

Phylogeographic mitogenomics of Atlantic cod *Gadus morhua*: Variation in and among trans-Atlantic, trans-Laurentian, Northern cod, and landlocked fjord populations

Linda A. Lait^{1,2}  | H. Dawn Marshall¹ | Steven M. Carr¹

¹Genetics, Evolution, and Molecular Systematics Laboratory, Department of Biology, Memorial University of Newfoundland, St. John's, NL, Canada

²Centre for Biodiversity Genomics, Department of Integrative Biology, University of Guelph, Guelph, ON, Canada

Correspondence

Linda A. Lait, Centre for Biodiversity Genomics, Department of Integrative Biology, University of Guelph, Guelph, ON, Canada.
Email: llait@uoguelph.ca

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Abstract

The historical phylogeography, biogeography, and ecology of Atlantic cod (*Gadus morhua*) have been impacted by cyclic Pleistocene glaciations, where drops in sea temperatures led to sequestering of water in ice sheets, emergence of continental shelves, and changes to ocean currents. High-resolution, whole-genome mitogenomic phylogeography can help to elucidate this history. We identified eight major haplogroups among 153 fish from 14 populations by Bayesian, parsimony, and distance methods, including one that extends the species coalescent back to ca. 330 kya. Fish from the Barents and Baltic Seas tend to occur in basal haplogroups versus more recent distribution of fish in the Northwest Atlantic. There was significant differentiation in the majority of trans-Atlantic comparisons ($\Phi_{ST} = .029-.180$), but little or none in pairwise comparisons within the Northwest Atlantic of individual populations ($\Phi_{ST} = .000-.060$) or defined management stocks ($\Phi_{ST} = .000-.023$). Monte Carlo randomization tests of population phylogeography showed significantly nonrandom trans-Atlantic phylogeography versus absence of such structure within various partitions of trans-Laurentian, Northern cod (NAFO 2J3KL) and other management stocks, and Flemish Cap populations. A landlocked meromictic fjord on Baffin Island comprised multiple identical or near-identical mitogenomes in two major polyphyletic clades, and was significantly differentiated from all other populations ($\Phi_{ST} = .153-.340$). The phylogeography supports a hypothesis of an eastern origin of genetic diversity ca. 200–250 kya, rapid expansion of a western superhaplogroup comprising four haplogroups ca. 150 kya, and recent postglacial founder populations.

KEYWORDS

bottlenecks, fish, founder effect, mitogenomics, phylogeography, Pleistocene glaciations

1 | INTRODUCTION

An understanding of population genetic structure, particularly in species threatened with extinction, is critical to conservation and preservation of biodiversity. Genetic structure can be influenced by a number of factors including habitat loss, changes to environmental

conditions, overexploitation, and the introduction of invasive species (Frankham, 1995; Wilson, 1988). The marine environment has been particularly impacted by overexploitation and environmental change (Alheit & Hagen, 1997; Carpenter et al., 2008; Hoelzel, 1999; Lluch-Belda et al., 1992; Schultz, Baker, Toonen, & Bowen, 2009). For example, the most recent Pleistocene glaciations (ca. 110–12 kya) disrupted

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