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Changes in stock composition of annual Atlantic salmon catches in the Baltic Sea on basis of DNA-microsatellite data and Bayesian estimation

Marja-Liisa Koljonen

Abstract

DNA level information, an 8-loci microsatellite baseline database of 26 Atlantic salmon (*Salmo salar L.*) stocks, has been analysed using a Bayesian estimation method to estimate stock and stock group proportions of Finnish catches in the Baltic Sea area. The proportions of five stock groups important in terms of fisheries management were assessed in catch samples taken in three years (2000, 2002 and 2003). The catch samples were representative of Finnish fishery in the Gulf of Bothnia and Gulf of Finland. In the Gulf of Bothnia area, catches are composed of three major units: wild fish, Finnish hatchery fish and Swedish hatchery fish. Owing to decreasing amounts of hatchery fish, the proportion of wild fish shows a rising trend in catches from the Åland Sea, increasing from 43% to 76% in 2000-2003. In the eastern Gulf of Finland, the largest contribution was made by local hatchery fish, the Neva salmon, which is released by Finland, Russia and Estonia. Both wild and hatchery fish occurred in the northern Gulf of Bothnia in 2003, but not in 2002. In the western part of the Gulf of Finland, fish originating from the Main Basin made a substantial contribution. The threatened, eastern, Estonian wild stocks were recorded only in the western part of the Gulf, with a 4% proportion.

Keywords: Atlantic salmon, stock mixture analysis, DNA, microsatellites

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Introduction

Mixed harvesting of populations can easily lead to the extirpation of minor stocks when harvest rates are high and the productivity of salmon stocks is unequal. Sustainable fisheries management requires a proper balance to be achieved between sufficient protection of weak stocks and effective harvest of strong stocks. Information on spatial and temporal variations in stock composition in mixed-stock fisheries is therefore essential for effective fisheries management and conservation (Begg *et al.*, 1999; Shaklee *et al.*, 1999). In most of the Atlantic salmon fishery in the Baltic Sea, fish are caught in mixtures of river stocks and also in mixtures of wild and hatchery-reared stocks. The management goals for wild and hatchery-reared fish differ and they may need to be managed with different intensities and with different harvest strategies. It is therefore important to know by which fisheries and in what amounts the wild fish stocks are exploited.

Genetic differences among fish stocks can be used for estimating stock proportions. Unlike external tags, genetic tags have the following advantages for the estimation of stock proportions: there are no costs associated with the actual tagging, no tags are lost, and there is no need to consider the possible effects of the external tags on the viability and catchability of the fish. Moreover, all fish are tagged for life, and studies can therefore be conducted on fishes that cannot be tagged by other methods, *e.g.* wild fish in remote areas or newly hatched fish in releasing programmes. Wild stocks in particular can be studied on an equal basis with hatchery stocks. With genetic stock identification, the time and place of sampling can be chosen more freely and precisely than with external tagging, as these are not dependent on preceding tag and release programmes. Further, there is no need to consider changes in the probability of the tags being returned by fishermen. In addition, genetic data can be combined with non-genetic data (*e.g.* scale characteristics and smolt age). Limitations to genetic mixed stock analysis are set only by limited genetic differentiation among baseline stocks. Genetic stock structure information can also be used to define management units based on genetic similarities between stocks (Koljonen *et al.*, 1999; Koljonen 2001).

Mixed stock analysis (MSA) has traditionally been based on allozyme data and maximum likelihood estimation (MLE) (Fournier *et al.*, 1984, Pella and Milner 1987). The method determines the relative contributions of baseline stocks with the highest likelihood of providing the observed multilocus genotypic frequencies in the catch sample. Today, allozyme data are often replaced by DNA microsatellite data, and MLE by Bayesian methods; both replacements increase the resolution power. Allozyme variation and the MLE have also been used to estimate stock proportions in Baltic Sea catches (Koljonen and McKinnell 1996, Koljonen and Pella 1997). In recent years, the analysis of DNA variation has greatly increased the amount of genetic information available for Baltic salmon stocks, too. The average mean heterozygosity is more than 10 times as great at microsatellite (0.692, present data, Koljonen *et al.* 2004a) as at allozyme loci (0.058, Koljonen *et al.* 1999). The number of alleles was generally only 2 or 3 at each allozyme locus, whereas the number of alleles ranges from 8 to 32, with a mean of 17.8, alleles per microsatellite locus within Baltic Sea Atlantic salmon populations. Such high allelic diversity at a sufficient number of loci can easily result in a greater number of possible multilocus genotypes than the actual number of individual fish comprising the populations. In simulation studies for Baltic Sea Atlantic salmon stocks, the precision was over three times as high for microsatellite data (3.8%) as for allozyme data (13.7%) when assessed as the mean standard error in MLE (Koljonen *et al.* 2004b).

A new estimation method using Bayesian statistics has been developed for stock composition estimation by Pella and Masuda (2001). In this method, posterior distribution combines the information on baseline stocks with that on the stock-mixture sample to estimate both the stock composition of the mixture sample and the genotypic composition of the baseline stocks. The stock

group proportion estimates are expressed in terms of probability distributions, which can be included in the fisheries management assessment model. However, direct information on the stock proportions in the catch is valuable as such by telling about the migration behaviour of the stocks and about the occurrence and proportions of river stocks and stock groups in different fisheries.

When conditional maximum likelihood (CML) estimation and the Bayesian method were compared using the same microsatellite data in self-assignment tests, the mean percentage of correct estimation over the baseline stocks improved by 10%, from about 87% for CML to 97% for the Bayesian method. The maximum downward bias for an individual baseline stock was 23% for CML estimation and only 8% for the Bayesian method. The mean error for CML was 12.9% and for the Bayesian method 3% (Koljonen et al. 2004a). Self-assignment tests are optimistic with respect to the bias and precision of estimation as compared with test samples drawn independently from the baseline stocks. Nevertheless, they provide valid comparisons of estimation methods. The Bayesian method improved the estimates notably in the most difficult cases, *i.e.* in stock pairs of high similarity. The proportion of correct estimation for the Tornionjoki stock was 70% with CML and 91% with the Bayesian method when an extra test sample of 100% Tornionjoki stock was used (Koljonen et al. 2004a).

This work demonstrates the power and use of microsatellite data and the Bayesian method in assessing stock and stock group proportions in the Atlantic salmon catches in the Baltic Sea fishery.

Materials and methods

Sampling of fish

The baseline data of potentially contributing salmon stocks were gathered by taking tissue samples of 1708 fish belonging to 26 Atlantic salmon stocks from rivers draining into the Baltic Sea (Figure 1, Table 1).

The catch samples were collected in three years (2000, 2001 and 2003) from Finnish Atlantic salmon catches in the Baltic Sea (Figure 1, Table 2). In 2000, three areas in the Gulf of Bothnia were included; in 2002 and 2003, samples were also collected from two sites in the Gulf of Finland and from one in the Baltic Main Basin fishery. The samples from the Gulf of Bothnia and Gulf of Finland were regarded as representative of Finnish catches.

