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DNA barcoding applications in aquaculture

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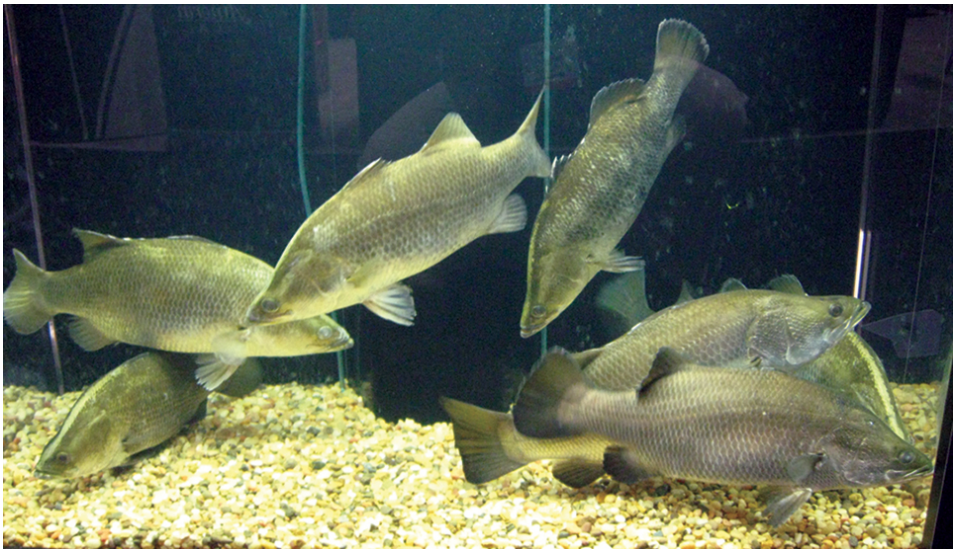
Method provides efficient, standardized species identification



The barcode sequence for barramundi would be CCTATACCTAATCTTCGGAGCATGAGCGGGCATGGTAGGC, as shown in the inset.

DNA barcoding has been adopted as a global biological identification system for animals in recent years. DNA barcoding first came to the attention of the scientific community in 2003, when Paul Hebert's research group at the University of Guelph published a paper titled "Biological Identifications Through DNA Barcodes." So far, scientists from over 30 different countries have participated in this international plan.

The goal of this international effort is to establish an easy and cost-effective way of species identification by reading a standardized region of DNA in a biological sample. In this technique, a short genetic marker in an organism is used to identify the species to which a plant, animal, fish or fungus belongs.

DNA barcoding has the potential to be a practical method for identification of the estimated 10 million species of eukaryotic life on earth. It will be of great utility in conservation biology and biodiversity surveys.

DNA barcoding in fish

DNA barcode sequences are very short relative to the entire genome and can be obtained reasonably quickly and cheaply. The cytochrome c oxidase subunit 1 mitochondrial region is emerging as the standard barcode region for higher animals.

The ability of barcoding to identify samples from whole or part specimens has important implications for fish retailing; fish management such as bycatch monitoring; sustainable fisheries; identification of threatened, endangered and protected species; and fish invasions such as recognition of range changes associated with climate change. The technology can unambiguously identify not only whole fish, but also fish eggs and larvae, fish fragments, fish fillets and processed fish.

It is anticipated that DNA barcoding will generate extensive data on ecology, geographic ranges of fisheries resources, nursery areas and spawning grounds. Barcoding studies could provide more detailed information about aquatic trophic chains, revealing which fish species are preyed upon by other fish species or sea birds. This ecological information could then be incorporated into models as well as provide new data for use in management and conservation.

Potential forensic applications of fish DNA barcoding include the monitoring of fisheries quotas and bycatch inspection of fisheries markets and products, the control of trade in endangered species and improvements in the traceability of fish products. DNA barcoding could also be used to detect fraudulent species substitutions and identify undesirable animal or plant material in processed foodstuffs.

Standardized reference

Once established, a standardized library of digital barcodes will provide an unambiguous reference that can be applied by non-specialists to facilitate identifying species across the globe and through centuries. The library will make possible identification of all species – whether abundant or rare, native or invasive – engendering appreciation of biodiversity locally and globally.

Compiling the library of barcodes will begin with the millions of specimens in museums, herbariums, zoos and gardens, and will strengthen ongoing efforts to preserve Earths' biodiversity. Barcoding links biological identification to advancing frontiers in DNA sequencing, miniaturization in electronics and computerized information storage that will include hand-held barcode devices.

Disadvantages

The DNA barcoding system relies on greater cytochrome c oxidase gene I (COI) sequence divergence (Fig. 1) species than within species. However, plants have a much slower rate of COI evolution than animals. Therefore, a more suitable marker is needed for use in DNA barcoding these groups.

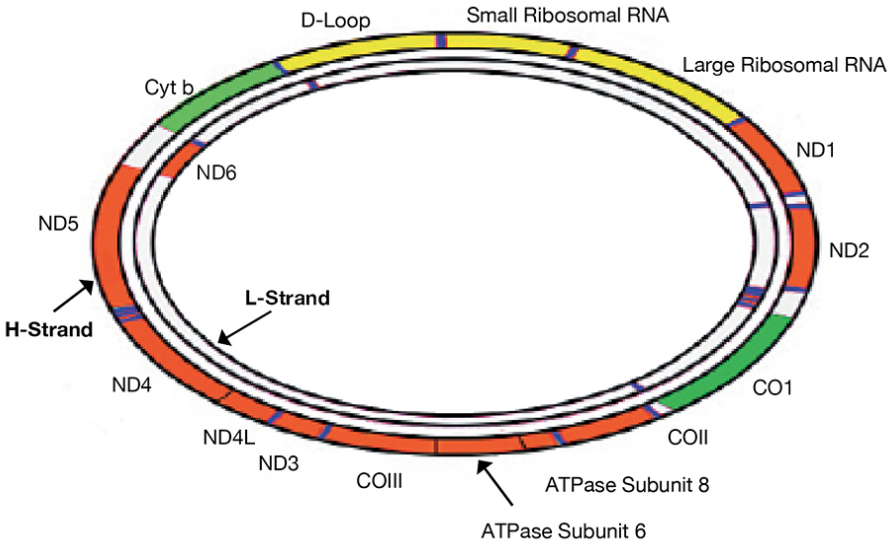


Fig. 1: The mitochondrial genome, COI-animal barcode target.

Chloroplast genes such as rbcl have been proposed as a barcode candidate for plants. No single gene will work for all taxa. The single-gene approach is less precise than using multiple genes and may introduce unacceptable errors.

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