Genetic Stock Assessment of Yukon Delta Bering Cisco Harvest

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Abstract

Bering cisco *Coregonus laurettae* are anadromous salmonids with known spawning populations only in the Yukon, Kuskokwim, and Susitna rivers in Alaska. Rearing Bering cisco are found in the coastal lagoons and estuaries of western Alaska, from Kuskokwim Bay to the Colville River delta, where they are actively harvested in subsistence fisheries. A commercial fishery for Bering cisco was recently initiated at the mouth of the Yukon River and the product is being marketed to the kosher community in New York City. The fishery has been limited to an annual harvest of about 4,500 kg; approximately 10,000 Bering cisco. A much larger allocation has been requested, suggesting that the fishery would expand if permitted to do so. The commercial harvest of Bering cisco at the mouth of the Yukon River is most likely a mix of Kuskokwim and Yukon River populations. Our primary objective here was to estimate the proportional composition of the annual commercial harvest from known Bering cisco populations using genetics methods, the results of which will provide direction to future population monitoring activities. To accomplish this objective, we began development of a genetic baseline for the three Bering cisco populations. Tissue samples were collected from the three spawning populations during 2009, 2010, and 2011. During the 2011 season primers that provide effective baseline markers capable of distinguishing among spawning populations were developed and optimized. Mixed-population samples from the fishery are currently being processed and analyzed. Beginning in 2010, the genetic samples from the north Delta harvest were kept separated from the samples from the south Delta harvest. Because there may be differences in population composition between regions of the Delta, these are the samples that are being processed. Analysis of samples collected during the 2010 season are almost complete and final analysis of the results will be forthcoming within the next few weeks. Processing of the 2011 samples began in late April, 2012. One additional season of genetics collections from the harvest are planned during fall 2012, which will provide three years of mixed population data to evaluate the consistency of population composition in the harvest.