The samples from the coastal fishery in the Gulf of Bothnia were taken in three important fishing areas (Åland Sea (sample 1, Figure 1), Bothnian Sea (2) and Bothnian Bay (3)) along the Finnish coast during the main fishing season and along the route of the northward spawning migration from the Baltic Main Basin across the Åland Sea to the northern rivers in Sweden and Finland. In the Gulf of Finland, the samples were taken separately from the Finnish coastal fishery in the east (4) and west (5) of the gulf in 2002 and 2003. The lengths of the captured fish from each of these areas were measured and daily scale samples were taken from a subsample stratified by size. Fish ages were determined by reading the scales, and the DNA subsample was taken from the fish stratified by sea-age (1-3 years). In addition, in 2002 and 2003 random samples were taken from the Baltic Main Basin fishery from catches landed at Bornholm Island (6).

Microsatellite DNA analysis

Multilocus genotype frequencies of baseline stocks and catch samples were needed to estimate the stock compositions of the catches. Total genomic DNA was extracted from muscle tissue samples,

adipose fins or scales following to the method described by Taggart *et al.* (1992) or by using the QIAGEN Tissue Sample Kit (Qiagen). The variation was determined at 8 to 9 microsatellite loci: Ssa85, Ssa289 (McConnell *et al.* 1995), Ssa171, Ssa197, Ssa202 (O'Reilly *et al.* 1996), SSOSL85, SSOSL311, SSOSL417 (Slettan *et al.* 1995) and SSOSL438 (Slettan *et al.* 1996). Locus SSOSL311 was used only for the analysis of the catch in 2003.

Genotypes were assayed by polymerase chain reaction (PCR) and polyacrylamide gel electrophoresis, either with radioactive labelling and autoradiography as previously described by Koljonen *et al.* (2002) or with fluorescent labelling. In the fluorescent method, the primers were labelled with infrared dyes as follows: IRD-700 (Ssa202, Ssa289, SSOSL85, SSOSL417, SSOSL438) and IRD-800 (Ssa85, Ssa171, Ssa197, SSOSL311). PCR was performed in a 10 μ l reaction volume with 15 ng of genomic DNA, 0.1 pmol of fluorescent labelled primer, 5 pmol of each forward and reverse primer, 200 μ M dNTPs, 10 mM Tris HCl (pH 9.0), 1.5 mM MgCl₂, and 0.25 U of Taq DNA polymerase (Pharmacia Biotech). PCR products were separated on 25 cm, 7% denaturing polyacrylamide gels and detected using an LI-COR automated DNA sequencer (LI-COR, Inc., Lincoln, NE, USA). Microsatellite genotypes were analysed with Gene ImagIRTM fragment analysis software (version 3.52 Scanalytics).

Genetic methods

The genetic differentiation between stocks for 8 loci was quantified with Nei *et al.*'s (1983) D_A distance. The neighbour-joining (NJ) method (Saitou and Nei 1987) was used to construct the dendrogram. The bootstrap test over loci was performed for the NJ tree by recalculating the distance for all loci 1000 times. Distance analysis and mean heterozygosities (Nei 1973) were computed with the DISPAN package (Ota 1993).

Estimation method

For genetic MSA, mixture modelling with the Bayesian estimation method was implemented with the BAYES program (Pella and Masuda 2001). The program calculates posterior probability distributions for unknown stock proportions in the mixed catch samples. The posterior distribution for the stock proportions combines the prior baseline information with the information on the mixed catch sample to estimate the stock composition of the mixture sample while at the same time updating the multilocus genotype distributions of the baseline stocks. Samples of the posterior distributions are drawn by Markov chain Monte Carlo (MCMC) sampling.

The baseline data were coded to provide the total allele counts at each locus for each stock, and the mixture data were coded to provide the multilocus genotype for each individual. Zeroes for baseline allele frequencies were assumed to be only sampling zeroes, and were estimated to have positive values. The multilocus genotype frequencies for the baseline stocks were estimated from the allele frequencies under the assumptions of Hardy-Weinberg and linkage equilibriums.

A total of 26 chains of samples were run per application (each catch sample) until the posterior probability distributions for the stock proportion estimates were stable and the chains had converged. To monitor the convergence of the chains to the posterior distribution, the univariate shrink factor (Gelman and Rubin, 1992) was computed for each of the stock proportions. The shrink factor compares the variation within a single chain with the total variation among the chains. Depending on the iterations needed for convergence of the chains, the last 1000 or 2000 MCMC draws of each chain were combined (26,000 or 52,000 draws) and used to describe the posterior

distributions of stock proportions. Proportions were estimated for each baseline stock and also for 5 or 7 stock groups important from the management point of view.

Results

Genetic differentiation between baseline stocks

Genetic differentiation between the baseline stocks varied substantially. In general, the genetic distances between stocks formed a pattern (Figure 2) similar to that noted earlier in allozyme data (Koljonen *et al.* 1999). Northern Baltic stocks from Finland and Sweden formed one compact branch. Eastern and southern Baltic Sea stocks from Russia, Estonia and Latvia formed another branch. Two stocks from southern Sweden (Emån and Mörrumsån) from rivers draining into the southern Baltic Main Basin formed a distinct intermediate branch (more detailed analysis in Säisä *et al.* 2004).

Stock proportions

Gulf of Bothnia: In the Gulf of Bothnia area, Atlantic salmon catches are composed of three major groups: (1) wild fish originating from Gulf of Bothnia rivers, (2) hatchery fish originating from Finland and (3) hatchery fish originating from Sweden (Figure 3a, 3b, 3c). The proportion of other stock groups originating from the Gulf of Finland and the Baltic Main Basin combined was less than 3% in all years, and they are not shown in the figures for Gulf of Bothnia catches. The proportion of wild stocks in the catches is important from a management point of view. The major components in the wild stock group were Tornionjoki and Kalixälven stocks.

The proportion of wild fish has been increasing since 2000. In the southern part of the Gulf of Bothnia, the Åland Sea, the proportion of wild fish rose from 43% (95% probability interval 37 – 50%) to 76% (95% PRI: 64 – 86%) between 2000 and 2003. At the same time the proportion of Swedish hatchery fish decreased from 41% to 7%, whereas that of Finnish hatchery stocks was more or less constant (15 – 17%) (Figure 3a). The clearest decline was in the proportion of Swedish Luleälven fish.

In Bothnian Sea catches the major contributor has been Finnish hatchery fish, 45 – 57% in 2000 – 2002. However, in 2003 its contribution fell to 23%, and that of Swedish hatchery fish to zero (Figure 3b). Correspondingly, the proportion of wild stocks increased from 35% (PRI: 25 – 47%) in 2000 to 76% (PRI: 64 – 86%) in 2003. Hatchery Neva salmon, released into the area, has made a marked contribution.

