

Fish Population Modeling Approaches for Assessing Direct Effects and Recovery Following Mitigation of a Pulp Mill Effluent in Jackfish Bay

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We present an approach to link chemically-induced alterations in molecular and biochemical endpoints to adverse outcomes in whole organisms and populations. A predictive population model was developed to translate changes in fecundity measures of white sucker (*Catostomus commersoni*) collected at Jackfish Bay, Lake Superior to alterations in population growth. Individual-level responses of fish exposed to pulp mill effluent were used to demonstrate the model's capability to project alterations in population status, both in terms of ongoing impact and subsequent recovery after stressor mitigation associated with process changes at the mill. Long term monitoring data from the Jackfish Bay site includes biochemical endpoints, such as steroid measurements, relevant to an adverse outcome pathway (AOP) resulting in decreased fecundity. In combination with population modeling, the AOP framework can be used as an organizing principle by which mechanistic data (e.g. circulating steroid concentrations) can be effectively translated into endpoints meaningful to ecological risk (e.g. population status). Extrapolation of the population modeling construct demonstrated at the Jackfish Bay site can be made to characterize white sucker population trends at other sites that are less data rich. This abstract does not necessarily reflect U.S. EPA Policy.