



Genetic mixed stock analysis of an interceptory Atlantic salmon fishery in the Northwest Atlantic

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ABSTRACT

Interceptory fisheries represent an ongoing threat to migratory fish stocks particularly when managed in the absence of stock specific catch and exploitation information. Atlantic salmon from the southern portion of the North American range may be subject to exploitation in the commercial and recreational salmon fisheries occurring in the French territorial waters surrounding St. Pierre and Miquelon off southern Newfoundland. We evaluated stock composition of Atlantic salmon harvested in the St. Pierre and Miquelon Atlantic salmon fishery using genetic mixture analysis and individual assignment with a microsatellite baseline (15 loci, 12,409 individuals, 12 regional groups) encompassing the species western Atlantic range. Individual salmon were sampled from the St. Pierre and Miquelon fishery over four years (2004, 2011, 2013, and 2014). Biological characteristics indicate significant variation among years in the size and age distribution. Nonetheless, estimates of stock composition of the samples showed consistent dominance of three regions (i.e., Southern Gulf of St. Lawrence, Gaspé Peninsula, and Newfoundland). Together salmon from these regions accounted for more than 70% of annual harvest over the decade examined. Comparison of individual assignments and biological characteristics revealed a trend of declining fresh water age with latitude of assigned region. Moreover, locally harvested Newfoundland salmon were ten times more likely to be small or one sea winter individuals whereas Quebec and Gaspé Peninsula salmon were two-three times more likely to be harvested as large or two sea winter salmon. Estimates of region specific catch were highest for salmon from the southern Gulf of St. Lawrence region ranging from 242 to 887 individuals annually. This work illustrates how genetic analysis of interceptory marine fisheries can directly inform assessment and management efforts in highly migratory marine species.

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1. Introduction

Mixed stock fisheries target admixtures of populations and are common for many migratory anadromous or marine fish species (Chase, 2003; Schindler et al., 2010; Utter and Ryman, 1993). These fisheries risk a reduction of biodiversity and the over exploitation

of rare constituents as the stock composition of mixed harvests are often unknown (Crozier et al., 2004; Saunders, 1981). A variety of approaches have been used to disentangle the composition of mixed stock fisheries including the application of physical tags (Candy and Beacham, 2000; Reddin et al., 2012; Weitkamp and Neely, 2002), morphometric analysis (e.g., Reddin and Friedland, 1999; Shepard et al., 2010), geochemistry (Campana et al., 1999; Fraile et al., 2015; Jónsdóttir et al., 2007), and molecular genetic approaches (Araujo et al., 2014; Ensing et al., 2013; Ruzzante et al., 2000). Despite obvious risks, dramatic reductions in catch variation

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have been observed in mixed stock fisheries over time as productivity can be buffered by intraspecific diversity (Hilborn et al., 2003; Schindler et al., 2010). Given the complexity and potential risks and benefits, understanding contributions to mixed stock fisheries remain an ongoing challenge for fisheries management and conservation.

Mixed stock fisheries have been extensively studied in anadromous salmonids, particularly Pacific salmon species, where genetic stock identification has been used to manage coastal fisheries (Beacham et al., 2004; Shaklee et al., 1998). However, as genetic baselines are established in more species, such as Atlantic salmon, *Salmo salar* (e.g., Bradbury et al., 2015; Ensing et al., 2013; Griffiths et al., 2010; Moore et al., 2014), new opportunities exist for broader application. Atlantic salmon, have traditionally been subject to mixed stock harvests during the marine phase of their life history, commonly associated with marine feeding areas or migratory routes (e.g., Chase, 2003; Saunders, 1981). In the western Atlantic, salmon migrate to the Labrador Sea or the waters west of Greenland to feed (Pippy, 1982; Reddin, 1988; Reddin and Short, 1991; Ritter, 1989) and although, most commercial marine fisheries for Atlantic salmon have ceased, three remaining marine fisheries may exploit mixed stocks of wild Atlantic salmon in the Northwest Atlantic. These include the Labrador subsistence food fisheries, the fishery at West Greenland, and a fishery in the waters surrounding the French islands of St. Pierre and Miquelon (ICES, 2015). Previous genetic based mixture analysis of the Labrador and West Greenland harvests have revealed contrasting patterns in stock composition consistent with their location on migratory routes of salmon at sea; the Labrador salmon fisheries harvesting predominantly Labrador origin salmon (96%, Bradbury et al., 2015) and the west Greenland fishery harvesting a mixture of stocks from eastern North America as well as from Europe (Gauthier-Ouellet et al., 2009; Sheehan et al., 2010). However, the stock composition of the St. Pierre and Miquelon Atlantic salmon fishery has to date not been determined and remains of concern to management and conservation efforts.

