

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-

cally, COI as a barcoding tool helps to identify an organism based on DNA sequence variability and assignment to a certain species previously described [10]. Also the DNA barcode sequences can be used as a DNA taxonomy tool to perform prediction and classification of potentially new species. Although the approach remains controversial, [14,18–22], barcoding datasets are rapidly accumulating as part of the worldwide campaign for inventories of global biodiversity [12,23–27]. The impacts of DNA barcoding is extended well beyond biodiversity science. By assembling sequence information for a single gene region from all species, in contrast to the usual focus of large scale genomics projects which acquire sequence information for all genes in single taxa, DNA barcodes can provide a quick preview of recent evolutionary history [28]. For example, data have revealed key features of the mitochondrial genome with implications on the role of selection, as well as highlighting taxonomic groups or species with unusual nucleotide composition or evolutionary rates [28,29]. The growing volume of barcode records has revealed that sequence variability within species is generally much lower than divergence among species, commonly referred to as the “barcoding gap”, a pattern that occurs in diverse lineages, suggesting a pervasive evolutionary process [12,17,23]. The barcode region is a genomic sentinel; shifts in the nucleotide composition of the barcode region in the animal kingdom closely mirror those in the rest of the mitochondrial genome. The classical pairwise distance method such as Neighbour Joining (NJ) based on Kimura 2-parameter distance (K2P) is currently the predominant approach used to analyse patterns of diversity with COI barcode region. It has been informative at the species-level discrimination across a variety of groups from terrestrial, marine and freshwater environments [30–35]. The accuracy of such results depends especially on the delineation between intraspecific variation and interspecific DNA sequence divergence, [36,37]. A threshold barcoding gap was proposed to define species boundaries of around 10 times the mean value for within species variation for the focal group [37–39]. More specifically, the proposed threshold value of 2% COI sequence divergence [12], and 0.16 patristic distances for species delimitation in Crustacea [10] may, however, be problematic in some cases (i.e., heteroplasmy, hybridization, incomplete lineage sorting, nuclear introgression of mtDNA [38–42]) because DNA barcoding follows the typological species approach and species are entities continue to evolve. To cope with such limitations, DNA barcode sequences have been analysed based on other species concepts [38], and referred to as Recognizable Taxonomic Units [43], or Molecular Operational Taxonomic Units [44].

Barcode sequences can be used to flag species whose mitochondrial genomes show unusual nucleotide composition and rates of amino acid change, thereby identifying lineages that merit more investigation. Other approaches of diversity assessment involve the examination of variation of nucleotide GC content across taxonomic groups to detect unusual variation in mitochondrial GC content [28,29,35]. However, the question of the functional significance of this GC variation remains controversial. It is not clear if it has adaptive significance, a by-product of neutral evolutionary processes or if it has actually any significant impact on the phenotype [45].

Decapods are the most recognizable of all crustaceans [46,47], and include the “true” crabs (Brachyura), hermit crabs and their relatives (Anomura), shrimps (Dendrobranchiata, Caridea and Stenopodidea), and lobsters (Astacidae, Thalassinidea), among other lesser known groups [47]. Establishing a robust DNA barcoding framework for decapods is particularly relevant because the order contains over 17,000 species [46], some of which support seafood and marine industries worth billions of dollars each year to

the global economy. Estimates by the Food and Agriculture Organization of the United Nations (FAO), indicated that landings of crustaceans represented about 7% of the total marine fish production in 2007, of which 83% were marine decapods.

Conservation and management of decapods have long been entirely focused on crustacean fisheries [48,49], but they also form a dominant functional group of megabenthic invertebrates on the Atlantic continental shelf and slope [50–54], encompassing a wide range of trophic levels [55] and a variety of feeding habits [56]. In view of their collective ecological importance and potential community interactions, the unambiguous delimitation of species becomes even more urgent.

Of the 17635 morphologically described freshwater and marine extant species [46], only 5.4% are represented by COI barcode region sequences. There is no global campaign yet to barcode crustaceans or decapods, as exists for other animal groups (e.g., fish, birds and lepidopterans). It therefore remains a challenge to compile regional databases that enable analysis of the extent and patterns of decapod diversity throughout the world. Here, using the most comprehensive COI data set for decapods so far examined, we analyse patterns of COI variability partitioning within and among species, genera and families. The combined dataset includes GenBank published sequences, COI barcode projects from the Barcode of Life Database (BOLD), [57] and new data generated herein (Table 1). Collectively, the combined dataset provide barcoding coverage for 1572 sequences of 528 species, 213 genera, and 67 families. Our molecular systematic assessment affords an opportunity to examine the utility of COI DNA barcodes for species recognition in a taxonomically complex and ecologically important group of organisms. We encompass in our study specimens with a range of different shapes (shrimp, lobsters, crayfish and crabs) and sizes (e.g., small crab (Porcellanidae: *Petrolisthes* spp) and big crab (Majidae: *Hyas* spp). Comprehensive biogeographic representation of species was achieved by including species from continental freshwater (e.g., Atyidae and Parastacidae family), brackish (e.g., Palaemonidae and Panopeidae) and marine realms with a high range of latitudinal distribution. On the basis of their latitudinal distribution, decapods from temperate or cold (e.g., Lithodidae: *Lithodes* spp) to tropical waters (e.g., Xiphocarididae: *Xiphocaris* spp) across a range of depth distribution (e.g., Galatheidae) were compared. Species with diverse ecological habits, including such sex reversal (e.g., Palaemonidae), association of shrimps (e.g., Palaemonidae) and crabs (e.g., Pagurus) with other animals and dispersal behaviour (e.g., Pandalidae and Portunidae) were also represented in our analysis. Despite the relatively small proportion of decapods that are considered here, the samples analysed collectively encompass the breadth of morphological and ecological diversity of the order.

Results

Data acquisition: new sequencing

Here we created new COI sequences of 497 specimens from a total of 101 species, 72 genera and 46 families (Table S1), of which 81 species, 48 genera and 13 families are exclusive of our generated data. The number of sequences per species varied between 1–32, with a mean of 5, and an average length of 620 base pairs (bp). Within this newly-generated dataset, 3.6% of the species barcodes conflicted with the assigned morphological taxonomic identification. Such cases were distributed throughout the Decapoda, including the long legged crabs *Macropodia longipes* (A. Milne Edwards & Bouvier, 1899) and *M. tenuirostris* (Leach, 1814) (Brachyura:Majidae) and the marbled rock crabs *Pachy-*

Table 1. Combined data set derived from new data generated herein and publicly available DNA barcoding projects from the Barcode of Life Database.

| Projects | Code | No. of sequences | Species | Citation |
|--|------------------------------------|------------------|---------|------------|
| BOLD public projects title | | | | |
| Genbank Crustacea Malac - Decapoda | GBCMD | 894 | 349 | GenBank |
| Genbank Crustacea Malac - Decapoda - Atyidae | GBCDA | 85 | 23 | GenBank |
| Genbank Crustacea Malac - Decapoda - Palaemonidae | GBCDP | 89 | 39 | GenBank |
| Genbank Crustacea Malac - Decapoda - Parastacidae | GBCPA | 161 | 59 | GenBank |
| Crustaceans of the St. Lawrence Gulf | WWGSL | 130 | 30 | [132] |
| Decapods of Pacific and Atlantic | FCDPA | 118 | 57 | [35] |
| Campaign Marine Life (MarBOL) | | | | |
| Decapods of Norway, Svalbard, U.K (Scotland), U.K (Wales and England), Mediterranean Sea | JSDN; JSDSV; JSDSC; JSDDUK; JSDDME | 159 | 52 | This study |
| Campaign Portugal – Aquatic Life | | | | |
| Decapods of Portugal (Hermes, Ipimar, IpimarX, Azores) | FCDPH; FCDOP; JSDDPX; JSDDAZ | 270 | 82 | This study |

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grapsus maurus (Lucas, 1846) and *P. marmoratus* (Fabricius, 1787) (Brachyura: Grapsidae) are represented by two “mixed” clades in a NJ tree (Figure S1).

