

Phylogeny of coleoid cephalopods based on complete mitochondrial genomes and cryptic species identification



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INTRODUCTIONS

Octopodidae is the largest family in Cephalopoda. Although octopods display a wide diversity in skin coloration, behavior and life strategies, the hard structures for specimens are insufficient. This caused difficulties to investigate the phylogenetic relationships only through morphological characteristics. In addition, the higher-level systematic relationships within the octopod group remain unclear and are difficult to establish based on only morphological data. Besides barely octopods fossil record, higher-level systematic relationships within the octopod group species limits and identification are difficult to establish.

Effective methods for the explanation of phylogenetic relationships and cryptic species delimitation are urgently needed. Automatic Barcode Gap Discovery (ABGD) and Bayesian implementation of the PTP model (bPTP) provide a high-throughput solution to identify the cryptic or undiscovered species. Besides, complete mtDNA was utilized to study the phylogenetic position and higher-levels systematic relationships of octopods. Compared to partial mt genes, complete mtDNA sequence can uncover more information about gene rearrangement and other variation at the genome level for all phyla, and are especially powerful for displaying sufficient interspecies sequence variability and describing species specificity.

OBJECTIVES

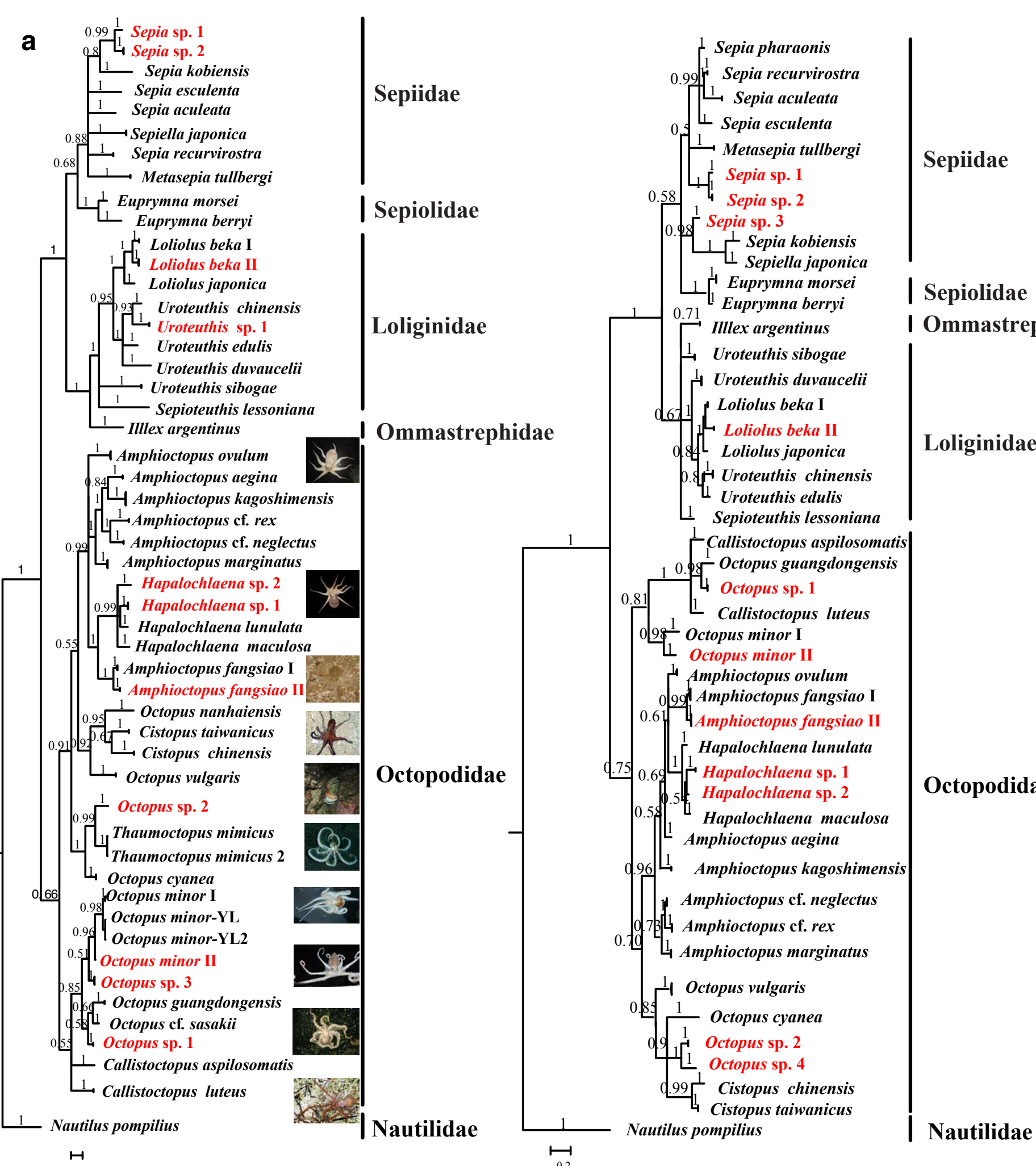
Identify the cryptic or undiscovered species with high-throughput methods based on DNA barcoding

