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## Data Article

## Data for praying mantis mitochondrial genomes and phylogenetic constructions within Mantodea



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## ABSTRACT

In this data article, we provide five datasets of mantis mitochondrial genomes: (1) PCG123: nucleotide sequences of 13 protein-coding genes including all codon positions; (2) PCG123R: nucleotide sequences of two rRNAs and 13 protein-coding genes including all codon positions; (3) PCG12: nucleotide sequences of 13 protein-coding genes without third codon positions; (4) PCG12R: nucleotide sequences of two rRNAs and 13 protein-coding genes without third codon positions, and (5) PCGAA: amino acid sequences of 13 protein-coding genes. These were used to construct phylogenetic relationships within Mantodea and the phylogenetic trees inferred from Bayesian analysis using two data sets (PCG12R, PCGAA) and Maximum Likelihood analysis using four data sets (PCG123, PCG12, PCG12R and PCGAA). We also provide initiation codon, termination codon, amino acid length and nucleotide diversity (Pi) of protein-coding genes among 27 mantises. The whole mitochondrial genomes of 27 praying mantises were submitted to GenBank with the accession numbers KY689112–KY689138.

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### Specifications table

|                            |  |
|----------------------------|--|
| Subject area               | Biology  |
| More specific subject area | Phylogenetics; Mitochondrial Genomics  |
| Type of data               | Figure, text file, graph and table   |
| How data was acquired      | Sanger DNA sequencing  |
| Data format                | Phylogenetic trees are in figure format (.eps) and newick format (.nwk) and mitochondrial DNA sequence alignments are in paup format (.nexus).   |
| Experimental factors       | Total genomic DNA was extracted from leg muscle. DNA sequences were acquired by PCR and Sanger sequenced by Sangon Biotech Company.  |
| Experimental features      | Sequence fragments were assembled using DNASTAR Package v.6.0. Nucleotide sequences and amino acids sequences of 13 protein-coding genes were used to construct phylogenetic trees by MrBayes 3.2 and RAxML 8.2.0.             |
| Data source location       | Specimens were collected from Africa, China, Indonesia and Malaysia.   |
| Data accessibility         | Five datasets (.nexus files) used to construct phylogenetic trees and newick tree files (.nwk files) are provided here. The whole mitochondrial genomes are available in GenBank with the accession numbers KY689112–KY689138. |