Data validation

From a theoretical point of view, two main factors may bias our intraspecific assessment of COI divergence: disequilibrium in the representation of some taxa or incorrect taxonomic classification (i.e., cryptic (morphological indistinguishable, but genetically distinct), or non-monophyletic species). The analysis of the combined GenBank and our novel data (Table S2) indicated the existence of sample bias ($p < 0.05$) as shown in Figure 1 (case A_R , for the entire symbols definition see Methods section). However when putative cryptic (16 species), non-monophyletic (47 species) and con-generic species with unusually low genetic distance (13 species under 2% K2P) were removed from the dataset (case B_R) (Table S3), the sample bias was lost ($p > 0.05$). Assuming an intraspecific barcode threshold of maximum 2% (K2P), the success of achieving congruent species assignments (Additional File 5) was 97.3% and 98% when mean intraspecific divergences values were compared (in case B_R vs B_M , Figure 1).

In order to reduce the impact of artefacts in our divergence assessment, statistical tests were performed among: raw data A_R vs B_R , mean data A_M vs B_M and between different data A_R vs A_M and B_R vs B_M proposed by Lefebvre *et al.*, [10]. The first three comparisons revealed sampling bias due to incorrect taxonomic classification and non-monophyletic taxa ($p > 0.05$) and B_R vs B_M showed no sample bias ($p < 0.05$) indicating a balanced design.

COI divergence assessment

COI barcode nucleotide divergences were calculated for the validated dataset from 1572 sequences of 528 species, 213 genera, and 67 families (B_R) (Table S4) to reduce the impact of artefacts in our divergence assessment. Sample sizes and mean divergences at various taxonomic levels are given in Table 2. As expected, genetic divergence increased with higher taxonomic rank: 0% to 4.6% within species, 2.5% to 32.7% within genera, and 6.6% to 48.3% within families. Although these ranges overlap, intraspecific (S), intragenus (G) and intrafamily (F) distances (Figures 2 and 3), were significantly different ($p < 0.001$). Patterns within families (Table 3 and Figure 3) 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%. The Galatheidae showed the lowest divergence within species (0.285%), and Lithodidae showed the lowest divergence within genus (6.376%) and within family (11.392%) distances: the highest values were observed within the Pandalidae (within genus: 20.924%) and Parastacidae (within species: 1.375% and within family: 25.617%). The Crangonidae showed the highest range of divergences within a family, the Pandalidae within genus and Parastacidae within species (Figure 3). No sample bias was detected in the within family analysis ($p > 0.05$). The Parastacidae was the only family exhibiting sample bias ($p < 0.05$), arising from the unbalanced distribution of data with 53% of the sequences being derived from the *Euastacus*, and 21% from the *Cherax* genera.

The majority (97%) of mean distance values within species were less than 2%, though the scale of divergence appears to vary extensively between species: all 10 specimens of *Goneplax rhomboides* (Linnaeus, 1758) (Brachyura: Goneplacidae) share the same haplotype, and *Cherax preissii* (Erichson, 1846) (Astacidea: Parastacidae) exhibited the highest mean intraspecific value of 2.61 ± 0.193 K2P distance.

GC content divergence assessment

Our second line of inquiry involved assessing the GC content in diverse lineages as a measure of nucleotide diversity. The frequency of the occurrence of GC-content can be a useful metric for understanding species diversity and evolutionary processes [58]. Nucleotide composition varied greatly, ranging from 30.8% to 49.4% of GC content (Table 4). In all cases, GC content decreased from the first to the third codon position with mean values of 50.90%, 42.92% to 21.73% respectively. The pattern of variance (standard error) confirmed that the highest range in GC content was observed in the third codon position: the second position displayed the least variation (Table 4). The proportion of nucleotides throughout 1572 sequences in case B_R was T = 34.7%, C = 20.1%, A = 26.9%, and G = 18.3%, respectively. Nucleotide bias did not occur at the first codon position (1st), though at the second codon position (2nd), there was marked bias in T and C, and favouring A against C at the third codon position (3rd). The

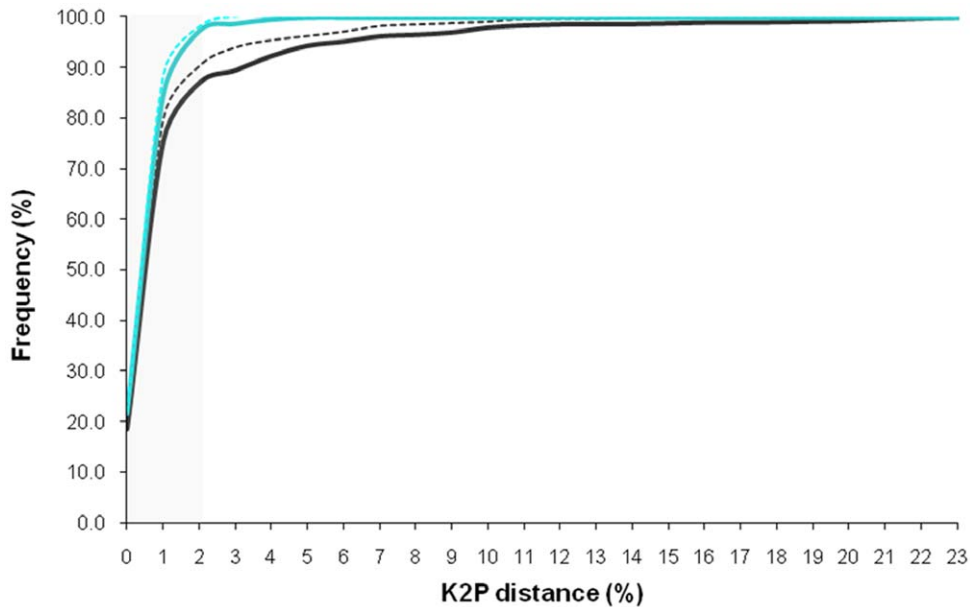


Figure 1. Intraspecific diversity assessment: the effect of sampling bias, non-monophyletic clades, putative cryptic species and congeneric species with low genetic distance. Solid lines represent the raw data for the total data set (A_R , black lines) and for the dataset in which non-monophyletic clades, putative cryptic species and congeneric species with low genetic distance were removed (B_R , blue lines). The dashed lines represent results for the data in which all taxa have the same weight (mean values of genetic distance), for the total (black, A_M) and trimmed (blue, B_M) datasets respectively.

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average frequency (R) of transitional (A/C and C/T) and transversal (A/T; A/C; C/G; G/T) rates are: COI barcode region R = 1.02; for 1st codon R = 2.7, for 2nd codon R = 1 and for 3rd codon position R = 0.8.

Our observations reveal considerable variation in the range of GC values within and among decapod families (Figure 4). Such variation leads to a zone of overlap covering even the most GC rich values in Pandalidae (49.4 % GC), and the lowest values in Chirostylidae (35.6% GC). The highest GC% content was observed in the Atyidae with a mean value of 42.40 ± 0.3465 , and the lowest in Chirostylidae of 33.05 ± 0.1392 (Figure 4), mostly reflecting a marked difference at the third codon base with 30.83 ± 0.9582 and 6.811 ± 0.3289 . All 11 families examined were significantly different ($p < 0.05$), but with considerable overlap (Figure 4). No sample bias effect was observed ($p > 0.05$), except for the Palaemonidae ($p < 0.05$), which also exhibited the highest standard error variation (SE) value.

