

Inferring marine distribution of Canadian and Irish Atlantic salmon (*Salmo salar* L.) in the North Atlantic from tissue concentrations of bio-accumulated Caesium 137

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Atlantic salmon returning from marine migrations to eastern Canada and western Ireland during 2002 and 2003 were analysed for tissue concentrations of bio-accumulated caesium 137 (^{137}Cs). Salmon from Canadian and Irish waters demonstrated concentrations ($0.20 \pm 0.14 \text{ Bq kg}^{-1}$ and $0.19 \pm 0.09 \text{ Bq kg}^{-1}$, mean \pm s.d., respectively) suggesting similar oceanic feeding distributions during migration. Canadian aquaculture escapees had a similar mean tissue concentration ($0.28 \pm 0.22 \text{ Bq kg}^{-1}$), suggesting migration with wild salmon. However, significantly higher concentrations in 1-sea-winter (1SW) escapees ($0.43 \pm 0.25 \text{ Bq kg}^{-1}$) may alternatively suggest feeding within local estuaries. High concentrations in some Canadian 1SW salmon indicated trans-Atlantic migration. Low concentrations of Canadian multi-sea-winter (MSW) salmon suggested a feeding distribution in the Labrador and Irminger Seas before homeward migration, because those regions have the lowest surface water ^{137}Cs levels. Estimates of wild Canadian and Irish salmon feeding east of the Faroes ($\sim 8^\circ\text{W}$) were 14.2% and 10.0% (1SW, 24.7% and 11.5%; MSW, 2.9% and 0.0%), respectively. We propose that most anadromous North Atlantic salmon utilize the North Atlantic Gyre for marine migration and should be classified as a single trans-Atlantic straddling stock.

Keywords: aquaculture and wild Atlantic salmon, Caesium 137, Canada, Ireland, North Atlantic Gyre, trans-Atlantic migration.

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Introduction

Marine mortality has been suggested as a major contributing factor to the decline of wild Atlantic salmon populations (Cairns, 2001; Hutchinson *et al.*, 2002; Lacroix and Knox, 2005). This mortality is proposed to happen within a salmon's first months at sea (Holm *et al.*, 2003). However, a recent study indicated good survival rates nearshore of Atlantic salmon post-smolts (Lacroix *et al.*, 2005). As a result, numerous researchers have proposed that research effort should focus on investigating factors that affect salmon survival offshore (Hutchinson *et al.*, 2002; Lacroix and Knox, 2005). Determining the cause of marine mortality requires a thorough understanding of the spatial and temporal distribution of Atlantic salmon during their oceanic feeding phase (Friedland, 1998; Jonsson and Jonsson, 2004). Unfortunately, Atlantic salmon migration routes and oceanic distribution patterns are poorly known (Hansen and Quinn, 1998; Holm *et al.*, 2003).

The currently accepted model for open-ocean migration of Atlantic salmon is based on past tag returns (Templeman, 1967;

Jensen, 1980a, b; Swain, 1980; Meister, 1984; Baum, 1997; Jacobsen *et al.*, 2001), mixed stock discrimination studies (Reddin *et al.*, 1984a; Reddin, 1987; Reddin and Freidland, 1999, Jacobsen *et al.*, 2001), and the distribution of commercial high seas fisheries (Christensen and Lear, 1980; Jensen and Lear, 1980; Hansen and Pethon, 1985; Reddin, 1986; Reddin and Dempson, 1986; Jakupsstovu, 1988; Scarnecchia *et al.*, 1991; Vigfússon and Ingólfsson, 1993). Southern European stocks ($<62^\circ\text{N}$) are proposed to migrate in relatively straight lines from natal rivers to feeding grounds off West Greenland (Went, 1973; Swain, 1980). Alternatively, northern European stocks ($>62^\circ\text{N}$) are proposed to migrate to feeding grounds off the Faroe Islands and Iceland, and in the Norwegian Sea (Hansen *et al.*, 1993, Jacobsen *et al.*, 2001), so may be subject to alternative causes of mortality. All North American stocks are thought to migrate directly to waters off West Greenland in the warmer months and to overwinter in the Labrador Sea and off the Grand Banks east to 44°W longitude (Reddin, 1986).

Environmental tracers, such as caesium-137 (^{137}Cs), have been utilized over a range of spatial scales to infer migratory behaviour of marine fish and mammals (Born *et al.*, 2002; Tolley and Haldal, 2002), including Atlantic salmon (Tucker *et al.*, 1999). Globally dispersed during the later half of the 20th century as a nuclear fission byproduct, ^{137}Cs formed a highly pronounced east–west gradient in the North Atlantic as a consequence of anthropogenic inputs from nuclear reprocessing facilities, Sellafield in the Irish Sea and La Hague in the English Channel, and fallout from the 1986 Chernobyl accident (Tucker *et al.*, 1999). Environmental concentrations decrease from point sources with distribution largely controlled by oceanographic processes (Marine Institute, 1999). Discharges of ^{137}Cs from Sellafield and La Hague peaked in the 1970s and 1980s, but have since been reduced by more than two orders of magnitude (Povinec *et al.*, 2003), decreasing concentrations in the Irish Sea (Marine Institute, 1999) and the eastern Atlantic (Povinec *et al.*, 2003). However, bioavailability of ^{137}Cs still exists from the water column and through remobilization from contaminated sediments (Povinec *et al.*, 2003).

Here, we infer the marine distribution of Atlantic salmon based on relative bio-accumulated ^{137}Cs concentrations found in the tissues of migrant salmon returning to Canadian and Irish rivers, compared with known ^{137}Cs levels in surface waters of the north Atlantic Ocean. On the basis of these data and past research, we propose an alternative hypothesis that Atlantic salmon utilize the North Atlantic Gyre for their marine migration (Figure 1). Our information will be crucial to the development of hypotheses concerning marine migration patterns and the causes of marine mortality of Atlantic salmon.

Material and methods

Wild, adult salmon were collected opportunistically from fishers or researchers in Atlantic Canada and western Ireland. Aquaculture salmon, to be used as western and eastern Atlantic controls, were obtained from salmon farms in the Bay of Fundy (BF), Canada, and Killery Fjord, western Ireland, respectively. Wild Canadian parr and Irish smolts were collected from the same watersheds as adults, if possible. Returning aquaculture escapees were obtained from researchers in the Bay of Fundy, Canada.

