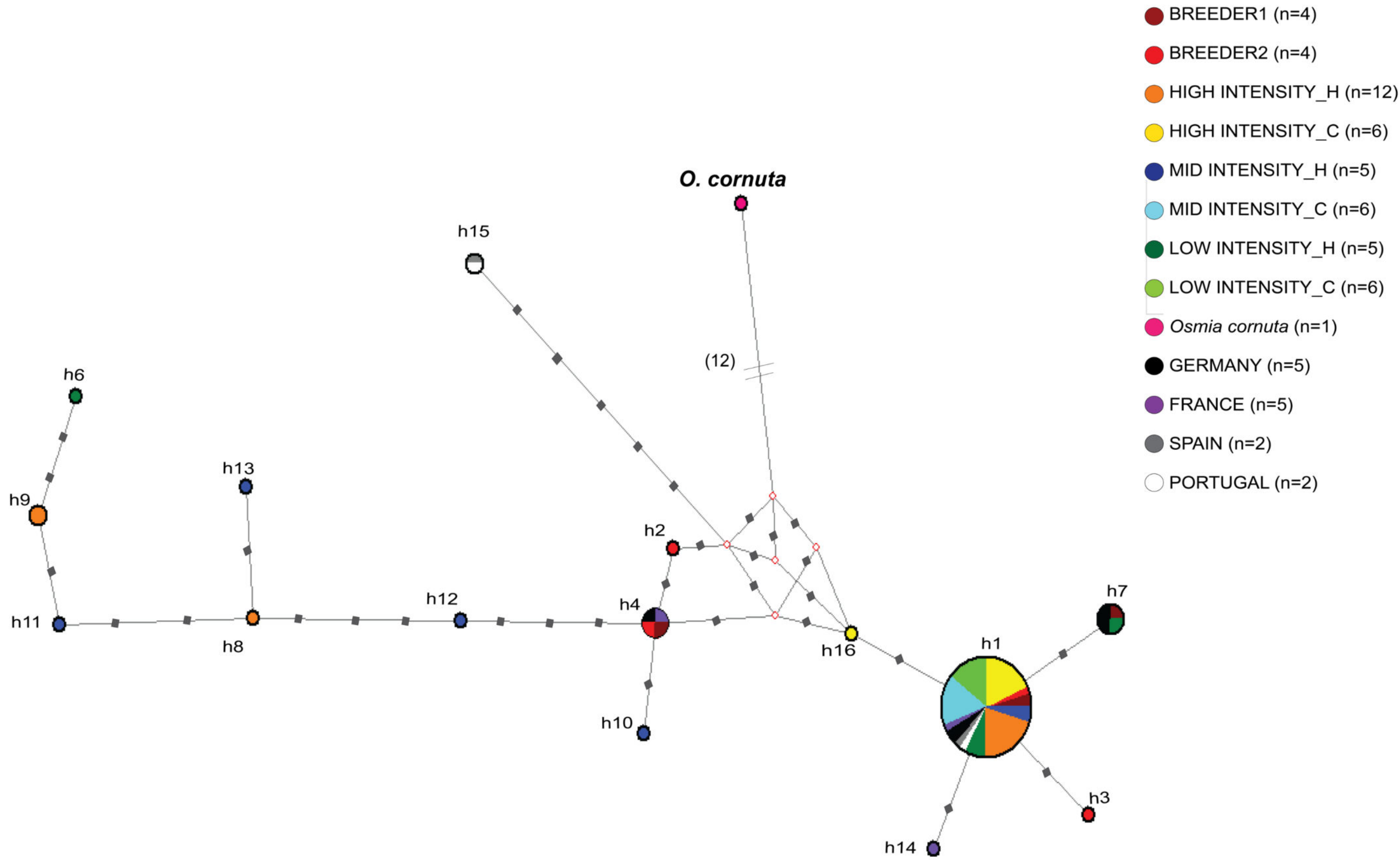
Haplotype network

INTRO

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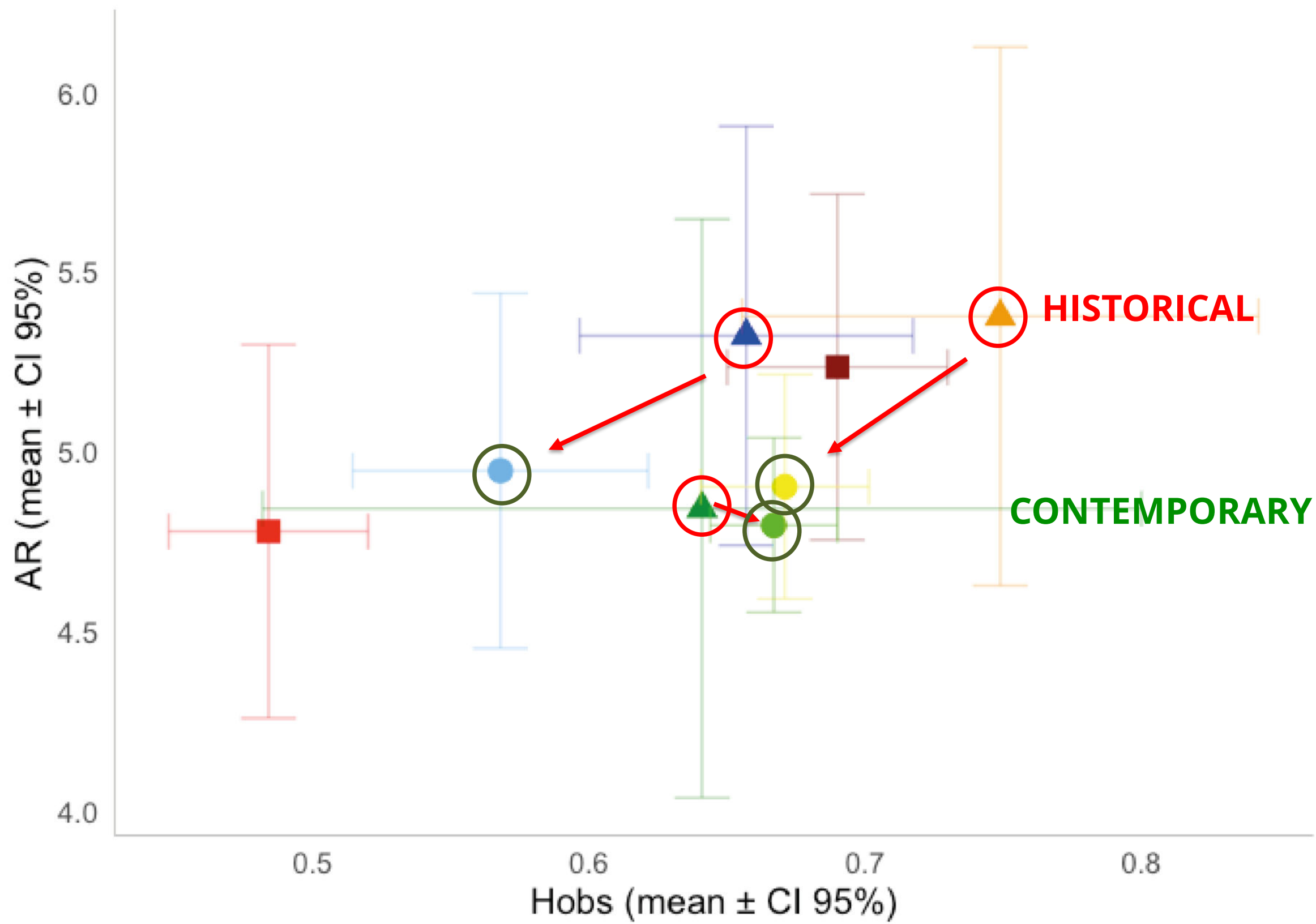
RESULTS

DISCUSSION



Nuclear DNA diversity

Allelic richness(AR) and observed heterozygosity (Hobs)



- SPACE:**
- No differences in Ho and AR between sampling areas
- TIME:**
- Loss of genetic diversity over time

