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Integrative Taxonomy, a New Tool for Fisheries Conservation

Adela Roa-Varon
Virginia Institute of Marine Science

Eric J. Hilton
Virginia Institute of Marine Science

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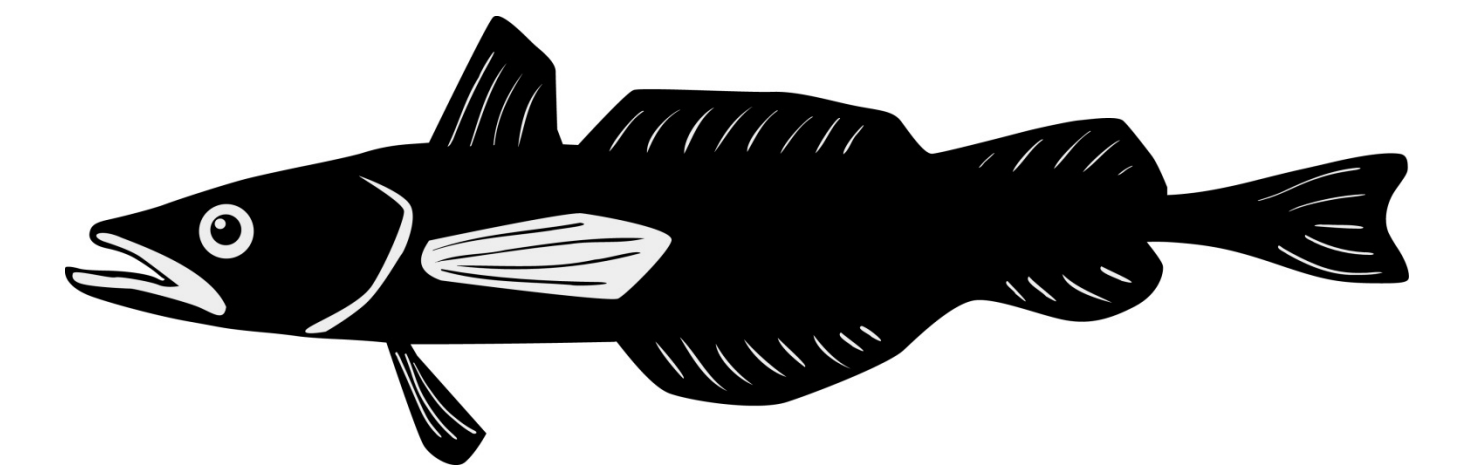
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Integrative Taxonomy: a New Tool for Fisheries Conservation

Adela Roa-Varon and Eric Hilton

Virginia Institute of Marine Science, William & Mary College

aroavaron@vims.edu, ehilton@vims.edu



What is Integrative Taxonomy?