Morphometrics and scale samples were taken at collection. Fork length (FL) of salmon was measured to the nearest 0.1 cm and wet body mass (WT) to the nearest 0.1 kg. When only heads were available, fork lengths and wet body weights were calculated from FL to WT and head length (HL) to FL ratios from whole body adult samples ($n = 113$ and 161, respectively). Scales samples were collected and stored as in Shearer (1992). If no scales were available ($n = 71$), otoliths were used for age determination. Heads of adult fish were removed and stored frozen in individual plastic bags before analysis.

Laboratory analysis

Frozen heads were thawed and head length (tip of snout to posterior edge of the opercle bone; Hubbs and Lagler, 1964) was measured to the nearest 0.1 cm, using calipers. Unknown head lengths from partial or unmeasured heads were estimated from HL:FL relationships for all adult samples. Otoliths were removed with non-contaminated Teflon forceps, cleaned, and stored in acid-washed polyethylene tubes. Head tissue weights were

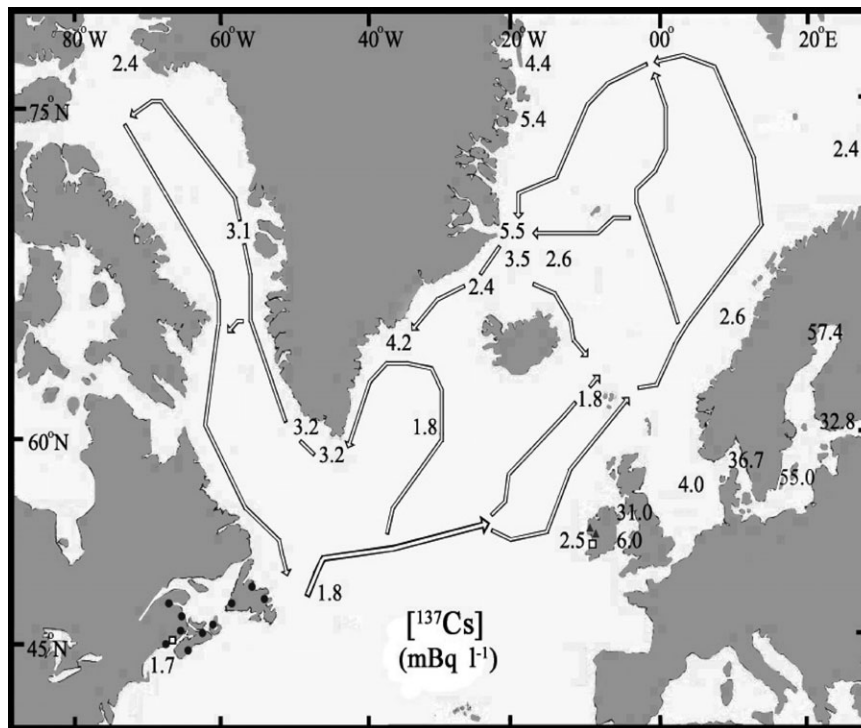


Figure 1. North Atlantic Gyre (open arrows; compiled from Krauss, 1986; Hansen and Osterhus, 2000; Lavender *et al.*, 2000; Jakobsen *et al.*, 2003) showing redistribution of mean surface seawater levels of ^{137}Cs (mBq l^{-1}) in the north Atlantic Ocean for the period 2000–2003 (compiled from RPII, 2002, 2003; NRPA, 2003, 2004; STUK, 2003, 2004; Dahlgaard *et al.*, 2004; HELCOM, 2004; J. Smith, pers. comm.; I. Sværen, pers. comm.). Atlantic salmon sample sites for 2002 and 2003 are indicated (black dots, Canada; black triangles, Ireland, open squares, aquaculture sites).

obtained to the nearest 0.1 g, using an electronic balance unless otherwise specified. Head wet weights (HWt_0) were taken before initial drying, which was done at 175°C for 24 h. Dentary, maxillary, operculum, parietals, pectoral fins, and dorsal process of the shoulder girdle were removed and weighed together (HWt_b). Remaining bones and soft tissue were dried at 175°C for 48 h and subsequently ashed at 450°C for 12 h or until a fine, grey powder ash was obtained (Morinville, pers. comm.). Individual ashed samples were homogenized with a mortar and pestle, weighed to the nearest 0.001 g, and stored in glass vials at sub-zero temperatures until shipment for gamma ray spectroanalysis. Parr whole-body wet samples (BWt_x) were weighed to the nearest 0.01 g. Samples were dried at 175°C for 72 h, then frozen until shipment. Smolt whole-body samples followed parr procedures, but were subsequently ashed for 6 h at 450°C.

Scales were cleaned, mounted between two glass slides, and aged using a projection microscope. Ages were determined by consensus from readings obtained by two separate investigators. Samples lacking appropriate scales for analysis were aged from whole otoliths read with a dissecting microscope, using a two-investigator reading procedure as well. Scale and otolith annuli were counted according to guidelines outlined by Shearer (1992) and Chilton and Beamish (1982), respectively. Disagreements over presumed ages were resolved by re-reading samples with both investigators present. Sea age for samples without collected scales or otoliths was estimated using the FL:sea age relationship for all the adult samples collected.

Gamma ray spectrometry

Ashed samples were weighed to the nearest 0.001 g and loaded into polyethylene cylinders for one-time counting using a high-purity germanium (HPGe) coaxial well gamma ray detector located at École Polytechnique, Montréal. Individual juvenile samples <15 g wet weight ($n = 44$) and below detection limits were pooled and counted just once. Counted samples were returned and stored at sub-zero temperature. Both minimum and

maximum concentrated samples and a further nine randomly selected samples were recounted to validate results, using two HPGe gamma ray spectrometers at McGill University, Montréal.

