

Genetic variation and population structure of saithe, *Pollachius virens*, in Icelandic waters.

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Saithe, *Pollachius virens*, is common all around Iceland, although it is more common in the warm waters off the south and west of the country. Saithe is found along the east coast of Canada and off the south part of Greenland. The northern most part of the distribution is in the Barent Sea and it is found along the coast of Norway, and also around Faroe Islands and Great Britain and south to Bay of Biscay. Tagging experiments have shown that saithe migrates in large schools long distances for spawning or search of food. Saithe is mostly pelagic and is commonly found at 200m depth or less, but is found at 450m the deepest. Spawning of saithe takes place around Iceland from late January to late March. The saithe population size around Iceland has fluctuated over the past few decades. The population size was large in 1970, estimated to be 700 thousand tonnes. Saithe is an important commercial fish in Iceland and the biggest catch was around 100 thousand tonnes in 1991. After this the catches decreased and have been around 40 thousand tonnes in the last decade until recent years it has increased again, with total catches of 60 thousand tonnes in 2004.

Genetic variation and populations structure of saithe around Iceland has not been studied and such research could shed new light on its biology. In the present study direct DNA sequencing of two mitochondrial genetic marker are used to analyse the populations structure of saithe, 300bp part of the cytochrome B gene (CytB) and 450bp part of the cytochrome oxidase I gene (COI). It will be analysed if environmental factors affect the genetic variation observed or if spawning populations differ genetically among different localities around Iceland. Effective population size (N_e) will be estimated and compared to information on other related fish species.

Samples of 540 individual saithe where collected in two surveys of the Icelandic Marine Institute around Iceland in September 2004 and in April 2005. The analysis of results is ongoing. Preliminary results suggest deeper haplotype tree for saithe compared to Atlantic cod, *Gadus morhua*. This could be explained by lower variance in progeny number by each female, but other explanations might also apply.

Further, it is planed to extend the present study by analysing the genetic variation of saithe throughout its distribution. The comparison might assist in explaining population size fluctuations and migration of saithe.