

Ecological opportunity promotes diversifying selection and facilitates rapid phenotypic divergence in Icelandic Arctic charr



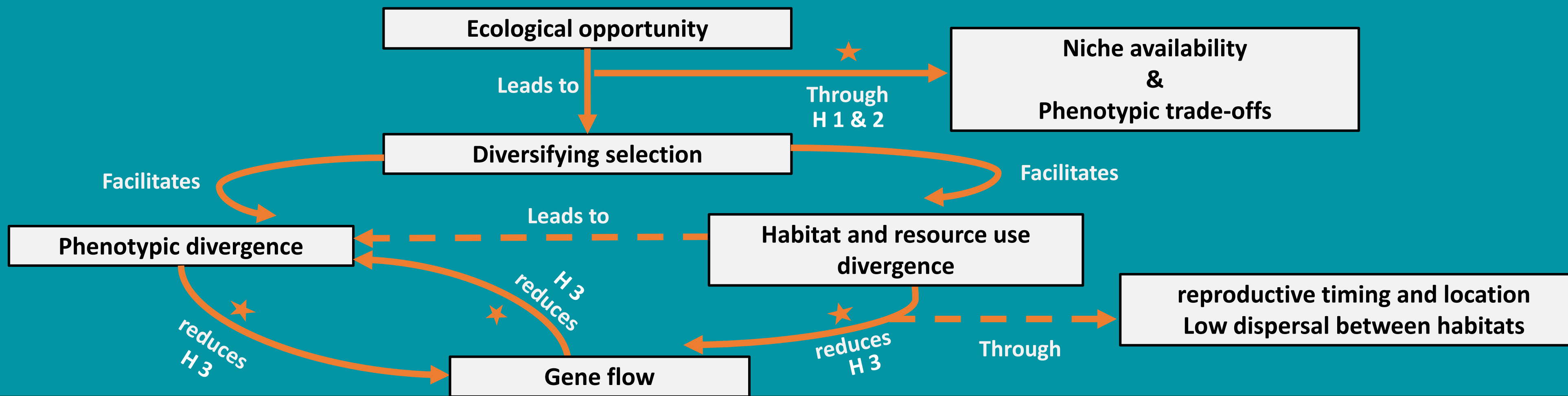
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