Data analysis

Tissue concentrations of ^{137}Cs (Bq kg^{-1} wet weight) for respective Canadian and Irish Atlantic salmon samples were regressed against wet body weight (WT). All samples were grouped by year of capture, continent of origin, oceanographic region of natal river drainage, natal river, and category (aquaculture, escapee, wild). Both generalized linear models (GLM ANOVA) and analysis of variance (ANOVA) followed by a *post hoc* Tukey test were used to examine overall trends between ^{137}Cs burden, duration at sea (sea age, FL, WT), and grouping variables (SYSTAT, 2004). Outliers, as defined by SYSTAT (2004), were removed for statistical analyses based on sample means and for the plotting of box plots comparing ^{137}Cs concentrations. However, outliers were considered to be critical data points and evidence for the development of a trans-Atlantic migration hypothesis. A significant trend between sea age cohorts and ^{137}Cs concentrations (ANOVA, $p < 0.001$) allowed separation of 1-sea-winter (1SW) and multi-sea-winter (MSW) wild Canadian samples pooled by oceanographic region of natal river drainage. The pooled samples were then compared with pooled samples from endangered inner Bay of Fundy (iBoF) populations using a *post hoc* Tukey test. Any region with a sample size (n) of < 3 was excluded from the analysis. Fork length and ^{137}Cs burden for wild migrants was regressed, using both raw and log-transformed data. Log-transformed ^{137}Cs burden data yielded an even lower value of r^2 value compared with a raw data regression. Therefore, raw data trend-line values (Figure 2) were subtracted from originals [^{137}Cs] to calculate Cs residuals to be used to de-trend data and to increase sample sizes for natal river comparisons within oceanographic river drainage regions: Atlantic coast (AT), BF, and Gulf of St Lawrence (GSL) in Canada and the west coast of Ireland (WC). Cs residuals for each

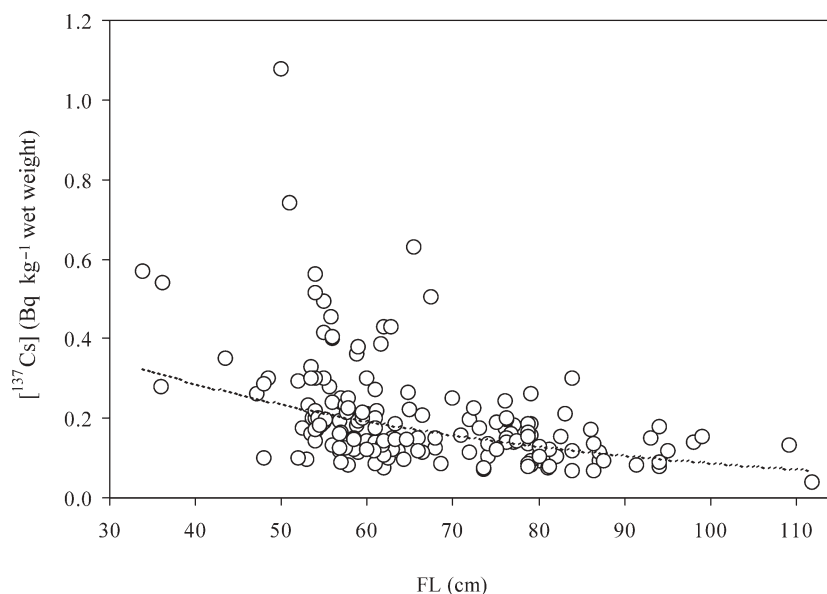


Figure 2. Tissue concentration of ^{137}Cs (Bq kg^{-1} wet weight) in relation to fork length (FL, cm) of wild adult Atlantic salmon sampled in 2002 and 2003 [$r^2 = 0.26$, $y = 0.6409 \exp(-0.0199x)$].

sample were calculated using

$$\text{Cs residual} = [^{137}\text{Cs}] - [0.6409 \exp(-0.0199\text{FL})],$$

where $[^{137}\text{Cs}]$ is the ^{137}Cs concentration (Bq kg^{-1} wet weight) and FL is fork length (cm) at capture. Individual ($n = 16$) and pooled ($n = 44$) juvenile ^{137}Cs burden data were compared using a Z-test. A two-sample Kolmogorov–Smirnov test was used to compare ^{137}Cs concentration frequency distribution of wild North American samples collected in 2002 and 2003 with the 1995/1996 study of the Ste Marguerite River Atlantic salmon population (see Tucker *et al.*, 1999).

Results

In all, 173 wild, adult salmon were collected in Atlantic Canada ($n = 143$) and western Ireland ($n = 30$) between September 2002 and November 2003. A further 12 aquaculture salmon controls were obtained from a farm in the BF, Canada (October 2002), and 10 from Killery Fjord in western Ireland (July 2003). Wild Canadian parr ($n = 44$) and Irish smolts ($n = 16$) were collected from the same watersheds as adult samples where possible. In all, 26 returning aquaculture escapee adults were obtained from research operations in watersheds of the BF, Canada (Table 1).

Of the 11 samples recounted for tissue concentrations of ^{137}Cs (test of analytical accuracy), there was no significant difference

between original and re-count results (GLM ANOVA, $p = 0.130$, two outliers removed). Overall analysis of Atlantic salmon returnees sampled in 2002 and 2003 revealed a trend for exponential decline of ^{137}Cs concentrations with increasing time away at sea (Figure 3). There was no significant difference between tissue ^{137}Cs concentrations and collection year (GLM ANOVA, $p > 0.05$), so 2002/2003 Canadian samples were pooled for subsequent analyses. There were significant differences between Canadian samples categorized by origin (wild, aquaculture escapee or aquaculture; GLM ANOVA, $p < 0.05$), but not between Irish wild and aquaculture samples. Analysis of wild returnee cohorts revealed that 0-sea-winter (OSW) salmon ($n = 3$) had significantly higher mean tissue ^{137}Cs burdens than older cohorts (ANOVA *post hoc* Tukey, $p < 0.001$, $n = 158$, 16 outliers removed). Grilse (1SW, $n = 84$) had significantly higher mean ^{137}Cs tissue burdens than 2-sea-winter (2SW) salmon ($n = 61$) (ANOVA *post hoc* Tukey, $p = 0.015$). There was no significant difference between 2SW and all older cohorts (Figure 2; ANOVA *post hoc* Tukey, $p > 0.535$).

Tissue concentrations of ^{137}Cs in wild Atlantic salmon returning to Canadian rivers in 2002 and 2003 ranged from 0.04 to 1.08 Bq kg^{-1} wet weight. Returning aquaculture escapees ranged from 0.07 to 0.82 Bq kg^{-1} wet weight. There was a significant difference between 1SW wild and escapee Canadian salmon (ANOVA, $p = 0.008$). Canadian aquaculture salmon (controls) had significantly lower tissue ^{137}Cs concentrations than 1SW wild

Table 1. Sampling locations and tissue concentrations of ^{137}Cs (Bq kg^{-1} wet weight) in Atlantic salmon collected from Canada and Ireland in 2002 and 2003 ($n = 282$), assigned to either wild (W), aquaculture (A), or aquaculture escapee (AE) origin, and age groups of 0-sea-winter (OSW), 1-sea-winter (1SW), and multi-sea-winter (MSW) fish by scale or otolith examination.