The stock group proportions of the three main groups seemed to be more stable in the most northern area, Bothnian Bay, and near the spawning rivers than in the southern areas. Swedish hatchery fish accounted for about 10%, the rest being divided between wild stocks and Finnish hatchery stocks. An increasing trend in the wild stock proportions could be seen there, too, and slightly over half of the catch was composed of wild fish in 2003 (52%, PRI: 42 – 63%) (Figure 3c).

Gulf of Finland: The composition of catches was more diverse in the Gulf of Finland than in the Gulf of Bothnia and all five potential groups made some contribution to the catches. The stock composition differed in the eastern and western parts of the Gulf. In both areas, however, a clear majority of the catches has usually been from Finnish hatchery releases as in 2002. In 2003, however, the northern wild fish, originating from the Gulf of Bothnia, also occurred in the eastern

Gulf of Finland catch, its proportion being as high as 36% (PRI: 30 – 42%) (Figure 3d). Similarly, some fishes from northern hatchery releases occurred in these eastern catches.

In the Gulf of Finland, local Estonian wild fish were observed only in the western part of the Gulf, with a contribution of about 4% in both years studied (4.6% in 2002 and 4.1% in 2003) (Figure 3e). In addition to Finnish hatchery releases, a clear contribution to this Finnish autumn fishery was made by salmon stocks of the eastern Main Basin (35% in 2002 and 41% in 2003). A decreasing trend, from 53% to 31%, in the proportion of Finnish hatchery fish was recorded there, too, from 2002 to 2003.

Samples from the Baltic Main Basin were not taken in relation to catches, but they still give some indication of the stock group composition of this fishery (Figure 3e). The main component, and at least half of the catches, has come from the northern wild stocks, mainly the Tornionjoki and Kalixälven stocks, but fish from other wild stocks, e.g. the Swedish Byskeälven and Vindelälven, were also caught. No eastern Gulf of Finland stocks were observed, although fish from rivers draining into the eastern and western Main Basin made some contribution (together 9-12%). In contrast to Finnish catches in the Gulf of Bothnia area, Swedish hatchery stocks (42%) seem to have made a greater contribution to these Main Basin catches than Finnish hatchery stocks (6%), even in 2003.

However, the increasing trend in the proportion estimate of the wild stocks is not necessarily solely due to increasing smolt production in the wild stocks. The catch numbers decreased markedly during the study, and when the proportions are counted from the catch numbers, we find that the number of wild fish caught did not increase at the same rate (Table 3, Figure 3). In the Åland Sea, for example, there seems to have been a clear decreasing trend over the four years in the amount of Swedish hatchery fish caught in this Finnish drift-net fishery in June, but the number of wild fish caught remained at about the same level.

Discussion

The 8 to 9 locus DNA-microsatellite data seemed to offer sufficient accurate stock composition estimates for Atlantic salmon stocks in the Baltic Sea to be useful for fisheries management. The 95% probability intervals were roughly symmetric about the point estimates and were usually less than 10%. For management, the maximum uncertainty of 10% is recommended, which could be achieved for the wild group with a mixture sample size of about 300 fish. In addition, the majority of the individual stocks were identified with high accuracy in the catches analysed.

The stock composition of the catches varied considerably in different areas of the Baltic Sea, notably in the Gulf of Bothnia and the Gulf of Finland. The same stocks tended to occur in the same areas over the years, but some migration changes were also apparent and the proportions of the stocks varied from one year to the next.

The stock proportion estimates do not directly indicate the amount of fish caught. The increasing proportion of wild fish does not mean larger wild catches and was thus a result not only the increasing wild production, but also of the increased mortality of the hatchery fish. Some change in migration behaviour might also explain the decreasing proportion of Swedish hatchery fish on the Finnish coast. The proportion of Swedish hatchery fish does not seem to have decreased so clearly in Main Basin catches.

Neither does the information on stock proportions in catches reveal the stock proportions in the total population. Fish stocks are not evenly distributed in the sea and fishing is not random sampling. The temporal and spatial distribution of fishes, and their migration routes and feeding areas may vary and this will be seen as changes in the stock compositions of catches. Even differences between stocks in migration routes and timing are known. Fishing is dependent on regulations and other fishing possibilities, even ice conditions, and the weather changes may change the fishery. The current samplings were planned to describe stock compositions in Finnish Atlantic salmon catches in the Gulf of Bothnia and Gulf of Finland. The sampling site in the Åland Sea is expected to cover all northward migrating stocks in the spring relatively well, if the timing of migration and fishing coincide.

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Table 1. Attributes of the microsatellite data set for 8 loci from Atlantic salmon of the Baltic region: the baseline stocks, sampling year, country of origin, sample sizes of individual fish (N), average sample sizes assayed per locus (\bar{N}), and the main mode of propagation, wild or hatchery-reared.

	Stock	Sampling year	Country	N	\bar{N}	Propagation
1	Tornionjoki, W	2000	Finland, Sweden	117	114.0	Wild
2	Tornionjoki, H	1997	Finland	119	111.0	Hatchery
3	Simojoki	1997	-"	59	56.6	Wild
4	Iijoki	1997	-"	61	59.6	Hatchery
5	Oulujoki	1997	-"	59	56.4	Hatchery
6	Kalixälven	2002	Sweden	169	168.5	Wild
7	Luleälven	1995,1997	-"	60	59.8	Hatchery
8	Byskeälven	1994	-"	77	73.4	Wild
9	Skellefteälven	1995, 1996	-"	51	45.4	Hatchery
10	Vindelälven	1993, 1995	-"	50	50.0	Wild
11	Umeälven	1995	-"	50	48.4	Hatchery
12	Lögdeälven	1995	-"	49	45.3	Wild
13	Ångermanälven	1995	-"	60	57.9	Hatchery
14	Indalsälven	1995, 1997	-"	64	63.8	Hatchery
15	Ljungan	1998	-"	51	49.0	Wild
16	Ljusnan	1999	-"	53	51.5	Hatchery
17	Dalälven	1999	-"	60	59.3	Hatchery
18	Emån	1999	-"	54	50.3	Hatchery
19	Mörrumsån	1999	-"	42	40.8	Wild
20	Neva	1997	Russia	60	56.6	Hatchery
21	Kunda	1996	Estonia	60	55.1	Wild
22	Keila	1997	-"	53	47.6	Wild
23	Pärnu	1997	-"	26	22.0	Wild
24	Gauja	1998	Latvia	70	65.0	Hatchery
25	Daugava	1996	-"	68	65.5	Hatchery
26	Venta	1996	-"	66	52.8	Wild
	<i>Total</i>			<i>1708</i>	<i>1625.2</i>	

Table 2. Catch site, calendar days of sampling, ICES statistical area, and sample sizes of DNA samples (N/DNA) from Finnish Atlantic salmon catches in 2000, 2002 and 2003.