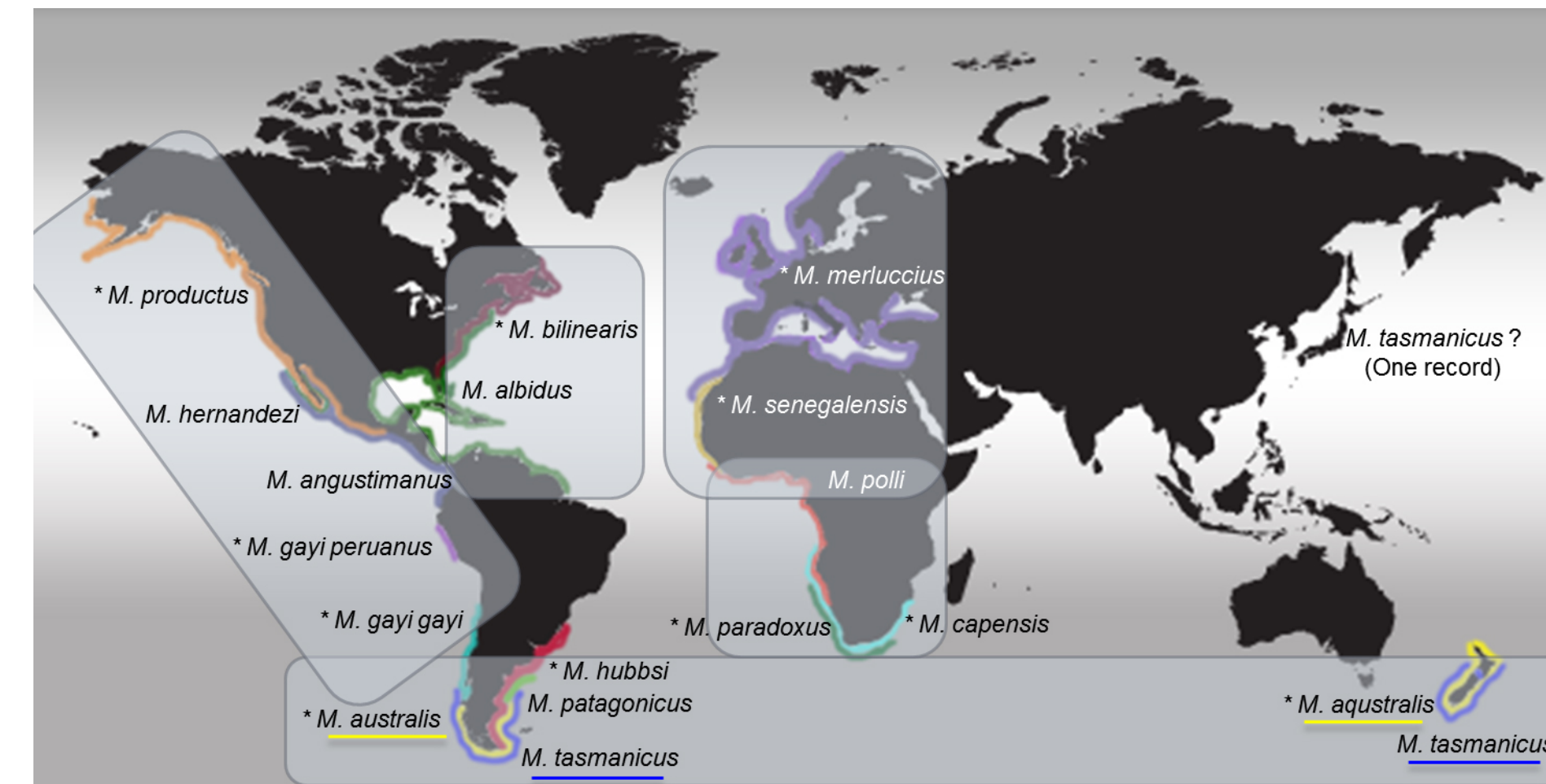
Species play a central role in nearly all disciplines of biology. Therefore delimitation of species has broad implications for efforts ranging from biological conservation to comparative evolutionary analyses. The rise of new genomic and bioinformatics tools led for **species delimitation** is becoming increasingly objective and integrative. **Gene capture** in combination with **Next generation Sequencing (NGS)** approaches allow collection of 1000s of loci for 100s of individuals. These new approaches also allow integration of genetic and non-genetic data in a unified framework.

We use **integrative taxonomy** to provide a more rigorous species delimitation by incorporating morphological and molecular data. Using **hakes** (Merlucciidae), an ecologically and commercially important family of fishes, as a model, this study aims to:

- 1) Identify species using integrative taxonomy
- 2) Reconstruct their phylogenetic relationships using a multispecies coalescent approach.
- 3) Investigate the global biogeography and diversification of hakes.

Due to the dramatic declines in abundance and commercial landings, preserving the biodiversity requires precise knowledge of the taxonomy of hakes.

