## C18 Pacific Salmon and the Endangered Species Act: Using STR DNA Analyses to Determine the Population of Origin of Fish Carcasses

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After attending this presentation, attendees will understand how forensic DNA analyses can be applied to wildlife and environmental management.

This presentation will impact the forensic community and/or humanity by demonstrating the wide range of capabilities DNA and STR analyses.

Pacific salmon and steelhead are an anadromous (fresh and marine water) fish with a complex life-cycle that spans a variety of fresh and saltwater habitats. Salmon are hatched in freshwater streams and rivers, migrate to coastal estuaries, and disperse into ocean waters to grow. Once mature they return through the estuaries and migrate upriver to their natal streams to reproduce. NOAA Fisheries Service received a petition in 1991 to list Pacific Northwest salmon populations under the Endangered Species Act (ESA). The ESA allows listing of “distinct population segments” of vertebrates and for salmon the distinction was established as “evolutionarily significant unit,” or ESU. NOAA Fisheries Service conducted a biological review of all anadromous salmon species on the West Coast and identified 52 ESUs, and evaluated whether they were at risk of extinction and should be considered for listing as threatened or endangered under the ESA. Currently there are 26 Sockeye, Chinook, Coho, Chum, and Steelhead ESUs listed as endangered or threatened “species” under the ESA. NOAA Office of Law Enforcement (NOAA OLE) is mandated to enforce the Endangered Species Act (ESA). Endangered Species Act violation investigations often require forensic molecular genetic expertise to positively identify carcasses to ESU of origin. Species identification of adult salmon is easily determined using diagnostic morphological and genetic markers. Although in some cases the question is: Which ESU did this fish carcass come from? The small amount of individual straying of individuals or geneflow between populations precludes the use of unique genetic characters to identifying ESUs; nonetheless, the ESU of origin can be ascertained by using population genetic analyses because of the extensive reproductive isolation between ESUs and populations within a species. In order to identify individuals to an ESU, a substantial amount of genetic information much be collected across the geographic range of that species. This genetic baseline is then used to evaluate the likelihood that an “unknown” fish carcass is from a specific ESU. Many investigations of illegal kills of endangered or threatened salmon involve wild Chinook salmon. The evidence is usually fillets or whole fish from a defendant’s freezer or cooler. NOAA OLE requires forensic genetic analyses to verify the illegally caught fish were actually from an endangered or threatened ESU. Because there are no diagnostic genetic markers to identify the ESU of origin, baseline genetic allele frequency data across all Chinook salmon populations to identify ESU of origin are relied on.

The genetic baseline from Chinook salmon contains data from 15,975 individuals from 109 populations across the geographic range of the species in North America. This includes but is not limited to the 17 Chinook salmon ESUs, of which nine are endangered or threatened to be extinct. Thirteen STR or microsatellite markers were used to collect the allele frequency data across all Chinook populations in the genetic baseline. The baseline allele frequency data essentially provides the empirical data signature, which will be used to identify the ESU of origin for an unknown fish carcass. The author will present data from forensic validation studies of the Chinook microsatellite (STR) baseline and provide examples of how to determine the ESU of origin using likelihood statistics to provide confidence values for the ESU assignment. Although current capabilities are for Chinook salmon ESU identification, genetic baselines for Chum salmon, Coho salmon, and Steelhead are being developed. Forensic casework involves identifying the species first and then determining the multilocus genotype of the Chinook salmon individual(s) for population genetic analyses. Determination of ESU involves a statistical analysis that first calculates the probability of assignment for an individual genetic profile to each population in the Chinook genetic baseline. These probabilities are used to calculate overall likelihoods of assignment to the ESU in question. The ESU assignment statistics utilize a partial Bayesian statistical method to determine the probability of assignment to population for each genetic profile at 13 microsatellite (STR) markers. This method employs a Monte Carlo simulation to generate a distribution of likelihoods from the simulated genetic profiles for each potential source population in the baseline. Based on these empirical distributions, the probability of the genetic profile for an unknown individual coming from each population is evaluated using the exclusion significance test described by Cornuet et al. (1999). The overall likelihood for a genetic profile to be assigned to an ESU is calculated by summing the probability of assignments for all populations in the ESU in question divided by the sum of all probability of assignments for all populations in the genetic baseline. This creates a likelihood ratio of the ESU in question compared to all populations in the Chinook genetic baseline.

**Endangered Species ACT, Pacific Salmon, DNA**