Country	Region/River	Origin	Stage	n	$[^{137}\text{Cs}]$ (Bq kg^{-1} wet weight)		CL (95%)
					Mean	s.e.	
Canada	GSL	W	Parr	44 ^a	0.30	–	–
Canada	AT	W	OSW	3	0.47	0.08	0.37
Canada	AT	W	1SW	26	0.21	0.04	0.08
Canada	BF	W	1SW	12	0.20	0.03	0.07
Canada	BF	A	1SW	12	0.09	0.01	0.03
Canada	BF	AE	1SW	12	0.43	0.07	0.16
Canada	iBoF ^b	W	1SW	8	0.21	0.04	0.10
Canada	Black R.	W	1SW	2	0.21	0.01	0.13
Canada	Gaspereau R.	W	1SW	4	0.20	0.08	0.25
Canada	Big Salmon R. ^c	W	1SW	2	0.23	0.13	1.59
Canada	GSL	W	1SW	35	0.28	0.03	0.05
Canada	AT	W	MSW	1	0.07	–	–
Canada	BF	W	MSW	7	0.17	0.02	0.04
Canada	BF	AE	MSW	14	0.15	0.02	0.03
Canada	GSL	W	MSW	60	0.14	0.01	0.02
Canada	iBoF ^b	W	MSW	4	0.15	0.02	0.06
Canada	Gaspereau R.	W	MSW	1	0.15	–	–
Canada	Big Salmon R. ^c	W	MSW	3	0.15	0.03	0.11
Ireland	WC	W	Smolt	16	0.53	0.04	0.08
Ireland	WC	W	1SW	26	0.19	0.02	0.04
Ireland	WC	A	1SW	10	0.23	0.04	0.08

^aSamples ($n = 44$) pooled and counted only once by gamma ray spectrometry.

^biBoF pools Big Salmon, Black, and Gaspereau River samples.

^cAccording to Amiro (2003), the Big Salmon River is considered iBoF, whereas the Black, Gaspereau, and Irish River populations are excluded based on a high proportion of virgin, MSW salmon.

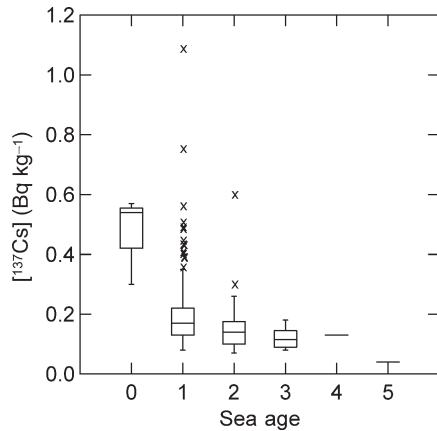


Figure 3. Relationship between sea age and tissue concentrations of ^{137}Cs (Bq kg^{-1} wet weight) for all wild Atlantic salmon samples collected in 2002 and 2003 ($n = 157$, 17 outliers removed). Outliers (crosses) removed for statistical analyses and plotting of this Figure are shown.

and escapee salmon (Table 1; GLM ANOVA, $p < 0.03$). Standardized frequency distributions of tissue ^{137}Cs concentrations for wild, returning Atlantic salmon sampled from the Ste Marguerite River, Quebec, in 1995/1996 (Tucker *et al.*, 1999) and all wild Canadian samples collected in 2002 and 2003 resulted in a significant difference (Kolmogorov–Smirnov two-sample test, $p = 0.01$).

Comparisons of ^{137}Cs concentrations in wild 1SW salmon grouped according to natal river drainage within Atlantic Canada oceanographic regions (AT, BF, and GSL) revealed no significant differences (ANOVA, $p = 0.56$, $n = 54$, 18 outliers removed). Tissue concentrations of iBoF fish also showed no significant difference from fish from the three other regions (Figure 4a; ANOVA, $p = 0.61$, $n = 54$, 18 outliers removed). Comparisons of wild MSW fish showed that BF fish ($n = 7$) had significantly higher tissue concentrations than GSL fish ($n = 58$, ANOVA, $p = 0.029$). When iBoF fish were compared as a separate region, only BF fish ($n = 3$) had significantly higher tissue concentrations than GSL fish ($n = 58$, ANOVA *post hoc* Tukey test, $p = 0.024$). There was no regional difference between the iBoF and the BF or GSL populations (Figure 4b; ANOVA *post hoc* Tukey, $p > 0.257$). River-by-river comparisons yielded no significant differences among ^{137}Cs residuals within the AT (Figure 5a; GLM ANOVA, $p = 0.214$, $n = 20$, five outliers removed), BF (Figure 5b; GLM ANOVA, $p = 0.132$, $n = 13$, one outlier removed), or GSL (Figure 5c; GLM ANOVA, $p = 0.414$, $n = 77$, 11 outliers removed) regions.

Tissue concentrations of ^{137}Cs in wild salmon returning to Irish rivers ranged between 0.09 and 0.52 Bq kg^{-1} wet weight. Aquaculture controls ranged from 0.09 to 0.41 Bq kg^{-1} wet weight (Table 1). There was no significant difference between 1SW wild ($n = 26$) and aquaculture ($n = 10$) Irish Atlantic salmon tissue ^{137}Cs concentrations (GLM ANOVA, $p = 0.108$, one outlier removed). Irish adult Atlantic salmon returning to the Corrib River had significantly higher Cs residuals (mean $[^{137}\text{Cs}] = 0.24$) than home-bound migrants caught in the inshore Achill fishery (mean $[^{137}\text{Cs}] = 0.14$, GLM ANOVA, $p < 0.001$, $n = 25$, five outliers removed). There was no significant difference in tissue ^{137}Cs concentrations between wild Canadian and Irish

