Prospects on the Application of DNA Barcoding on Soil-Transmitted Helminths in Children

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Abstract

Since more than a decade, DNA barcoding has been widely used to examine biological samples and differentiate species, as well as employed in ecological and conservational studies. There is a growing interest of DNA barcoding, particularly in medical parasitology, but its potential utility in soil-transmitted helminths (STHs) remains unclear. Therefore, in this article, we review the studies using DNA barcoding and its applications in medical parasitology with special focus on STHs such as *Ascaris lumbricoides*, *Ancylostoma duodenale*, *Necator americanus*, and *Trichuris trichiura*. DNA barcoding is reliable for identifying STH species as well as its cryptic species. In addition, epidemiological data and the impacts of STH infections on children are discussed. This article further discusses the paucity of STH DNA barcodes (partial cytochrome oxidase subunit 1 [COI] mitochondrial DNA [mtDNA] sequences) in two gene banks; National Center for Biotechnology Information (NCBI) and Barcode of Life Data (BOLD) Systems. It also highlights the future prospects of DNA barcoding including primer designing and reference library on STHs.

Keywords
- children
- cryptic species
- DNA barcoding
- PCR
- soil-transmitted helminths

Introduction

What is DNA Barcoding?

DNA barcoding is a molecular identification tool that relies on "universal" primers using polymerase chain reaction (PCR) that amplifies a short fragment of mitochondrial DNA (mtDNA, 650 bp of cytochrome c oxidase subunit 1, COX1 or COI) for species identification.[1] This technique is widely used in ecological and conservation studies as morphological study is impractical.[2] One of the taxonomic challenges of morphological study is the introduction of cryptic species (two or more morphologically identical species grouped as a single species).[3] Fortunately, DNA barcoding can overcome this impediment. Using DNA barcoding, at least 10 cryptic species of a neotropical skipper butterfly species (*Astraptes fulgerator*) were revealed in northwestern Costa Rica; cryptic species are prevalent in the tropical regions.[4] Furthermore, some genetic markers of certain taxa are not suitable for species identification. For example, 18S ribosomal DNA (rDNA) and 28S rDNA of free-living marine nematodes are usually unable to identify these nematodes up to the species level.[5] Hence, DNA barcoding was used that reliably identified a wide range of free-living marine nematodes up to the species level.[5] DNA barcoding benefits a lot of organizations that are involved with invasive species, control of agricultural pests, and food safety for human health.[6] DNA barcodes are publicly available in the Barcode of Life Data (BOLD) Systems[7] for the general access of biological attributes and names of any species worldwide.[6] Due to DNA degradation, full length of DNA barcodes is hard to obtain.[8] Hence, primers that target a shorter fragment of COI (100–344 bp) have been designed and used on degraded samples, such as museum samples,[8] gut contents,[9] and stool samples.[10] With all the advantages, nevertheless, there are few disadvantages of using DNA barcoding.[11,12,14,17] A few authors[11,12] suggested that nuclear mitochondrial pseudogenes (numts, copies of nonfunctional mtDNA found in the nucleus) are problematic for DNA

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