	Catch site	Sampling days	ICES area	N/DNA
2000				
1	Åland Sea	May 29 - June 28	29	413
2	Bothnian Sea	June 18 - August 6	30	293
3	Bothnian Bay	June 22 - August 4	31	298
			<i>Total</i>	<i>1004</i>
2002				
1	Åland Sea	May 4 – June 27	29	218
2	Bothnian Sea	May 29 – August 7	30	179
3	Bothnian Bay	May 23 – August 22	31	180
4	Gulf of Finland: East	July 3 – August 9	32	150
5	Gulf of Finland: West	October 16 – December 4	32	136
6	Baltic Main Basin	December 3	25	71
			<i>Total</i>	<i>934</i>
2003				
1	Åland Sea	May 22 – June 26	29	209
2	Bothnian Sea	May 20 – September 17	30	218
3	Bothnian Bay	June 23 – September 1	31	203
4	Gulf of Finland: East	May 30 – September 25	32	448
5	Gulf of Finland: West	May 20 – December 3	32	148
6	Baltic Main Basin	February 18, October 3, November 18	25	215
			<i>Total</i>	<i>1441</i>

Table 3. Number of individuals in each Atlantic salmon stock group in the Finnish Åland Sea catch, estimated from total number of fish caught.

Stock group	Number of individuals			
	2000	2001	2002	2003
<i>1. Gulf of Bothnia, wild</i>	4 552		5 496	3 827
2. Gulf of Bothnia, Finnish hatchery	1 533		1 315	817
3. Gulf of Bothnia, Swedish hatchery	4 334		1 057	334
4. Gulf of Finland	5		3	5
5. Baltic Main Basin	88		118	30
<i>Total</i>	<i>10 512</i>		<i>7 989</i>	<i>5 014</i>

Fig. 1. Map of the Baltic Sea showing locations of salmon rivers and the six catch sampling sites (★).

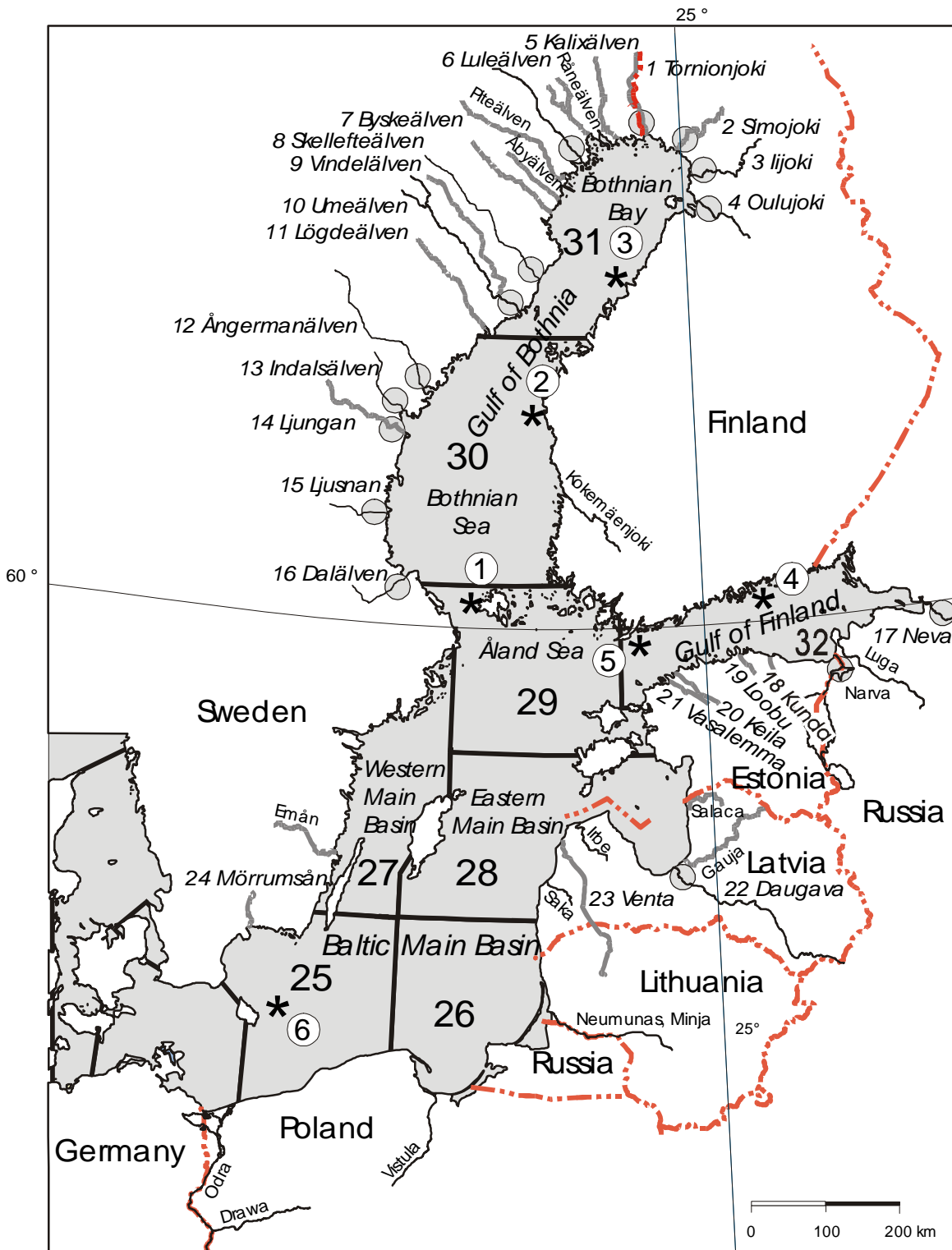


Fig. 2. Genetic D_A distances (Nei et al. 1983) between the 26 Atlantic salmon baseline stocks of the Baltic Sea represented with a neighbour joining tree (Saitou and Nei 1987). Distances are based on 8 microsatellite loci. Country of origin and ICES statistical area (25 – 32 see Fig. 1.) at the salmon river mouth are indicated.