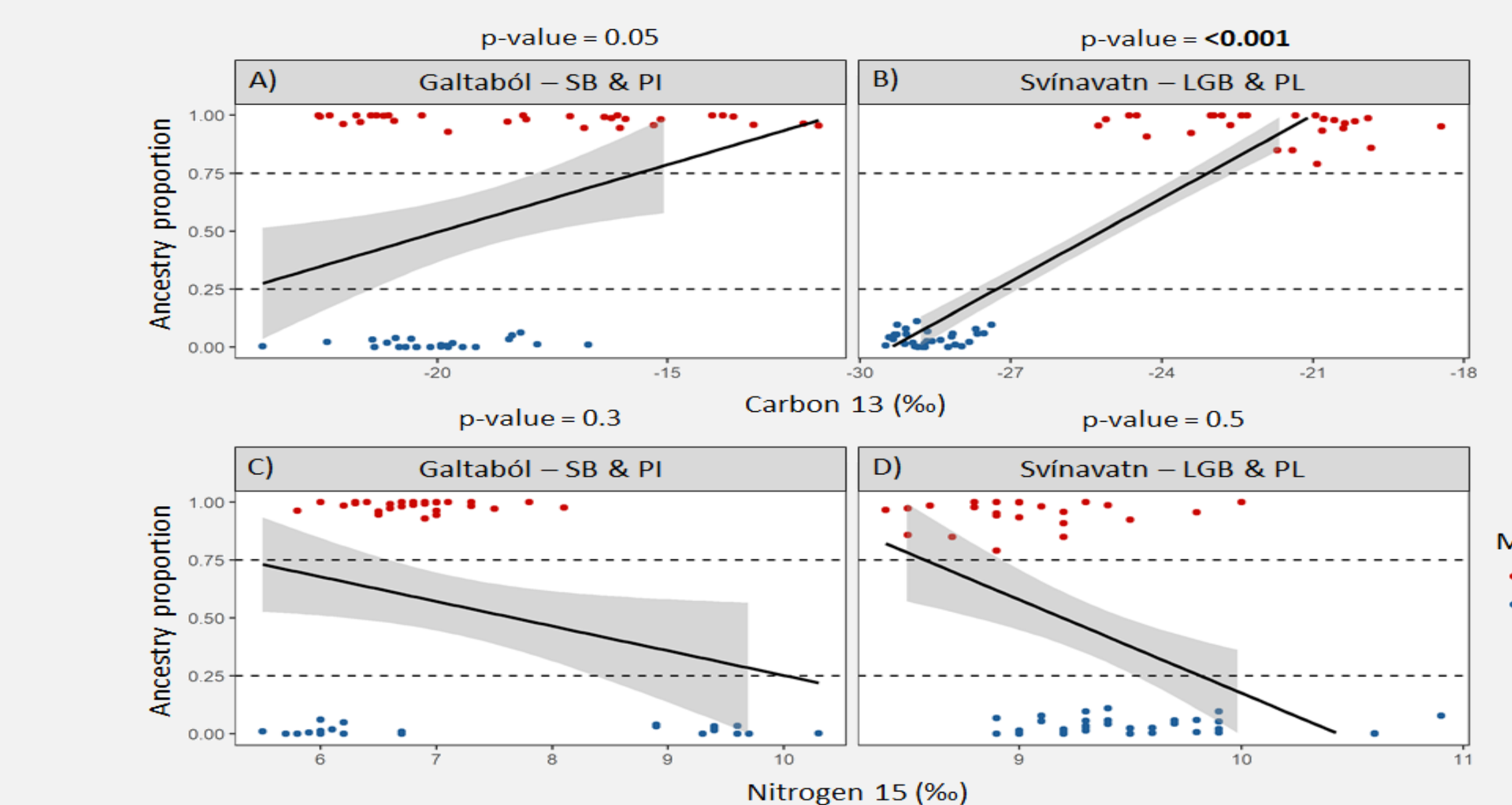
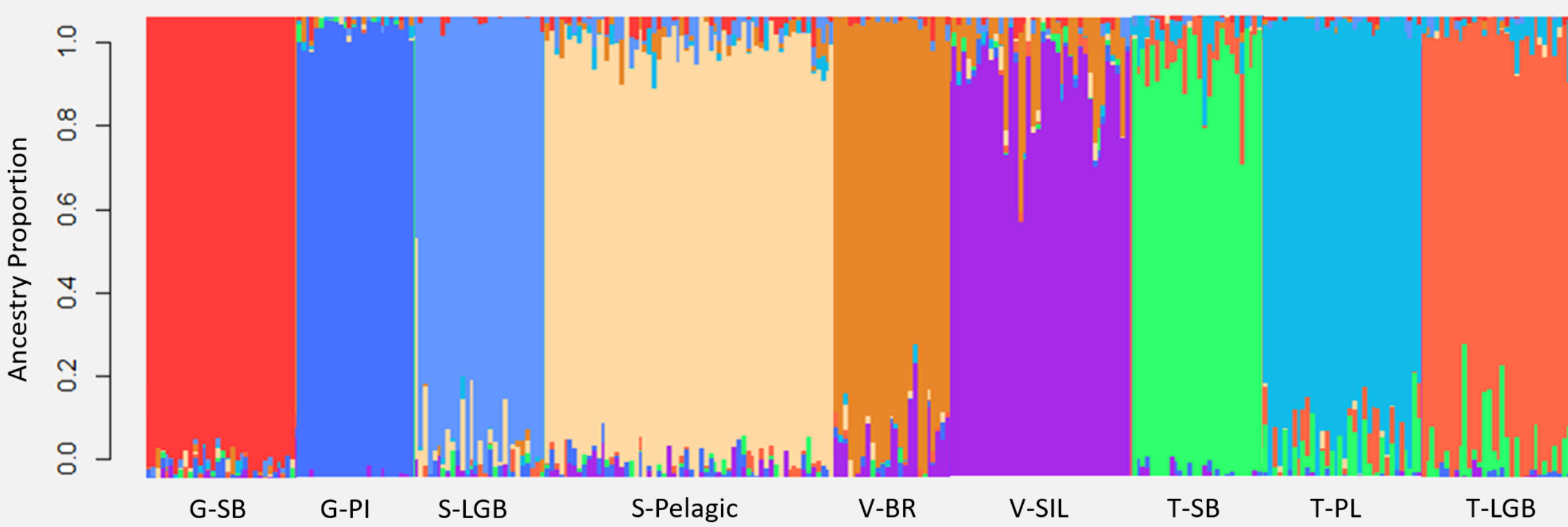
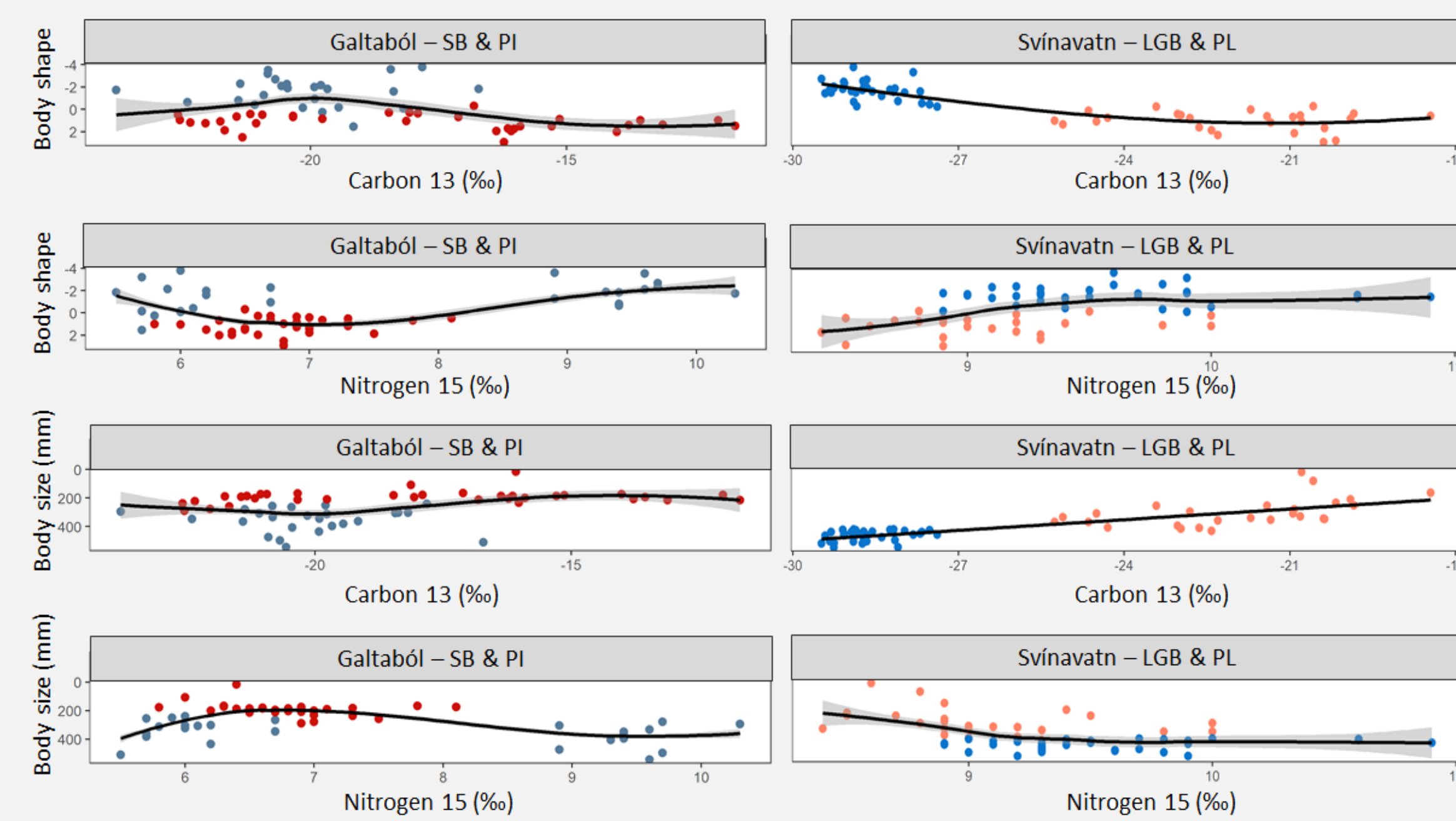