The Atlantic salmon fishery in the French territorial waters around St. Pierre and Miquelon is a commercial and recreational gillnet fishery reported to harvest as much as 5 ton or 2300 individuals annually in recent years (ICES, 2015). In the absence of salmon producing rivers in St. Pierre and Miquelon, the fishery is entirely interceptory in nature, likely targeting southern stocks migrating around southeastern Newfoundland. As many of these regions to the south have experienced dramatic declines and record lows in productivity (COSEWIC, 2011; DFO, 2013a,b; Fay et al., 2006), concerns persist regarding possible inception and exploitation in this fishery. Atlantic salmon stocks in the southern Newfoundland portion have declined by as much as 70% and were recently assessed as threatened, whereas stocks in the New Brunswick and the USA are at risk of extinction (COSEWIC, 2011; DFO, 2013b; Fay et al., 2006; Robertson et al., 2013). The threat this fishery may pose to persistence and recovery of these stocks ultimately remains to be quantified and continues to be an issue of concern (COSEWIC, 2011; DFO, 2013a,b).

The goal of this work was to determine the origin of the salmon intercepted in this mixed stock gill net fishery for Atlantic salmon in the waters surrounding St. Pierre and Miquelon and to quantify potential impacts on those salmon populations. The main objective was to estimate the stock composition of salmon harvested in this fishery using genetic stock identification and to examine the temporal stability of the catch composition. The work builds directly on recent initiatives to develop a North American microsatellite baseline for Atlantic salmon, including samples from two additional rivers of the eastern USA. Using this baseline, accurate mixture analysis and individual assignment to 12 regional North American reporting groups is possible. In conjunction with catch logs, these

estimates of stock composition will allow the magnitude of fishery harvest for the various contributing stocks to be estimated.

2. Methods

2.1. Baseline samples

Baseline samples encompassed 12067 individuals spanning 194 individual rivers ranging from Ungava Bay in the north to the Sheepscot River in Maine to the south (Fig. 1, Table 1). Data included in the baseline represented a combination of previously analyzed datasets (see Bradbury et al., 2014; Dionne et al., 2008 for regional analyses and further details) and new data (see Bradbury et al., 2015; Moore et al., 2014 for methods and database details). The baseline differs from previous analyses in that two additional rivers were included to better represent US salmon populations. These were the Sheepscot River and the Narraguagus River, both located in the state of Maine (Fig. 1). Baseline accuracy for mixture analysis and individual assignment have been extensively explored previously (see Bradbury et al., 2015; Moore et al., 2014), but limited re-analysis has been conducted here to assess the impact of the inclusion of the two additional populations.

2.2. Fishery samples

The St. Pierre and Miquelon (SPM) Atlantic salmon fishery is comprised of commercial and recreational gill net harvests occurring in the French coastal waters surrounding St. Pierre and Miquelon. The fishery generally occurs from May 1st to July 31st annually (Goraguer, 2011). The dominant gear type consists of 5 inch gill nets of 360 m length for commercial fishers and 180 m length for recreational fishers. Although fishing may occur around the islands, the majority of fishing occurs close to the southeast portion of St. Pierre (Goraguer, 2011). Sampling of the Atlantic salmon fishery at St. Pierre and Miquelon was conducted by Ifremer (i.e., French Research Institute for the Exploration of the Sea) in 2004, 2011, 2013, and 2014 as early as 24 May in 2013 to 7 July in 2011. Adipose fin clips for 3–11% of the harvest were collected in 2011, 2013 and 2014 for genetic stock identification whereas scale samples were used in 2004. Biological characteristics information collected included length (cm), weight (guttled, kg), and scale samples were used for interpretation of river age, sea age, and spawning history.

2.3. DNA extraction and genotyping fishery samples

DNA extraction and microsatellite genotyping of all fishery samples were carried out at the Aquatic Biotechnology Laboratory (Fisheries and Oceans Canada). DNA was extracted using the Qiagen DNeasy 96 Blood and Tissue extraction kit (Qiagen) following the guidelines of the manufacturer. DNA was quantified using QuantIT PicoGreen (Life Technologies) and diluted to a final concentration of 10 ng/μL in 10 mM Tris (Buffer EB, Qiagen). Microsatellite polymorphisms were scored at the following 15 loci: Ssa85, Ssa202, Ssa197 (O'Reilly et al., 1996), SSOSL417 (Slettan et al., 1995), SsaD85 (King, unpublished), SsaD58, SsaD71, SsaD144, SsaD486 (King et al., 2005), MST-3 (hereafter referred to as U3) (Presa and Guyomard, 1996), SSsp2201, SSsp2210, SSsp2215, SSsp2216 and SSspG7 (Paterson et al., 2004). Genotyping of fishery samples followed the methods outlined in Bradbury et al. (2015) and Bradbury et al. (2014). In short, loci were multiplexed into three panels either by combining loci amplified individually prior to electrophoresis, or by multiplexing at the PCR stage. The PCR reactions for single locus amplification were set up in a 10 μL volume containing 20 ng DNA, 1X PCR buffer (KCl buffer or (NH₄)₂SO₄ (Fermentas) (Table S4)), 1.5–2.5 mM MgCl₂ (Fermentas), 0.2 mM

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