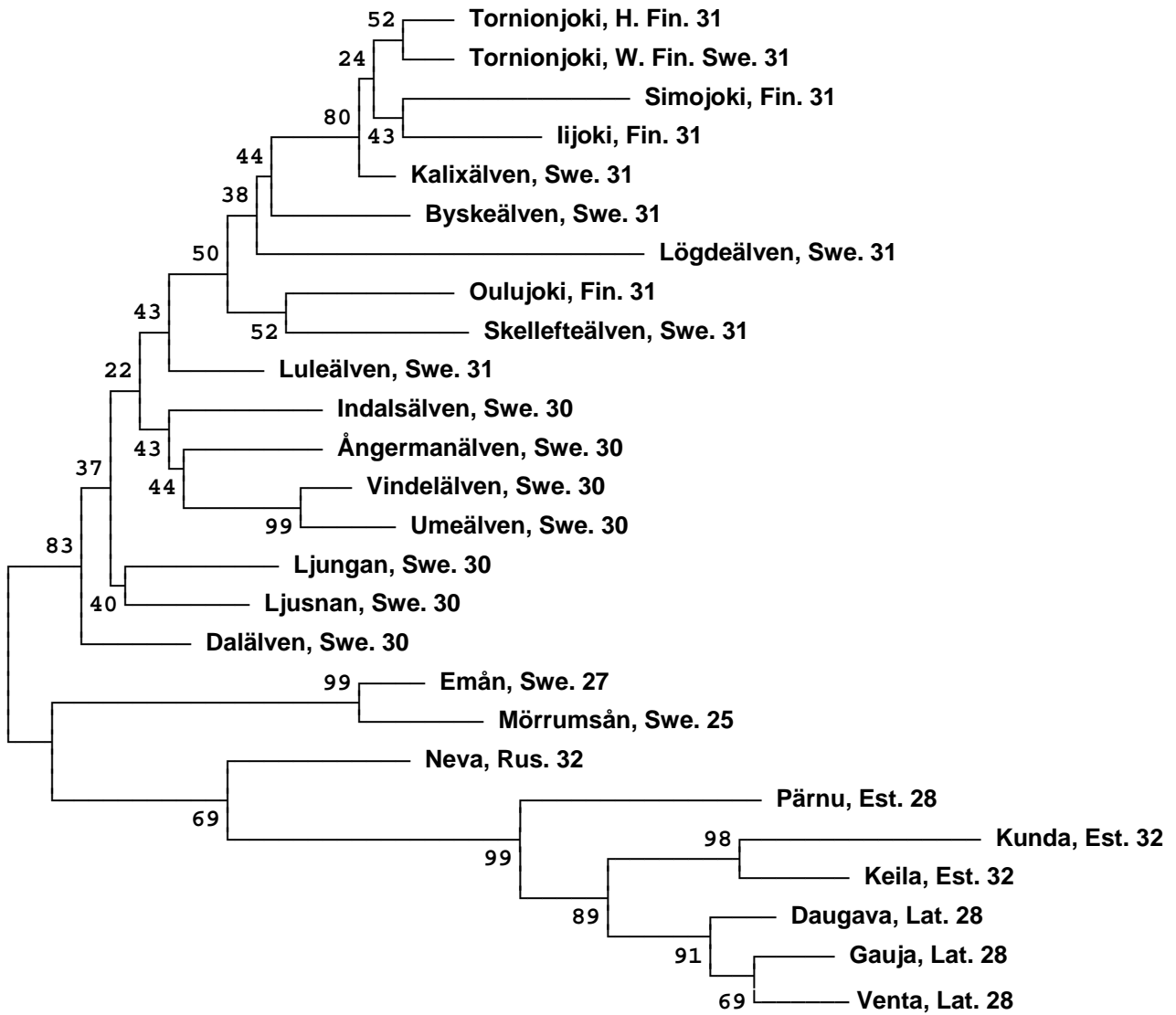
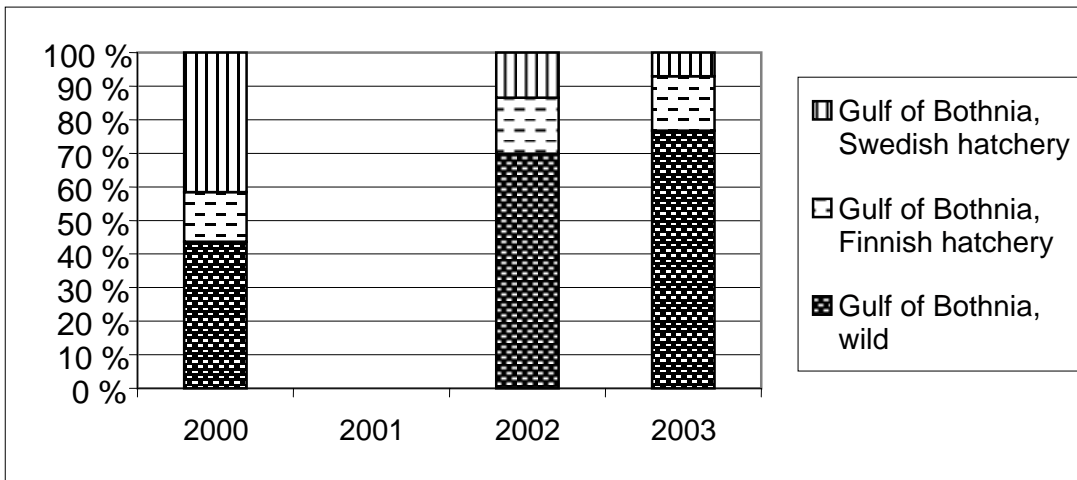
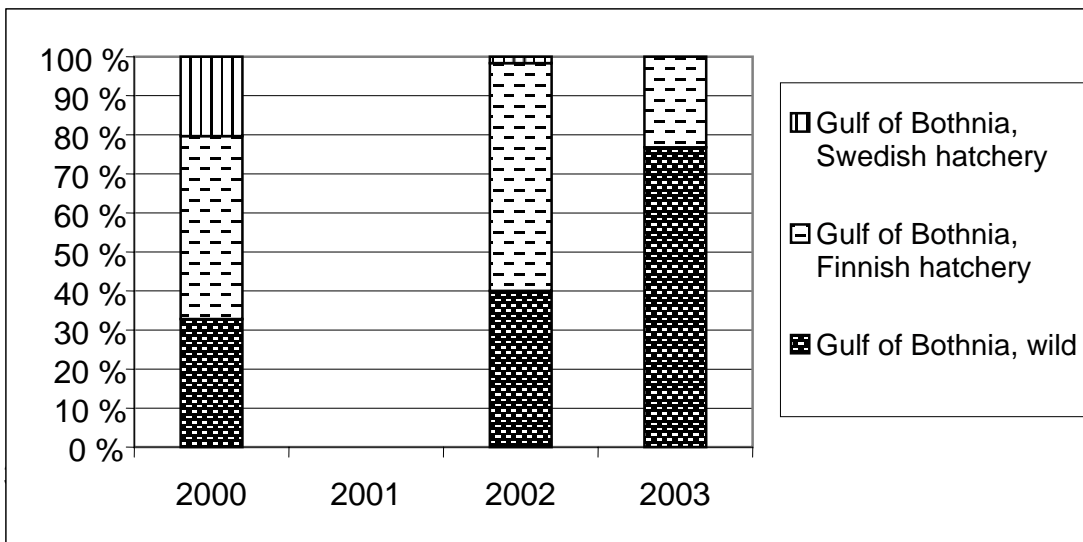


Figure 3. Stock group proportion estimates of Finnish Atlantic salmon catches with DNA microsatellite method.