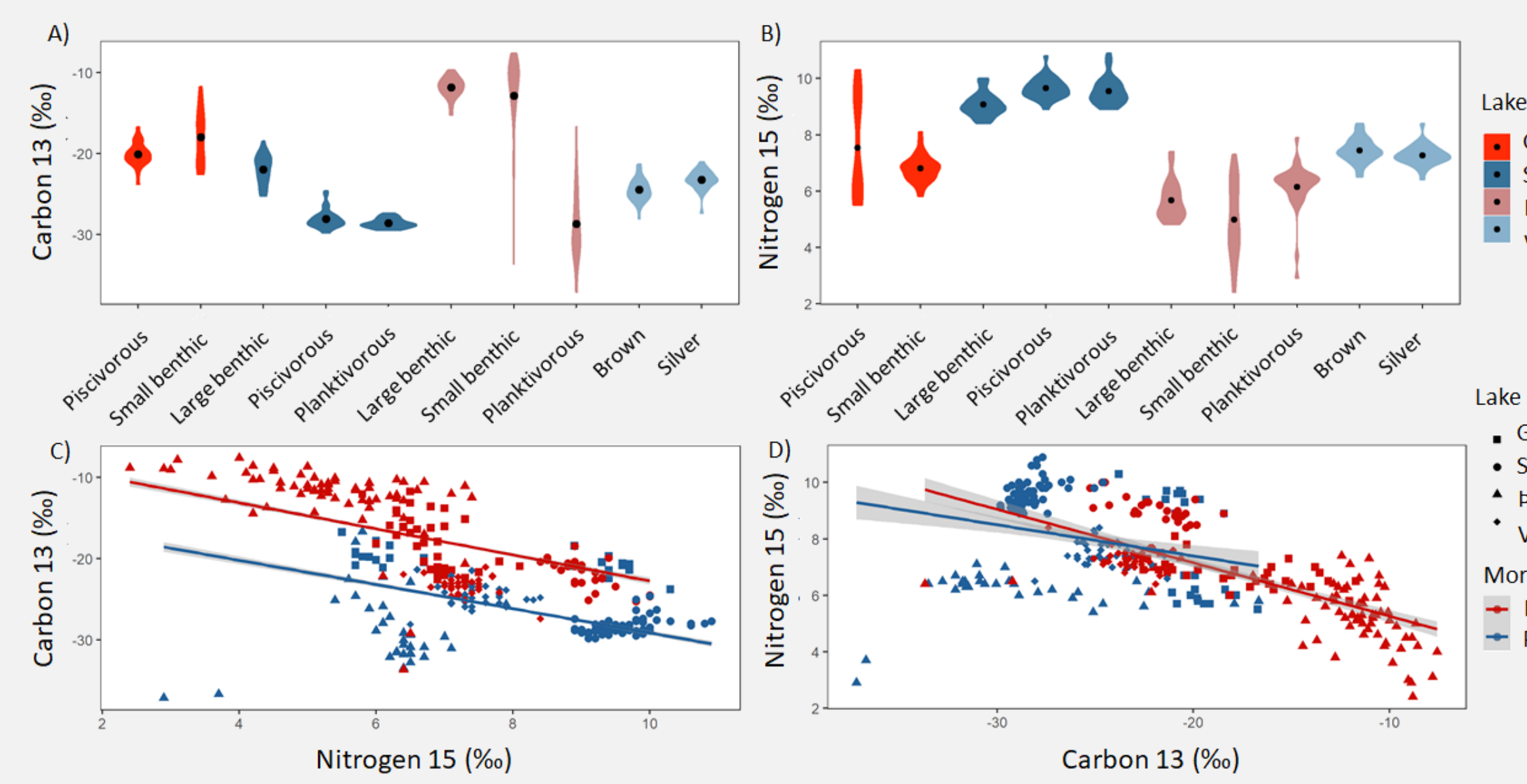
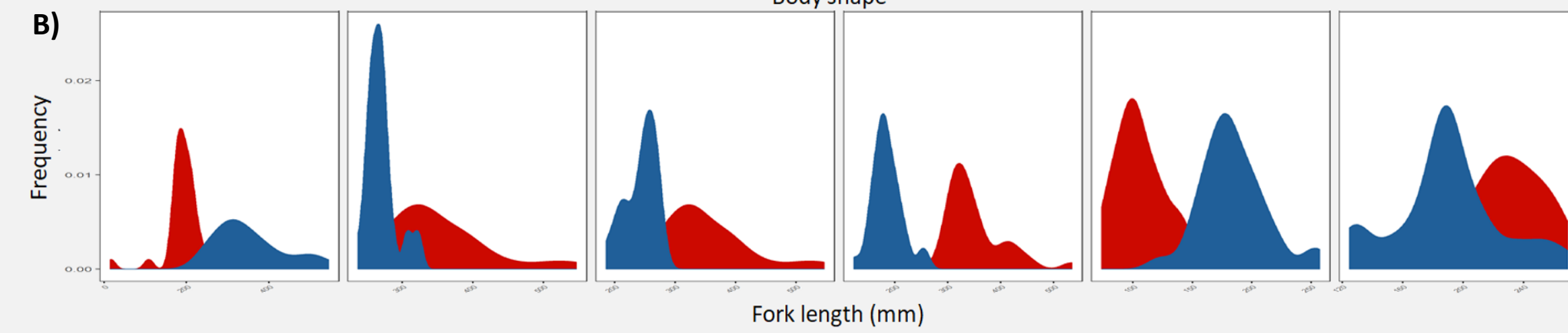
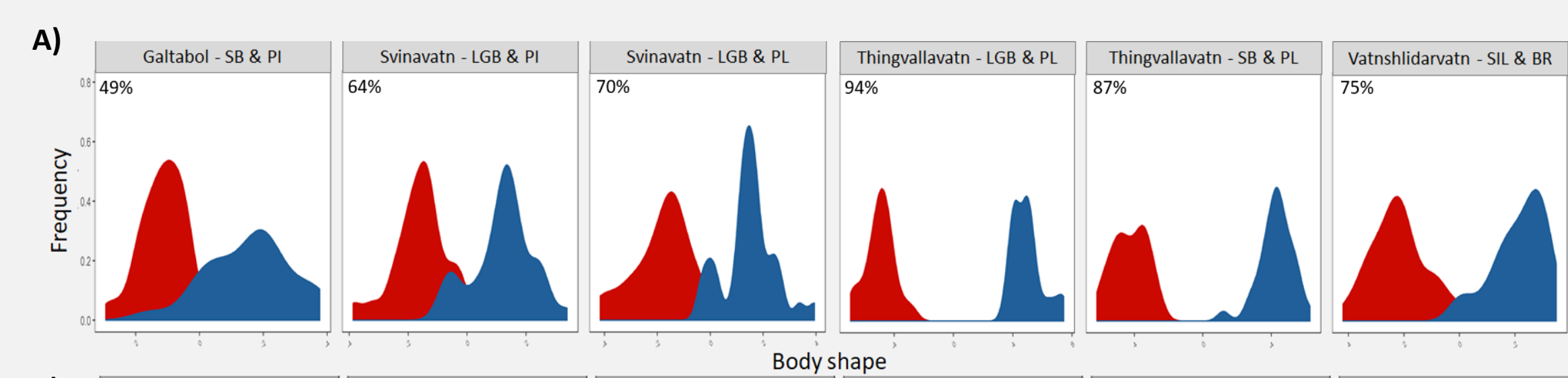
1. Overall goal