Discussion

The COI gene appears to be an informative molecular marker at several taxonomic scales, but particularly at the species level. Our analysis shows a general increase in the molecular divergence of COI with taxonomic rank, a trend that suggests that morphological taxonomy is roughly in agreement with DNA evolution. Yet, this relationship is not entirely consistent, and the distribution of divergences at different taxonomic scales sometimes overlaps. The COI gene tree was used in this study to present our results and to allow comparison with previously defined species groups within decapods. However other genes and phylogenetic methods are required to evaluate the evolution information contained in the barcode region of COI [59]. It is worthwhile emphasizing that it was not within the scope here to generate new insights into decapods species evolutionary relationships, but rather to analyse patterns of COI variability among decapods.

Table 2. Pairwise COI barcode nucleotide divergences for the Decapoda using K2P distances (%).

| Decapoda ^a | No. of comparisons | Min Dist | Mean Dist ^b | Max Dist |
|--|--------------------|----------|------------------------|----------|
| (1572 seq ,528 sp, 213 gen, 67 fam) | | | | |
| Intraspecies | 3577 | 0 | 0.541 ± 0.01 | 4.605 |
| Intragenus | 18077 | 2.509 | 15.49 ± 0.04 | 32.75 |
| Intrafamily | 35422 | 6.694 | 22.325 ± 0.023 | 48.348 |
| Intraorder | 1176159 | 8.509 | 26.07 ± 0.003 | 54.994 |

^aNumber of sequences, species (sp), genera (gen) and families (fam) are shown in parentheses.

^bData reported as K2P distances (%) \pm SE.

doi:10.1371/journal.pone.0019449.t002

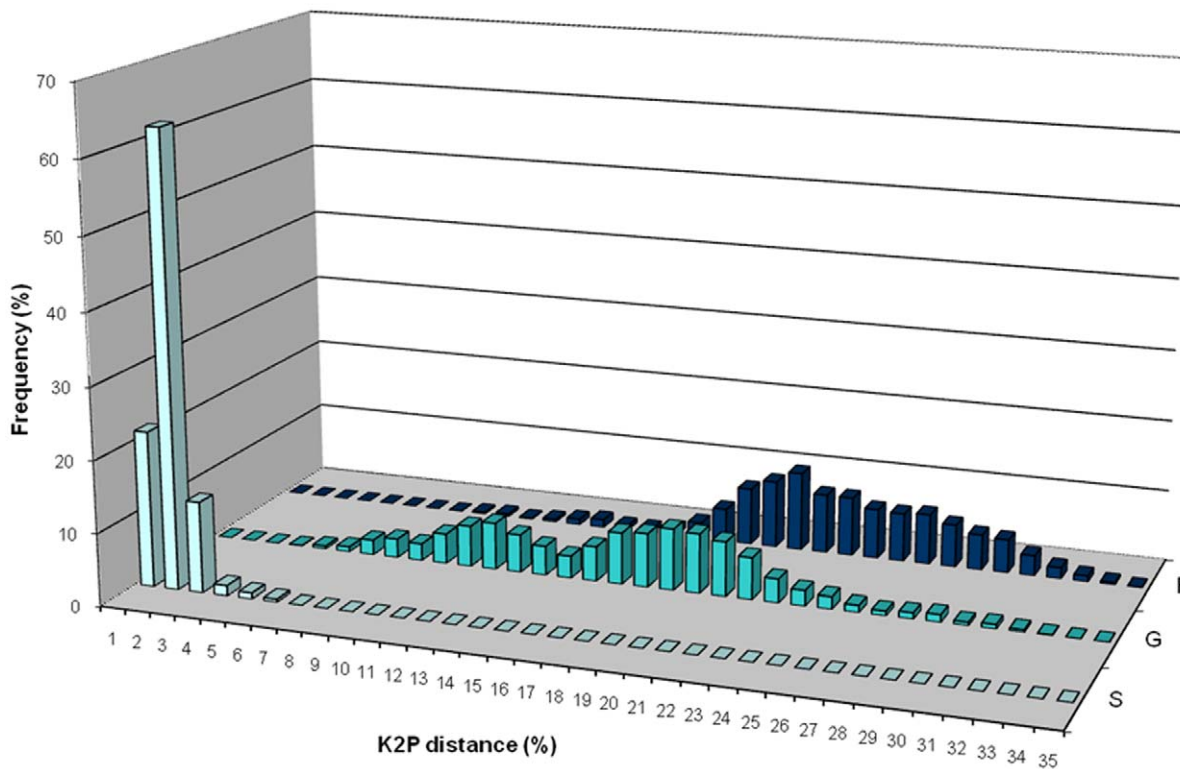


Figure 2. Frequency distribution of COI K2P distances (%) intraspecific (S), intrageneric (G), and intrafamilial (F) from 302 species, 154 genera, and 58 families.

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New data acquisition

Our data further supports the validity of DNA barcoding for species identification in marine decapods. The ratio of within species to between species variation (21X) was much higher than the threshold (10X) proposed by Hebert *et al.*, [37] as a potential species' boundary. Therefore, assigning specimens to species was usually straightforward with no overlap between within species – and between species distance (95% of the cases).

COI divergence assessment

It has been discussed whether COI barcoding sequence variation will defer yield new insights into the evolutionary relationships among different taxonomic metazoan groups, once complete barcode data are available. Whereas each family apparently coincides with the expected molecular hierarchy, the scale of divergence at each taxonomic level appears to vary extensively between and within families.

The highest values of F (Figure 3) belong to families of infraorder Caridea (Atyidae, Pandalidae, Palaemonidae, Crangonidae), representative of the currently recognized natant lineages of the suborder Pleocyemata [60]. Such high values of genetic distance reflect possibly the remarkable range of adaptation and biological diversity within the infraorder Caridea [46,61–63]. Many caridean families inhabit both shallow and deep water marine environments [62], hydrothermal vents [64], freshwater lakes and mountain streams [63], caves [65], and commonly establish temporary or lifelong associations with other taxa [66–68]. The phylogeny of the infraorder Caridea based on mitochondrial and nuclear genes has suggested that the Caridea is monophyletic [61], underpinned by a possible radiation in the

Triassic period [60]. Apparent polyphyletic and paraphyletic compositions of some Caridean families have, however, been reported by morphological and molecular studies [61]. Also multi-locus genes, including both mitochondrial and nuclear genomes and additional taxa, will need to be analysed to provide informative characters to resolve the phylogeny among Caridean groups.

The economically important Lithodidae and Pandalidae exhibit markedly contrasting patterns of intrafamilial divergence (Figure 3). The typically cold-water Lithodidae king crab comprises weakly divergent species, suggesting either that the family represents an extreme situation of rapid morphological diversification, and/or slow molecular evolution, reflecting a slow metabolism found in organisms that inhabit cold environments [69,70], or possessing larger body sizes [71,72] or both [73–75]. Moreover, distribution, and therefore opportunities for population differentiation, in these groups remains constrained by the stressful effects of temperature extremes on early life-history stages [76]. However, the phylogeny of the family Lithodidae is controversial [77,78], and molecular and adult and larval morphological data remain equivocal [79,80].