The Process of Integrative Taxonomy



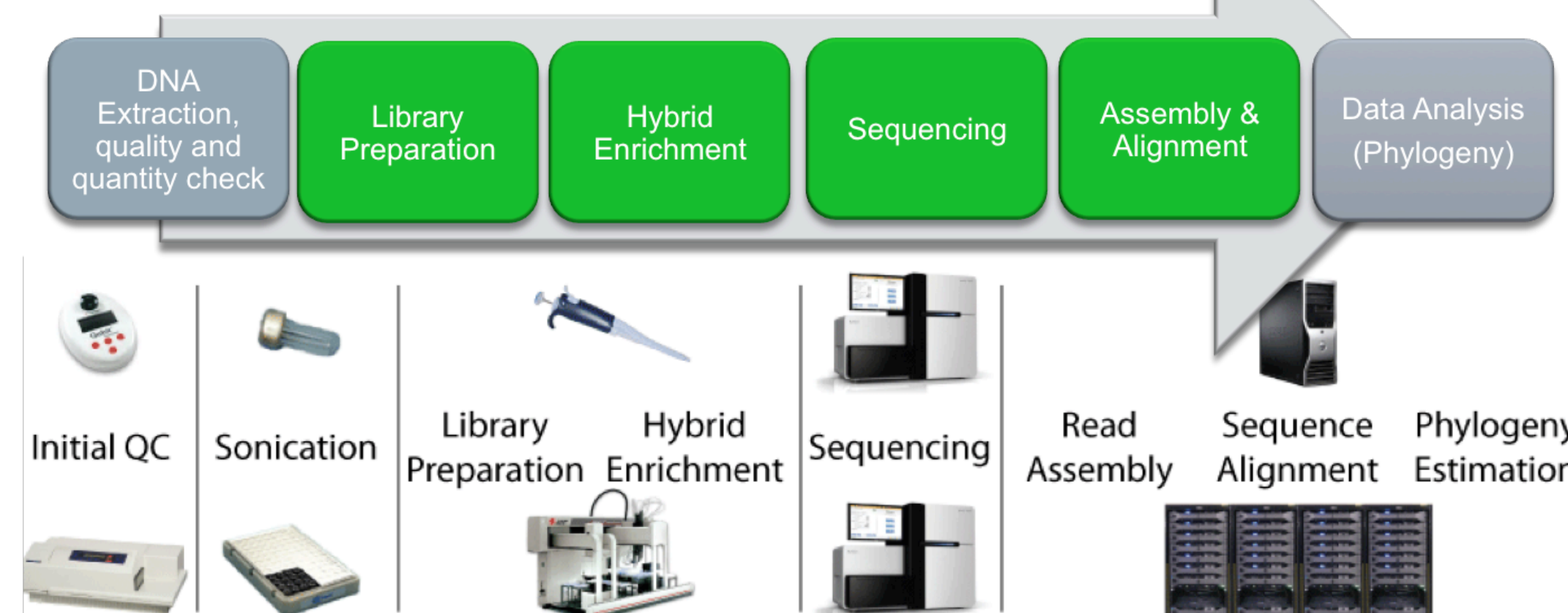
Global distribution of *Merluccius* spp.