Adaptive diversification in sympatry requires niche availability and phenotypic trade-offs to facilitate diversifying selection combined with reduced gene flow between diverging populations. We assessed these three requirements for diversification in Icelandic Arctic charr (*Salvelinus alpinus*)

2. Hypotheses



4. Results – Morphology, resource use, and gene flow



Morphological divergence in body shape (A) and size (B) between benthic and pelagic morphs. % = correct classification from LDA

Hypothesis 1: Morphs show similar patterns of niche availability across populations

- A) Consistent differences in $\delta^{13}\text{C}$ signatures between morphs within populations
- B) Weaker effects of $\delta^{15}\text{N}$ signatures, morphs do not always differ in trophic position
- C) & D) Variation in resource use across populations, morphs are diverging along similar benthic and pelagic trajectories based on $\delta^{13}\text{C}$ signatures but not $\delta^{15}\text{N}$ signatures

Hypothesis 2: Resource use is a significant predictor of morphological divergence – potential for phenotypic trade-offs and diversifying selection.

Consistent effects of $\delta^{13}\text{C}$ signatures on body shape (A: 6/6 morph pairs) and size (C: 5/6 morph pairs)

Weaker effects of $\delta^{15}\text{N}$ signatures on body shape (B: 1/6 morph pairs) and size (D: 2/6 morph pairs)