The Oregoniidae also exhibits very low mean divergences within taxa (S = 0.66%; G = 5.56%; F = 12.96%), here represented by five deep water species from two genera. Nucleotide substitution rate is the ultimate source of genetic variation and it is the substrate for molecular evolution. The metabolic rate hypothesis [81,82] has been proposed to explain mtDNA substitution rate variations in animals. Correlation between metabolic rate and nucleotide substitution may be mediated by (i) the mutagenic effects of oxygen radicals that are abundant by-products of aerobic respiration, and (ii) increased rates of DNA

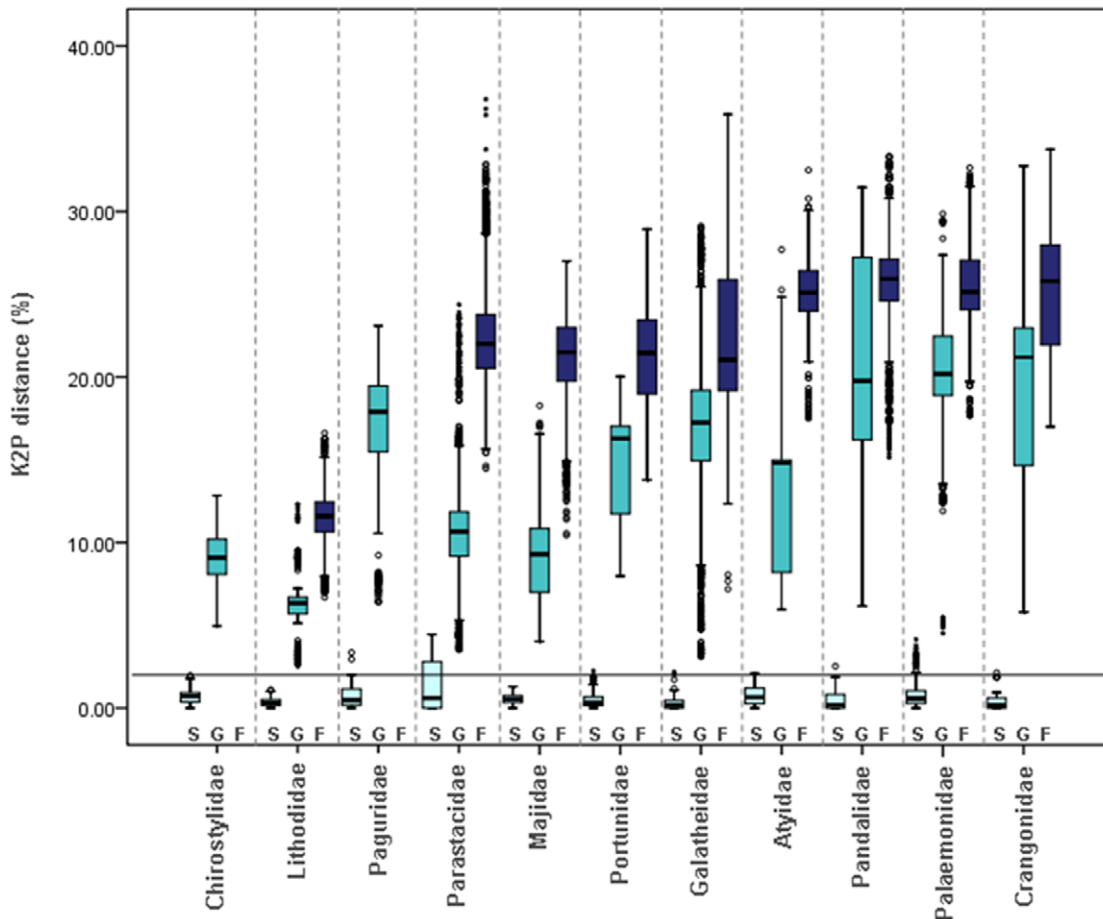


Figure 3. Boxplot distribution of 11 selected families of the Decapoda order intraspecies (S), intragenus (G), and intrafamily (F) COI K2P distances (%). The plot summarises median (central bar), position of the upper and lower quartiles (called Q1 and Q3, central box), extremes of the data (dots) and very extreme points of the distribution that can be considered as outliers (stars). Points are considered as outliers when they exceed $Q3+1.5(Q3-Q1)$ for the lower part, where $(Q3-Q1)$ is the inter quartile range. The number of sequences, species, and genera per family are given in Table 3. Mean K2P distance (%) \pm SE within taxa are: Chirostylidae S=0.701 \pm 0.028 and G=8.999 \pm 0.039; Lithodidae S=0.416 \pm 0.021, G=6.376 \pm 0.137 and F=11.392 \pm 0.063; Paguridae S=0.686 \pm 0.045 and G=17.173 \pm 0.084; Parastacidae S=1.375 \pm 0.131, G=11.017 \pm 0.078 and F=22.681 \pm 0.064; Majidae S=0.547 \pm 0.028, G=9.643 \pm 0.214 and F=21.084 \pm 0.061; Portunidae S=0.453 \pm 0.024, G=14.826 \pm 0.311 and F=28.929 \pm 0.047; Galatheidae S=0.285 \pm 0.017, G=16.839 \pm 0.04 and F=22.355 \pm 0.033; Atyidae S=0.758 \pm 0.041, G=13.475 \pm 0.352 and F=25.218 \pm 0.056; Pandalidae S=0.49 \pm 0.042, G=20.924 \pm 0.213 and F=25.617 \pm 0.07; Palaemonidae S=0.812 \pm 0.055, G=20.157 \pm 0.108 and F=25.398 \pm 0.048; Crangonidae S=0.344, G=19.991 \pm 0.514 and F=25.241 \pm 0.103. doi:10.1371/journal.pone.0019449.g003

synthesis and nucleotide replacement in organisms with higher metabolic rates [82]. The general hypothesis assumes that deep-sea animals exhibit hypo-metabolism [83–85], which is characterised by abnormally low level metabolic rates. The theory holds that limited light with depth reduces visual predation pressure and selects for reduced locomotory ability and metabolic capacity [86]. Although this theory applies predominantly to pelagic animals, deep-sea benthic animals (including crustaceans) exhibit metabolic rates also typically an order of magnitude lower than their shallow-water counterparts [70,86]. While this phenomenon in deep-sea benthic crustaceans may simply be a function of very low temperatures at depth in areas of steep thermal gradients [86], reduced metabolic rates observed in deep-sea benthic crustaceans may still be ecologically relevant to their rate of molecular evolution.

The Pandalidae is one of the most species-rich families due to extensive diversification in the genus *Plesionika*. Our data set showed the highest nucleotide divergences within the genus, represented by the genera *Plesionika*, *Pandalus*, *Pandalopsis* and the

Table 3. Number of Decapoda sequences, species, genera and families analyzed in the present study.

| Family | Species | Genus | Sequences |
|---------------|---------|-------|-----------|
| Atyidae | 16 | 9 | 59 |
| Chirostylidae | 13 | 1 | 66 |
| Crangonidae | 16 | 7 | 58 |
| Galatheidae | 84 | 10 | 220 |
| Lithodidae | 12 | 6 | 52 |
| Majidae | 24 | 14 | 67 |
| Paguridae | 11 | 1 | 57 |
| Palaemonidae | 32 | 5 | 87 |
| Pandalidae | 19 | 5 | 74 |
| Parastacidae | 43 | 8 | 98 |
| Portunidae | 22 | 10 | 90 |

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Table 4. Variation of GC content in the COI barcode region and codon position among the Decapoda and from 11 selected families.

