

GENERAL  
BIOLOGY

## The Allozyme ESTD\* Locus as a Marker of Genetic Differentiation between European and North American Populations of the Atlantic Salmon (*Salmo salar* L.)

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The Atlantic salmon (*Salmo salar* L.) is an anadromous fish that spawns in rivers of Europe and North America [1] and performs feeding migrations to the northern regions of the Atlantic ocean [2].

More than three decades ago, in conjunction with extensive catches of Atlantic salmon in the North Atlantic, the problem of identifying salmon populations of European and American origin arose. This problem has still not been solved (see reviews [3–6]).

In this article, we show the possibility of efficient discrimination between the North American and European populations of the Atlantic salmon based on ESTD\* locus polymorphism. This locus codes for esterase D (EC 3.1.1.-). The suggested approach resulted from studies of the genetic structure of Canadian populations of the Atlantic salmon and a comparison with analogous characteristics of the European populations.

Young Atlantic salmon specimens were collected in 1994–1995 in five Canadian rivers: Freshwater ( $n = 20$ ); Highlands ( $n = 25$ ); Restigouche ( $n = 13$ ); Little Southwest Miramichi ( $n = 12$ ); and its tributary, the Catamaran ( $n = 13$ ) (Fig. 1). Atlantic salmon specimens from the White Sea were used as controls. Electrophoresis in polyacrylamide and starch gels was performed as described in [7, 8]. The data on the genetic polymorphism of the ESTD\* locus are published in [8].

The figure shows sector diagrams of frequencies of the ESTD\* locus alleles in the Canadian and previously studied European populations [7] of the Atlantic salmon. The ESTD\*100 allele dominates in the European populations (frequency, 0.759–1.000), whereas in

the samples from the Canadian Freshwater, Little Southwest Miramichi, and Catamaran rivers, the alternative allele ESTD\*92 was fixed. This allele also dominated in the other two Canadian populations. Only one heterozygote ESTD\*92/100 was found in the sample from the Restigouche River (ESTD\*100 allele frequency, 0.039), and two ESTD\*92/100 heterozygotes were discovered in the Highlands River (ESTD\*100 allele frequency, 0.040).

Therefore, these Canadian populations are fixed (or almost fixed) with respect to the ESTD\*92 allele, whereas the previously studied Norwegian populations and populations of the Arctic Ocean and the Baltic Sea are fixed with respect to the ESTD\*100 allele (or this allele at least dominates in them) [7–9]. In view of this, the ESTD\* locus may serve as a genetic marker for identifying European and North American populations of the Atlantic salmon in the North Atlantic.

Earlier, differences in the allele frequencies of other protein-encoding loci were found between European and North American salmon specimens (see reviews [3–5]); however, these differences were not as pronounced as the differences between the frequencies of the ESTD\* locus alleles.

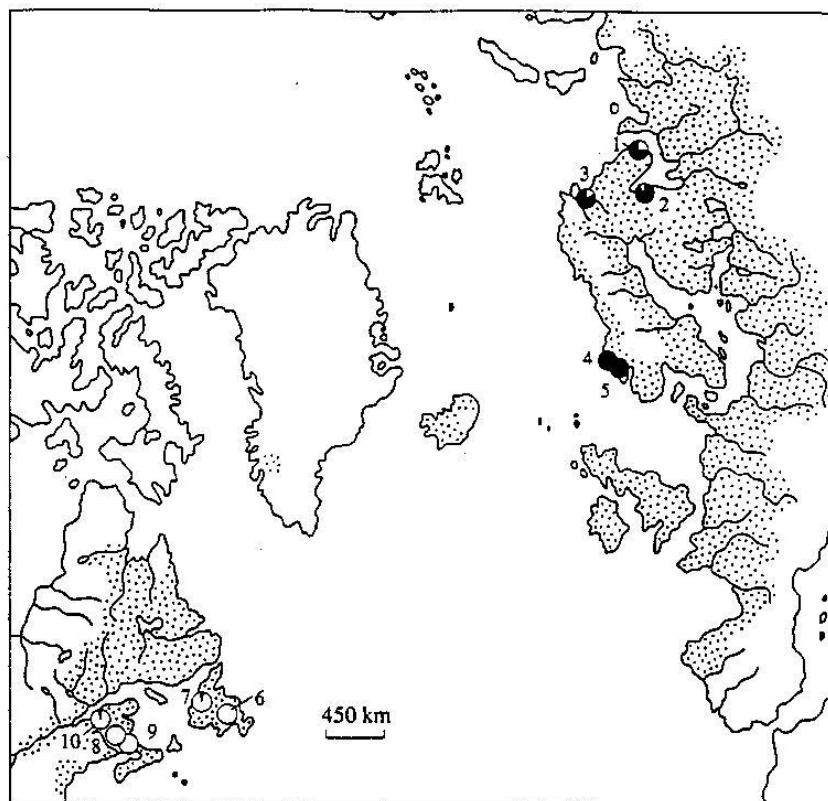
Specimens of European and American origin may be almost fully identified by analysis of DNA variability [6, 10–14]. However, this analysis is complex, expensive, and time-consuming, whereas the analysis of ESTD\* locus polymorphism is simple and only takes several hours. This locus is expressed in several tissues, including the adipose fin; therefore, the salmon genotype may be identified by a biopsy.