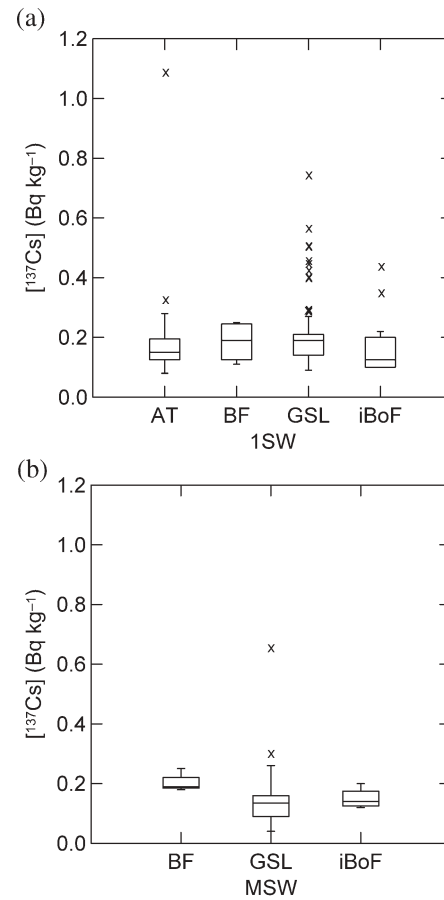


Figure 4. Wild Canadian Atlantic salmon tissue concentration of ^{137}Cs pooled by oceanographic regions of natal river drainage (AT, BF, and GSL) compared with the iBoF populations for (a) 1SW (18 outliers removed) and (b) MSW salmon (two outliers removed). Outliers (crosses) removed for statistical analyses and plotting of these Figures are shown.

salmon (Figure 6a; GLM ANOVA, $p = 0.277$, three outliers excluded). However, comparison of Canadian 2002 ($n = 12$) and Irish 2003 ($n = 10$) aquaculture salmon showed a significant difference (Figure 6b; GLM ANOVA, $p = 0.001$).

Tissue ^{137}Cs concentrations of Irish smolts ranged from 0.34 to 0.91 Bq kg^{-1} wet weight (Table 1). Their mean tissue concentration of 0.53 Bq kg^{-1} wet weight was significantly higher than Canadian parr (0.30 Bq kg^{-1} wet weight, one-sample Z-test, $p < 0.001$). Tissue concentrations of Canadian grilse returning after only spending summer months at sea (0SW) ranged from 0.30 to 0.57 Bq kg^{-1} wet weight and were also significantly higher than parr (one-sample Z-test, $p = 0.027$), but not significantly different from Irish smolts (GLM ANOVA, $p = 0.539$, one outlier removed).

Discussion

Similar ranges of tissue ^{137}Cs burdens in all sea age cohorts of wild, Canadian, and Irish salmon indicated that similar feeding grounds were utilized during marine migration. The significant relationship between duration at sea and declining tissue ^{137}Cs concentrations indicated that different sea age cohorts (1SW,

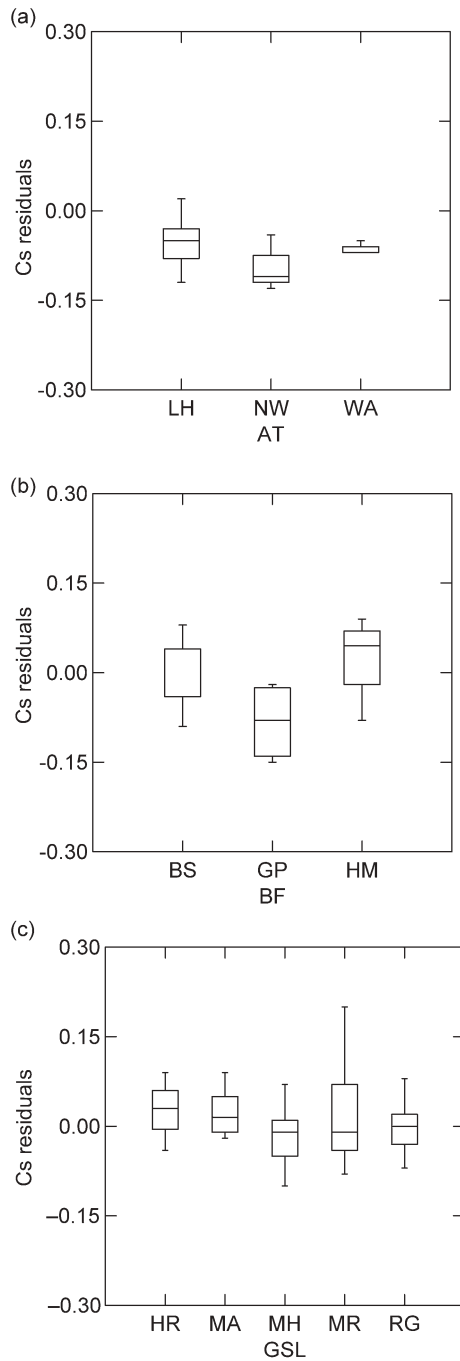


Figure 5. (a) River-by-river comparison within (a) Canada’s AT region (four outliers removed), (b) the BF region (one outlier removed), and (c) the GSL (nine outliers removed) of wild Atlantic salmon ¹³⁷Cs residuals. Rivers analysed include the LaHave (LH), Northwest (NW), Western Arm (WA), Big Salmon (BS), Gaspereau (GP), Hammond (HM), Harry’s (HR), Margaree (MA), Merrigomish Harbor (MH), Miramichi (MR), and Restigouche (RG).

MSW) of salmon may utilize different marine feeding grounds, and therefore follow different migratory routes within an overall migration pattern. High mean tissue ¹³⁷Cs concentrations in some Canadian ISW salmon suggested that they were distributed east of the Faroes before initiating homeward spawning migration, whereas the lower mean tissue concentrations of MSW salmon