| Taxon | Min. | Mean | Max. | Codon position | | |
|-------------------------------------|-------|-------------|-------|----------------|-------------|-------------|
| | | | | 1st | 2nd | 3rd |
| Order | | | | | | |
| Decapoda | 30.8 | 39.39±0.085 | 49.4 | 50.90±0.062 | 42.92±0.021 | 21.73±0.213 |
| (1572 seq, 528 sp, 213 gen, 67 fam) | | | | | | |
| Families | | | | | | |
| Atyidae | 35.30 | 42.40±0.346 | 47.00 | 52.76±0.170 | 43.51±0.099 | 30.83±0.958 |
| (59 seq, 16 sp, 9 gen) | | | | | | |
| Chirostylidae | 31.50 | 33.05±0.139 | 35.60 | 49.54±0.129 | 42.78±0.508 | 6.81±0.328 |
| (66 seq, 13 sp, 1 gen) | | | | | | |
| Crangonidae | 34.60 | 39.33±0.361 | 47.60 | 50.46±0.227 | 43.17±0.083 | 24.36±0.904 |
| (58 seq, 16 sp, 7gen) | | | | | | |
| Galatheididae | 33.20 | 37.24±0.169 | 45.50 | 50.56±0.148 | 43.03±0.037 | 18.11±0.493 |
| (220 seq, 84 sp, 10 gen) | | | | | | |
| Lithodidae | 34.40 | 36.31±0.226 | 40.40 | 48.82±0.107 | 43.76±0.097 | 16.36±0.621 |
| (52 seq, 12 sp, 6 gen) | | | | | | |
| Majidae | 30.80 | 35.37±0.253 | 38.70 | 48.29±0.244 | 42.22±0.066 | 15.61±0.574 |
| (67 seq, 24 sp, 14 gen) | | | | | | |
| Paguridae | 32.40 | 36.34±0.197 | 41.00 | 49.80±0.262 | 43.07±0.051 | 16.14±0.608 |
| (57 seq, 24 sp, 14 gen) | | | | | | |
| Palaemonidae | 36.40 | 41.01±0.404 | 48.60 | 52.70±0.311 | 43.83±0.094 | 26.51±0.884 |
| (87 seq, 32 sp, 5 gen) | | | | | | |
| Pandalidae | 35.20 | 41.93±0.274 | 49.40 | 51.39±0.163 | 43.32±0.066 | 31.06±0.740 |
| (74 seq, 19 sp, 5 gen) | | | | | | |
| Parastacidae | 37.30 | 40.39±0.186 | 48.60 | 51.25±0.110 | 43.34±0.063 | 26.53±0.550 |
| (98 seq, 43 sp, 8 gen) | | | | | | |
| Portunidae | 31.90 | 38.31±0.334 | 44.20 | 50.44±0.243 | 41.87±0.056 | 22.60±0.866 |
| (90 seq, 22 sp, 10 gen) | | | | | | |

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monospecific *Dichelopandalus* and *Stylopandalus*. The genus *Pandalus* (Leach, 1814) is retained as a possible paraphyletic group [87], and the phylogeny of *Pandalopsis* remains to be described. The phylogenetic relationship between members of the genus *Plesionika* is still to be established and in spite of recent taxonomic revisions [88–90], our data endorse the need for additional effort.

Taxonomic classification

One of the factors that may bias our divergence assessment is the possibility of incorrect or uncertain taxonomic classification. The COI barcodes grouped together the two spider crab specimens (0% distance) *Macropodia longipes* and *M. tenuirostris* (Leach, 1814). Such genetic similarity, if generally supported, emphasizes the idea that these two species should be considered as one based on similar morphological characteristics of adults and larval stages [91–95]. Combined data presented herein suggests that *M. longipes* is in fact a synonym of *M. tenuirostris*.

Low divergence levels were observed (0.065%) also between *Pachygrapsus maurus* and *P. marmoratus*. *Pachygrapsus marmoratus* can be distinguished from related species *P. maurus* by the presence of two lateral post-orbital teeth, whereas *P. maurus* possesses one [96]. *Pachygrapsus marmoratus* and *P. maurus* are considered sister species and are genetically clearly distinct to other species of the genus

[97]. Ecologically, these two species share the some rocky intertidal area and were collected from Flores Island in the Azores Archipelago. Our data might indicate hybridization or a misidentification. In our study *P. maurus* was represented by two juvenile specimens, and in spite of the evident differences in adult morphology [98] the diagnostic features can be hard to distinguish in juvenile specimens. Further molecular (e.g. AFLP or microsatellites [99]) and morphological analyses should be combined to identify species and between species hybrids within the *Pachygrapsus* species.

Cryptic and young species

For decapods, COI resolves relationships among the more closely related species within genus, and can be used to address the question of whether species groups based on morphological, ecological and biogeographical characters represent evolutionary lineages. The described levels of intraspecific variation must be considered preliminary, since several species were characterized based on only up to ten specimens – sufficient for a valid barcode, but not sufficient to accurately capture genetic diversity of the species. However pairwise sequence differences derived from 10 specimens per species reflected differences in the range of diversity. DNA sequences for additional specimens collected across the

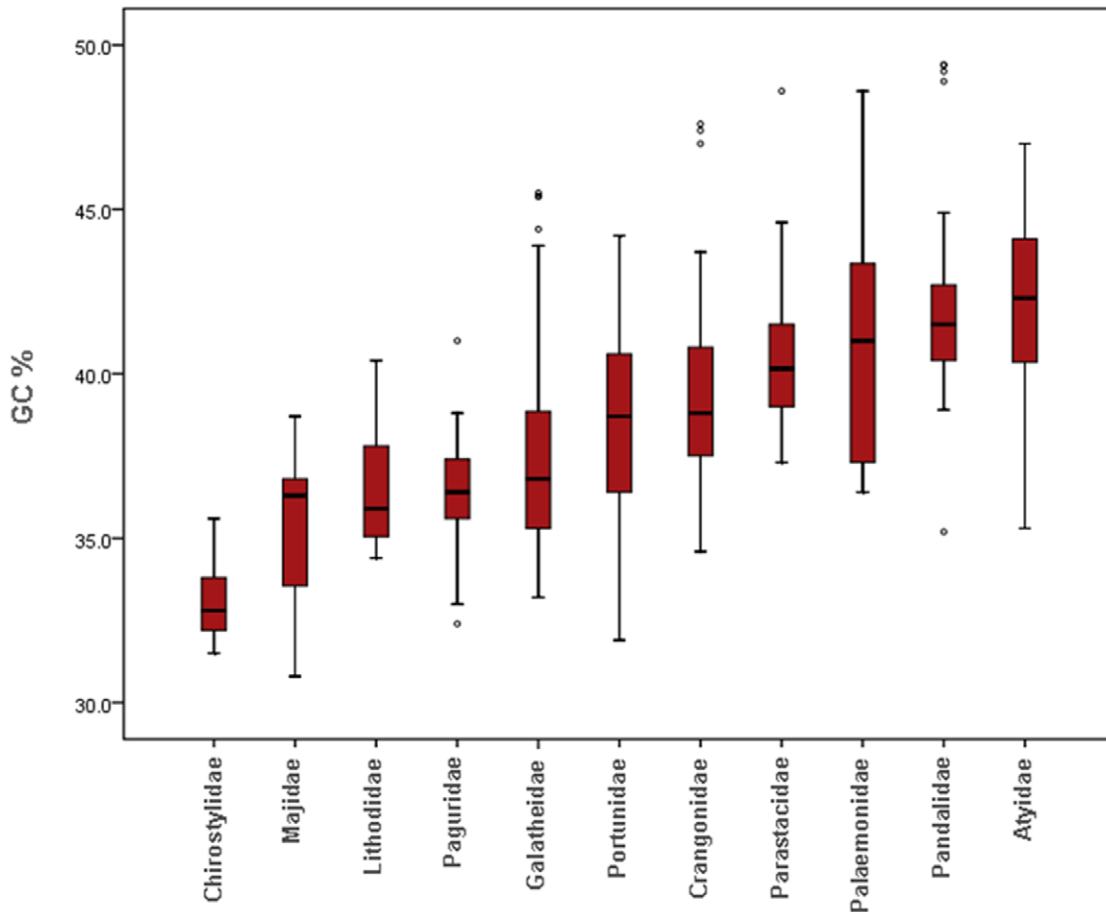


Figure 4. Boxplot distribution of ascending GC content (%) from 11 selected families. The number of sequences, species, and genera per family is indicated in Table 3 and statistic values in Table 4. doi:10.1371/journal.pone.0019449.g004

geographic ranges of additional species are needed to test and validate this result. In some cases, higher levels of intraspecific variation may reflect underlying population structure. For example, the freshwater crayfish *Cherax preissii* (Erichson, 1846) (Astacidea: Parastacidae) showed highest divergence values with a maximum of 4.45% genetic distance (0.5 patristic distance) between two main populations from the North and South of Australia. A recent systematic study of the genus *Cherax* suggested that the taxonomy of *C. preissii* should be re-examined [88], even if the diversity between Australian populations reveals evidence of contemporary, but not ongoing, gene flow during pluvial Pleistocene periods [89]. However, extensive cryptic species have been documented in freshwater crayfish taxa, concurring with the increased discovery of diversification in freshwater taxa [66,100–104]. Another example is the species *Macrobrachium nipponense* (De Haan, 1849) (Caridea: Palaemonidae) with a maximum distance of 4.15% (0.4 patristic distance). The genus *Macrobrachium* has more than 100 species described, distributed exclusively in freshwater and brackish habitats (except *M. intermedium* (Stimpson, 1860)) [105,106]. The species of this genus exhibits significant intra-population and intra-individual variation in egg size [107] and larval characters [108]. *Macrobrachium nipponense* exhibits high tolerance of variation in water parameters, having the ability to change in three generations to full freshwater [109], and together with its popularity in the aquarium trade, renders it an effective invasive species [110,111]. Taxonomic complexity is associated

with morphological plasticity of taxonomically important (e.g., the rostrum and/or the second periopod) changes in relation to growth [112] and environmental variation [113]. The morphological characters are extremely conservative and molecular systematic data from the genus *Macrobrachium* suggests that the uses of traditional morphological characters and molecular data are essential to diagnose accurately natural species groups [100].