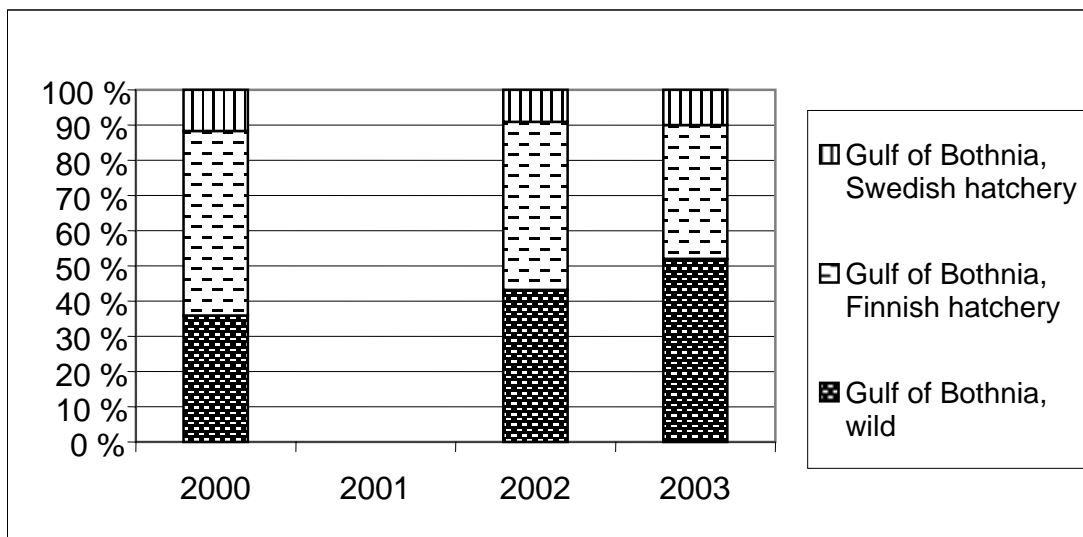
3a. Proportions of Atlantic salmon stock groups in Finnish Åland Sea catches.



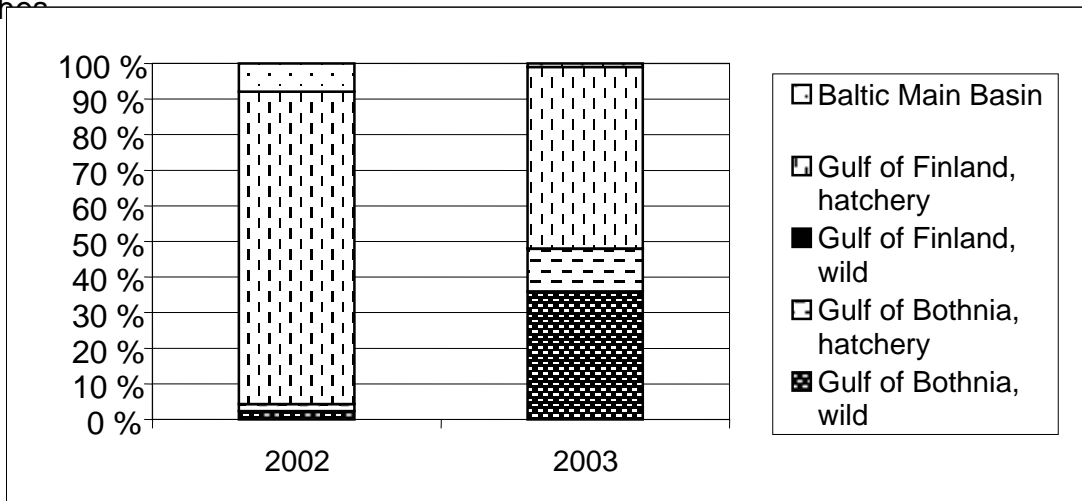
3b. Proportions of Atlantic salmon stock groups in Finnish Bothnian Sea catches.



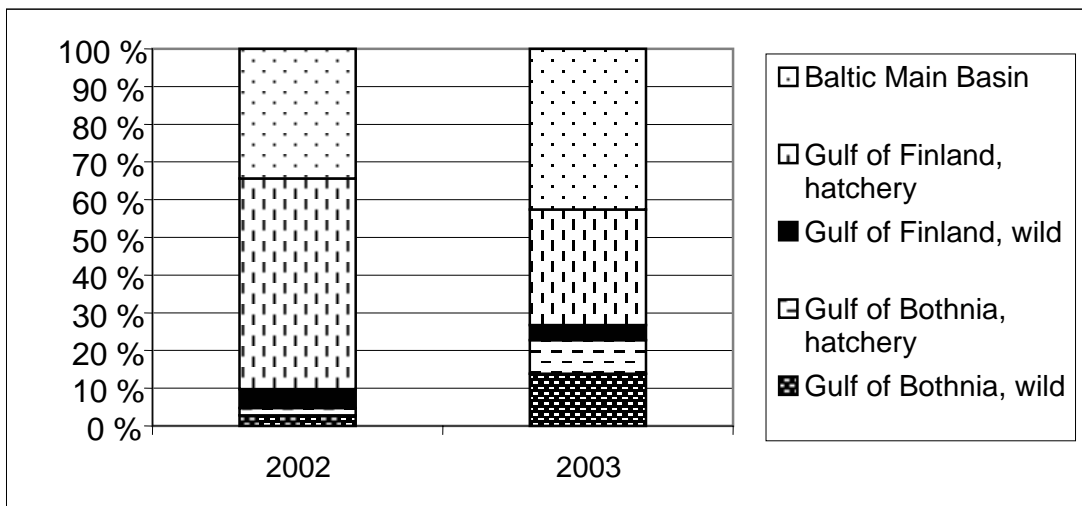
3c. Proportions of Atlantic salmon stock groups in Finnish Bothnian Bay catches.



3d. Proportions of Atlantic salmon stock groups in the Finnish eastern Gulf of Finland catches.



3e. Proportions of Atlantic salmon stock groups in the Finnish western Gulf of Finland catches.



3f. Proportions of Atlantic salmon stock groups in the Finnish Main Basin catches.



Figure 4. Proportions of Atlantic salmon stock groups and number of individuals in the Finnish Åland Sea catch.

