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DNA IDENTIFICATION OF FISH SPECIES

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International growth in the trade and consumption of fish has led to an increased potential for species substitution or mislabeling. Mislabeling of an endangered species could lead to market exploitation and interfere with fisheries conservation and management programs. Mislabeling fish species could expose consumers unknowingly to health risks that are associated with certain species, such as allergens or toxins. Additionally, fish species substitution can be a form of economic deception, where a species of lower quality is mislabeled as a higher-quality species that commands a greater market price. In all cases, the occurrence of species substitution can lead to consumer mistrust and confusion, ultimately resulting in a general avoidance of fish products. Therefore, the ability to regulate fish species substitution is essential to ensure public confidence and trust in the food supply.

Previously, the majority of species identification methods were based on protein analysis, such as isoelectric focusing and immunoassays. However, DNA-based methods are growing in popularity due to their increased specificity, sensitivity and ability to be effective in heavily processed food products. Within the field of DNA-based species identification, there are numerous gene targets and detection methods available, each with its own advantages and disadvantages. For the most part, research groups have thus far worked independently to develop methods for detection of fish species within groups of commercial interest. While it is beneficial to have a variety of techniques and gene targets available, there is currently a lack of standardized protocols for fish species identification. Improving the coordination of research efforts will greatly facilitate progress in this rapidly growing discipline and help standardize DNA-based fish and seafood species identification. This presentation will include a brief discussion of current DNA-based techniques and gene targets, followed by an examination of major collaborative research efforts working towards DNA-based fish species identification.

Research at the Oregon State University Seafood Research Laboratory and the University of Guelph Barcode of Life Program will also be described. Investigators determined the sequences coding for a portion of the cytochrome oxidase subunit I gene (COI) for over 900 fish representing seven salmon species. The barcode region was found to be well-conserved within species, with a mean intra-species divergence of 0.25%, ranging from 0.04% to 0.39%. Variation between species was higher, with an average genetic distance of 6.0% between a species and its nearest neighbor. The ratio of inter- to intra-species variation was higher than 1:1 for all seven commercial salmonid species (i.e., Chinook salmon, Atlantic salmon, pink salmon, chum salmon, sockeye salmon, coho salmon, and rainbow trout), indicating that these species may be differentiated using DNA barcodes. Furthermore, the results suggest that the barcode region is an appropriate genetic target for the development of species-specific PCR assays for the identification of salmon in commercial food products.