Explore optimal DNA barcodes in Octopodidae.

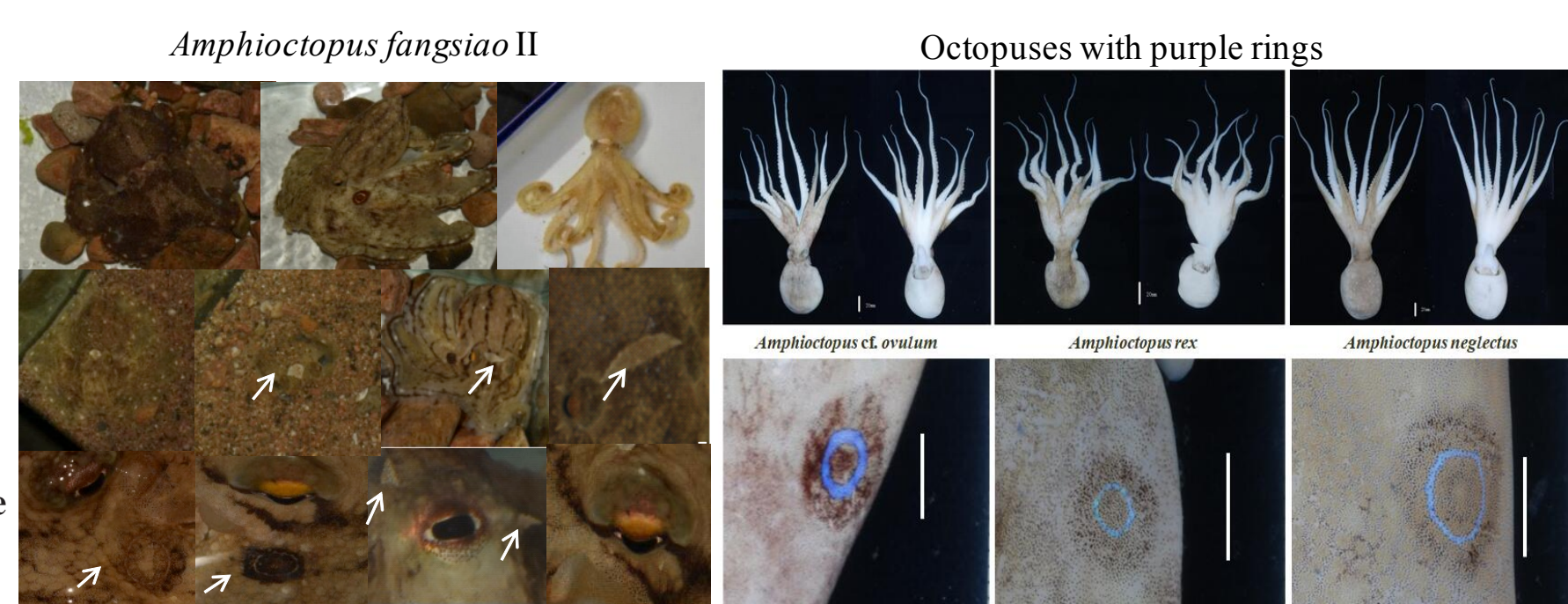
Analyze phylogenetic relationship of coleoid cephalopods based on mitochondrial DNA sequences

Analyze relationships between relative species by comparing morphological and mitochondrial genome characteristics comprehensively.