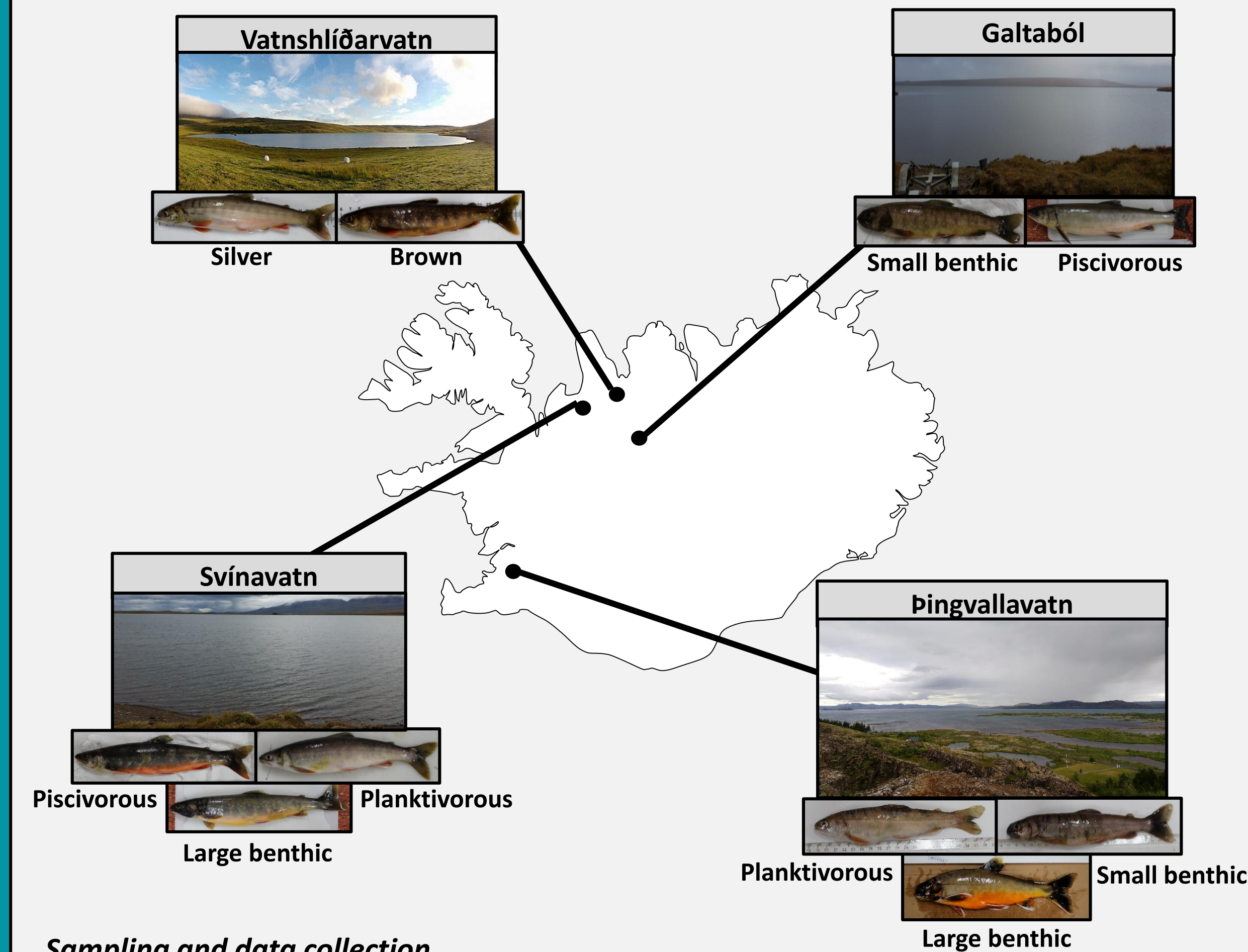
Hypothesis 3: Phenotypic divergence and resource use are significant predictors of genetic divergence – habitat and phenotypic divergence leads to reduced gene flow

Most sympatric morphs and all populations are genetically differentiated ($K = 9$)

Significant relationships between $\delta^{13}\text{C}$ signatures and body shape and size with the proportion of benthic and pelagic alleles

