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MAR 3 - 2011

Ms. Alexandra Morton
< gorbuscha@gmail.com >

Dear Ms. Morton:

This is in response to your correspondence of January 14, 2011, addressed to your Member of Parliament, Mr. John Cummins, regarding the recently published research of Dr. Kristina Miller and her colleagues at Fisheries and Oceans Canada (DFO) and the University of British Columbia.

As you indicate, the work is impressive and represents an important contribution toward developing a comprehensive understanding of the biological and environmental factors affecting salmon spawning success.

In response to your concerns for possible human health implications, please be assured that the results of this study and those of previous studies to which you refer give no indication of any cause for concern for human health. I have attached a summary of the recent paper written by Dr. Miller *et al* and an overview on *plasmacytoid leukemia syndrome* (PLS) for your reference, and I will take this opportunity to clarify some misconceptions presented in your correspondence.

In terms of the quotation from Newbound and Kent (1991), "Experimental interspecies transmission of *plasmacytoid leukemia* in salmonid fishes," you imply that they demonstrated that PLS had been shown to infect cells of humans and other higher vertebrates. This is incorrect and based on a misquote. Newbound and Kent refer to a 1976 study citing the capacity of *bovine leucosis* (a virus that causes only mild disease in cows) to infect the *cells* of other species *in vitro* (i.e., in a Petri dish). They made no statements linking PLS to humans, and were in no way insinuating that this syndrome was cause for concern for human health.

The statement "DFO has known about this potential virus for four years..." is also incorrect. The sockeye salmon that were studied were sampled in 2006, but the tissue was not analyzed until 2008 and 2009, and the hypothesis that the results indicated possible exposure to a virus was not made until mid-2009.

It is important to recognize that Dr. Miller *et al* did not identify a specific virus and that, until a specific virus is identified, it is only proposed that a virus is responsible for the genomic signature identified. Molecular testing of these samples has been ongoing to identify if there is an infectious agent associated with this distinct signature. These tests have included all characterized viruses known to affect Pacific salmon.

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In addition, the fact that a potential virus is unknown would not infer that it is new to salmon, especially given that data on the prevalence or effects of viruses in wild salmon populations are quite limited. Moreover, if a pathogen is not culturable in the lab, as is the case for many viruses, it is difficult to recognize and study, and may be missed. Therefore, we cannot assume that all newly discovered infectious agents in wild salmon are, in fact, new to the population.

However, once "new" infectious agents are discovered, epidemiological research (tracking the geographic distribution of variations in DNA sequences) can help researchers make that determination. Again, we should be clear that Dr. Miller's research is still at the discovery stage and has not identified a specific infectious agent responsible for the genomic signature associated with premature mortality of salmon in the river.

Your letter suggests a possible connection between the genomic signature discovered in this research and salmon farms. DFO has not conducted research associated with this gene expression signature and salmon farms, and will not speculate on such a link. However, the signature associated with river-mortality in adult salmon was present in salmon migrating through both Johnstone Strait, where there are salmon farms, and Juan de Fuca Strait, where there are no salmon farms. As well, our unpublished data shows that the signature is present as far north as Haida Gwaii, where there are no salmon farms.

The publication of Dr. Miller's research is an example of the Department's commitment to open and transparent scientific research on the health of Pacific salmon. On the basis of Dr. Miller's findings, DFO continues its research into whether an infectious agent is contributing to the premature mortality of Fraser River sockeye salmon.

Please be assured that the Department takes your concerns seriously. Thank you for taking the time to write to me and I hope this letter has helped to clear up any misunderstandings on this matter.

Sincerely,

A handwritten signature in black ink, appearing to read "Gail Shea", written in a cursive style.

Gail Shea, P.C., M.P.

Attachments (2)

c.c.: Mr. John Cummins, M.P.