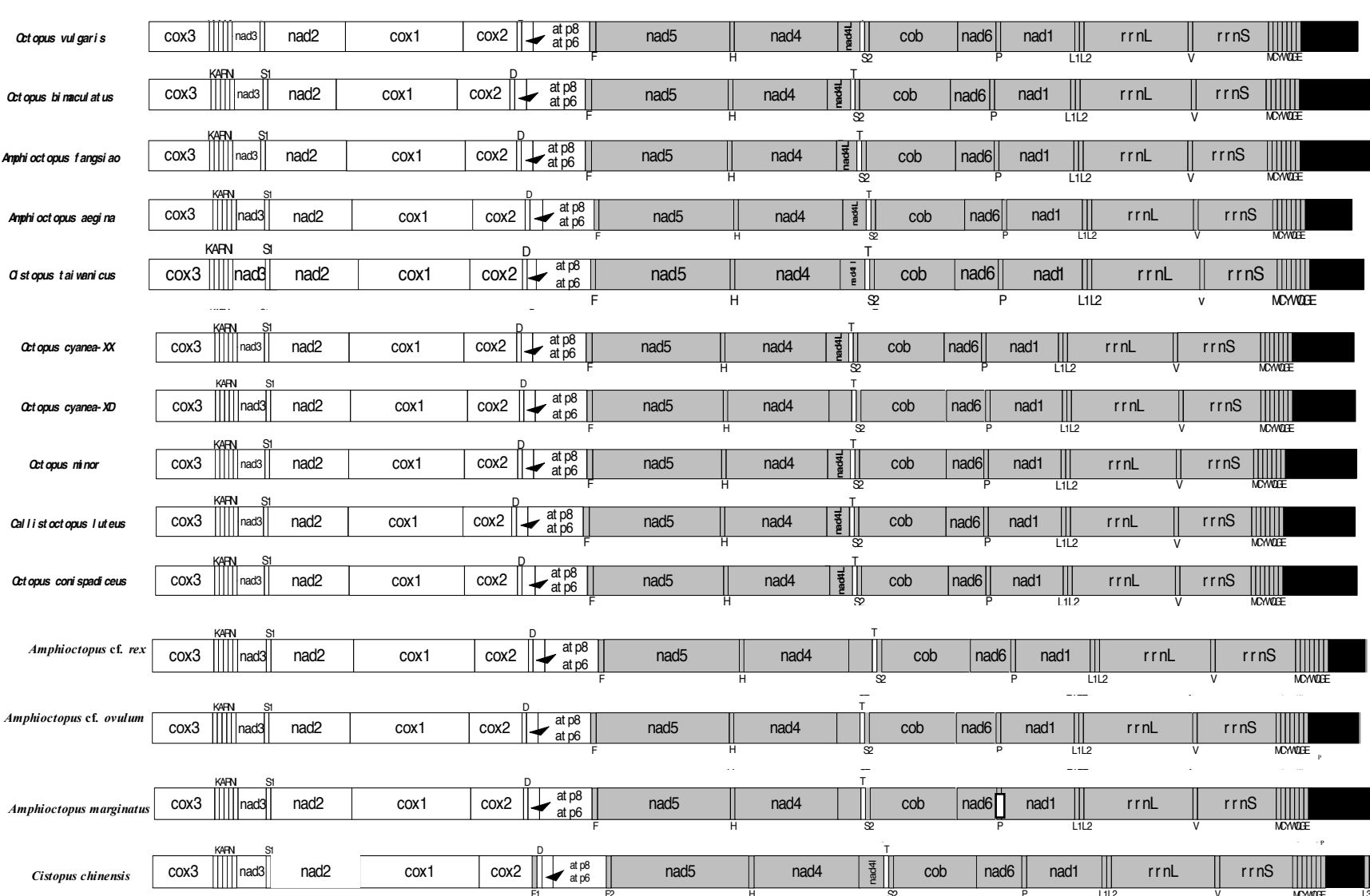
RESULTS



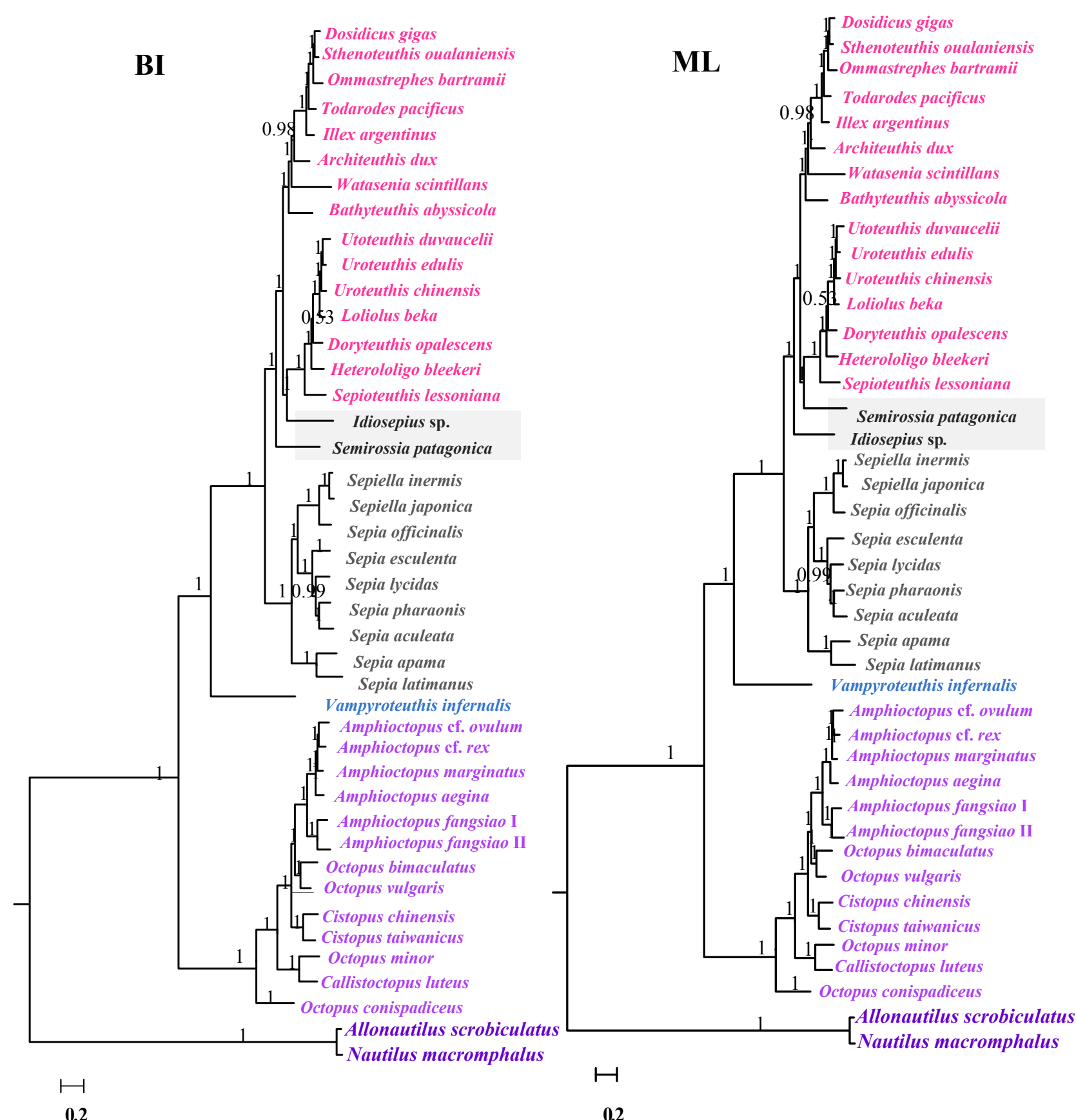
ABGD and bPTP methods based on COI (a) and 16S (b) reveal cryptic species and undiscovered species in coleoid cephalopods. Two methods detected the clear discrimination of at least 9 cryptic species or new species.