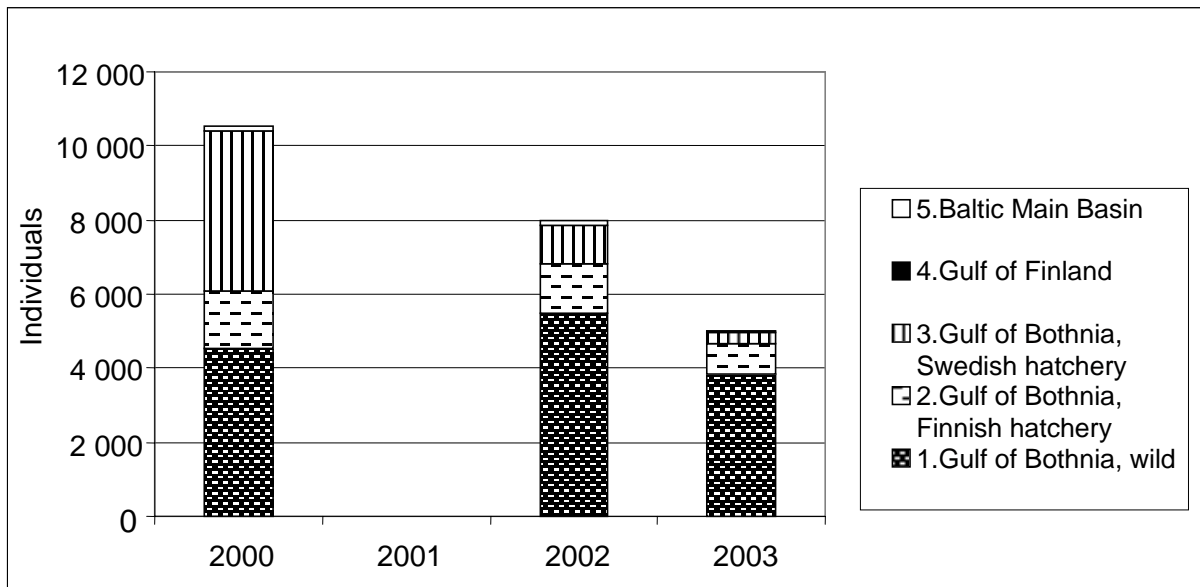


Table 4. Stock group proportions (%) in Atlantic salmon samples from Finnish catches in 2000 based on genetic analysis, using the variation at 8 DNA microsatellite loci and Bayesian estimation program, Bayes (Pella and Masuda 2001).

1. Åland Sea

Origin of stock group	Mean	SD	2,50 %	Median	97,50 %
1. Gulf of Bothnia, wild	43.3	3.4	36.6	43.3	49.9
2. Gulf of Bothnia, Finnish hatchery	14.6	2.9	9.3	14.4	20.7
3. Gulf of Bothnia, Swedish hatchery	41.2	3.1	35.3	41.2	47.3
4. Gulf of Finland, wild	0.1	0.1	0.0	0.0	0.5
5. Baltic Main Basin	0.8	0.5	0.2	0.8	2.0
	100.0			99.7	

2. Bothnian Sea

Origin of stock group	Mean	SD	2,50 %	Median	97,50 %
1. Gulf of Bothnia, wild	35.7	5.8	24.8	35.6	47.2
2. Gulf of Bothnia, Finnish hatchery	44.6	5.8	33.3	44.7	55.9
3. Gulf of Bothnia, Swedish hatchery	19.2	3.1	13.5	19.1	25.6
4. Gulf of Finland, wild	0.0	0.1	0.0	0.0	0.4
5. Baltic Main Basin	0.5	0.4	0.0	0.4	1.6
	100.0			99.7	

3. Bothnian Bay

Origin of stock group	Mean	SD	2,50 %	Median	97,50 %
1. Gulf of Bothnia, wild	39.5	5.2	29.7	39.3	49.8
2. Gulf of Bothnia, Finnish hatchery	49.3	5.5	38.2	49.4	59.6
3. Gulf of Bothnia, Swedish hatchery	10.8	2.7	5.9	10.6	16.6
4. Gulf of Finland, wild	0.3	0.5	0.0	0.1	1.6
5. Baltic Main Basin	0.2	0.3	0.0	0.0	1.0
	100.0			99.4	

Table 5. Stock group proportions (%) in Atlantic salmon catch samples in 2002 based on genetic analysis, using the variation at 8 DNA microsatellite loci and Bayesian estimation program, Bayes (Pella and Masuda 2001), and the proportion of wild fish estimated by scale reading method.

1. Åland Islands, 60°10'N, 19°20'E, May 4 - June 27, 2002. Sample size = 218.

Origin of stock group	Mean	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	68.8	5.1	58.4	68.9	78.6
2. Gulf of Bothnia, Finnish hatchery	16.5	4.4	8.6	16.2	25.8
3. Gulf of Bothnia, Swedish hatchery	13.2	3.2	7.3	13.1	19.8
4. Gulf of Finland, wild	0.0	0.1	0.0	0.0	0.4
5. Baltic Main Basin	1.5	0.8	0.3	1.3	3.5

2. Bothnian Sea, 62°15'N, 21°15'E, May 29 - August 7, 2002. N = 179.

Origin of stock group	Mean	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	38.9	6.0	27.1	39.0	50.3
2. Gulf of Bothnia, Finnish hatchery	56.8	6.1	45.1	56.7	69.0
3. Gulf of Bothnia, Swedish hatchery	1.6	1.8	0.0	1.0	6.2
4. Gulf of Finland, wild	0.6	0.6	0.0	0.4	2.2
5. Baltic Main Basin	2.1	1.1	0.5	1.9	4.7

3. Bothnian Bay, 63°45'N, 22°30'E, May 23 - August 22, 2002, and 65°00'N, 24°30'E, N = 180

Stock group	Mean	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	43.1	5.2	32.9	43.1	53.4
2. Gulf of Bothnia, Finnish hatchery	47.6	5.2	37.7	47.5	57.9
3. Gulf of Bothnia, Swedish hatchery	9.1	3.3	3.3	8.9	16.1
4. Gulf of Finland, wild	0.0	0.2	0.0	0.0	0.5
5. Baltic Main Basin	0.1	0.3	0.0	0.0	1.0

4. Gulf of Finland (east), 60°20'N, 27°00'E, July 3 - August 9, 2002. N = 150

Origin of stock group	Mean	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	2.3	1.6	0.2	2.0	6.3
2. Neva stock (Finland, Russia and Estonia)	88.0	2.9	81.9	88.2	93.1
3. Gulf of Bothnia, Swedish hatchery	1.7	1.3	0.0	1.5	4.8
4. Gulf of Finland, wild	0.1	0.3	0.0	0.0	1.0
5. Baltic Main Basin	7.9	2.4	3.9	7.7	12.9

5. Gulf of Finland (west), 59°40'N, 23°30'E, October 16 - December 4, 2002. N = 136

Origin of stock group	Mean	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	2.8	1.5	0.6	2.6	6.4
2. Neva stock (Finland, Russia and Estonia)	56.0	4.4	47.3	56.1	64.6
3. Gulf of Bothnia, Swedish hatchery	2.2	1.3	0.3	1.9	5.4
4. Gulf of Finland, wild	4.6	2.2	1.2	4.3	9.5
5. Baltic Main Basin	34.5	4.4	26.2	34.4	43.2

