

Anthropogenic transport of species within across ranges: Unpredictable genetic and evolutionary consequences



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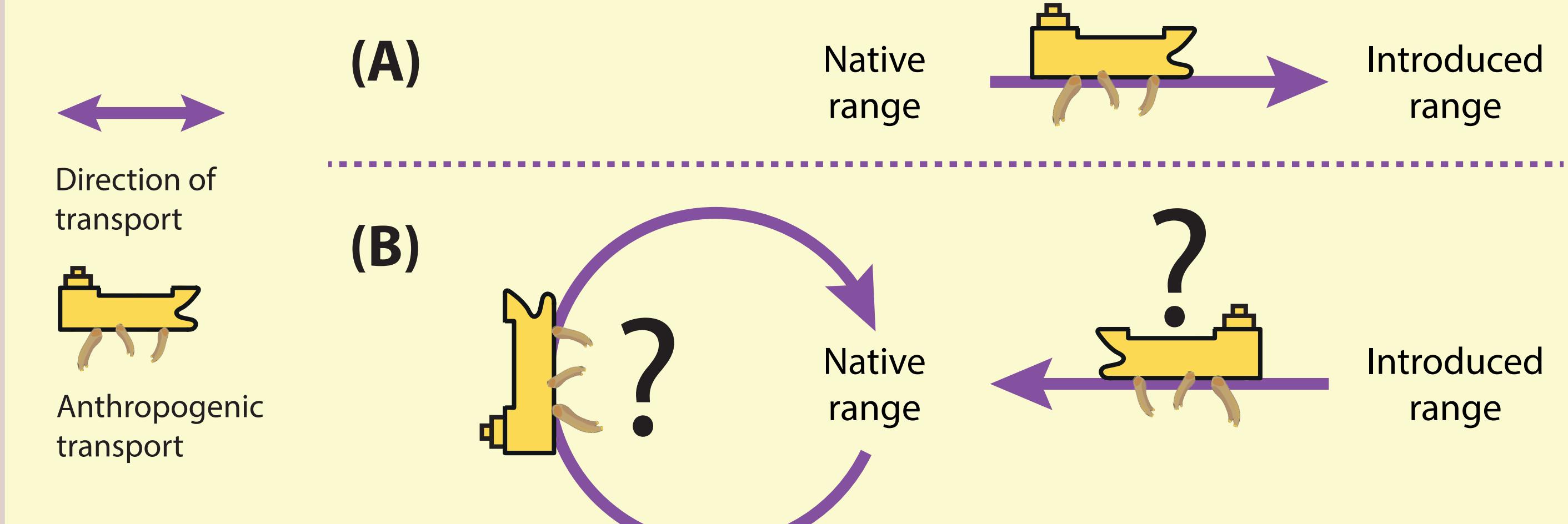
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- Natural dispersal of organisms is limited by movement capabilities of adults and/or propagules.
- Human activities can translocate organisms, **altering natural dispersal and gene flow**.
- Understanding the magnitude and scale of connectivity among populations is fundamental for understanding **biogeography, ecology and evolutionary history**.



Study organism

- *Ciona intestinalis* is a **sessile** invertebrate (Asciidae, Tunicata).
- Native to **north-east Atlantic**, but has been introduced and is **invasive** in the **western Atlantic** where it is a prominent **biofouler**, and can cause serious damage to **aquaculture facilities**.
- Extremely **short pelagic larval phase** (<24 hours) limits natural dispersal capabilities.