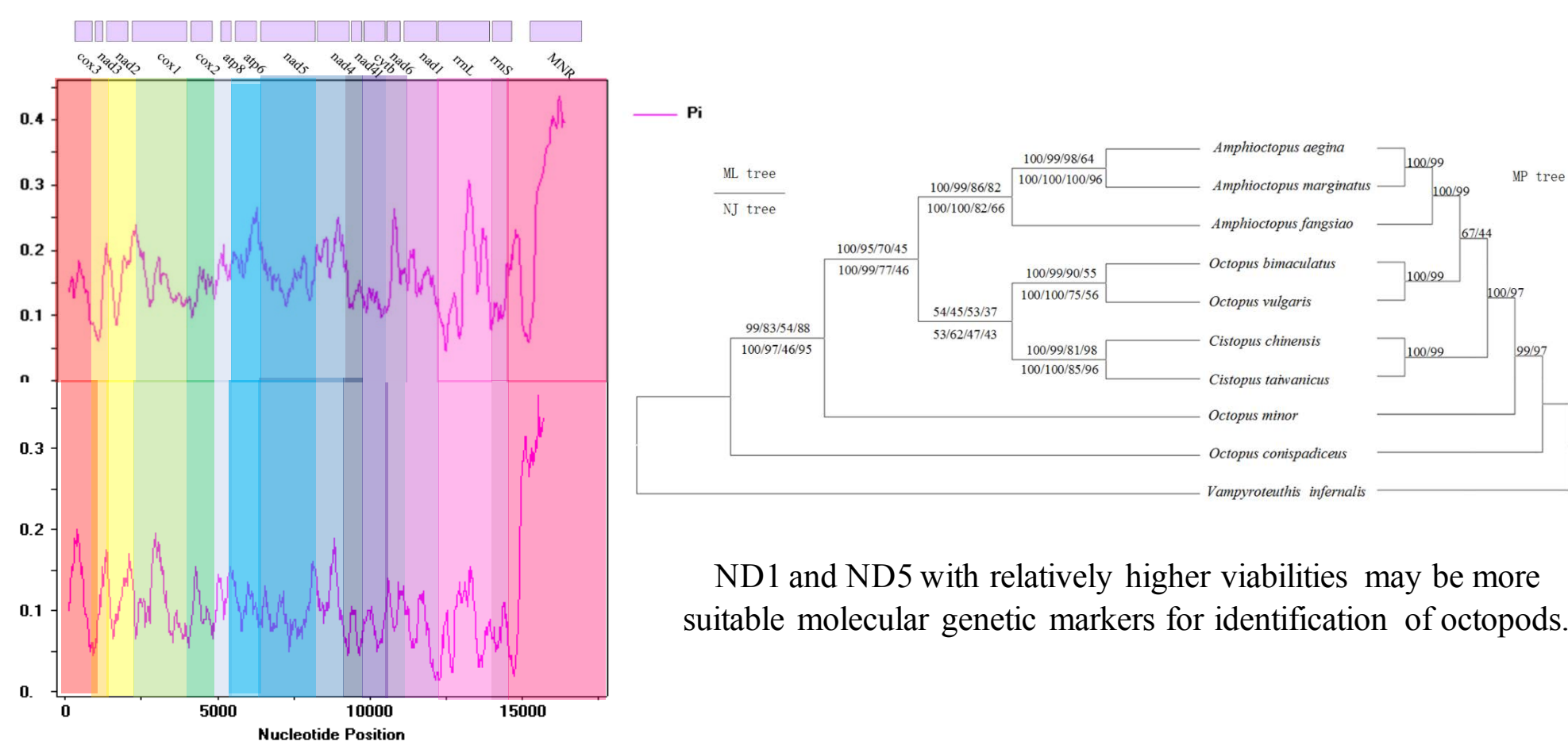
Potential cryptic species morphological identification after discrimination by ABGD and bPTP analysis.



Octopods shared highly consistent gene arrangement and re-arrangement. Small changes only presented in tRNAs. The trnP in *Amphiocotopus cf. rex* was absent, which moved backward in *A. ovalum* and *A. marginatus*. In addition, *Cistopus chinensis* was the only one showing trnL replication.



Phylogenetic analysis within Cephalopoda based on amino-acids of 13 protein-coding genes. *Amphiocotopus* genus and *Cistopus* genus were two monophyletic groups. *Octopus* genus was divided into two clusters, which was further demonstrated its polyphylietism. *O. minor* showed a very closer relationship to *C. luteus*, but exhibited a distant relationship to the other species in *Octopus sensu stricto* genus.



ND1 and ND5 with relatively higher viabilities may be more suitable molecular genetic markers for identification of octopods.

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Photographs