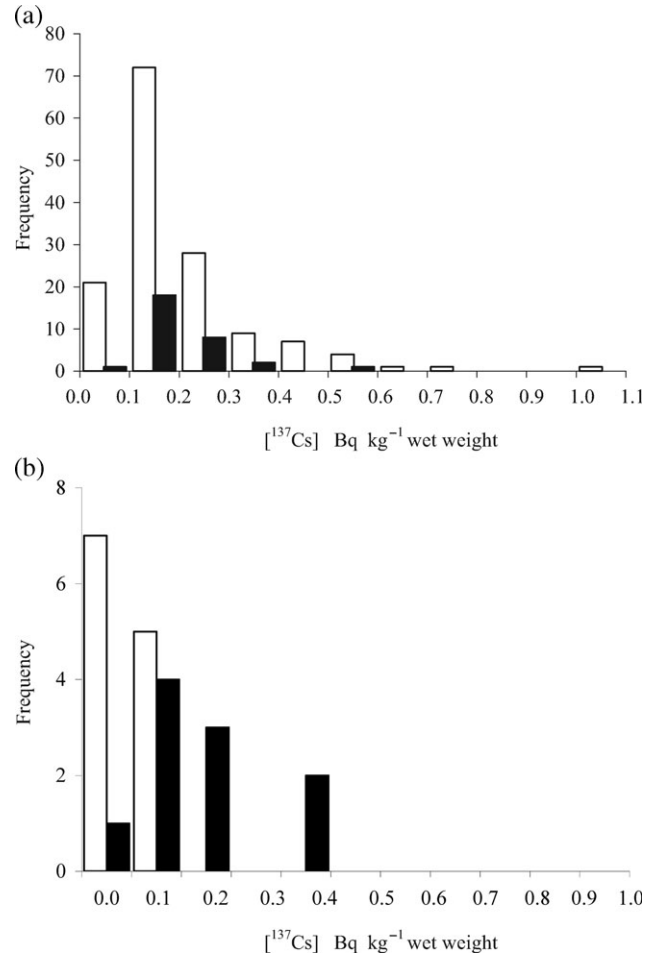


Figure 6. (a) Frequency distribution of tissue ¹³⁷Cs concentrations (Bq kg⁻¹ tissue wet weight) for (a) wild Atlantic salmon from Canada (2002 and 2003; open bars, *n* = 144, mean = 0.20) and Ireland (2003; solid bars, *n* = 30, mean = 0.19) and (b) aquaculture Atlantic salmon from Canada (2002; open bars, *n* = 12, mean = 0.09) and Ireland (2003; solid bars, *n* = 10, mean = 0.23).

suggested a more northern distribution in the Labrador and Irminger Seas, corresponding to regions of low surface water ¹³⁷Cs levels. Caesium clearance rates in tissue decrease with increasing animal size (Rowan and Rasmussen, 1994), so concentrations in larger fish would be expected to be higher, but this is not shown by our results. Atlantic salmon actively select colder sea surface temperatures with increasing body size (Jensen, 1967; Reddin and Shearer, 1987; Jakupsstovu, 1988; Holm *et al.*, 2003), and bio-accumulation of ¹³⁷Cs is positively correlated to water temperature (Rowan and Rasmussen, 1994), so cooler SSTs could be a contributing factor to declining ¹³⁷Cs concentrations with increasing sea age.

Overall ¹³⁷Cs concentrations in Canadian aquaculture escapees (0.28 ± 0.22 Bq kg⁻¹ wet weight) were similar to those in wild fish (0.20 ± 0.14 Bq kg⁻¹ wet weight), although 1SW escapees may display an alternative behaviour to wild migration patterns. Between 21% and 40% of salmon caught around the Faroes during the 1990s were aquaculture escapees (Hansen *et al.*, 1999; Hansen and Jacobsen, 2003), suggesting that escapees may revert to wild migration patterns. This is likely the case for escapees maturing as MSW salmon, because they would have a longer

period to revert to wild migration patterns and consequently demonstrate ^{137}Cs levels as their wild counterparts (Table 1). In contrast, significantly higher concentrations in 1SW escapees may suggest feeding within local estuaries (Jonssen *et al.*, 1993; Carr *et al.*, 1997). Even MSW escapees, depending on the timing of their escape, may move to adjacent river mouths to await spawning runs (Gausen and Moen, 1991), and subsequently only increase their already low ^{137}Cs burdens slightly to levels resembling wild returnees, because most of their body mass would have been derived from farm feed. Timing of escapes for aquaculture fish, relative to specific life stages (i.e. post-smolt, 1SW, or MSW), may determine the ultimate path of marine migration.

Bio-accumulation of ^{137}Cs in fish is greater in freshwater than in saltwater (Rowan and Rasmussen, 1994). This relationship was demonstrated by the increasing mean ^{137}Cs concentrations from parr (0.30 Bq kg⁻¹ wet weight) to smolts (0.53 Bq kg⁻¹ wet weight) and the significant decline of tissue concentrations in returning 1SW and MSW salmon. High tissue concentrations of ^{137}Cs (0.47 Bq kg⁻¹ wet weight) in 0SW post-smolts returning to spawn can be explained by their relatively short time spent at sea. The biological half-life of ^{137}Cs in large fish is hundreds of days to several years (Rowan and Rasmussen, 1994), so returning 0SW salmon should still display ^{137}Cs tissue concentrations reflecting freshwater residence, rather than recently bio-accumulated ^{137}Cs from marine sources.

Comparing the frequency distribution of tissue ^{137}Cs concentrations of wild Canadian returnees (1SW and MSW) from 1995/1996 (Tucker *et al.*, 1999) with 1SW and MSW herein (2002 and 2003) revealed a dramatic decrease in tissue concentration range between these time periods. Although frequency distributions of both data sets were significantly different, a similar Poisson trend with a few extreme outliers was observed. In both data sets, extreme outliers indicated trans-Atlantic migrants that had fed for extended periods of time in regions of high ^{137}Cs contamination. The overall decline of the North Atlantic ^{137}Cs east-west gradient (Povinec *et al.*, 2003) and redistribution of radioisotopes via the North Atlantic Gyre towards polar regions and East Greenland (Figure 1; Dahlgard *et al.*, 2004) was reflected in the changes observed between the salmon tissue ^{137}Cs concentrations found by Tucker *et al.* (1999) and our results. Overall, our results agree with those of Tucker *et al.* (1999) and with their 1995/1996 observations inferring pan-Atlantic migration of salmon returning to the Ste Marguerite River in Quebec.

There were no significant regional differences of mean ^{137}Cs burdens in tissue from 1SW Canadian salmon originating from three Atlantic Canadian oceanographic regions based on natal river drainage, which indicated that all migrants had followed similar migration routes and/or fed in similar regions before homeward migration. Endangered iBoF river Atlantic salmon consist of 35 or more rivers from the Black River near the Saint John estuary in New Brunswick, around the inner bay to the Cornwallis River in Nova Scotia (Anon., 2001; Amiro, 2003). Genotype data group the Gaspereau, Black, and Irish Rivers with iBoF stock (Verspoor *et al.*, 2002), but Amiro (2003) states that these rivers do not belong to the iBoF complex based on a high proportion of MSW virgin fish. Inner Bay of Fundy salmon have been hypothesized to remain within the BF and Gulf of Maine during their marine migration (Amiro, 2003), but our results revealed no significant differences of mean ^{137}Cs in tissue from 1SW or MSW salmon originating from the iBoF and the three other Canadian oceanographic regions. Atlantic salmon feeding

and migrating solely within the BF and Gulf of Maine would be expected to bio-accumulate maximum tissue concentrations of 0.23 Bq kg⁻¹ wet weight based on a bio-accumulation factor of 130 (Rowan and Rasmussen, 1994) relative to ambient ocean levels (1.7–1.8 mBq l⁻¹; Table 2). The range of tissue ^{137}Cs concentrations measured for iBoF populations (0.10–0.43 Bq kg⁻¹ wet weight) exceeded this maximum expectation, even after excluding Gaspereau and Black River samples (0.10–0.35 Bq kg⁻¹ wet weight). Therefore, our results do not support the hypothesis that iBoF salmon remain in the BF and Gulf of Maine during their marine phase. Our data suggests that iBoF salmon exit the BF to follow migration routes and/or feed in regions similar to most other Canadian Atlantic salmon. Further evidence is provided by the recent work of Lacroix and Knox (2005), who demonstrated that most post-smolts exit the BF rapidly unless they are caught in the large mid-bay gyre.