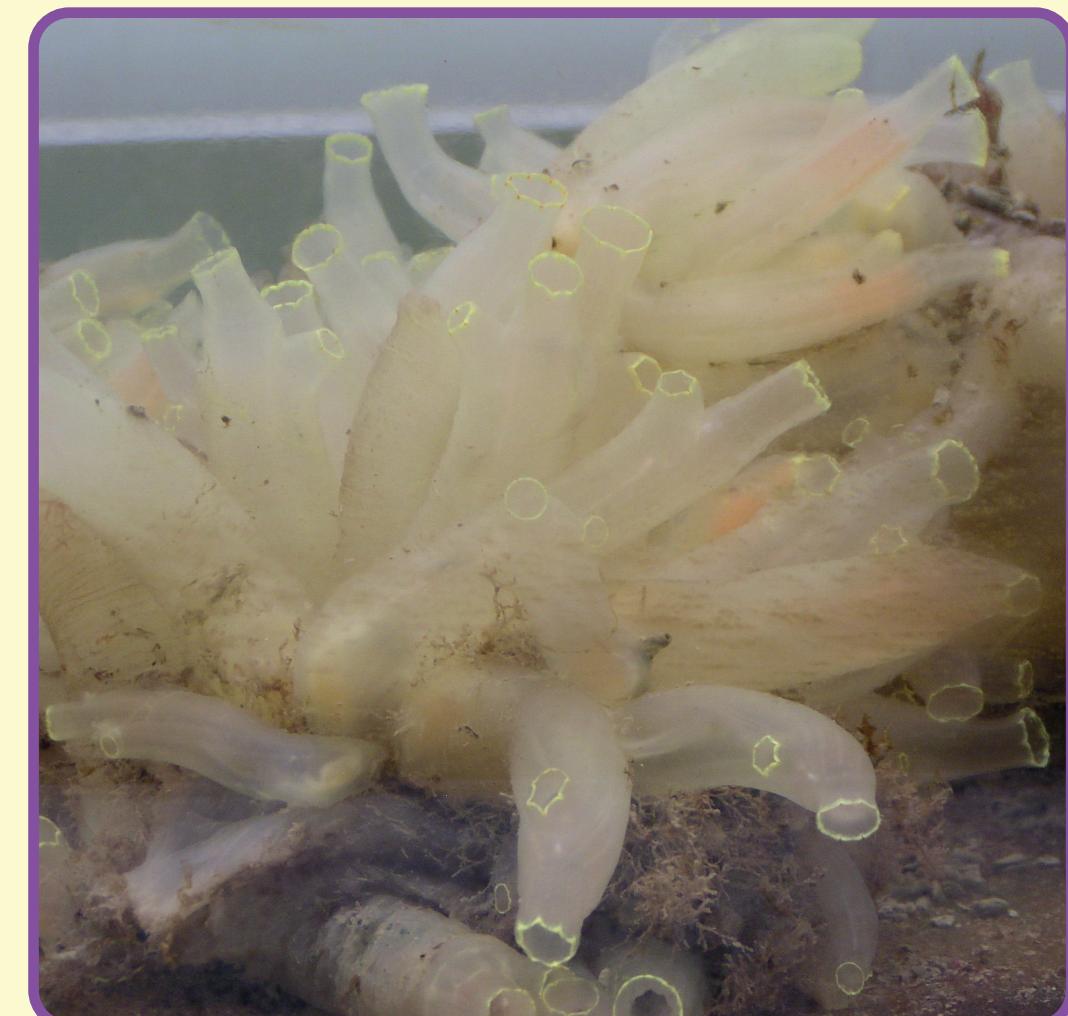


Figure 2 | *Ciona intestinalis*
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Figure 1 | (A) Most invasion genetics research has focused on the genetics of the **introduced range** to understand **post-invasion dynamics & evolutionary consequences**. (B) Despite this, we need to understand the genetic signatures in the **native range** to accurately infer the identity of the **source population, reconstruct the history + routes of invasion**, and test if **anthropogenic transport is affecting the genetic composition of the native range**.

What did we do?

- Sampled **484 individuals** from **15 artificial sites** in north west France, south England, and an island inbetween, Jersey, between June and December 2014.
- Genotyped **nine microsatellite loci** from Viard & Dubois (unpublished) and Zhan *et al.* (2010).