It seems likely that cryptic species will be discovered among geographically widespread decapods species. Here, two shrimp species *Palaemon elegans* (Rathke, 1837) and *Pasiphaea tarda* (Kreyer, 1845) from the Northeast Atlantic Ocean showed non-monophyletic patterns when compared with their con-specifics from other oceanographic regions. For the first example, *P. elegans*, the mean distance within species was 5.296% (0.530 patristic distances). Previously, three morphological types for the cosmopolitan species *P. elegans*, have been suggested (see for review [93]), supported by high allozymic divergence within the Mediterranean Sea [114]. This species is adapted to extremely variable salinities, temperatures and oxygen [115,116]. A surprisingly complex population structure within *P. elegans* has been recently discovered comprising three haplogroups [117][142] from: Atlantic and Alboran Sea, Mediterranean Sea and the Black Sea, Caspian and Baltic Sea. The Baltic Sea population revealed high levels of nucleotide divergence suggesting the existence of a cryptic species that originated in the late Miocene period when ancestral Baltic populations of *P. elegans* were isolated from Atlantic popula-

tions [117][142]. It is likely, however, that the occurrence of this species in the Baltic Sea represents an introduced invasive species rather than an effect of natural expansion [117,118]. Based on such a scenario, it is possible that specimens from the Baltic Sea from Costa *et al.* [35] represent a cryptic species, or that hybridization is taking place between *P. elegans* and *P. intermedius* [117]. Interestingly we had only found difference in one amino acid positions between Northeast Atlantic Ocean and Baltic populations. Although this difference cannot be considered as indicating species separation, it does suggest the need for a re-examination of specimens [119].

Most marine species the preponderance of pelagic larval stages and the absence of obvious distribution barriers suggests a high level of gene flow with populations predicted to be genetically homogeneous [120]. However high levels of genetic differentiation between populations over small spatial scales were described [121,122] suggesting that marine ecosystems may not be as interconnected as they seem [123,124]. *Pasiphae tarda* revealed a maximum intraspecific distance of 4.913 % (0.509 patristic distance). In relation to the data presented here for the cosmopolitan species *P. tarda*, it is possible that limited larval dispersal/gene flow is associated with deep genetic breaks between populations between the North Pacific Ocean and the North Atlantic. Several comparative phylogeography studies in marine taxa, including corals, decapods and bryozoans, have suggested various ages of the genetic discontinuities, ranging from the Miocene to the Pliocene during episodic marine regressions [125–129]. These authors showed concordance of genetic structure across multiple taxa combined with temporal discordance suggesting that regional genetic structures have arisen from common physical processes operating over extended time periods. The presence of intraspecific genetic structure, as well as deeply divergent lineages, strongly suggests that such overarching processes promote lineage diversification [125–129].

The presence of intraspecific genetic structure is furthermore supported by high amino acid diversity within species showing variation in four amino acid positions between Pacific and Atlantic populations.

Whether *C. preissii*, *M. nipponense*, *P. elegans* and *P. tarda* exhibit taxonomically significant geographic variation and/ or comprise cryptic species should be reviewed with additional morphological, as well as population genetic and molecular systematic studies with multi-locus genes. Based on the taxonomic incongruence identified here, such approaches can explore further the levels of cryptic speciation and reproductive isolation across putative species [130].

The utility of COI as a tool for rapid identification depends on the genetic variation among species exceeds intraspecific variation to such an extent that a clear “barcoding gap” exists. However, the gap might be absent in younger species (incomplete lineage sorting) and species with hybrid zones because of the insufficient variation to be determined as distinctly different using only barcodes [36,131]. Our data further support the incomplete lineage sorting of the genus *Hyas* reported between *H. araneus* (Linnaeus, 1758) and *H. coarctatus* (Leach, 1815), [132]. These species are morphologically distinct from larval stages to adulthood [133], indicating that misidentification is highly unlikely, and incomplete lineage sorting is more plausible. We found low levels of divergence (0.778%) between one specimen of *Hyas lyratius* (Dana, 1851) from Costa *et al.*, [35] and *H. coarctatus* supporting the recent evolution of the genus. However additional analyses among nuclear rDNA genes will be necessary to confirm the hypothesis of recent evolution and identification or delineation at to species of the genus *Hyas*.

Nuclear mitochondrial pseudogenes (numts)

COI has been the preference for species identification/delineation due the traditionally accepted advantages of mtDNA. However, it is also well recognised that analysis of mtDNA sequence variation can be distorted by the inclusion of nuclear mitochondrial pseudogenes (numts). Because the DNA barcoding initiative attempts to barcode all life forms, the potential impact of numts issue cannot be ignored [134–136]. Numts are non-functional copies of mtDNA in the nucleus that have been found in major clades of eukaryotic organisms, e.g., arthropods [134,137], crustaceans [136] and decapods [135,138,139]. Their proportion varies greatly depending on the organism, life style, and on the genome properties (i.e., rates duplication, mutation, deletion, and retrotransposition, see [140,141] for review). Numt sequence can be highly divergent from the orthologous COI sequences. Additionally, high genetic divergences are used to indicate possible new species that may be nested within species complexes. Buhay [136] reported a list of potential cases of numts in Crustacea when she found reading frame problems without the occurrence of stop codons. Even though the proportion of adenine – thymine (numts have a significantly lower AT% compared with the orthologous mtDNA [134]) did not differ between specimens, there is increasing concern about the potential overestimation of species richness [134] by inclusion of numts. Here, we have discussed the occurrence of high nucleotide divergences within species, e.g., *Cherax preissii* [104]. As an example here, we cannot ignore the possibility of dealing with numts sequences even if our quality controls failed to detect them (see Methods). Also other studies showed that mitochondrial cytochrome *b* gene fragments in the freshwater crayfish, *Cherax destructor* (Clark 1936) had numts [139]. They reported of four closely related crayfish species (*Orconectes* spp.) the presence of numts of the COI gene and how barcoding methods would incorrectly infer single individuals belonging to multiple, unique species [134]. Moreover, we found high amino acid diversity among *C. preissii* species showing difference from three amino acid positions. More than two amino acid intraspecific changes could represent a radical change [142] at highly conserved COI gene and as they are likely caused by sequencing error [119]. Especially when numts were already reported for this genus or even for members of the family Parastacidae, it is worthwhile for the scientific community to analyse additional morphological characters and molecular markers other than mitochondrial genes. Characterization of numts is important to understand genome dynamics and evolution, and their significant increases when several genomes of related organisms can be compared. It is thereby important to ensure that numts sequences are not discarded, but recognized, labelled, and submitted as such [136,138].

GC content divergence assessment

For decapods, substantially more nucleotide changes were observed at the 3rd codon position than the 1st, and more at the 1st than the 2nd: the SE of the GC % of the 3rd, 1st and 2nd bases of Decapoda were 0.213, 0.062 and 0.021, respectively (Table 4). Such values indicate the fact that most synonymous mutations occur at the 3rd position, with a few at the 1st position and none at the 2nd as also observed in Australian fish [143].