**Summary of "Genomic signatures predict migration
and spawning failure in wild Canadian salmon,"
by Kristina M. Miller *et al.* (2011), *Science*, vol 331, pp 214-17.**

In the past decade, Fraser sockeye salmon have experienced high and fluctuating levels of premature mortalities, both en route to spawning areas and on spawning areas. This study looked at possible factors that could have resulted in the unpredicted mortalities, with the ultimate goal of helping managers better predict salmon returns. One known factor going into the study was a link between mortality and water temperatures. Seven of the last 10 summers have been the warmest on record for the Fraser River, and biotelemetry (wireless monitoring of fish) has revealed high losses of migrating sockeye in regions of elevated river temperature.

For the study, adult salmon caught in the ocean, in-river and at the spawning area were either tagged or implanted with a radio transmitter and biopsied for blood, gill, muscle, and fin tissue. The tagged fish were then tracked through ocean and river environments. Physiological variation in the health and condition of salmon at the time of sampling was examined by analyzing the expression of thousands of genes in gill tissue. Researchers then compared the expression of genes in individual salmon that made it to spawning grounds to salmon that died prematurely. A number of distinct gene expression (genomic) signatures were analyzed for their association with successful migration and spawning, but only one was found to correlate with premature mortality.

The study yielded new insight into one potential physiological mechanism associated with survivorship during return migration. Researchers identified the same pattern or "genomic signature" that was correlated with a significantly increased risk of the salmon dying before spawning – whether the salmon were tagged in the ocean, river, or at spawning grounds. These data imply that salmon were already physiologically compromised (i.e., in poor condition) before they entered the river, and that river conditions *alone* were not likely responsible for all mortality in the river.

However, we cannot assume that an association with mortality is evidence that the genomic signature *caused* the mortality, and there is still the very real possibility that elevated temperature and physiological predisposition may together impact survivorship in the river.

The genomic signature associated with premature mortality showed an elevation of the type of immune response stimulated when an infectious agent is causing damage inside the cells (where viruses and intracellular parasites would reside).

Moreover, 65 percent of affected biological processes were consistent with responses to viral infections. Researchers also noted linkages with genes associated with responses to leukemia-like diseases. Leukemia-like diseases often result from retroviral infections, but not always. However, from this single gene expression study, there is not enough evidence to conclude that sockeye salmon have leukemia or are infected with retroviruses; this will require further study. The researchers hypothesize that the genomic signature associated with elevated mortality is in response to a virus infecting fish before river entry and that persists to the spawning areas. It is important to note that the study identified a pattern of change or genomic signature, and did not identify an infectious agent.

This study is the "discovery" stage in understanding factors that may compromise the fitness of salmon. Research is ongoing to identify if there is a viral infectious agent associated with this signature. To date, molecular testing of these samples has yielded no evidence of viruses known to affect Pacific salmon associated with this signature.

The full study can be found online at
< <http://www.sciencemag.org/content/331/6014/214.full> >.

Appendix: *Plasmacytoid leukemia syndrome (PLS)*

Leukemia is a broad term covering a spectrum of diseases, typically related to blood disorders or anemic blood diseases. Leukemia does not have one causative agent.

Plasmacytoid leukemia or *Plasmacytoid leukemia syndrome (PLS)* is a leukemia-like disease of chinook salmon that was originally identified in wild and cultured chinook salmon in British Columbia in the late 1980s. The cause of this syndrome is not known and, while it is speculated that the cause is viral, a possible virus associated with PLS has still not been identified or "characterized." Therefore, while salmon with advanced stages of PLS can be identified through histology (which assesses macroscopic changes in cells and tissues), researchers cannot test for the presence of a virus or other agent causing PLS.

As reported by Newbound and Kent (1991), it was possible, by injection, to cause chinook and sockeye salmon to show signs of this disease in the laboratory.

PLS does not affect Atlantic salmon. Researchers have attempted to infect Atlantic salmon in experimental challenges, but they were shown to be highly resistant and have never shown any signs of the disease.

It has been suggested in the media and by members of the public that past DFO research has inferred that the presence of PLS in salmon may be harmful to humans. As noted earlier in my response, statements regarding the capacity of *bovine leucosis* (which generally causes only mild disease in cows) to infect the cells of other species *in vitro* (i.e., in a Petri dish) were misquoted. Researchers made no statements linking PLS to humans and in no way insinuated that PLS was cause for concern for human health.