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Comparison of growth in Atlantic cod (*Gadus morhua*) originating from the northern and southern coast of Iceland reared under common conditions

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ABSTRACT

Counter-gradient variation in growth has been documented for several commercial fish species. This phenomenon was tested for Atlantic cod (*Gadus morhua*) when forming the base population for a cod-breeding program in Iceland. In 2004, wild brood fish from five locations off the Icelandic coast were captured using gillnets from commercial fishing vessels. The eggs were hatched at the Marine Research Institute (MRI) and transferred to sea cages at 322 days post hatch dPH. Growth rate, maturation and conditional factor were measured at a commercial scale among the fishes originating from these five locations. The measurements taken at 322 days post hatch (dPH) showed a significant different in weight, but measurements taken at 729 and 952 dPH showed no difference in growth rate, length or maturation.

Analysis of gene diversity among the brood fish showed a significant genetic structure, but all F_{ST} were below 0.006 and were significant. Moreover, the hatching success among the females from these locations was not significant.

The main conclusion is that Atlantic cod originating from the North and South coast of Iceland show no quantitative differences in growth, proportion of maturation or length. These results need to be considered when forming the base population of Atlantic cod.

1. Introduction

The hypothesis that fish vary in growth performance and other life history traits on a latitudinal scale was put forward by Conover (1990) and Conover and Present (1990). According to the hypothesis, northern populations should display higher growth performance at higher temperatures. This variation is explained by adaptation to the different growth conditions, such as day length and average annual temperature, at different latitudes. Counter-gradient variation in growth (CnGV) has been documented for several commercial species, including turbot (*Scophthalmus maximus*), largemouth bass (*Micropterus salmoides*) (Williamson and Carmichael, 1990), Atlantic salmon (*Salmon salar*) (Nicieza et al., 1994) and striped bass (*Morone saxatilis*) (Conover et al., 1997). Temperature and light varies considerably through the distribution range of Atlantic cod (*Gadus morhua*), giving the potential for local variation in growth patterns (Brander, 1995; Suthers et al., 1999).

Recent studies have found considerable geographical variation in the life history and genetic structuring of Atlantic cod populations, even at small geographical scales (Arnason et al., 2009; Knutsen et al., 2007; Pampoulie et al., 2006; Salvanes et al., 2004). Population variation in growth has also received recent interest. Svåsand et al. (1996) found different growth performances in Norwegian coastal cod and Arcto-Norwegian cod. Another study on Norwegian cod found evidence for counter-gradient variation in life history traits, including growth and feeding performance (Salvanes et al., 2004). Similarly, growth experiments of cod populations from the North American coast found that cod from a cold environment had better growth performance at colder temperatures and an overall broader range of optimal growth temperature (Dutil et al., 2008). However, a recent study on juvenile cod from the same area did not find evidence for CnGV, although growth patterns appeared genetically determined (Wijekoon et al., 2009).

In general, the effect of temperature on the growth patterns of cod has been well documented during different life stages (Björnsson and Steinarsson, 2002; Imsland et al., 2005). According to the model of Björnsson and Steinarsson (2002) for the growth of wild cod, the optimal temperature varies with weight from 17 °C for a juvenile of 2 g to approximately 7 °C for a two kg cod. The sea temperature around Iceland varies in both longitude and latitude; for example, there are 1100 more degree days in one year (days multiplied by average sea temperature) in the southwest than in the northwest (Astthorsson et al., 2007). Based on the growth model, 150 g juveniles transferred to sea-cages in spring will take approximately 32 months to reach a 4 kg slaughter size (Björnsson and Steinarsson, 2002). As for cod farming, optimizing growth in sea-cages is important and moreover, recent reports of geographical variation in Atlantic cod highlight the need to record geographical

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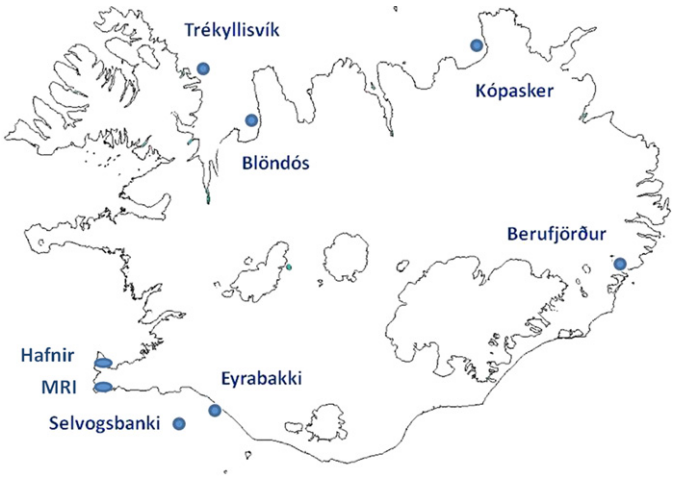

Fig. 1. Overview over the origin of the base population sampled in 2004 and the rearing location at Marine Research Institute (MRI), land-based station in Hafnir and in cages at Berufjörður.

variation in growth and other economical important traits under industrial conditions.

The main objective of this study was to estimate any variation in growth, condition and maturation of Atlantic cod from five locations around Iceland (northeast, northwest and south) and their performance in sea-cages to select individuals for creating the base population of a cod breeding program.