Despite the commonly held view that invertebrate mitochondria are AT-rich, while chordate mitochondria are GC-rich [12,29,144] with a mean value up to 45% GC content [29], our observations reveal considerable variation in the range of GC values (31–50% GC) within decapods (Figure 4), with a mean value of 38%. Similar values have been reported in independent Decapoda COI assessments, but also for total mtDNA diversity

within the order [29]. Appraising a wider taxonomic breadth, Clare *et al.*, [29] also detected large shifts in GC content (up to 8%) even at the generic level in the Insecta, highlighting that heterogeneity in mtDNA GC content is not restricted to our current observations.

The wide range of GC content in some families in our analysis is intriguing, though observations here must be treated cautiously as most sequences originated from GenBank, a source where sequencing error and misidentifications have been well documented [136]. Nevertheless, the wide range among families was largely due to 3rd codon positions as also observed in fish species [143]. Several explanations for genome shifts in nucleotide composition exist, which can be categorized into theories of mutational bias (observation that purine to purine or pyrimidine to pyrimidine changes -transitional- occur with greater frequency than purine to pyrimidine or vice versa - transversional [145] and natural selection [144]). There remains a strong interest in exploring the environmental context of such shifts, including fluctuations in temperature, salinity, pressure [75,146–152], and biological factors such as population size, generation time, body size, larval dispersal, mutation rate and parasite behaviour [74,153–160]. It is important to underline that the families with higher GC values belong to the oldest Pleocymata lineage Caridea [60]. It is known that DNA sequences with similar GC content may be grouped together if phylogenetic analysis is performed on DNA sequences [161]. GC-rich DNA is assumed to produce a more heat-stable helix [162] and thus can be selectively advantageous in animals with high metabolic regulation induced by environmental drivers such as light, temperature, salinity, oxygen, and pH. Recently a study [145] showed the existence of a strong positive correlation between hydrophobicity and genomic GC content in prokaryotic organisms. Although the importance of hydrophobicity on the stability of proteins has been observed in most of the protein families [163], GC increment may be related to the structural and functional changes of the encoded proteins [145] in Caridea, suggesting that natural selection is the main force influencing mutation patterns.

Sample size and geographical coverage for species diversity assessment

Early in the DNA barcode initiative the question of how many specimens are needed to create a reliable reference for specimen identification and diversity assessment remained largely unresolved. A sample size of 12 individuals per species was proposed by [164], but it has been correctly asserted that a reference sequence sample for all species seems pointless without taking the evolutionary characteristics of each species into account [165]. Zang *et al.*, [165] showed that there is no significant correlation between samples size and the percentage of the total number of haplotypes observed, and the effort of finding new haplotypes varies considerably over different species/populations. In our data the pattern of diversity found among species is very diverse, but it remains unclear how representative it is as an estimate of genetic/variation diversity based on a sample of 10 individuals. As an example we have the species *G. rhomboides* represented by 7 individuals from the Portuguese west coast and three from Great Britain sharing a unique haplotype. Such data suggest that we should have better randomized sampling from the whole geographical distribution of a species in DNA barcoding projects to better encompass the diversity of the species. Nevertheless, the trends disclosed, together with the high levels of concordance overall between previous indications of taxonomic anomalies and links to coarse environmental features, does suggest that data presented here are broadly representative of contemporary

biodiversity patterns. Indeed, examination of diversity at the COI region yields an informative framework to identify and explore priority issues, demanding in turn a fully integrative approach utilising additional molecular, distributional and ecological information.

Conclusions

Although our study is limited to decapods, and the sampling is limited to a small proportion of the entire order (5.4% of the 17635 extant species described), it is unlikely that the general patterns observed have been biased by our sampling or taxonomic coverage. Here with our range of molecular data we have contributed to the assessment of decapods biodiversity in several ways, including: revealing putative cryptic species (e.g., *Palaemon elegans*); assigning correct species names of taxa with different life history stages (*Pachygrapsus marmoratus*); confirming the existence of the synonymy names (*Macropodia tenuirostris*); facilitating a rapid assessment of taxon diversity in groups that have until now received limited morphological and systematic examination (*Macropodia*), and we also flag taxonomic groups (Caridea; Lithodidae and Pandalidae) with unusual nucleotide composition or evolutionary rates. Intraspecific genetic diversity has a fundamental role in delimiting species boundaries. The burgeoning record of barcode records, in conjunction with additional ecological and molecular approaches, is likely to enhance understanding of the history and evolutionary trajectory of decapod species. It has become essential that species are accurately delineated, cryptic species are identified and/or conservation units are proposed on the basis of sound phylogenetic and phylogeographic variation in space and time. Efforts to conserve biodiversity should work to preserve both existing biodiversity as well as the evolutionary processes shaping genetic diversity, the core determinant evolutionary potential for adaptation to changing environments.

Materials and Methods

Data sampling

We collected 516 decapods specimens from the North East of the Atlantic, the Gulf of Cadiz and the Mediterranean Sea between 2005 and 2008. The specimens encompassed 101 species in 74 genera from 42 families of the order Decapoda. Deep-water specimens were collected by the National Institute of Biological Resources (INRB-IPIMAR) with nets and by the IOC-UNESCO Training through Research programme and the EU funded project Hotspot Ecosystem Research on the Margins of European Seas (HERMES) with two dredges and three box-cores. Littoral specimens were collected at low tide using dip nets, baited traps and scuba diving. Samples were stored in 70% ethanol (2001–2005) and in 100% ethanol (2006–2008). Morphological identifications were undertaken and confirmed by taxonomists. Scientific names followed the Integrated Taxonomic Information System (www.its.gov). In most cases, the whole specimen was stored as a morphological voucher for future reference (Table S1). For some large decapod species, only tissue (legs or abdominal muscle) was obtained for barcoding and the samples were stored as tissue vouchers, accompanied by photographs taken prior to DNA extraction. All details regarding taxonomy, vouchers and collection sites with geographical coordinates can be found in the Barcode of Life Data System website (BOLD, www.barcodinglife.org) under two campaigns, Marine Life (MarBOL) and Portugal – Aquatic Life (Table 1). In order to ensure adequate geographical coverage, multiple specimens (at least two per site) from different geographical areas of target species were examined.

