

Systematic and Evolutionary Insights Derived from mtDNA COI Barcode Diversity in the Decapoda (Crustacea: Malacostraca)

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Abstract

Background: Decapods are the most recognizable of all crustaceans and comprise a dominant group of benthic invertebrates of the continental shelf and slope, including many species of economic importance. Of the 17635 morphologically described Decapoda species, only 5.4% are represented by COI barcode region sequences. It therefore remains a challenge to compile regional databases that identify and analyse the extent and patterns of decapod diversity throughout the world.

Methodology/Principal Findings: We contributed 101 decapod species from the North East Atlantic, the Gulf of Cadiz and the Mediterranean Sea, of which 81 species represent novel COI records. Within the newly-generated dataset, 3.6% of the species barcodes conflicted with the assigned morphological taxonomic identification, highlighting both the apparent taxonomic ambiguity among certain groups, and the need for an accelerated and independent taxonomic approach. Using the combined COI barcode projects from the Barcode of Life Database, we provide the most comprehensive COI data set so far examined for the Order (1572 sequences of 528 species, 213 genera, and 67 families). Patterns within families show a general predicted molecular hierarchy, but the scale of divergence at each taxonomic level appears to vary extensively between families. The range values of mean K2P distance observed were: within species 0.285% to 1.375%, within genus 6.376% to 20.924% and within family 11.392% to 25.617%. Nucleotide composition varied greatly across decapods, ranging from 30.8 % to 49.4 % GC content.

Conclusions/Significance: Decapod biological diversity was quantified by identifying putative cryptic species allowing a rapid assessment of taxon diversity in groups that have until now received limited morphological and systematic examination. We highlight taxonomic groups or species with unusual nucleotide composition or evolutionary rates. Such data are relevant to strategies for conservation of existing decapod biodiversity, as well as elucidating the mechanisms and constraints shaping the patterns observed.

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Introduction

In recent decades, the loss of biodiversity has been recognized as a major global environmental problem, with much effort being targeted at biodiversity conservation [1–5]. Yet, a major obstacle in studying the human impact on the biosphere is what has often been referred to as the 'taxonomic impediment': a lack of taxonomic expertise in many groups of living organisms [6] and also the morphological variability associated with such phenotypic plasticity [7,8] or dimorphism [9]. Biodiversity assessments that are based primarily on morphological characters not only are

labour intensive, but risk also under – or over-estimation of biodiversity [10]. To overcome such problems, a short, standardized 650 bp sequence of the cytochrome *c* oxidase subunit 1 (COI) mitochondrial DNA (mtDNA) has been proposed as a barcoding tool, or at least to confirm species delimitation for taxonomic, ecological and evolutionary studies [11–17]. The NCBI GenBank molecular database demonstrates that, amongst others (e.g. 16 S, with >7000 entries), COI is one of the most frequently used genes (>10 000 nucleotides entries) for ecological and evolutionary studies of Decapoda, and augmenting these records will enhance the comparative value of such standardised approaches. Specifi-