

DNA sequence variation of a mitochondrial cytochrome *b* region in Haddock, *Melanogrammus aeglefinus*

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Sequence variation of a 381 base pair fragment of the mitochondrial cytochrome *b* gene was studied using polymerase chain reaction and direct sequencing of 97 haddock, *Melanogrammus aeglefinus*, from Iceland, 14 from the Faroe Islands and six from the Irish Sea, respectively. Nineteen variable nucleotide sites define 22 haplotypes. Three of these were non-silent resulting in two non-conservative and one conservative amino acid replacement. The amount of variation was high ($\hat{h} = 0.69$; $\hat{\pi} = 0.25$ per 100 bp) with two haplotypes at polymorphic frequencies greater than 5%, some rare haplotypes with a wide distribution and a large number of singleton haplotypes. The genealogical tree among haplotypes shows homoplasy and it is relatively shallow. Net nucleotide differences among localities are in some cases different from nil. Geographic locality explains some of the variation among areas within Iceland, among areas between Iceland and the Faroe Islands and between countries, correspondingly. Regular clines in frequency were observed for the two high-frequency haplotypes with each of them reaching its highest frequency in a particular area within Iceland. Results are presented and compared and contrasted with published mtDNA results from Atlantic cod.