Failure of Population Recovery in Relation to Disease for Pacific Herring in Prince William Sound

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Rapid declines in wild fish populations are often associated with disease, but the role of disease in prolonged depression of fish populations is poorly understood. Three pathogens are commonly associated with disease of marine fish: the mesomycetozoean Ichthyophonus hoferi, filamentous bacteria (*Tenacibaculum maritimum*), and viral hemorrhagic septicemia virus (VHSV). We show that following a severe 1993 disease outbreak in the Pacific herring (*Clupea pallasi*) population of Prince William Sound, Alaska, U.S.A., population recovery has been impaired by epidemics that have cycled through the adult population about every 4 years. Comprehensive epidemiological study from 1994 through 2002 resulted in time series of two disease indices related to these parhogens. The series were augmented to 2006 using data from two lesions skin ulcers (associated with filamentous bacteria) and white foci in the heart (associated with *I. hoferi*) collected by field biologists from 2003 through 2006. The time series indicated that decreasing severity of epidemics of filamentous bacteria and VHSV in 1993/1994 and 1998 were replaced by epidemics of I. hoferi that peaked in 2001 and 2005. The impact of disease on population abundance was quantified by updating an age-structured assessment model with data from 2001 through 2006. The best model scenario modeled mortality as a function of the filamentous-bacteria/VHSV index for ages 3 4 with the total prevalence of I. hoferi for all ages. From 1993 through 2006, estimated natural mortality was significantly greater than background natural mortality of 0.25. The overall pattern in estimated age 3 recruitment was a strong pulse every four years (1983, 1987, 1991) and then persistently low numbers after 1992. However, projections from the model showed that the low recruitment after 1992 was sufficient for population recovery if the effect of disease had not been present. This study shows that disease information can be used to explain and predict changes in populations that have confounded traditional fisheries assessment.