The distribution of Atlantic salmon at sea based on ^{137}Cs concentrations in tissue suggests that salmon feeding west of the Faroe Islands (8°W), in the Labrador and Irminger Seas, or east of the Grand Banks would be expected to bio-accumulate levels <0.23 Bq kg⁻¹ wet weight. Atlantic salmon feeding off West and East Greenland would be expected to bio-accumulate higher levels, ranging from 0.40 to 0.72 Bq kg⁻¹ wet weight (Table 2). West Greenland feeding grounds are only occupied by predisposed MSW salmon in summer and autumn (Jensen, 1980a, b; Jensen and Lear, 1980; Swain, 1980; Reddin, 1986). Migrants feeding off East Greenland are hypothesized to continue moving within the Irminger/East Greenland Current into the Labrador Sea, where ^{137}Cs levels are considerably lower, and therefore dilute high concentrations bio-accumulated in the East Greenland Current. Atlantic salmon feeding east of the Faroe Islands (excluding the Baltic Sea) would be expected to bio-accumulate levels up to 4.0 Bq kg⁻¹ wet weight. The highest ^{137}Cs burdens in the eastern North Atlantic would be for salmon feeding in the North Sea or close to the Irish Sea, where maximum estimates range from 1.3 to 4.0 Bq kg⁻¹ wet weight, respectively. These expected levels of ^{137}Cs in salmon are consistent with results from resident piscivorous fish in the northeast Atlantic (up to 10.0 Bq kg⁻¹ wet weight; Table 2). On the basis of Irish aquaculture controls and expected and measured bio-accumulation levels, a conservative estimate for ^{137}Cs concentrations in tissue of Atlantic salmon feeding east of the Faroe Islands (8°W) was ≥ 0.3 Bq kg⁻¹ wet weight.

Of 73 wild Canadian grilse sampled, 24.7% had tissue ^{137}Cs concentrations of ≥ 0.3 Bq kg⁻¹ wet weight. Grilse from all Atlantic Canadian oceanographic regions based on natal watersheds were represented (AT, BF, and GSL). A tissue ^{137}Cs concentration of 1.08 Bq kg⁻¹ wet weight from a 1SW salmon caught in the Northwest River, Newfoundland, provided sound evidence of trans-Atlantic migration. Of 68 MSW salmon sampled, just 2.9% were inferred to have fed east of the Faroes before returning as maiden spawners. Of 141 Canadian wild Atlantic salmon sampled, 14.2% (24.7% 1SW, 2.9% MSW) were inferred to have spent a significant period feeding in the northeast Atlantic before homeward migration. Whether or not 1SW aquaculture escapees follow similar migration patterns to wild 1SW salmon, 50% of 1SW escapees sampled had tissue concentrations > 0.3 Bq kg⁻¹ wet weight. No escapees returning as MSW salmon had tissue concentrations > 0.3 Bq kg⁻¹ wet weight, suggestive of a similar migration to wild MSW salmon.

Our estimate of 14.2% for wild Canadian salmon undertaking a migration beyond the Faroes may be an underestimate when the

Table 2. Minimum–maximum, mean levels of ¹³⁷Cs in surface water (mBq ¹³⁷Cs l⁻¹), wild Atlantic salmon tissue (Bq kg⁻¹ wet weight) based on a bio-accumulation factor of 130 relative to seawater levels (Tucker *et al.*, 1999), and resident piscivorous fish tissue (Bq kg⁻¹ wet weight) in the North Atlantic from 2000 to 2003.

Region	Surface water [Cs ¹³⁷] (mBq l ⁻¹)	Estimated salmon tissue [Cs ¹³⁷] (Bq kg ⁻¹ wet weight)	Resident fish tissue [Cs ¹³⁷] (Bq kg ⁻¹ wet weight)	Source
Bay of Fundy	1.7–1.8, 1.7	0.22–0.23, 0.22	–	J. Smith (pers. comm.)
Grand Banks, Labrador Sea	1.8	0.23	–	J. Smith (pers. comm.)
West Greenland	3.1–3.2, 3.2	0.40–0.42, 0.42	–	Dahlgaard <i>et al.</i> (2004)
Irminger Sea	1.8	0.23	–	Dahlgaard <i>et al.</i> (2004)
East Greenland	4.2–5.5, 4.9	0.55–0.72, 0.64	–	Dahlgaard <i>et al.</i> (2004)
Denmark Strait, Iceland Sea	2.4–3.5, 2.8	0.31–0.46, 0.36	–	Dahlgaard <i>et al.</i> (2004)
Faroe Islands	1.8	0.23	0.1–0.2, 0.2 ^a	Dahlgaard <i>et al.</i> (2004); NRPA (2004)
Norwegian Sea, Barents Sea	1.8–5.7, 2.7	0.23–0.74, 0.35	0.1–1.2, 0.3 ^b	NRPA (2003, 2004); I. Sværen (pers. comm.)
Greenland Sea	4.4–5.4, 4.9	0.57–0.70, 0.64	–	Dahlgaard <i>et al.</i> , 2004
West coast of Ireland	2.0–3.0, 2.5	0.26–0.39, 0.33	0.1–0.8, 0.3 ^b	RPII (2002, 2003)
Irish Sea	6.0–31, 14	0.78–4.0, 1.82	0.1–10, 0.5 ^b	RPII (2002, 2003); NRPA (2004)
North Sea	2.1–10, 4.7	0.27–1.3, 0.61	0.1–2.1, 0.5 ^b	NRPA (2003, 2004)
Baltic Sea	25–70, 49	3.3–9.1, 6.37	1.2–32, 9.3 ^c	HELCOM (2003); NRPA (2003, 2004); STUK (2003, 2004)

^aCod and haddock.