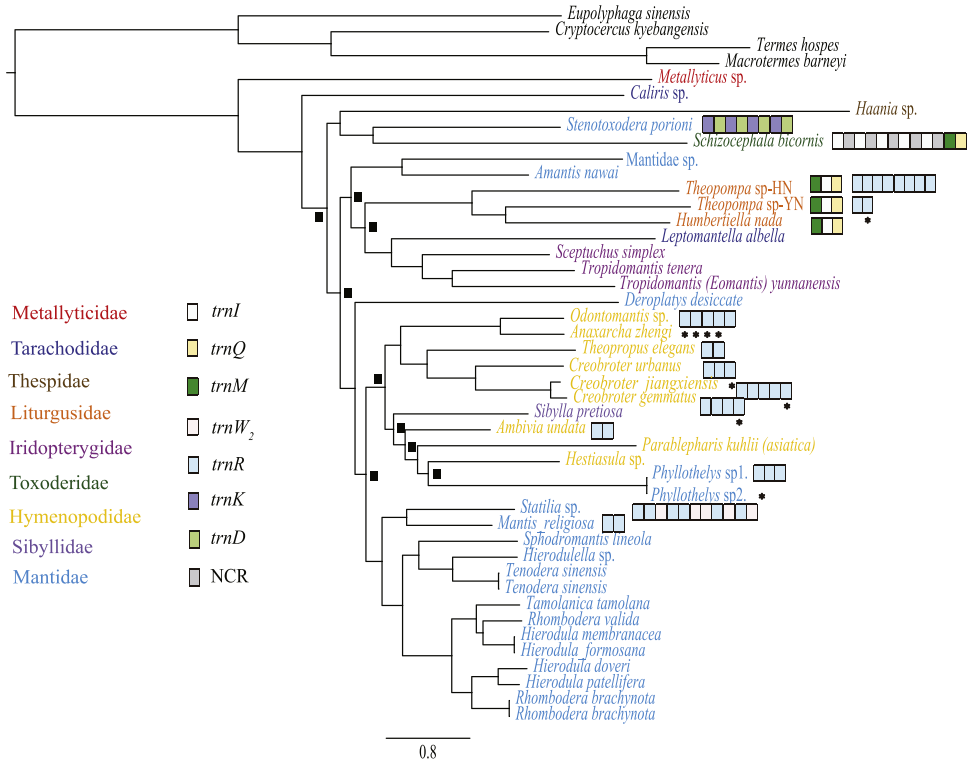
### Value of the data

- The mitochondrial genomes of praying mantises are good models for future study of gene rearrangements and gene duplications.
- The primer strategy used to amplify the mantis mitochondrial genomes could be widely used for other insect mitochondrial genomes and this strategy can greatly reduce the experimental workload needed to acquire whole genome sequences.
- The phylogenetic relationships within Mantodea inferred from BI analyses using 2 data sets (PCG12R, PCGAA) and ML analysis using four data sets (PCG123, PCG12, PCG12R and PCGAA) show a few differences with the phylogenetic relationships reported in the main text, which is worthy of further discussions.
- The data presented here will be useful to solve the phylogenetic relationships within Mantodea.

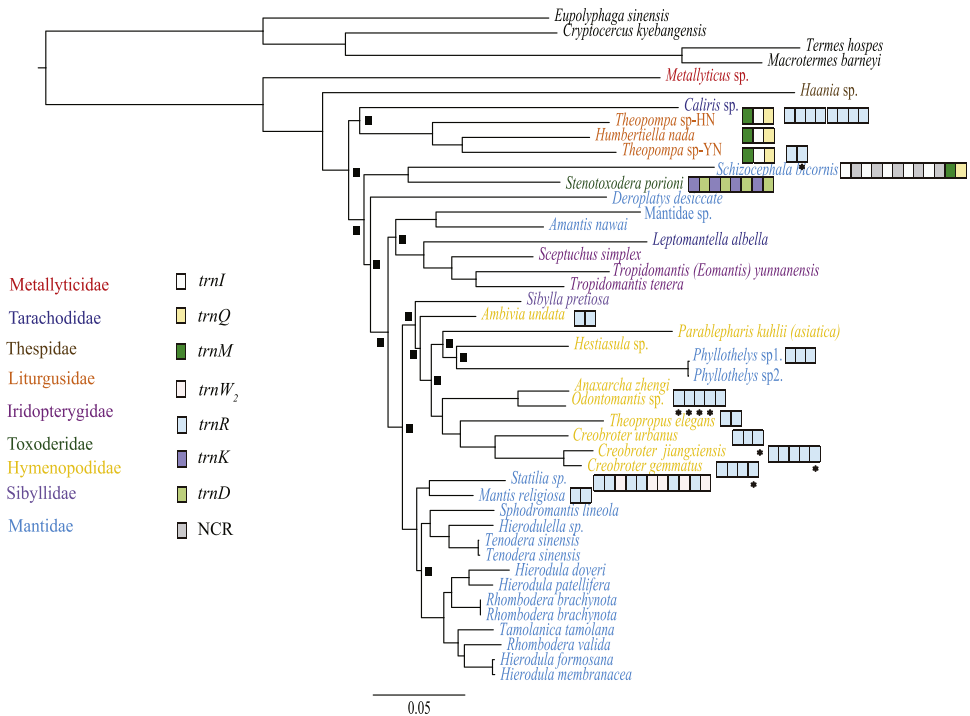
### 1. Data

The data presented here originate from a study of higher tRNA gene duplication in the mitogenomes of praying mantises (Dictyoptera, Mantodea) and the phylogeny within Mantodea [1], including genome statistics and phylogenetic trees. The monophyly of Mantodea is supported [2–6] whereas the phylogenetic relationships within Mantodea are under suspicion especially in two large families: Mantidae and Hymenopodidae [7,8]. Our study supported the monophyly of Liturgusidae and Iridopterygidae and the paraphyly of Hymenopodidae, Mantidae and Tarachodidae [1].

