

# Genetic Status of Atlantic Salmon in Maine

Interim Report from the  
Committee on Atlantic Salmon in Maine

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Board on Environmental Studies and Toxicology

Ocean Studies Board

Division on Earth and Life Studies

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*Conclusions* 47

Stocking clearly has not been completely effective, as shown by declining run sizes over the last 30 years. Whether today's genetic differences represent a remnant of salmon population structure that predates human intervention, following thousands of years of natural selection and genetic drift, typical of salmon occupying different habitats with a variety of environmental circumstances, or whether they represent five to six generations of genetic drift, exacerbated by an increasingly serious population collapse over a short period, is a question that we cannot answer by genetic characterization of neutral genetic markers alone. Any conclusions we draw about the selection/drift dichotomy will necessarily be circumstantial. Suffice it to say that the patterns of variation we see are typical of wild salmon exhibiting the effects of both selection and drift.

Maine Governor Angus King, in his presentation to the committee on June 12, 2001, asked whether we are dealing with Maine salmon or merely salmon in Maine. The distinctiveness of Maine salmon is important, but it is not the whole question, which we consider to have two parts. For the first part, the genetic evidence available for review indicates that wild salmon swimming in Maine's DPS-designated rivers are genetically distinct from salmon swimming in Europe, from those in Canada, and from those used in the Maine aquaculture industry. Collectively, the data are persuasive on these points, from which we conclude that the natural salmon spawning in Maine's DPS-designated rivers are "Maine salmon," not just "salmon in Maine."

The second part of the question is whether these Maine salmon are mainly hatchery-created mixtures or the results of natural processes—including migration, colonization, natural selection, and genetic drift—that occur in network-connected watersheds. More specifically, the issue concerns the relative importance of natural selection over long periods, which influenced the differentiation of Maine's original salmon populations, versus recent genetic drift or a sampling effect related to small populations. Hatchery supplementation—including the movement and mixing of multiple stocks, adaptation to hatchery husbandry practice, and genetic drift—has the potential to alter the gene pool of wild populations. If salmon in Maine are merely the local "farm crop," rather than largely the result of natural processes, they might not be "Maine salmon." We do not have data to answer this question completely.

We can, however, draw some inference from comparisons of the watershed-specific samples of the current DPS rivers. If Maine salmon are an artificial construct of non-river-specific hatchery supplementation, then the separate watershed-specific populations should be genetically indistinguishable. The genetic evidence available for review indicates that the natural populations

are distinguishable from each other. Moreover, their degree of distinctiveness is typical of that found throughout the remaining world distribution of wild Atlantic salmon. The data suggest that current Maine salmon in the DPS rivers are not mainly hatchery mixtures but rather show the typical metapopulation structure that characterizes wild populations of salmon and their relatives in places where stocking has been absent or insignificant. Maine has wild salmon populations in the eight DPS rivers that are as divergent from Canadian populations and from each other as expected among wild salmon populations elsewhere in the Northern Hemisphere.