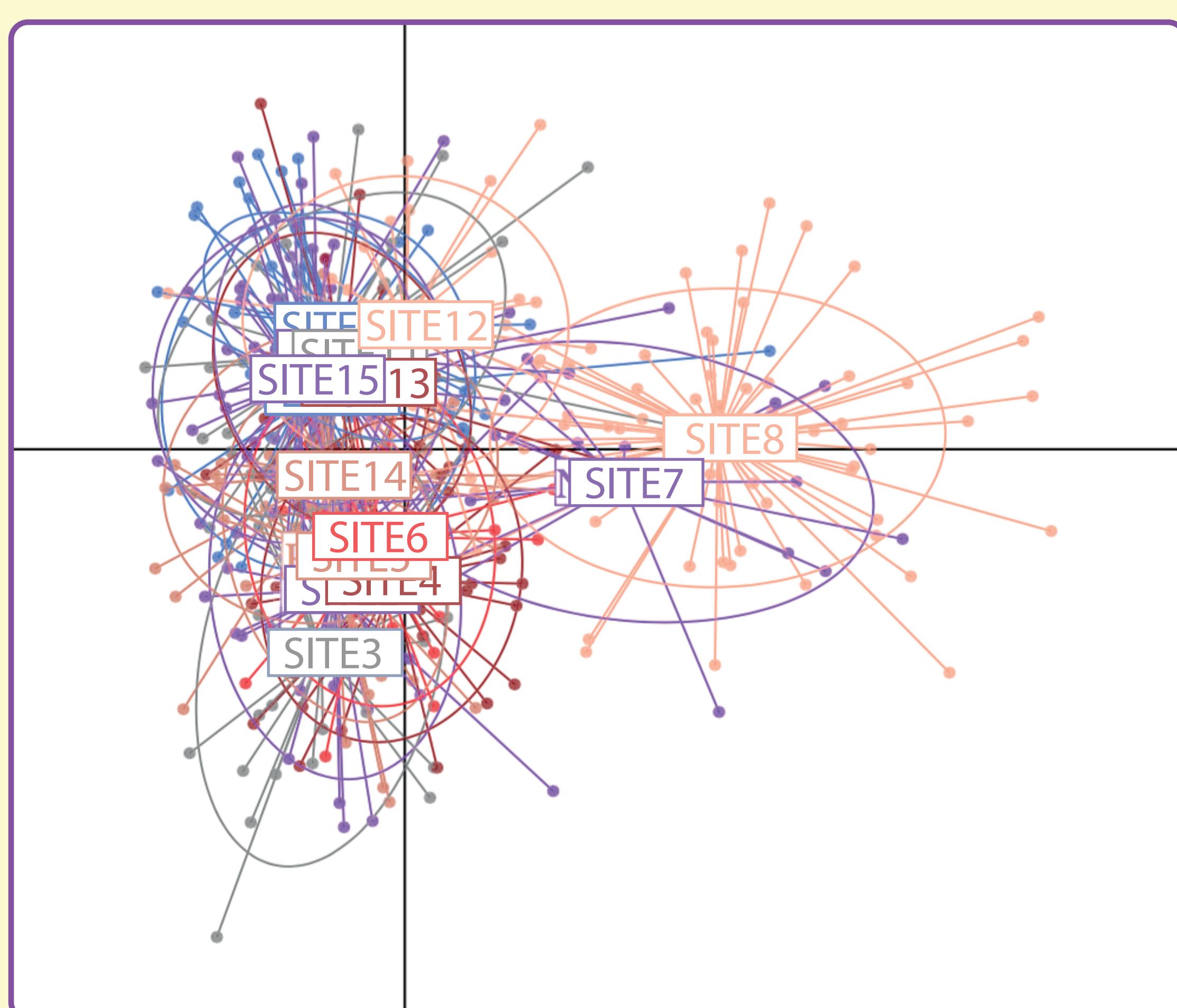


Figure 3 | Plot of the first two axes obtained by Discriminant Analysis of Principal Components. Labels are placed at the centre of each site, further delineated by inertia ellipses, with dots representing individuals.

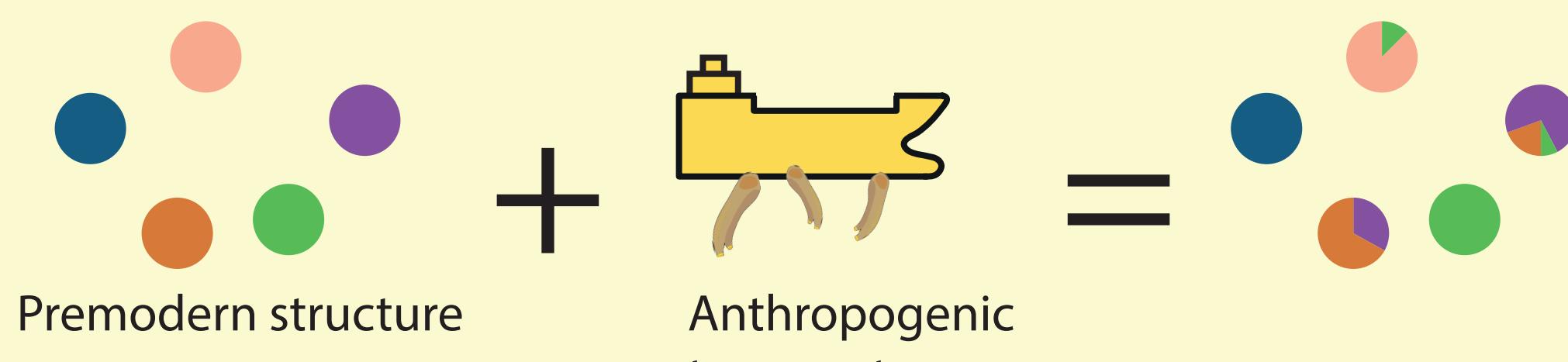
What did we find?

- Differentiation indices suggested both **anthropogenic transport** and other factors such as **natural dispersal or premodern population structure** may have shaped genetic patterns.
- DAPC and STRUCTURE analyses suggest both population structure and a mixing of genotypes (Fig. 3/4).
- **Isolation by distance** is evident when all sites are included, but not within sub-regional groups of populations within the native range.
- **Dissimilar patterns of population structure** could not be predicted based on geographical location, dispersal type/ intensity or the homogenising effect of artificial transport.



Figure 4 | Population structure at the 15 sampled sites with $K = 2$, as inferred by STRUCTURE.

Take home message



- Genetic patterns can be **unpredictable in highly urbanised native ranges** with **unknown consequences for species' evolutionary trajectories**.

Circle =
Population
Colour =
genotype

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Anthropogenic transport of species across native ranges: unpredictable genetic and evolutionary consequences

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References

Zhan A, MacIsaac HJ, Cristescu ME (2010) *Molecular Ecology*, **19**, 4678 - 4694.