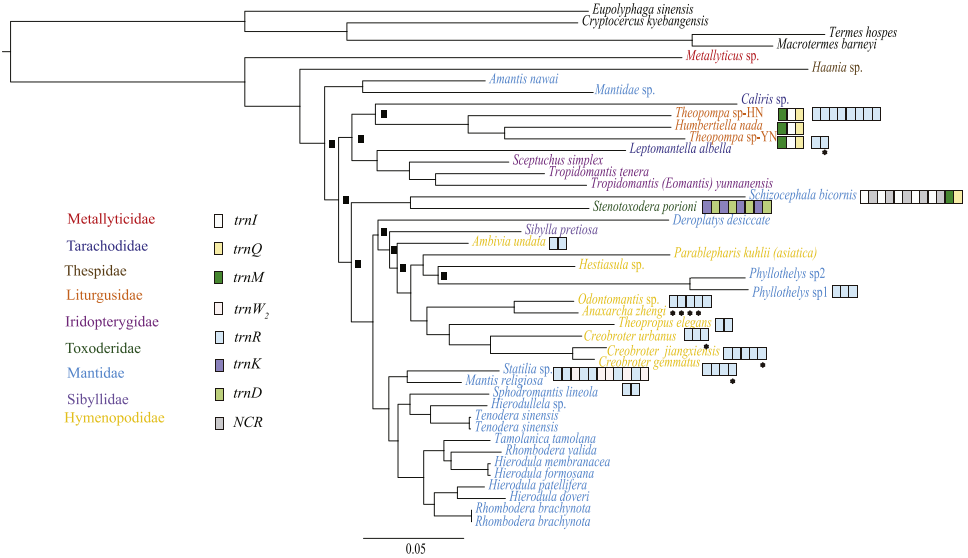
Five data sets were used to perform Maximum Likelihood analysis (ML) and Bayesian Inference (BI): (1) PCG123: 13 PCGs including all codon positions; (2) PCG123R: two rRNAs and 13 PCGs including all codon positions; (3) PCG12: 13 PCGs without third codon positions; (4) PCG12R: two rRNAs and 13 PCGs without third codon positions, and (5) PCGAA: amino acid sequences of 13 PCGs. The phylogenetic relationships inferred from BI analyses using 3 data sets (PCG123, PCG123R, PCG12) and ML analyses using the data set PCG123R shared the same topologies. Hence, we illustrated nodal supports from the four analyses together, which are data provided in the main text [1]. Here, we



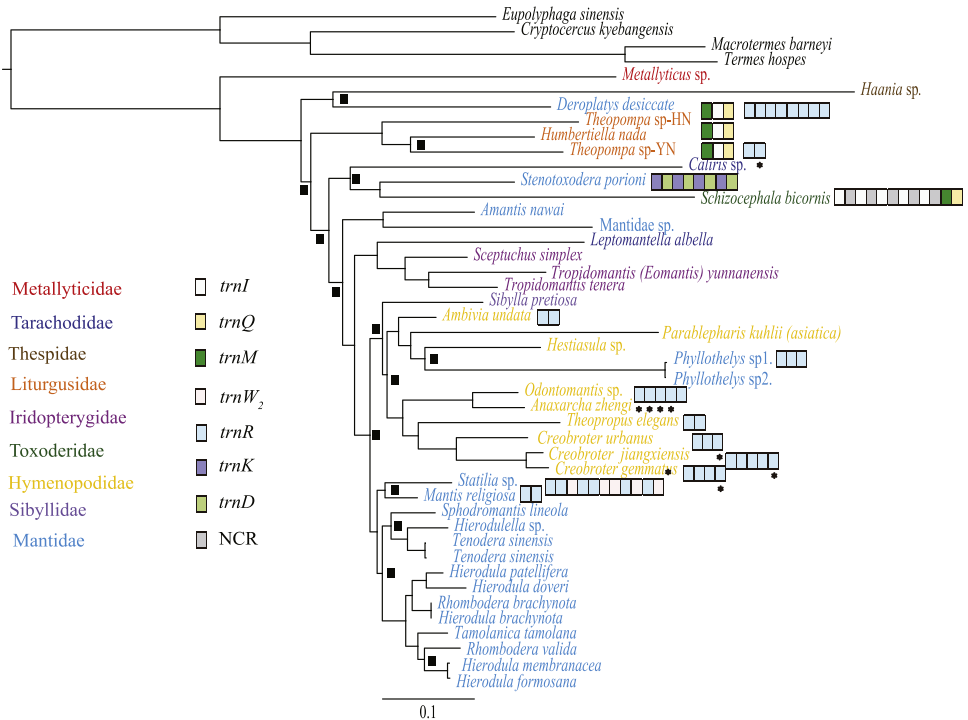
**Fig. 1.** Phylogenetic relationships of Mantodea analyzed with ML methods using the dataset 13PCG. At each node, the black box indicates BP < 75. Other small boxes represent tRNA genes and the box labeled with an asterisk represents a pseudogene.