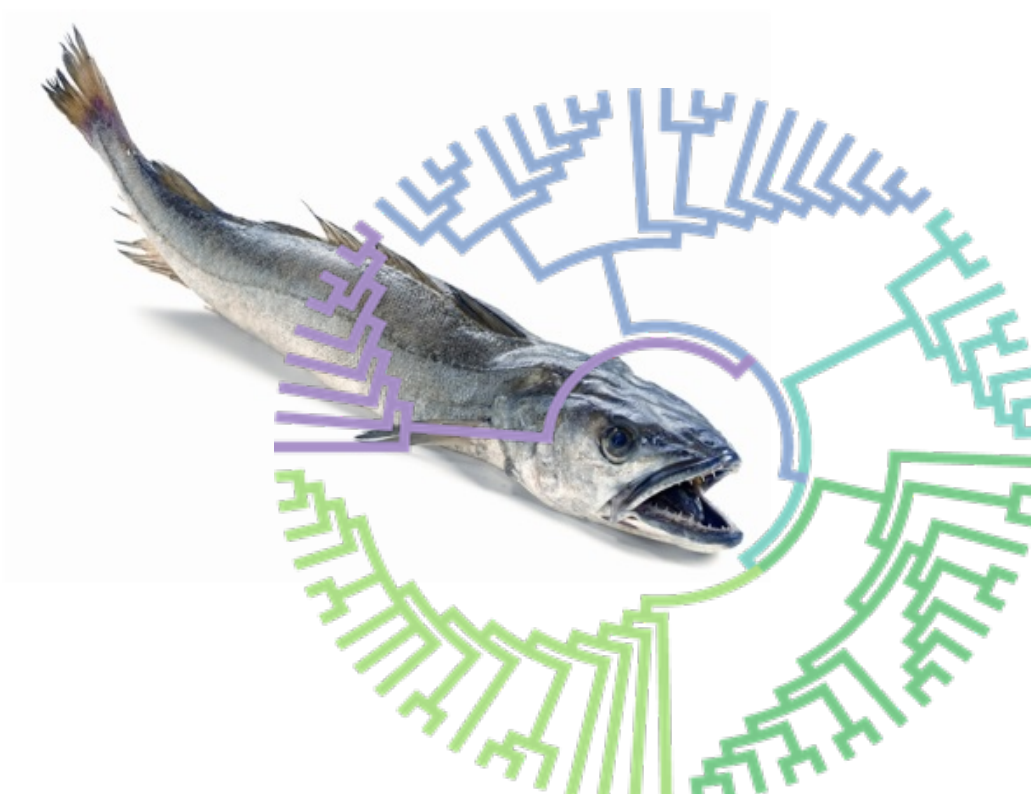
Molecular Data

Morphological data (meristic and morphometric data and internal morphology) are collected for at least 25 specimens from museum specimens and voucher specimens from our molecular sampling. Type specimens will be examined.

Genome-wide Genetic Data



DNA sequences from single-copy protein-coding genes shared across hakes were targeted using the gene capture method developed by Li et al (2013).



Expected Results

- 1) Phylogeny of the family Merlucciidae
- 2) Species delimitation of *Merluccius*
- 3) Biogeography of hakes

Results to Date

Baits libraries were designed based on candidate single-copy markers for *Gadus morhua* genome, using the MYBaits target enrichment system. A preliminary analysis was run to test the baits using *Merluccius bilinearis* and *Gadus morhua* as a positive control. Approximately, 1500 to 3000 target single-copy gene markers were identified. After corroborating the efficiency of the molecular technique, 70 species were sequenced, including 23 hakes representing all the species with exception of *Merluccius gayi-peruanus*. Data is in the early stages of analysis and at least 40 more samples are expected to be sequenced representing all the species in the genus. Morphological data are being collected and analyzed. This study will result in a better understanding of the evolution of commercially valuable fishes, which is necessary for effective fisheries management and conservation.

Reference

Li, C., Hofreiter, M., Straube, N., Corrigan, S., Naylor, G.J.P. 2013. Capturing protein-coding genes across highly divergent species. *BioTechniques* 54:321–26

Acknowledgments

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Glossary

Species are the fundamental taxonomic unit for a wide array of biological studies and applied fields such as conservation planning.

Species delimitation: the process of identifying species-level biological diversity from empirical data.

Integrative Taxonomy an approach to taxonomic research that aims to incorporate the diverse data types and methods used in systematic biology to document biodiversity and the evolutionary processes that promote divergence.

Hakes (*Merluccius*, Merlucciidae) are some of the most important commercially harvested fishes in the world. Identifying their species remains problematic due to similar morphology across species, which results in difficulties in assessing species distributions and stocks.

Gene Capture or DNA hybridization allows for hundreds of pre-specified genes to be targeted and isolated for sequencing in a single experiment.

Next Generation Sequencing (NGS) also known as high-throughput sequencing, is the term used to describe a number of different modern sequencing technologies including: Illumina, Roche 454, Ion torrent and SOLiD sequencing.