Total genomic DNA was extracted from small amounts of tissue (1 mm³ muscle tissue or whole legs for small specimens) using the Chelex dry release [166] or QIAGEN DNeasy tissue extraction kits (QIAGEN) for older or less well preserved samples. Prior to DNA extraction, the sample was washed overnight in 50 µl of QIAGEN Buffer AE (10 mM Tris-Cl; 0.5 mM EDTA; pH 9.0) in order to rehydrate the tissue. For the Chelex dry release extraction method tissue samples were added to 120 µl of a 10:2 mixture of Chelex buffer with Proteinase K (Sigma), incubated at 55°C for 8–12 hours and subsequently heated to 95°C for 20 minutes. The barcode region was amplified with alternative sets of primers depending on PCR reaction success. The primers used with forward direction were LCOI490 [167], CrustDF1 [132], CrustF1 [35], CrustF2 [35], and COL6 [138] and with the reverse primers HCO2198 [167]; CrustDR1 [132]; CrustR2 (5'-GGT AGA ATT AGA ATA TAC ACT T - 3', designed within the context of the BOLD-FCDDPA project), COH6 [138]. A cocktail of primers with M13 tails [168] was used with two forward and two reverse primers LCOI490; CrustF1; HCO2198; and CrustR2. All PCRs were performed in a 25 µl volume containing 1 X PCR buffer, 3 mM MgCl₂, 0.1–0.2 mM dNTP, 1U TAQ polymerase (Promega), 5–10 pmol of each primer, and 2–10 ng of DNA template. The thermal cycling conditions consisted of 94°C for 60 s; 35–40 cycles of 94°C for 30 s, 48–56°C for 90 s, and 72°C for 60 s; followed by a final extension of 72°C for 5 mins. Alternative thermal cycling conditions was consisted of 94°C for 60 s; 5 cycles of 94°C for 30 s, 45°C for 90 s, and 72°C for 60 s; 35 cycles of 94°C for 30 s, 50–56°C for 90 s, and 72°C for 60 s; followed by a final extension of 72°C for 5 mins. The thermal cycling was identical for all primer except the CrustF2/HCO primer set, which was as follows: one cycle of 94°C for 60 s; 35 cycles of 94°C for 30 s, 42°C for 90 s, and 72°C for 60 s; followed by a final extension of 5 min at 72°C. PCR products were visualized on precast 1% agarose gels using the E-gel 96 system (Invitrogen). Prior to sequencing 15 µl PCR products were cleaned with 1U shrimp alkaline phosphatase (Promega) to dephosphorylate residual deoxynucleotides and 0.5 U Exonuclease I (Promega) to degrade excess primers [169]. The purification thermal conditions consisted of 37°C for 45 min and 80°C for 15 min. Bidirectional sequencing was performed using BigDye Termination chemistry on an Applied Biosystems® 3730 sequencer by Macrogen Inc. (www.macrogen.com, South Korea). Sequences were manually checked for ambiguities and assembled in CodonCode Aligner version 1.3.0 (<http://www.codoncode.com/>). Sequences were aligned using CLUSTAL W [170] implemented in MEGA4 [171] and the amino acid translation was examined to ensure that no gaps or stop codons were present in the alignment. BLAST searches were performed for all sequences via interrogating GenBank's online nucleotide database using the megablast algorithm.

Genbank data set

To provide a comprehensive sister-species coverage and survey of intraspecific variation, our data set was complemented by COI sequences from GenBank, as available on 4th June 2009. Additional sequences were included from the Barcode of Life Data Systems website (<http://www.barcodinglife.org/>, as accessed on 4th June 2009). The BOLD platform allows us in our Project List page to have access not just to our full list of personal projects, but also all publicly accessible projects on BOLD, e.g., GenBank Animals (COI) and MarBOL compans. The BOLD system archives sequences located in COI barcode region from samples identified only to genus and species level being less than half of the COI entries in NCBI GenBank database. Sequences were omitted in our study if they were not allocated to a species, were from taxa with multiple denominations or taxonomic ranks, and suspected of being derived from misidentified,

mislabelled species or putative pseudogenes (when found intraspecific distances >10%, aberrant nucleotide composition, unusually long branches in our NJ tree and nonsensical systematic relationships [134,136]), exhibited stop codons or indels, were less than 500 bp in length within the COI barcode region and finally sequences that were not reported in scientific journals to avoid potential misidentifications that could possibly be derived from GenBank [172], we submitted these to a rigorous quality control. From public projects [57] we downloaded 5052 comprising 856 species from 249 genera and 83 families only 3187 COI barcode region sequences were selected from 520 species, 178 genera and 53 families with sufficient length and quality according to our stringent criteria.

Combined data set: sequence selection and data validation

Two main factors may bias divergence assessments. First, disequilibrium in the representation of some taxa could skew divergence distributions. Here we standardized taxon comparisons to maximum of 10 individuals per species [173] randomly selected reducing to 1906 sequences from 603 species, 225 genera and 68 families were included in the total data analyses. To test how patterns of genetic divergence at COI correspond to morphological species concepts, species diversity was estimated based on the similarity and clustering pattern in their COI barcodes independent of taxonomic assignments. A threshold of 2% sequence divergence was employed to draw boundaries for barcode haplotype clusters. This arbitrary threshold was selected based on the observation that intraspecific divergences observed in a variety of groups rarely exceed this value [12–16].

Secondly, the taxonomic classification may be incorrect or uncertain. Most common problems will result from cryptic species, and paraphyletic or polyphyletic taxa [10,174]. All sequences were aligned and a Neighbour Joining tree produced using BOLD platform. We identified, in this tree, all sequences clustering far from their known taxonomic or phylogenetic position, and removed the non-monophyletic, putative cryptic species and congeneric species with distance values lower than 2% evaluated from the literature. After such selective removal, we proceeded to analyse 1572 sequences from 528 species, 213 genera, and 67 families. Additionally we tested the possible artefact attributable to biased species representation by computing within mean species divergence and the influence of presumably non-monophyletic taxa on the divergence distribution. An assumption-free statistical test was proposed by Lefebvre *et al.*, [10] to directly measure the overlap between raw data (highly represented taxa have more impact than weakly represented ones) and a second set of data where each taxa was given the same weight by computing mean divergence through distance values. Comparing the frequency of intraspecific distances values (<3%) between the raw data and the mean data will indicate whether or not the divergence assessment is a result of a strong disequilibrium in the representation of some taxa. The divergence distribution was tested within species diversity between the initially dataset with 1906 sequences (case A) and the validate data set with 1572 sequences (case B). To obtain the first statistical indication of the overlap between divergence distributions, Mann-Whitney U Test were performed (Figure 1) among [10]: raw data A_R vs B_R , mean data A_M vs B_M ; and between different data A_R vs A_M and B_R vs B_M with the SPSS software version 16.0.2 [175].

Decapoda diversity assessment

The diversity assessments for the decapods and for the most represented families were analysed from the data set with 1572 sequences from 528 species, 213 genera, and 67 families (B_R). For statistical purposes only, families containing at least 50 sequences

[10,174] with more than 5 species were compared [10]. Nucleotide divergences of COI and variation in GC content were analysed between the 11 most representative families (Table 2).

The K2P has become the metric most widely used in barcoding studies and is deployed here. Genetic distances between specimens were calculated for each intraspecies (S), intragenus (G) and intrafamily (F) with the 'Distance Summary' command implemented by BOLD. Although distance distributions within families are not independent from each other, we performed the Kruskal–Wallis one-way analysis of variance between S, G, and F distributions to obtain a first statistical indication of the overlap between divergence distributions with GenStat [176].

In order to investigate the sensitivity of results to variations in matrices distances methods, Patristic distances were computed using the program PATRISTIC [177].

Our second line of investigation examined the diversity in GC content across multiple taxonomic groups. To ensure homology with the BOLD data (because the sequences are heterogeneous in length), all sequences (1572) were trimmed to 500 bases and GC content and nucleotide composition were calculated for 11 families using MEGA 4 [171].

Supporting Information

Figure S1 Taxon ID Tree of Decapoda generated by BOLD. Neighbour Joining tree (Kimura 2-parameter, uniform rates among sites, pairwise deletion) combining COI data from public BOLD projects and present study. A total number of 1906 sequences from 603 species, 225 genera and 71 families were used. (PDF)

Table S1 Novel COI decapod barcodes generated by the present study. (XLS)

Table S2 Accession numbers for the sequences used in this study. Specimens' list of 1906 COI sequences from 603 species, 225 genera and 71 families. (XLS)

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Table S3 Accession numbers for the sequences removed from the decapod diversity assessment analysis.

Specimens' list of 340 COI sequences from 79 species, 30 genera and 19 families.

(XLS)

Table S4 Accession numbers for the sequences used for assessment of decapod diversity. Specimens' list of 1572 COI sequences from 528 species, 213 genera and 67 families.

(XLS)

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Author Contributions

Conceived and designed the experiments: JMds SC FOC GRC. Performed the experiments: JMds. Analyzed the data: JMds. Contributed reagents/materials/analysis tools: AdS ACC MRC. Wrote the paper: JMds. Designed the study: JMds SC FOC GRC. Developed and performed molecular data analyses: JMds. Performed the decapoda taxonomy and morphology supervising and their identification: AdS ACC MRC. Drafted the manuscript: JMds SC AdS FOC GRC. All authors read and approved the final manuscript.

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