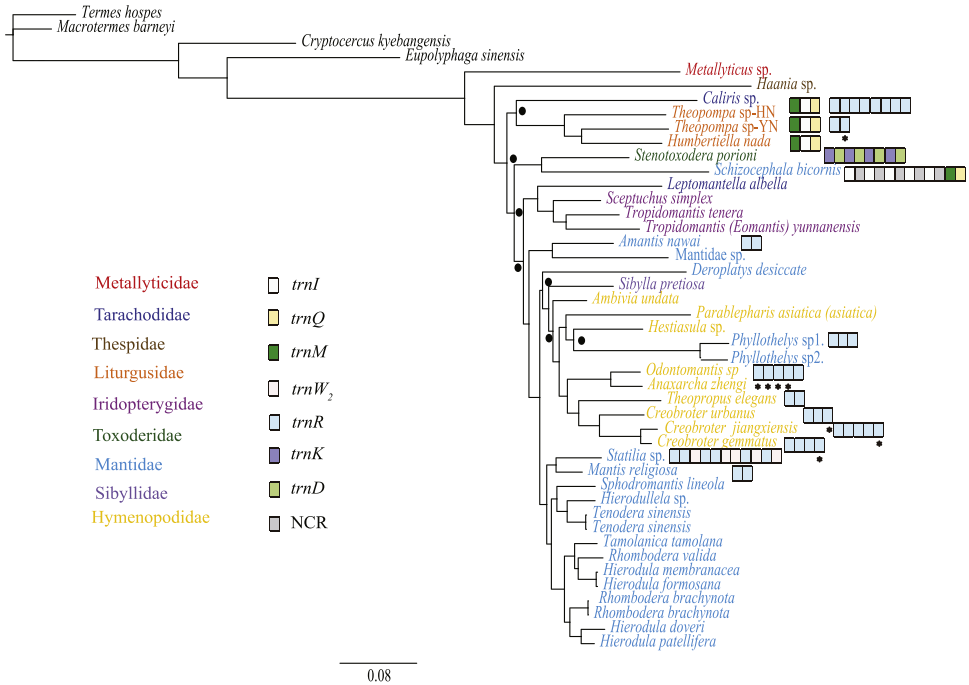
**Fig. 2.** Phylogenetic relationships of Mantodea analyzed with ML methods using the dataset 13PCG12. At each node, the black box indicates BP < 75. Other small boxes represent tRNA genes and the box labeled with an asterisk represents a pseudogene.



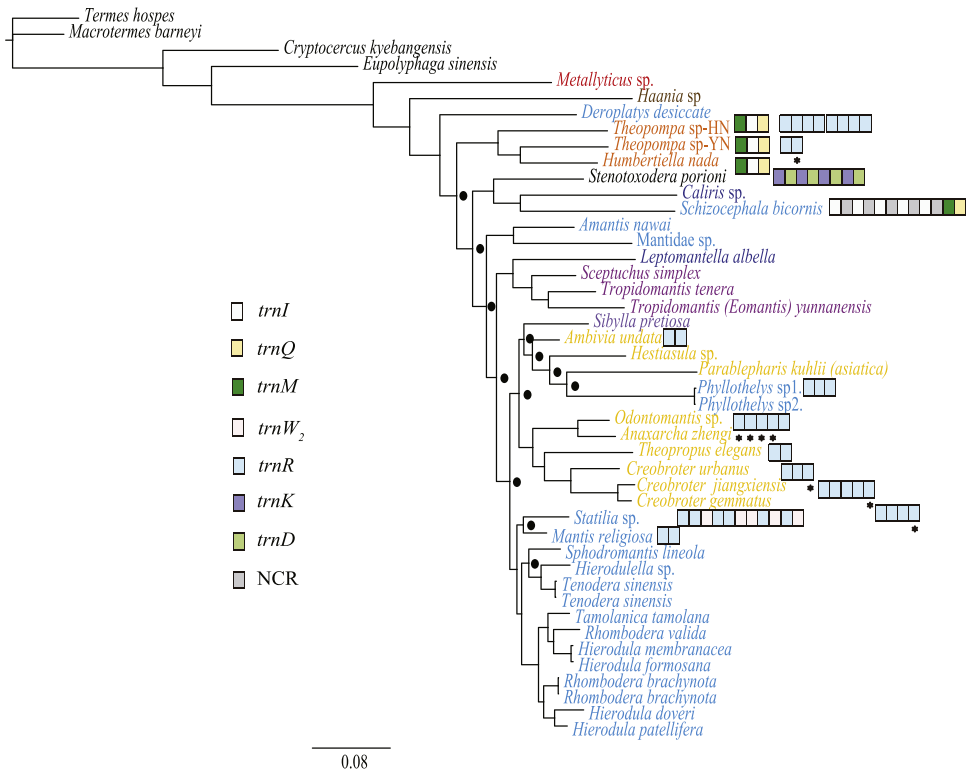
**Fig. 3.** Phylogenetic relationships of Mantodea analyzed with ML methods using the dataset 13PCG12R. At each node, the black box indicates BP < 0.75. Other small boxes represent tRNA genes and the box labeled with an asterisk represents a pseudogene.



