

# Local adaptation in Brook Trout



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# Neutral vs. adaptive genetic variation



- Allozyme, mitochondrial, and microsatellite DNA variation *is* indicative of *non*-selective population genetic processes, but *not* of *adaptive* variation within and between populations.
- *We'd really like to know of adaptive genetic variation!*
- What *do* we know of adaptive genetic variation in brook trout?
  - Some local-scale studies of brook trout *have* inferred adaptive variation...

# Background

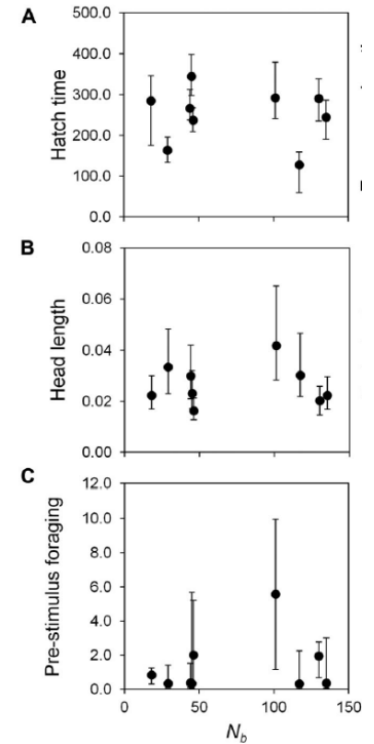
- All these studies were conducted in Canada, and all investigated the relations among population fragmentation and effective size and putatively adaptive variation.
  - Small, isolated populations might lose genetic variation more rapidly due to genetic drift than large populations, and drift might overcome selection as population size decreases.
- → *What are the implications for adaptive potential?*

# Habitat fragmentation, population size, habitat fragmentation, and adaptive variation

- Fraser et al. (2014) investigated SNP variation at genes encoding different biological functions in 14 fragmented Brook Trout populations of variable sizes in Newfoundland.
- Putatively adaptive differentiation was greater between small and large populations or among small populations than among large populations, *underlining the effect of drift*.
- The results suggest that:
  - fragmentation *does* affect natural selection, and
  - changes in adaptive genetic variation and differentiation of fragmented populations vary with population size.
- → Habitat fragmentation may affect population persistence independently of and perhaps *before* the effects of demographic and genetic stochasticity become apparent.

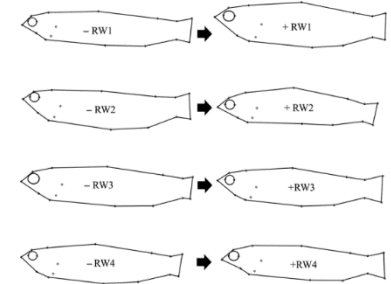
# Quantitative trait variation

- The Fraser group (Wood et al. 2017) examined additive genetic variation ( $V_A$ ) and quantitative trait differentiation ( $Q_{ST}$ ) for 15 traits among nine populations in Newfoundland populations that varied in census size ( $N = 179\text{--}8416$ ) and effective number of breeders ( $N_b = 18\text{--}135$ ).
- Across these traits, population size was only weakly related to quantitative genetic variation.
- This outcome suggests that:
  - Small populations may retain adaptive potential, and
  - Populations of all sizes experience a variety of environmental conditions in nature, and extremely large studies are required before any firm conclusions can be made.



Variation in hatch time, head length, and foraging activity as a function of  $N_b$

# Variation of body size, shape, and coloration

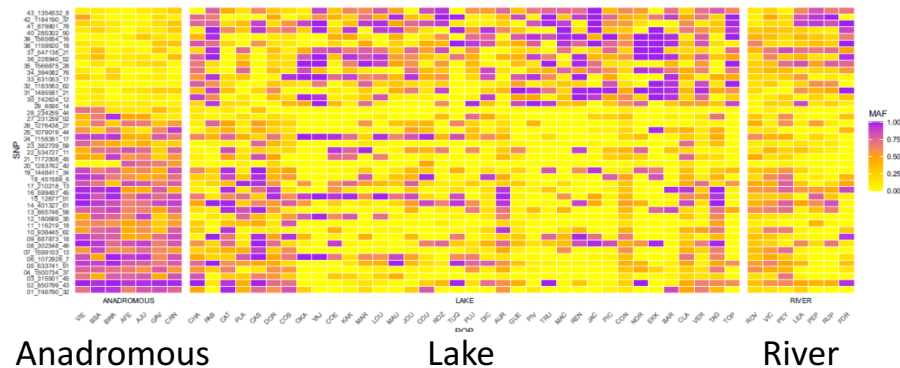


- The Fraser group (Zastavniouk et al. 2017) examined relationships between mature adult traits and ecological variables among 14 populations of brook trout in Newfoundland – these are naturally fragmented populations with shared ancestry that exhibit considerable variability in habitat characteristics and population size ( $49 < N_c < 10,032$ ).
- Body size, shape, and coloration differed among populations, with a tendency for more variation among *small* populations in trait means and coefficient of variation than among *large* populations.
- Phenotypic differences were more frequently and directly linked to habitat variation or sex ratio than to population size, suggesting that selection *can* overcome genetic drift at small population size.
- Phenotype–environment associations were stronger in females than males, suggesting that natural selection due to abiotic conditions may act more strongly on females.



# Adaptive and maladaptive genetic diversity in small populations

- They observed considerable accumulation of putatively deleterious mutations across populations, suggesting that genetic drift might be the main driver for accumulation of such variants.
- Lacustrine populations showed lower genetic diversity, but did not exhibit more deleterious mutations, suggesting that the negative effect of drift *can* be mitigated by purifying selection.
- They identified particular genomic regions associated with anadromy.



- They noted an over-representation of transposable elements associated with variation in environmental variables, suggesting the importance of transposable elements in adaptation.



# Bigger picture of state of knowledge

- This is a rather *limited* body of studies, with a rather limited scope (geography and traits considered).
- We would benefit from a deeper understanding of genomic regions associated with adaptive traits.
- Investigation of adaptive genetic variation has *not* yet been extended to brook trout populations in the Chesapeake Bay region.
- Further understanding of *adaptive* genetic variation would inform management of regional Brook Trout populations and help us conserve their long-term adaptive potential.



# References

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- Wood, J. L., D. Tezel, D. Joyal, and D. J. Fraser. 2015. Population size is weakly related to quantitative genetic variation and trait differentiation in a stream fish. *Evolution* 69(9):2303-2318.
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