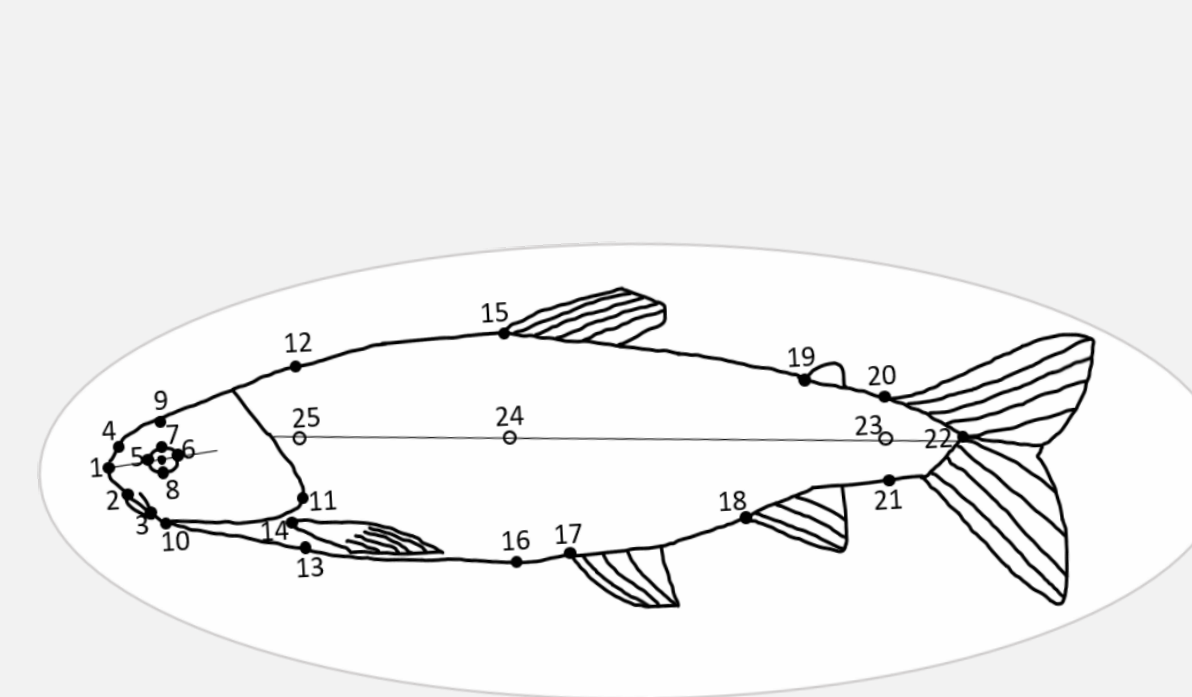
Ancestry proportion was related to $\delta^{13}\text{C}$ signatures for 5/6 morph pairs, with Galtaból being the only exception

3. Methods – Sampling and data



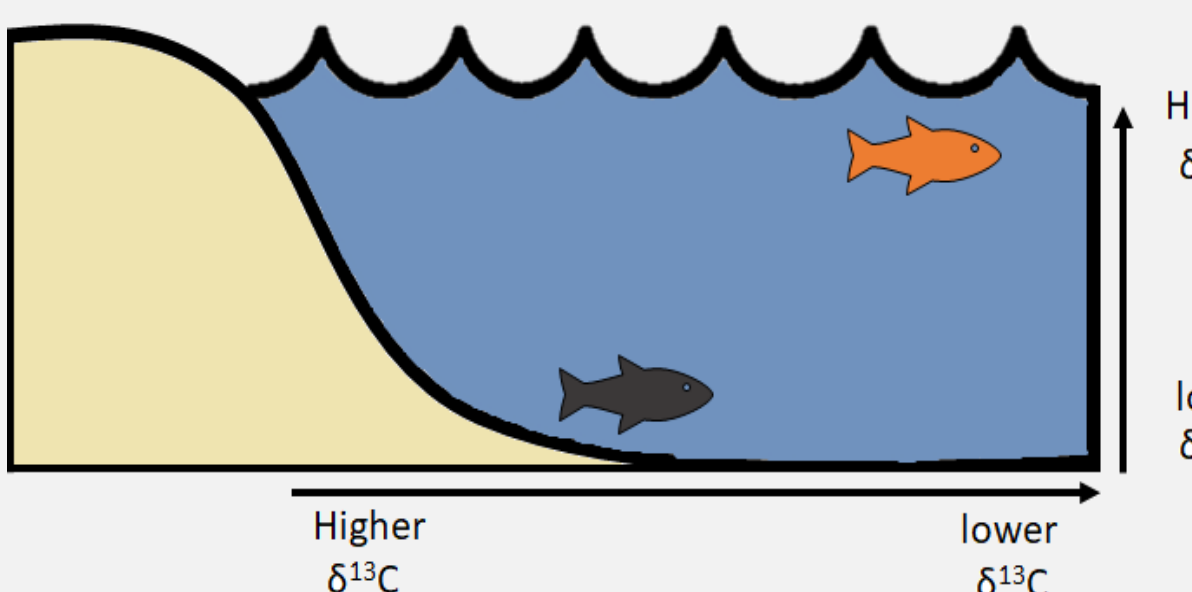
Sampling and data collection

- 316 fish (~32 per morph) were sampled during morph specific spawning periods from 2013-2015
- Morphs were identified based on body shape, size, craniofacial traits, and colour



Morphological divergence

- Geometric morphometrics based on 25 homologous landmarks
- Partial warp and uniform component scores were calculated after a generalized Procrustes superimposition
- Shape data was minimized for allometric effects
- Linear discriminant function analyses were used to quantify body shape along a benthic-pelagic axis
- Fork length was used as an estimate of body size