**Fig. 4.** Phylogenetic relationships of Mantodea analyzed with ML methods using the dataset 13PCGAA. At each node, the black box indicates BP < 0.75. Other small boxes represent tRNA genes and the box labeled with an asterisk represents a pseudogene.



**Fig. 5.** Phylogenetic relationships of Mantodea analyzed with BI methods using the dataset 13PCG12R. At each node, the black box indicates PP < 0.95. Other small boxes represent tRNA genes and the box labeled with an asterisk represents a pseudogene.



**Fig. 6.** Phylogenetic relationships of Mantodea analyzed with BI methods using the dataset 13PCGAA. At each node, the black box indicates PP < 0.95. Other small boxes represent tRNA genes and the box labeled with an asterisk represents a pseudogene.

**Table 1**

Initiation codon (I codon), termination codon (T codon) and amino acids length of protein-coding genes among 27 mantises.

| Species  |         | <i>nd2</i> | <i>cox1</i> | <i>cox2</i> | <i>atp8</i> | <i>atp6</i> | <i>cox3</i> | <i>nd3</i> | <i>nd5</i> | <i>nd4</i> | <i>nd4l</i> | <i>nd6</i> | <i>cytb</i> | <i>nd1</i> |
|--|---------|------------|-------------|-------------|-------------|-------------|-------------|------------|------------|------------|-------------|------------|-------------|------------|
| <i>Ambivia undata</i> (Hymenopodidae)                | No.     | 342        | 511         | 229         | 52          | 225         | 263         | 117        | 574        | 445        | 93          | 167        | 378         | 310        |
|  | I codon | ATG        | TTG         | ATA         | ATC         | ATA         | ATA         | ATC        | ATG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Hestiasula</i> sp. (Hymenopodidae)                | No.     | 342        | 511         | 230         | 52          | 225         | 263         | 117        | 575        | 445        | 93          | 167        | 377         | 310        |
|  | I codon | ATG        | TTG         | ATT         | ATT         | ATA         | ATA         | ATT        | ATG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | TAA         | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Odontomantis</i> sp. (Hymenopodidae)              | No.     | 342        | 512         | 229         | 52          | 225         | 262         | 117        | 573        | 445        | 93          | 167        | 378         | 313        |
|  | I codon | ATG        | TTG         | ATG         | ATC         | ATA         | ATG         | ATT        | ATG        | ATG        | ATG         | ATT        | ATG         | ATT        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | TAA        | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Parablepharis kuhlii asiatica</i> (Hymenopodidae) | No.     | 345        | 514         | 229         | 52          | 224         | 262         | 117        | 575        | 439        | 93          | 167        | 378         | 314        |
|  | I codon | ATG        | TTG         | ATG         | ATT         | ATA         | ATG         | ATT        | ATG        | ATT        | ATG         | ATG        | ATG         | ATA        |
|  | T codon | TAA        | TAA         | TAA         | TAA         | TAA         | TAA         | TAA        | T-         | TAG        | TAA         | TAA        | TAA         | TAA        |
| <i>Creobroter jiangxiensis</i> (Hymenopodidae)       | No.     | 342        | 513         | 229         | 52          | 225         | 262         | 117        | 575        | 445        | 93          | 167        | 377         | 310        |
|  | I codon | ATG        | ATC         | ATG         | ATT         | ATA         | ATG         | ATT        | ATG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Creobroter urbanus</i> (Hymenopodidae)            | No.     | 342        | 512         | 229         | 52          | 225         | 262         | 117        | 574        | 445        | 93          | 167        | 378         | 310        |
