



Barcoding of Canada freshwater fishes



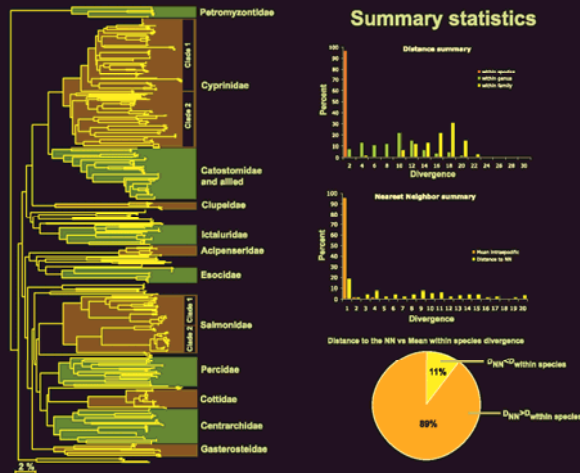
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Background - The freshwaters of Canada host 202 fish species including groups of high economic potential such as sturgeons, trouts and salmon. Owing to the steady increase of anthropogenic pressures during the last century, numerous fish species are facing drastic changes of their habitat. This fact called for an increased pace of biodiversity survey to track changes of abundance and distribution in nature. However, because of their high diversity and profound changes in appearance during development, fish identification is no easy task. In this context, the use of molecular tools to assign unknowns from any ontogenetic stages to a species is required. Barcoding consists in using a standardised fragment of the Cytochrome oxidase I gene (Cox1) from the mitochondrial genome for that purpose.



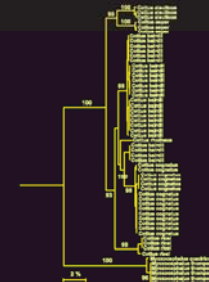
Coverage - Sequences of 652 bp from the Cox1 region have been generated for 1355 individuals belonging to 189 species from 86 genera and 28 families collected throughout the freshwaters of Canada. This set of 883,460 bp representing 94% of the overall fauna has been used to assess the potential of Cox1 barcodes to accurately identify freshwater fish species from Canada. The success of this approach depends mostly on the shape of the species genealogy at Cox1 region given that overlaps in the genealogy of two distinct species due to hybridisation and introgression or recent divergence and lineage sorting lead to assignment ambiguities at the species level.



Monophyletic - no overlap = Catostomidae



Polyphyletic - overlap = Salmonidae - Clade 2



Paraphyletic - no overlap = Cottidae

Barcoding freshwater fish species

- The families sampled constitute monophyletic groups and a steady increase of divergence is observed through hierarchical levels (species, genera, family).

- Overall, the nearest neighbour (NN) from the closest species is more divergent than conspecifics. The Cox1 barcodes generally tend to cluster according to the species limits.

- In 10% of the cases, the nearest neighbour (NN) from a distinct species is more closely related than conspecifics and species genealogies overlap. In these cases, assignment at the species level is ambiguous.

- The species genealogies tend to differ between families and three patterns are detected: 1) the species are monophyletic (Cox1 barcodes follow species limits); 2) some species are paraphyletic (Cox1 barcodes support more species than currently recognised); 3) some species are polyphyletic (inconclusive - hybridisation ? lineage sorting ? taxonomic errors ?)