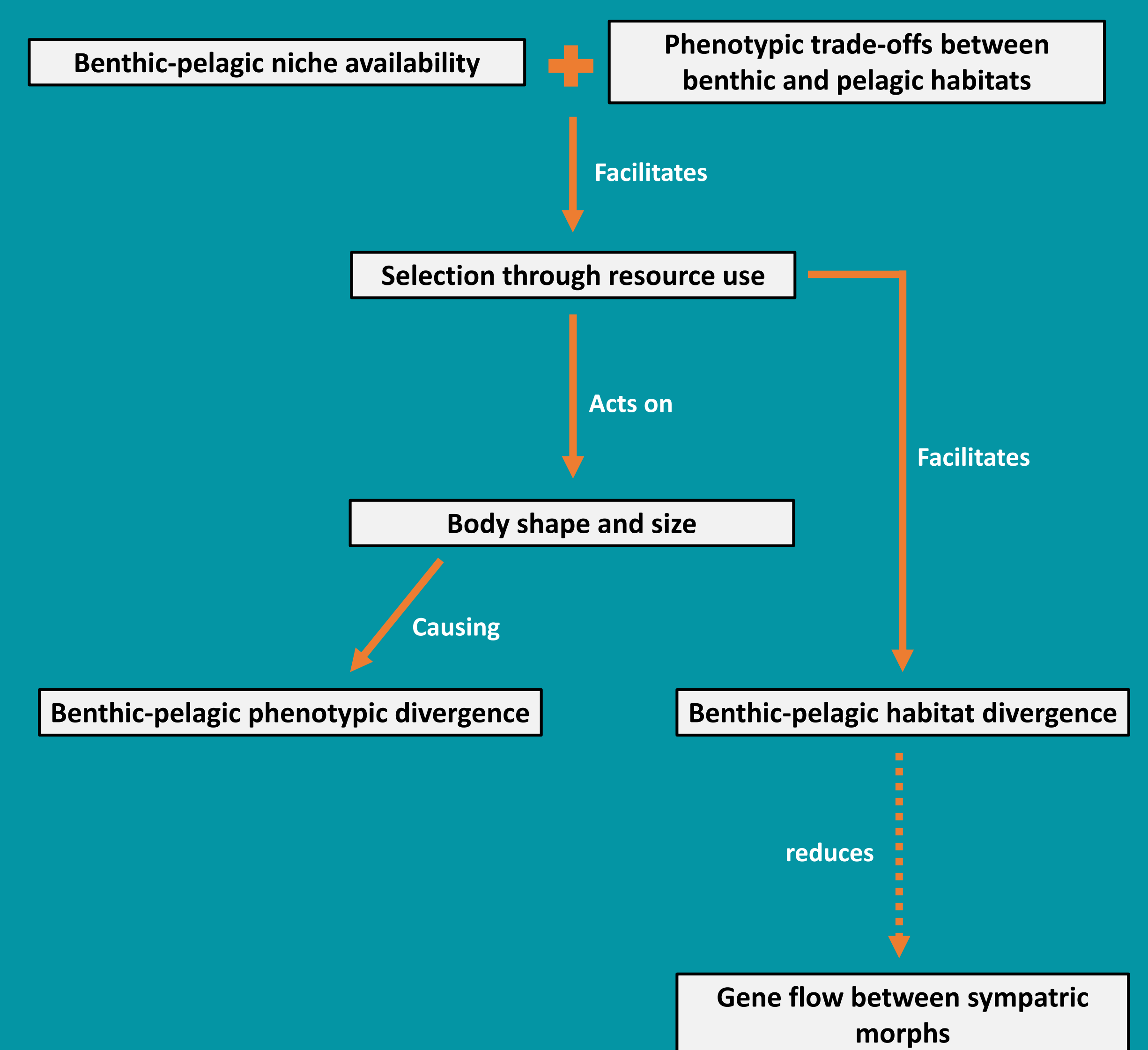
Resource use

- $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ stable isotopic signatures were used as a proxy for resource use

Genetic divergence and gene flow

- Genotypes at 14,187 polymorphic SNPs in 307 fish from an Arctic charr Affymetrix genotyping array
- The proportion of ancestry for each individual was quantified using q-values from sNMF, an unsupervised clustering method

5. Conclusions and take home message



Evidence that the interacting effects of niche availability, phenotypic trade-offs, and reductions in gene flow facilitate repeated patterns of rapid sympatric benthic-pelagic divergence in Icelandic Arctic charr