|  | I codon | ATG        | TTA         | ATG         | ATT         | ATA         | ATG         | ATT        | GTG        | ATG        | ATG         | ATT        | ATA         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAG         | TAA        |
| <i>Theopropus elegans</i> (Hymenopodidae)            | No.     | 342        | 511         | 229         | 52          | 225         | 262         | 117        | 574        | 445        | 93          | 165        | 377         | 310        |
|  | I codon | ATG        | ATG         | ATG         | ATT         | ATA         | ATG         | ATT        | GTG        | GTG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | TAG         | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Sceptuchus simplex</i> (Iridopterygidae)          | No.     | 342        | 511         | 228         | 52          | 225         | 262         | 117        | 574        | 445        | 93          | 167        | 377         | 310        |
|  | I codon | ATG        | TTG         | ATG         | ATT         | ATA         | ATG         | ATT        | GTG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | T-          | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Eomantis yunnanensis</i> (Iridopterygidae)        | No.     | 342        | 511         | 227         | 52          | 224         | 262         | 117        | 574        | 445        | 95          | 167        | 378         | 311        |
|  | I codon | ATG        | TTG         | ATG         | ATT         | ATA         | ATG         | ATT        | ATG        | ATG        | ATA         | ATT        | ATG         | ATG        |
|  | T codon | TAG        | TAA         | TAA         | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Tropidomantis tenera</i> (Iridopterygidae)        | No.     | 342        | 511         | 228         | 53          | 225         | 262         | 117        | 573        | 445        | 93          | 167        | 378         | 311        |
|  | I codon | ATG        | CTG         | ATG         | ATT         | ATA         | ATG         | ATC        | GTG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAG        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Amantis nawai</i> (Mantidae)                      | No.     | 342        | 511         | 228         | 52          | 225         | 262         | 117        | 573        | 445        | 93          | 165        | 377         | 311        |
|  | I codon | ATG        | CTG         | ATG         | ATA         | ATA         | ATG         | ATA        | GTG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Tenodera sinensi</i> (Mantidae)                   | No.     | 342        | 512         | 230         | 52          | 225         | 263         | 117        | 574        | 445        | 93          | 167        | 378         | 311        |
|  | I codon | ATG        | ATT         | ATC         | ATC         | ATA         | ATA         | ATT        | GTG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |
| <i>Sphodromantis lineola</i> (Mantidae)              | No.     | 342        | 511         | 228         | 52          | 225         | 263         | 117        | 574        | 445        | 93          | 167        | 378         | 311        |
|  | I codon | ATG        | CTG         | ATG         | ATC         | ATA         | ATA         | ATC        | ATG        | ATG        | ATG         | ATT        | ATG         | ATG        |
|  | T codon | TAA        | TAA         | T-          | TAA         | TAA         | TAA         | TAA        | T-         | TAA        | TAA         | TAA        | TAA         | TAA        |

