List of datasets: datasets utilized with description, best nucleotide model employed, analyses performed and number of specimens included.

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| --- | --- | --- | --- | --- |
| Dataset | Description | Best model selected by jModeltest (AIC/BIC) | Analysis | No of specimens in analysis |
| COI\_CHR\_alignment/tree | alignment/tree of COI sequences from the Central Hamersley Range specimens only | HKY+G | ABGD and PTP (results in Fig. 2) | 56 |
| 16S\_CHR\_alignment/tree | alignment/tree of 16S sequences from the Central Hamersley Range specimens only | GTR+G | ABGD and PTP (results in Fig. 2) | 36 |
| 28S\_CHR\_alignment/tree | alignment/tree of 28S sequences from the Central Hamersley Range specimens only | GTR+G+I | ABGD and PTP (results in Fig. 2) | 42 |
| COI-alignment for COI-16S-28S-Concatenate-analysis | COI alignment constructed for the concatenated COI-16S-28S analysis, comprising sequences from the Central Hamersley Range specimens, representatives of Pilbaranella, one specimen from the DeGrey catchment, and Bathynella sp from Slovenia | GTR+G+I | RaxML and MrBays (Supplementary material) | 63 |
| 16S-alignment for COI-16S-28S-Concatenate-analysis | 16S alignment constructed for the concatenated COI-16S-28S analysis, comprising sequences from the Central Hamersley Range specimens, representatives of Pilbaranella, one specimen from the DeGrey catchment, and Bathynella sp from Slovenia | GTR+G | RaxML and MrBays (Supplementary material) | 44 |
| 28S-alignment for COI-16S-28S-Concatenate-analysis | 28S alignment constructed for the concatenated COI-16S-28S analysis, comprising sequences from the Central Hamersley Range specimens, representatives of Pilbaranella and one specimen from the De Grey catchment | GTR+G+I | RaxML and MrBays (Supplementary material) | 49 |
| COI-alignment for COI-18S-Concatenate analysis | COI alignment constructed for the COI-18S analysis, comprising representatives of: the Central Hamersley Range, Pilbaranella and DeGrey catchment, Bathynellinae and Gallobathynellinae | GTR+G+I | RaxML and MrBays (not shown) | 25 |
| 18S-alignment for COI-18S-Concatenate analysis | 18S alignment constructed for the COI-18S analysis, comprising representatives of: the Central Hamersley Range, Pilbaranella and DeGrey catchment, Bathynellinae and Gallobathynellinae | GTR+G+I | RaxML and MrBays (not shown) | 31 |
| COI-16S-28S-Concatenate-tree | concatenate COI-16S-28S gene tree | - | RaxML and MrBays (Fig. 2) | 69 |
| COI-18S-Concatenate-tree | concatenate COI-18S gene tree | - | RaxML and MrBays (Fig. 3) | 33 |