2. Materials and methods

2.1. Sampling and rearing conditions of juveniles

Wild cod were captured in April–May 2004 (year class 2004) using gillnets brought onboard commercial fishing vessels. Five spawning areas located north and southwest of Iceland were chosen: Kópasker, (NE Iceland – N63°36′58.46″, W16°53′47.65″). Trékyllisvík (66°4′33.14″N, 21°22′8.13″W), Blöndós (65°41′54.52″N, 20°19′59.28″W) Eyrabakki (63°49′47.92″N, 21°9′35.01″W) and Selvogsbanki (63°28′33.61″N, 21°31′55.55″W) (Fig. 1.). All wild brood fish were hand-striped onboard the fishing vessels, and the eggs were fertilized 1/2 h later. The mating ratio was 1:2, with one male used to fertilize eggs from two females. Approximately 200 ml of eggs from each female were placed in a 1 l box, and after fertilization 800 ml of seawater was added. The eggs were then transferred to the Marine Research Institute (MRI) Hatchery at Staður, Grindavík. The brood fish were slaughtered and weighed and fin clips taken for genetic analysis.

The rearing temperature at the MRI was kept constant at 8 °C during the first week post-hatch, to optimize the yolk conversion and facilitate proper filling of the swim bladder, after which the temperature was gradually raised to 10–14 °C. The growth rate peaked at 5 weeks post-hatch (15–20%/day), while the length increment was largest at a size of 6–7 cm (up to 1.7 mm/day). The juveniles at the MRI were fully weaned at 8 weeks post-hatch (33 mm). During the rearing time at the MRI, tests were made to measure to survival of eggs from each female.

The 2004 year-class was transferred from the MRI to the land-based station at Hafnir in November 2004 at a size 30–40 g. The juveniles were reared in one 40-cubic-meter circular tank with a flow-through system of seawater. The rearing temperature was kept constant at 8.3 °C with a 100% oxygen saturation and a salinity of 30–32‰ with continuous light.

The 2004 year-class was transferred in May 2005 from the land-based farm to a 90-m round, 18-m-deep sea cage in Berufjörður at the east coast of Iceland (64°43′42.02″N, 14°23′56.06″W) (Fig. 1). During growth in the sea-cage, the cod were fed once each day from June to November and once every three days over the coldest period from late November to May using a commercially formulated feed from Fóðurblandan Ltd., Iceland, containing 18% fat and 45% protein. Feeding was regulated depending on appetite. The seawater temperature was measured twice weekly throughout rearing (Fig. 1).

2.2. Data handling and statistical analysis

The fish were measured three times during rearing. The first measurement was made on the 25th of March, 2005, at the land-based rearing stage in Hafnir, where random samples of 2794 individuals were measured. The second measurement was made on the 6th of May, 2006, where a random sample of 756 individuals taken from the sea-cage in Berufjörður were killed and measured. The last measurements were made on the 15th of December, 2006. A random sample of 755 individuals was taken from the sea-cage in Berufjörður and killed and measured. The weight, maturation length and condition factor were compared between individuals based on the original locations of the brood fish. The condition factor (CF) was calculated as ungutted body weight (g) × 100/(body length cm)^3. The maturation stage was determined visually on the 6th of May, 2006, and the 15th of December, 2006. The slaughtered fish were gutted and classified as mature if eggs or sperm were clearly observed.

The analysis data for body weight, length and CF were tested with one way ANOVA, and the proportion of maturation multiple proportions test (Newcombe, 1998). Interaction between groups and days of measurements were tested with two ways ANOVA with interaction. All statistics were calculated by using R 2.14.0 software (R Development Core Team, 2011). The growth of the 2004 year-class was compared with that predicted by Björnsson and Steinarsson (2002). The model is $G = (0.5735\mathrm{T}) \times W^{(-0.1934 \text{ to } 0.02001T)}$, where G = specific growth rate, T = rearing temperature and W = weight of the fish. The predicted weight Wt_2 after t days, then, is $Wt_2 = Wt_1 \times e^{(G \times t/100)}$, where G = specific growth rate and Wt_1 = present weight. The predicted values from the model versus the measurements were tested with two-sample t-tests in R 2.14.0. An α level of 0.05 was used to test for significant differences.

2.3. DNA profiling

In the beginning of the rearing, all eggs were mixed at 7 day, post fertilization, and at each measurement a tissue samples were collected from the measured fish. Tissue samples from brood-fish were collected when the fish was stripped. Pedigree was constructed using the microsatellite markers listed in chapter 2.4. The offspring were matched to their parentage, and their origin, based on their scoring and the record of mating (marker scoring was performed at Prokaria Ltd., Reykjavik). Parental assignment was performed using MasterBayes R software (Hadfield et al., 2006).

2.4. Genetic distance (F_{ST})

The genetic distance for the 2004 year-class was determined from sixteen microsatellites (Gmo8, Gmo19, Gmo37 (Miller et al., 2000), Tch11, Tch14 (O'Reilly et al., 2000), and Gmo38 (Jakobsdottir et al., 2006), PGmo38, PGmo49, PGmo61-FRb, PGmo71, PGmo74, PGmo87, PGmo94, PGmo100, PGmo124, and PGmo134 (Skirnisdottir et al., 2008)). Analysis of gene diversity in the subdivided populations was performed as described by Nei (1973) and using the algorithm in R (Goudet, 2005). Significant genetic structures among the populations were tested using the