

Juvenile growth and susceptibility to *Aeromonas salmonicida* subsp. *salmonicida* in Atlantic salmon (*Salmo salar* L.) of farmed, hybrid and wild parentage

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Abstract

Atlantic salmon of wild, hybrid and farmed parentage were established in November 2002 and hatchery-reared up to March 2004. At age 1+, farmed fish were significantly ($F=28.3$ $P<0.0001$) larger than wild fish, with hybrids intermediate (farm=38.1 g, hybrid=29.0 g, wild=21.9 g). A sample of fish from each group was fin clipped, mixed into two replicate tanks, then exposed to experimental challenge with the causative agent of furunculosis, *Aeromonas salmonicida* subsp. *salmonicida* via cohabitants. A third tank, containing only hybrids, was challenged with *A. salmonicida* in order to investigate the effects of individual fish size on susceptibility. Significant differences in mortality were observed among the groups ($G=7.9$ $P<0.022$). However, an effect of fish size on mortality was also observed, and, fish representing the three experimental groups were significantly different in size. When this effect was controlled for, initial differences in group-mortality were no longer significant. Consequently, under the given conditions, no significant differences in susceptibility to the bacteria *A. salmonicida* subsp. *salmonicida* were observed between salmon of farm, hybrid and wild parentage.

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1. Introduction

Escapement of farmed Atlantic salmon (*Salmo salar* L.) represents both an economic and environmental concern for the salmon culture industry. The presence (Gudjonsson, 1991; Lund et al., 1991; Crozier, 1998), successful spawning (Lura and Saegrov, 1991; Carr et al., 1997) and genetic integration (Crozier, 1993, 2000; Clifford et al., 1998) of escaped farmed Atlantic salmon

in native salmon populations have been documented. These observations give cause for concern for the ecological and genetic consequences that this may have on recipient native salmon populations. This is especially important considering that Atlantic salmon populations are often regarded as genetically adapted to the specific river they inhabit (reviewed by Taylor, 1991), there is a global decline in wild Atlantic salmon (Parrish et al., 1998; Kellogg, 1999; WWF, 2001) and the salmon farming industry continues to expand.

Farmed Atlantic salmon have been subject to domestic selection for a range of biological traits (e.g., Gjøen and Bentsen, 1997; Gjedrem, 2000). Farmed Atlantic

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salmon generally display a lower degree of genetic variation compared to native populations (Cross and Callanain, 1991; Youngson et al., 1991; Mjølnerød et al., 1997; Norris et al., 1999; Skaala et al., 2004). Under hatchery conditions, both Grisdale-Helland and Helland (1998) and Thodesen et al. (1999) observed significantly greater growth and feed conversion rates in salmon of 5th selected generation compared to wild salmon. Furthermore, Einum and Fleming (1997) also observed significantly greater hatchery growth for 7th generation selected salmon compared to wild salmon. Results of studies in natural habitats have demonstrated lower survival of offspring of farmed parentage compared to wild parentage (McGinnity et al., 1997, 2003; Fleming et al., 2000).

Despite evidence that offspring of farmed salmon display reduced survival in natural habitats when compared to offspring of wild salmon, there are significant gaps in current understanding of the actual mechanism(s) conferring these differences. Susceptibility to disease agents is associated with fitness, both in natural and domestic environments. Despite this, thus far, potential differences in susceptibility to disease agents between salmon of wild and domestic origin have been little explored. Glover et al. (2004) compared the susceptibility of Atlantic salmon of farm and wild parentage to the sea louse *Lepeophtheirus salmonis*. Although only moderate differences in susceptibility to this parasite were observed, with the largest differences being observed between two of the wild stocks, in a study of susceptibility to ISA virus, Nylund et al. (1995) observed a greater susceptibility of farmed salmon to this virus than wild salmon.

Furunculosis is a disease caused by the bacterium *Aeromonas salmonicida* subsp. *salmonicida* and has been extensively studied (e.g., Austin and Austin, 1987; Johnsen and Jensen, 1994). Although furunculosis induced mortality has been recorded in wild salmonids in Britain since the early 20th century (Mackie et al., 1930), the marine form of this disease was not detected in Norway until 1985. After its introduction to Norway, the disease was observed in both wild and domesticated salmon (Munro and Hastings, 1993; Bernoth, 1997) and spread rapidly along the Norwegian coastline infecting no less than 550 farms and 74 wild salmon populations by the end of 1992 (Johnsen and Jensen, 1994). Outbreaks of furunculosis on salmon farms have been fewer in later years due to effective vaccination (Brown and Bruno, 2002; Lillehaug et al., 2003).

A genetic component in susceptibility to furunculosis has been observed in Atlantic salmon (Gjedrem et al., 1991; Gjøen et al., 1997). This has been taken

advantage of by the Norwegian Atlantic salmon breeding program where selection for this trait has been practiced since the 5th generation (Gjedrem, 2000). As a consequence of the fact that there is a significant genetic component in susceptibility to furunculosis, this disease has a documented history of infection and mortality in both domesticated and wild salmon in Norway and well-established challenge models exist for this bacterium; it is suggested that this disease is a suitable candidate for studying potential differences among domesticated and wild salmon. The aim of the present study was to compare salmon of farmed, wild and hybrid parentage under identical rearing and challenge conditions for growth, and, susceptibility to furunculosis.

2. Materials and methods

The fish used in this study were the offspring resulting from the crossing of farmed and wild salmon. Adult farmed salmon used to produce progeny for this study were escapees of unknown farm origin that had entered and were captured by a variety of methods in the middle and upper reaches of the river Vosso (60°38'N, 5°57'E), on the west coast of Norway, in the late summer and autumn of 2002. These individuals were identified and verified as farmed salmon by the VESO laboratory, based upon established diagnostic characteristics (Lund et al., 1989, 1995, 1997; Lund and Hansen, 1991). Wild adult salmon used for this study were collected from the living GeneBank located in Eidfjord, west Norway. These fish are the F1 progeny of wild spawners that were collected from the river Lærdal (61°6'N, 7°28'E).

On 12.11.02, verified farmed salmon were stripped in the Voss hatchery to produce full sibling families. A vial of sperm from each male was retained at 4 °C for later use to create hybrids with the wild salmon. On 2.12.02, sperm and eggs were collected from wild Lærdal salmon at the GeneBank and then transferred to the Voss hatchery. Farmed male and wild female hybrid families were created, in addition, Lærdal full sibling families were created. All families were full sibling apart from hybrids which were either paternal or maternal half siblings with their respective parental stocks. Fertilized eggs were disinfected with buffodine and incubated in single-family incubators at the Voss hatchery. When the eggs reached the eyed stage on 3 April 2003, they were shocked, dead eggs removed and 200 viable eggs from each of 6 pure farm families, 6 hybrid families and 6 pure wild families were transported to the research facilities of the Institute of Marine Research,

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