^bFish tissue concentrations taken from observed mean levels in Atlantic salmon, cod, haddock, halibut, herring, mackerel, monkfish, plaice, pollack, sole, and whiting sampled within respective regions.

^cCod, herring, flounder, and plaice.

decline of the trans-Atlantic ¹³⁷Cs gradient (Povinec *et al.*, 2003) and range of northeast Atlantic resident piscivorous fish ¹³⁷Cs burdens (0.10–10.0 Bq kg⁻¹; Table 2) are considered. Even migrants with tissue ¹³⁷Cs concentrations ranging from 0.10 to 0.30 Bq kg⁻¹ could have fed and/or migrated within northeast Atlantic waters. Tucker *et al.* (1999) estimated 43% of returning migrants to the Ste Marguerite River, Quebec, had fed beyond Iceland, and that 59% of 1SW and 36% of 2SW salmon fed in the northeast Atlantic. In a study based on discriminant scale analysis of 247 2SW Atlantic salmon sampled from the Faroese fishery during 1981 and 1982, Reddin (1987) concluded that 1.2% were of Canadian origin, similar to our estimate of 2.4% of MSW salmon hypothesized to have undertaken trans-Atlantic migration. Unfortunately, 1SW salmon, which are abundant off the Faroes during the winter fishery (Jakupsstovu, 1988), were not examined in Reddin’s study.

Of 26 wild Irish grilse sampled during 2003, only 11.5% had tissue concentrations of ¹³⁷Cs ≥ 0.3 Bq kg⁻¹ wet weight. No Irish 2SW salmon sampled had tissue levels > 0.3 Bq kg⁻¹ wet weight. Recent studies of wild Norwegian Atlantic salmon returning during 2002 found mean ¹³⁷Cs tissue concentrations of 0.2 Bq kg⁻¹ wet weight (NRPA, 2004). These results suggest that most Irish and other European populations of Atlantic salmon follow the North Atlantic Gyre and spend a significant period feeding in the western Atlantic before migrating home again.

Our samples of aquaculture Atlantic salmon were intended as non-migratory controls, but this role may have been compromised because of the geographical origin of their feed. Feed for Canadian salmon aquaculture is obtained globally, the majority from Chilean and Peruvian anchovy fisheries (Saulier, pers. comm.).

The mean tissue concentration of 0.09 Bq kg⁻¹ wet weight we found for Canadian aquaculture salmon may not be the best indicator of average western North Atlantic tissue ¹³⁷Cs concentrations for Atlantic salmon. On the other hand, Irish aquaculture salmon are fed 60–70% marine products, the majority consisting of herring, sandlance, capelin, and Norwegian pout from the North Sea, Norwegian Sea, and Barents Sea (Grøttheim, 2002), and probably were a better indicator of average eastern North Atlantic tissue ¹³⁷Cs concentrations for Atlantic salmon. Decreasing levels of Cs¹³⁷ in the North Atlantic (Povinec *et al.*, 2003) has resulted in indistinct regional levels (Figure 1), making inferences about exact feeding grounds difficult. Many of our sample concentrations were low, and the detection limit for HPGe gamma ray spectrometers is only 0.1 Bq kg⁻¹ wet weight (NRPA, 2004), so inferences based on individual ¹³⁷Cs concentrations are not considered as powerful as inferences based on observed trends.

The currently accepted migration model has been contradicted by past tag returns and more recent research (Shelton *et al.*, 1997; Tucker *et al.*, 1999; Hansen and Jacobsen, 2000; Holm *et al.*, 2003). Two tagged smolts from Canada, one from the Matamec River in the GSL (Gibson and Côté, 1982), the other from the Saint John River in the BF (Reddin *et al.*, 1984b), were recaptured as MSW salmon off Norway in 1979. Two tagged smolts from the Liscomb River on Nova Scotia’s AT were subsequently recaptured in the Faroese fishery (Reddin, 1987), as were two from the Penobscot River, USA (Baum, 1997). Conversely, salmon tagged as smolts in Scotland were recaptured along the Labrador coast, and adults tagged off the Grand Banks were recaptured in Ireland and Scotland (Redden *et al.*, 1984b). A tagging study of

ocean-migrating Atlantic salmon north of the Faroes resulted in four recaptures from GSL rivers (Miramichi, $n = 3$; Kouchibouguac, $n = 1$; Hansen and Jacobsen, 2000). Recent research trawls in the northeast Atlantic caught post-smolts following the North Atlantic Gyre northeast into the Norwegian Sea and Greenland Sea (Shelton *et al.*, 1997; Holm *et al.*, 2000, 2003). This suggests that trans-Atlantic migration is not only undertaken by European stocks, but by North American stocks as well.

Although other researchers have suggested that Atlantic salmon undertake trans-oceanic migrations using the North Atlantic Gyre current system (Jensen, 1967; Stasko *et al.*, 1973; Reddin *et al.*, 1984b; Tucker *et al.*, 1999; Friedland *et al.*, 2001), ours is the first study that incorporated migrants from both sides of the Atlantic and used similar temporal scales to infer an overall migration model based on empirical data. Changes in the dumping regime of nuclear wastes from Sellafield into the Irish Sea (Kenny, 2003) has created other environmental tag options. ^{99}Tc has been increasing since the 1990s (Dahlgard *et al.*, 2004), and may reform another east–west gradient of radionuclides. To prove that Atlantic salmon utilize the North Atlantic Gyre for marine migration, further research on exact routing of salmon is required.

Ocean temperature selection based on natal latitudinal origin has been demonstrated in Atlantic (Jacobsen *et al.*, 2001) and Pacific salmon (Brannon, 1984), and if migration within the North Atlantic Gyre is the correct Atlantic salmon migration model, serious consideration should be given to the need to implement an international management scheme based on latitudinal and geographic origin of Atlantic salmon populations relative to the North Atlantic Gyre (Bisbal and McConnaha, 1998; Potter *et al.*, 2004). Certain Atlantic salmon populations, such as those from southern latitudes, need protection from fishing on oceanic feeding grounds when migration timing and SSTs suggest their presence. National management plans aiming to control salmon catches within EEZs may provide a measure of success, but to increase marine survival, managing human activities in international waters is crucial. We propose that anadromous Atlantic salmon (other than Baltic Sea stocks; Jutila *et al.*, 2003) be classified as a trans-Atlantic straddling stock, making international cooperation essential to ensuring their survival at sea.

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