

Chimeric mitochondrial genomes: a hazard for phylogenetics and environmental DNA identification of fishes

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Abstract

Chimeric mitogenomes are artifacts resulting from laboratory or sequence assembly errors. There have been no quantitative studies of chimeric DNA sequences in animals and their effects on phylogenetics and DNA identification have not been studied. We describe a new, simple strategy for detecting chimeras and apply this to a set of 123 mitogenomes of fishes of the subfamily Schizothoracinae. We detected seven chimeras (5.7%). The proportion of heterospecific nucleotides ranged from 7.5% to at least 99.2%. Six chimeras included heterospecific DNA fragments of at least one marker commonly used for environmental DNA identification of fishes (12S rRNA, 16S rRNA, COI, cytochrome b). Five chimeras were placed in an incorrect phylogenetic position in a mitogenome phylogeny. All seven sequences have been re-used in subsequent phylogenies and some have also been used in DNA identification studies. This study shows that chimeras may be common among published mitogenomes, and affect phylogenetic inference and environmental DNA identification. Our findings further suggest that chimeric mitogenomes may remain undetected even if commonly used DNA identification markers are used to verify their identity. Detecting such ‘cryptic’ chimeras requires additional effort, which currently is not routinely employed.

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