Genomic and physiologic predictors of condition of returning adult Chinook salmon (*Oncorhynchus tshawytscha*): implications of a warming ocean

Summary report *Prepared for:*

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ABSTRACT

Chinook salmon face a number of conservation threats, including fishing pressures, predation, habitat loss and environmental pollution. In addition, climate change looms as a significant threat to ocean productivity and natal stream hydrologic properties, presenting a stress to Chinook food webs and abundance. Not only is abundance of concern, but the nutritional quality of the fish is also important. For this study, we hypothesized that climate change (sea surface temperature-related ocean productivity) will have negative ramifications for Chinook salmon 'quality', and that measures of lipid content, lipid classes, proximate analysis and gene expression will provide quantitative measures of salmon condition. Our study involved both a field component and a captive component.

For the field component, we collected Chinook samples from two sites in British Columbia, namely Langara in the northern Queen Charlotte Islands, and April Point, in the Strait of Georgia. Fish collected at April Point Lodge were 3 and 4 year old fish from the Fraser River, the South Thompson River and rivers on the East coast of Vancouver Island, while the majority of fish collected from Langara were 4 and 5 year old fish (range 2-7) from a much larger range of stocks including local Queen Charlotte Island fish, West Coast of Vancouver Island fish and Coastal Washington and Oregon fish stocks. By intercepting salmon at two points in British Columbia, we expected a range of lipid values, and offering an opportunity to develop, apply and validate new approaches to evaluating condition (genomics and lipid measurements). Stable isotope ratios revealed seasonal differences in $\delta^{13}C$ and C:N ratios for fish caught at April Point but not Langara Island suggesting that early returning stocks to the Fraser River and S. Thompson River may be experiencing some early nutritional or fasting-related influences. However, seasonal differences in lipid content and caloric energy content were observed in fish collected at Langara Lodge but not April Point Lodge with significant decreases in lipid content and caloric energy content in fall fish from Langara. Lipid content levels and caloric energy content of fish from April Point were similar to fall fish from Langara, suggesting that fish caught at April Point had already lost the majority of their lipid stores as they neared their natal streams, while spring fish from Langara were likely still feeding in order to reach their much further destinations.

For the captive component, we conducted a nutritional stress experiment on captive Chinook in collaboration with Yellow Island Aquaculture research facility in an effort to help identify lipid and genomic markers that could be used as stress indicators for wild fish. Results of the controlled fasting study at Yellow Island demonstrated that $\delta^{13}C$ stable isotope ratios were higher in fasted fish relative to controls ($p < 0.001$). $\delta^{13}C$ ratios were inversely correlated to lipid ($r^2 = 0.56$), indicating that this isotopic ratio provides a clear signal of fasting stress. However, no changes in lipid content or caloric content were observed between the fasted and control groups indicating that other biological processes involved in fasting may take place prior to using lipid stores for energy. Results of microarray indicated that 21 genes related to lipid metabolic pathways were differentially expressed between the two feeding groups. Microarray analysis revealed a down-regulation in expression of 18 genes and up-regulation of 3 genes related to lipid metabolic pathways in response to fasting. The gene expression of four of these endpoints was correlated to lipid percent, providing evidence that these markers may provide useful gene targets for assessing Chinook condition. Eleven Chinook specific gene targets were further developed for gene expression analysis, using real-time PCR. These will be used to validate the results of the preliminary (non-

specific) microarray approach, and further investigate the expression of genes involved in the major lipid metabolic pathways in Chinook salmon. These markers, along with lipid measurements and stable isotope ratios, offer a promising means of linking condition and quality of salmon with potential successes of different year classes and stocks. This is especially important given increasing oscillations of sea surface temperature.