

Paige Robinson

Population genetics and phylogeography of Scottish Loch Brown Trout using mitochondrial DNA analysis

Recent genetic advances have meant that large scale population comparisons can be used to answer questions on phenotypic diversity and migration behaviour. Phenotypic diversity is the variation between different morphological features in a species, and migration behaviour describes the movement of different populations and how much they interact and reproduce with each other. In this study, the mitochondrial gene ND1 was used to see if brown trout, *Salmo trutta*, sampled from different areas of the Loch Maree and Loch Lomond catchments in Scotland were reproductively isolated. If this were the case, each area would have a slightly different genetic sequence, showing that the group only mates with other members of that population. Brown trout are a common freshwater fish throughout Scotland with 3 ecomorphs; standard brown trout, large piscivorous Ferox trout and anadromous sea trout which migrate to sea for a season, before returning to their spawning grounds to mate. Therefore it was also expected that morphs would be genetically distinct from one another. The results showed that there was not a significant difference for trout haplotypes from different locations, or for different ecomorphs. This implied that trout may be less specific about breeding site than thought, and that migrants between groups are common. It is also implied that these ecomorphs are not completely genetically distinct, however this may be a more subtle chance that would need a wider study to find. Further study is needed using more genes, a larger sample size taken from multiple lakes and equal ecomorph quantities to make results accurate and precise. If those results were consistent with this study, conservation efforts would have to be for Brown trout at a species level instead of ecomorphs like the Ferox trout, which is often the current strategy.