|  |         |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <i>Hierodulella</i> sp. (Mantidae)         | No.     | 342 | 511 | 228 | 52  | 225 | 263 | 117 | 570 | 445 | 93  | 167 | 378 | 311 |
|  | I codon | ATG | TTG | ATG | ATT | ATA | ATA | ATT | GTG | ATG | ATG | ATT | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Rhombodera brachynota</i> (Mantidae)    | No.     | 342 | 512 | 228 | 52  | 225 | 263 | 117 | 574 | 445 | 93  | 167 | 378 | 311 |
|  | I codon | ATG | ATA | ATG | ATT | ATA | ATA | ATT | GTG | ATG | ATG | ATT | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Hierodula chinensis</i> (Mantidae)      | No.     | 342 | 511 | 226 | 52  | 225 | 262 | 117 | 574 | 445 | 93  | 167 | 377 | 311 |
|  | I codon | ATG | CTG | ATG | ATT | ATA | ATG | ATT | ATG | ATG | ATG | ATT | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Hierodula membranacea</i> (Mantidae)    | No.     | 342 | 513 | 228 | 52  | 225 | 263 | 117 | 574 | 445 | 93  | 167 | 378 | 311 |
|  | I codon | ATT | ATT | ATG | ATC | ATA | ATA | ATT | ATG | ATG | ATG | ATA | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Deroplatys desiccata</i> (Mantidae)     | No.     | 343 | 511 | 227 | 53  | 226 | 262 | 117 | 573 | 445 | 93  | 171 | 377 | 311 |
|  | I codon | ATG | TTG | ATG | ATT | ATA | ATG | ATA | ATG | ATG | ATG | ATA | ATG | ATG |
|  | T codon | TAA | TAA | TAA | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Phyllothelys</i> sp1. (Mantidae)        | No.     | 343 | 512 | 228 | 52  | 225 | 262 | 117 | 574 | 445 | 94  | 167 | 377 | 310 |
|  | I codon | ATG | ATC | ATG | ATT | ATA | ATG | ATT | ATG | ATG | ATG | ATT | ATG | ATG |
|  | T codon | TAA | TAA | TAA | TAA | TAG | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Phyllothelys</i> sp2. (Mantidae)        | No.     | 343 | 512 | 228 | 52  | 225 | 262 | 117 | 574 | 445 | 94  | 167 | 377 | 310 |
|  | I codon | ATG | ATC | ATG | ATT | ATA | ATG | ATT | ATG | ATG | ATG | ATT | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAA | TAG | TAA | TAA | TAA | TAA | TAA | TAA | TAA | TAA |
| <i>Schizocephala bicornis</i> (Mantidae)   | No.     | 340 | 511 | 231 | 53  | 225 | 261 | 117 | 574 | 445 | 93  | 167 | 378 | 311 |
|  | I codon | ATG | TTG | ATT | ATT | ATA | ATG | ATT | ATG | GTG | ATG | ATT | ATG | ATA |
|  | T codon | TAA | TAA | TAA | TAA | TAA | T-  | TAA | T-  | TAG | TAA | TAA | TAA | TAA |
| <i>Mantidae</i> sp. (Mantidae)             | No.     | 342 | 511 | 239 | 53  | 225 | 264 | 117 | 574 | 445 | 93  | 167 | 379 | 312 |
|  | I codon | ATG | TTG | ATA | ATC | ATA | ATG | ATT | ATT | GTG | ATG | ATT | ATG | ATA |
|  | T codon | TAA | TAA | TAA | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Metallyticus</i> sp. (Metallyticidae)   | No.     |     | 513 | 230 | 52  | 226 | 261 | 118 | 575 | 449 | 93  | 169 | 376 | 311 |
|  | I codon |     | TTG | ATG | ATC | ATT | ATG | ATT | GTT | ATA | ATG | ATC | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAA | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAG | TAA |
| <i>Sibylla pretiosa</i> (Sibyllidae)       | No.     | 342 | 513 | 228 | 52  | 225 | 263 | 117 | 574 | 445 | 93  | 168 | 378 | 310 |
|  | I codon | ATG | TTA | ATG | ATT | ATA | ATA | ATT | ATG | ATG | ATG | ATT | ATG | ATG |
|  | T codon | TAA | TAA | T-  | TAG | TAA | TAA | TAA | T-  | TAA | TAA | TAA | TAA | TAA |
| <i>Caliris</i> sp. (Tarachodidae)          | No.     | 342 | 511 | 228 | 52  | 225 | 262 | 118 | 574 | 444 | 93  | 168 | 378 | 313 |
|  | I codon | ATG | GTG | ATG | ATT | ATA | ATG | ATA | ATG | ATG | ATG | ATG | ATG | ATA |
|  | T codon | TAA | TAA | TAA | TAA | TAA | TAA | TAA | T-  | T-  | TAA | TAA | TAA | TAG |
| <i>Haania</i> sp. (Thespididae)            | No.     | 511 | 228 | 52  | 223 | 260 | 117 | 572 | 443 | 94  | 166 | 377 | 311 |     |
|  | I codon |     | TTG | ATG | ATA | ATA | ATA | ATC | GTG | ATG | ATA | ATT | ATG | ATG |
|  | T codon | T-  | TAA | T-  | TAA | TAA | T-  | TAA | T-  | TAA | TAA | TAA | TAG | TAA |
| <i>Stenotoxodera porioni</i> (Toxoderidae) | No.     | 343 | 512 | 226 | 52  | 225 | 262 | 117 | 575 | 445 | 93  | 167 | 378 | 311 |
|  | I codon | ATG | TTA | ATG | ATC | ATA | ATG | ATG | GTG | ATG | ATG | ATC | ATG | ATG |
|  | T codon | TAA | TAA | TAA | TAA | TAA | T-  | TAA | T-  | TAA | TAA | TAA | TAA | TAA |