INTRO

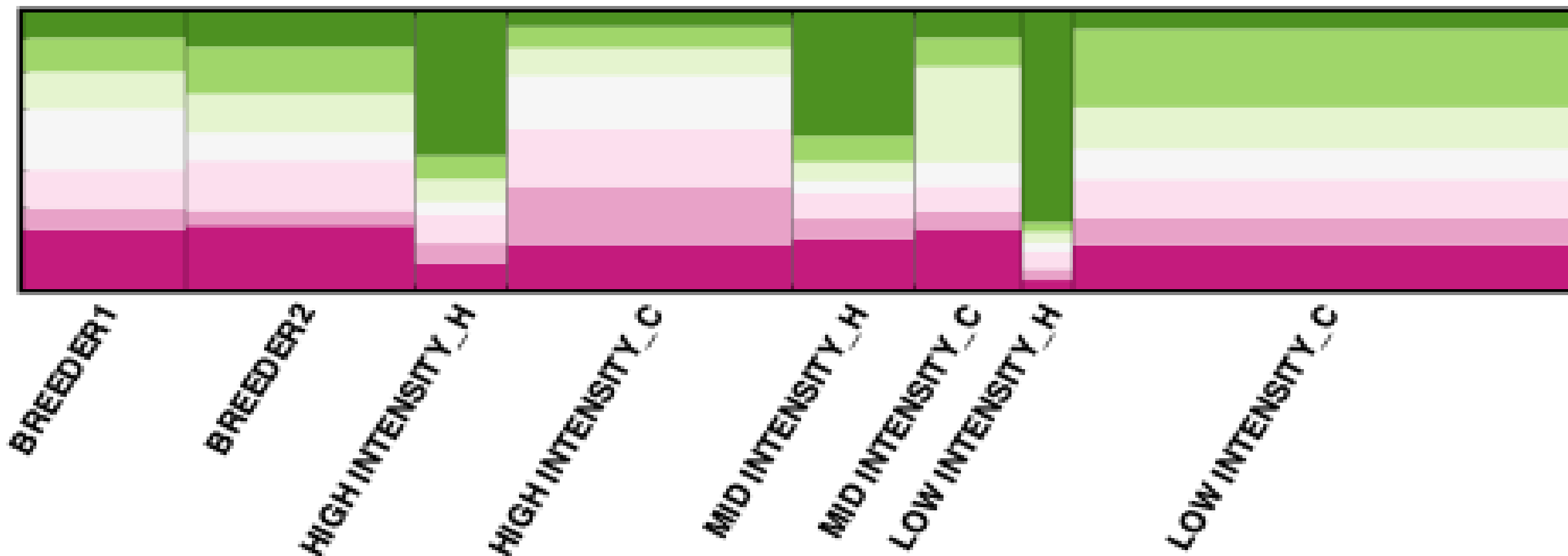
METHODS

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Nuclear DNA structure

Genetic clusters = 7



SPACE:

- Similar group assignment across sampling areas.

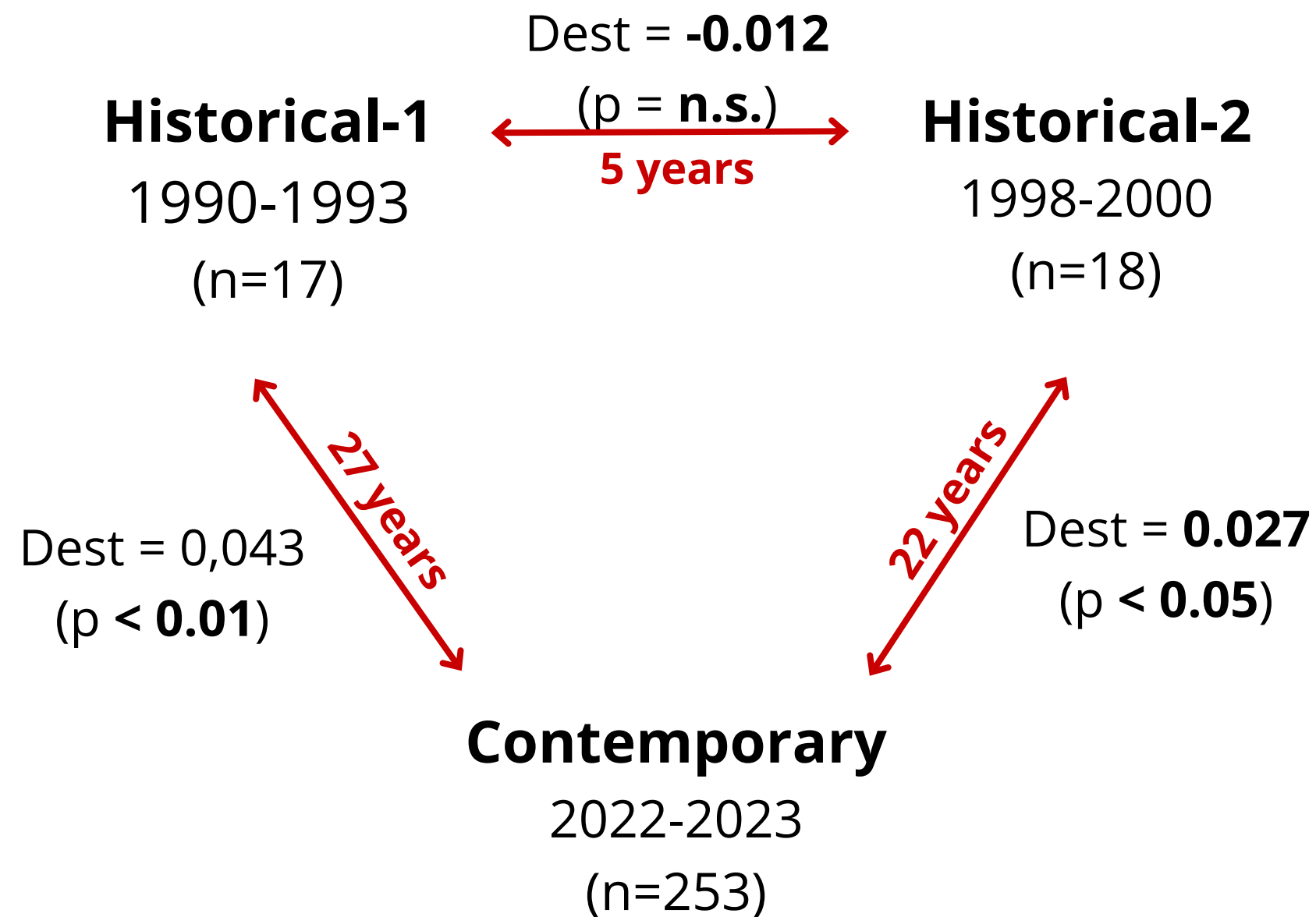
TIME:

- Shift in group assignment in the three sampling areas from historical to contemporary time period.

MANAGEMENT:

- Same genetic groups of historical and contemporary populations.

Genetic drift or management effect?



No change in time in historical samples = no strong effect of drift
=> **management effect**