

ICES CM 2012/ H:16 - Advances in the traceability of fish and fish products: from species to populations

Poster title: Consistency between management units and genetic structure in saithe (*Pollachius virens*)? Application of modern genetic tools to an exploited species in the Northeast Atlantic

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The identification of isolated populations in widely distributed marine species is complicated by low levels of genetic differentiation caused by large population sizes and recent separation. Modern genetic approaches now allow for the isolation of hundreds of genetic markers, therefore improving the power to identify biologically meaningful management units. Saithe (*Pollachius virens*) is a highly migratory and commercially important fish species in the North Atlantic. The species geographical range is divided into several management units on both sides of the Atlantic, though the genetic population structure is unknown. There are three management units of saithe defined in Northwest Atlantic waters (here named Pollock on St. Pierre Bank, the Scotian Shelf and in the Gulf of Maine), and six units in the Northeast Atlantic; west of Ireland, west of Scotland, off -Faroe Island, around Iceland, in the North Sea and finally the Northeast Arctic unit along the Norwegian coast (62°N). The question of consistency between management units and population genetic structure remains. The present study is aimed at testing for genetic structuring of the species within the Northeast Atlantic. We apply genome wide sequencing technologies to identify markers (Single Nucleotide Polymorphisms, SNPs) that are most discriminatory between sites across saithe geographical range. A SNP panel is used for a detailed analysis of population structure to measure the level of exchange of genetic material in this saithe complex.

Keywords: Population genetic structure, Single Nucleotide Polymorphisms, Stock identification, Northeast Atlantic

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