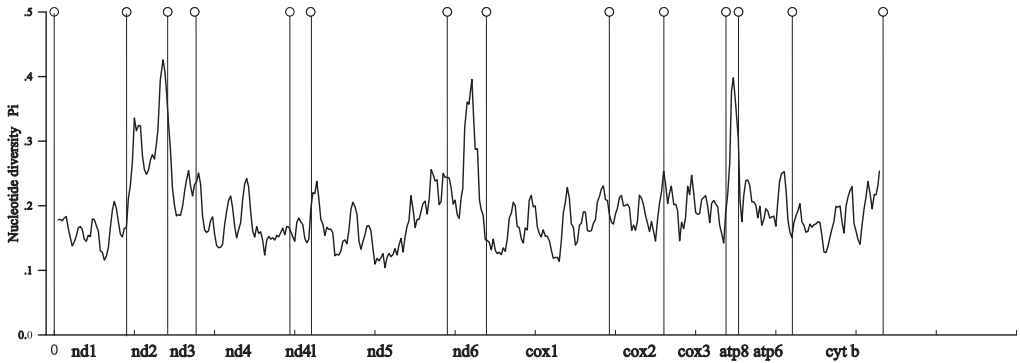


Fig. 7. Nucleotide diversity of protein-coding genes among 27 mantises.

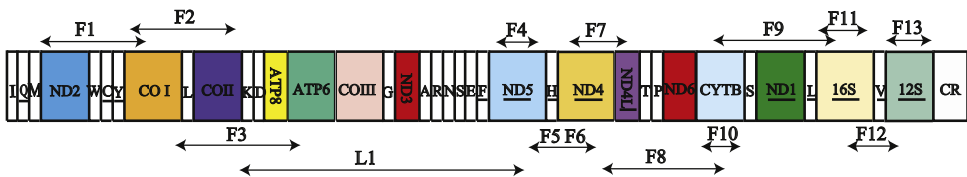


Fig. 8. The primer strategy. Double-headed arrows indicate the location of the fragment amplified by PCR with each pair of primers. See Table 1 in the main text [1] for the primer DNA sequences associated with each fragment.

present the phylogenetic relationships inferred from BI analyses using two data sets (PCG12R, PCGAA) and ML analyses using four data sets (PCG123, PCG12, PCG12R and PCGAA) (Figs. 1–6). These phylogenetic trees can be compared to trees presented in the main text. The sequences of the five datasets are also provided. The initiation codon, termination codon and amino acids length of protein-coding genes are compared among 27 mantises (Table 1) and the nucleotide diversity of protein-coding genes are calculated (Fig. 7).

## 2. Experimental design, materials and methods

Our routine experimental approach was as follows: acquisition of the whole mitochondrial genomes of 27 mantises using total DNA extraction, PCR and sequencing; sequence analyses including assembly, annotation and alignment; and construction of phylogenetic relationships. The primer strategy is shown in Fig. 8 and primer sequences are given in the main text [1]. Five data sets (PCG123, PCG123R, PCG12, PCG12R and PCGAA) of 46 samples including 15 previously sequenced mantis mitogenomes [9–13] were used along with the mitogenomes of two cockroaches [14] and two termites [15,16] as outgroups. ML and BI analyses were implemented in RAxML 8.2.0 [17] and MrBayes 3.2 [18], respectively. PartitionFinder 1.1.1 [19] was used to infer the optimal partitioning strategy and choose the best model. The nucleotide diversity of protein-coding genes among 27 mantises was calculated by DnaSP v5 [20]. A more detailed method and routine are provided in the main text [1].

## Acknowledgements

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## Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2018.10.070>.

## Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2018.10.070>.

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