6. Baltic Main Basin, 55°15'N, 16°00'E, December 3, 2002. N = 71

Origin of stock group	Mean	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	46.7	12.3	22.0	47.2	68.8
2. Gulf of Bothnia, Finnish hatchery	18.9	13.2	0.0	17.7	47.0
3. Gulf of Bothnia, Swedish hatchery	17.1	6.5	5.6	16.7	30.7
4. Gulf of Finland, wild	1.2	1.5	0.0	0.7	5.2
4b. Gulf of Finland, hatchery, Neva	4.4	2.5	0.9	4.0	10.5
5. Baltic Main Basin	11.7	3.9	5.2	11.4	20.2

Stocks included in the groups in genetic estimates:

1. Gulf of Bothnia wild: Tornionjoki W, Simojoki, Kalixälven, Byskeälven, Vindelälven, Lögde, Ljungan.
2. Gulf of Bothnia Finnish hatchery: Tornionjoki H, Iijoki, Oulujoki, (Neva).
3. Gulf of Bothnia Swedish hatchery: Luleälven, Skellefteälven, Umeälven, Ångermanälven, Indalsälven, Ljusnan, Dalälven,
4. Gulf of Finland, wild: Kunda, Keila
- 4b. Gulf of Finland, hatchery: Neva
5. Baltic Main Basin: Emån, Mörrum, Pärnu, Gauja, Daugava, Venta.

Table 6. Stock group proportions in Finnish Atlantic salmon catch samples in 2003 based on data of 9 DNA microsatellite loci. Samples 1 - 5 relative to Finnish catches.

1. Åland Islands, 60°10'N, 19°20'E. May 22 - June 26, drift net, N = 209.

Origin of stock group	% of catch	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	76.4	5.6	64.4	76.8	86.4
2. Gulf of Bothnia, hatchery, Finnish	16.3	4.8	8.1	15.9	26.7
3. Gulf of Bothnia, hatchery, Swedish	6.7	2.9	1.6	6.4	13.1
4. Gulf of Finland, wild	0.0	0.1	0.0	0.0	0.4
5. Gulf of Finland, hatchery	0.0	0.1	0.0	0.0	0.2
6. Western Main Basin, wild, Swedish	0.0	0.1	0.0	0.0	0.4
7. Eastern Main Basin	0.5	0.5	0.0	0.4	1.9

2. Bothnian Sea, 62°00'N, 21°15'E. May 20 - September 17, trap-net, N = 218.

Origin of stock group	% of catch	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	75.6	4.2	66.7	75.8	83.1
2. Gulf of Bothnia, hatchery, Finnish	22.9	4.1	15.6	22.7	31.7
3. Gulf of Bothnia, hatchery, Swedish	0.3	0.5	0.0	0.1	1.8
4. Gulf of Finland, wild	0.0	0.1	0.0	0.0	0.4
5. Gulf of Finland, hatchery	0.1	0.5	0.0	0.0	1.6
6. Western Main Basin, wild, Swedish	0.1	0.2	0.0	0.0	0.5
7. Eastern Main Basin	1.0	0.7	0.1	0.9	2.6

3. Bothnian Bay, 63°45'N, 22°30'E and 65°00'N, 24°30'E.

June 23 - September 1, 2003, trap-net, N = 203.

Stock group	% of catch	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	51.8	5.4	41.5	51.7	62.5
2. Gulf of Bothnia, hatchery, Finnish	38.4	5.2	28.2	38.4	48.5
3. Gulf of Bothnia, hatchery, Swedish	9.5	2.7	4.8	9.4	15.3
4. Gulf of Finland, wild	0.0	0.2	0.0	0.0	0.4
5. Gulf of Finland, hatchery	0.0	0.1	0.0	0.0	0.2
6. Western Main Basin, wild, Swedish	0.0	0.1	0.0	0.0	0.4
7. Eastern Main Basin	0.2	0.4	0.0	0.0	1.4

4. Gulf of Finland (east), 60°20'N, 27°00'E. May 30 - September 25, trap-net, N = 448.

Origin of stock group	% of catch	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	36.3	3.2	29.9	36.3	42.3
2. Gulf of Bothnia, hatchery, Finnish	11.0	10.3	4.6	9.0	60.3
3. Gulf of Bothnia, hatchery, Swedish	0.6	0.6	0.0	0.5	2.3
4. Gulf of Finland, wild	0.1	0.3	0.0	0.0	0.9
5. Gulf of Finland, hatchery	51.0	10.3	0.0	52.9	57.6
6. Western Main Basin, wild, Swedish	0.0	0.1	0.0	0.0	0.2
7. Eastern Main Basin	1.0	0.5	0.3	0.9	2.1

5. Gulf of Finland (west), 59°40'N, 23°00'E. May 20 - December 3, long-line, N = 148.

Origin of stock group	% of catch	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	13.5	3.5	7.1	13.4	20.6
2. Gulf of Bothnia, hatchery, Finnish	3.2	6.6	0.0	1.4	32.1
3. Gulf of Bothnia, hatchery, Swedish	5.3	2.2	1.7	5.1	10.2
4. Gulf of Finland, wild	4.1	1.9	1.2	3.9	8.4
5. Gulf of Finland, hatchery	31.3	7.2	0.0	32.3	40.2
6. Western Main Basin, wild, Swedish	1.4	1.0	0.2	1.2	3.9
7. Eastern Main Basin	41.1	4.1	33.3	41.1	49.3

6. Baltic Main Basin, 55°15'N, 16°00'E. Feb.18, Oct. 3. Nov. 18, drift-net, N = 215.

Origin of stock group	% of catch	SD	2.5%	Median	97.5%
1. Gulf of Bothnia, wild	60.7	5.3	49.7	60.9	70.7
2. Gulf of Bothnia, hatchery, Finnish	6.4	3.8	1.6	5.4	15.8
3. Gulf of Bothnia, hatchery, Swedish	24.1	4.2	15.3	24.2	32.2
4. Gulf of Finland, wild	0.0	0.2	0.0	0.0	0.5
5. Gulf of Finland, hatchery	0.4	0.5	0.0	0.1	1.9
6. Western Main Basin, wild, Swedish	5.1	1.6	2.4	5.0	8.7
7. Eastern Main Basin	3.4	1.2	1.4	3.2	6.1

Stocks included in the groups in genetic estimates:

1. Gulf of Bothnia wild: Tornionjoki W, Simojoki, Kalixälven, Byskeälven, Vindelälven, Lögde, Ljungan (7).
2. Gulf of Bothnia hatchery Finnish: Tornionjoki, H; Iijoki, Oulujoki, (Neva) (4).
3. Gulf of Bothnia Swedish hatchery: Luleälven, Skellefteälven, Umeälven, Ångermanälven, Indalsälven, Ljusnan, Dalälven (7)
4. Gulf of Finland, wild: Kunda, Keila (2)
5. Gulf of Finland, hatchery: Neva Fi, Neva Rus (2).
6. Western Main Basin: Emån, Mörrumsån (2).
7. Eastern Main Basin: Pärnu, Gauja, Daugava, Venta (4).