Differentiation of the European or American populations of the Atlantic salmon might be hindered by the fact that, in certain runs from rivers of the Arctic Ocean basin, the ESTD\*92 allele is present with a relatively high frequency (up to 0.29) [7–9]. It is known that salmon specimens from these rivers fatten in the Norwegian Sea, where only single specimens from the American populations were found [2]. Therefore, their

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Frequencies of ESTD\*100 (black sectors) and ESTD\*98 (white sectors) alleles in Atlantic salmon populations: (1) Kachakovka ( $n = 29$ ); (2) Nilma ( $n = 16$ ); (3) Neiden ( $n = 64$ ); (4) Hop ( $n = 11$ ); (5) Oyre ( $n = 19$ ) [7]; (6) Freshwater; (7) Highlands; (8) Catamaran; (9) Little Southwest Miramichi; (10) Restigouche. Dots denote the Atlantic salmon range.

identification is of little practical importance. Specimens with the ESTD\*92 allele in the Norwegian Sea appear to be migrants from European rivers of the Arctic Ocean basin.

The distribution of the ESTD\*92 allele in Atlantic salmon populations is rather unusual. This allele was found in two distant parts of the species range—in North America and in Europe in the Arctic Ocean basin. We suggest that this is a more ancient allele, which was displaced as a relict to the borders of the Atlantic salmon range by specimens with a more recent ESTD\*100 allele.

Further studies of ESTD locus genetic polymorphism in different parts of the Atlantic salmon range, in particular, in populations of the North Atlantic islands, would be of great scientific and practical interest.

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#### REFERENCES

1. MacCrimmon, H.R. and Gots, B.L., *J. Fish. Res. Board Can.*, 1979, vol. 36, pp. 422–457.
2. Bakhtanskii, E.L., Klovach, N.V., and Lepskaya, V.A., *Biotopicheskie osnovy raspredeleniya promyslovyykh i kormovykh morskikh zhivotnykh* (Biotopical Principles of Distribution of Marketable and Edible Marine Animals), Moscow, 1991, pp. 94–115.
3. MacCrimmon, H.R. and Claytor, R.R., *Aquacult. Fish. Manage.*, 1986, vol. 17, no. 1, pp. 1–17.
4. Stahl, G., *Population Genetics and Fishery Management*. Ryman, N. and Utter, F., Eds., Seattle: University of Washington Press, pp. 121–140.
5. Verspoor, E., *Present and Future Atlantic Salmon Management*, Savannah, Georgia, 1988, pp. 37–46.

6. Davidson, W.S., Birt, T.P., and Green, J.M., *J. Fish Biol.*, 1989, vol. 34, pp. 547-560.
7. Skaala, O., Makhrov, A.A., Karlsen, T., *et al.*, *ICES Statutory Meeting, Anadromous and Catadromous Fish Committee*, 1996.
8. Semenova, S.K. and Slyn'ko, V.I., *Dokl. Akad. Nauk SSSR*, 1988, vol. 300, no. 5, pp. 1239-1243.
9. Kazakov, R.V. and Titov, S.F., *J. Fish Biol.*, 1991, vol. 39, pp. 1-6.
10. Palva, T.K., Lehtvaslainen, H., and Palva, E.T., *Aquaculture*, 1989, vol. 81, pp. 237-244.
11. Bermingham, E., Forbes, S.H., Friedland, K., and Pla, C., *Can. J. Fish. Aquat. Sci.*, 1991, vol. 48, pp. 884-893.
12. Culter, M.G., Bartlett, S.E., Hartley, S.E., and Davidson, W.S., *Can. J. Fish. Aquat. Sci.*, 1991, vol. 48, pp. 1655-1661.
13. McConnell, S.K., O'Reilly, P., Hamilton, L., *et al.*, *Can. J. Fish. Aquat. Sci.*, 1991, vol. 52, pp. 1863-1872.
14. Taggart, J.B., Verspoor, E., Galvin, P.T., *et al.*, *Can. J. Fish. Aquat. Sci.*, 1991, vol. 52, pp. 2305-2311.