

# A new eyeless species of *Nicon* (Annelida: Nereididae) from the deep Northwest Pacific Ocean

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## Abstract

A new species of the nereidid annelid, genus *Nicon* Kinberg, 1866, from KIOST Seamount, Northwest Pacific deep water is described. *Nicon* is a genus characterized by lacking paragnaths or papillae on the pharynx and composed of nine species worldwide, distributed from shallow water to deep sea. *Nicon ablepsia* sp. nov. here described is characterized by the lack of eyes on the prostomium, prolonged tentacular cirri reaching to chaetiger 6, notochaetae homogomph spinigers, neurochaetae homogomph spinigers and heterogomph falcigers. Phylogenetic relationships of *Nicon* remain undetermined based on molecular data. In this study, we constructed molecular Maximum-Likelihood phylogenetic tree from 29 nereidid species based on four marker genes: mitochondrial 16S rRNA gene and cytochrome c oxidase subunit I (COI) gene; nuclear 18S rRNA gene and 28S rRNA gene. Our analysis suggest the *Nicon* is clustered within Nereidinae, and nereidinae is not recovered as monophyletic. A key to species of *Nicon* is provided.

**Key words:** deep sea, *Nicon*, new species, Gymnonereidinae, systematics

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## 1 Introduction

Nereidids are among the most diverse annelid families, with more than 535 species classified into 43 genera (Bonyadi-Naeini et al., 2017). This family is one of the most diverse groups in the deep sea (Paterson et al., 2009). Comparison with shallow-water species, some morphological and genetic changes has been considered to be an evolutionary adaptation to extreme environment (Zhang et al., 2017). According to Gonzalez et al. (2018), the colonization of Aphroditiformia to deep sea and cave environments seems to be related with the loss of eyes. Many nereidid species belonging to subfamily Nereidinae from deep water are reported as being eyeless. Four *Neanthes* species (*Neanthes abyssorum* Hartman, 1967, *N. kermadeca* (Kirkegaard, 1995), *N. typhla* (Monro, 1930), *N. shinkai* Shimabukuro et al., 2017) are known as having no eyes (Shimabukuro et al., 2017). These species are found at depths of more than 2 000 m, with the exception of *N. typhla*. *Neanthes abyssorum* was described from Bransfield Strait, Antarctic Ocean; *N. kermadeca* was from Kermadec Trench, South Pacific Ocean; *N. typhla* was from off South Georgia Island; *N. shinkai* was from São Paulo Ridge, Southwest Atlantic Ocean. *Nereis anoculopsis* Fauchald, 1972 and *N. anoculus* Hartman, 1960 were from California deep water. They also lacked eyes (Fauchald, 1972; Hartman, 1960). *Ceratocephale abyssorum* (Hartman and Fauchald, 1971) and *Nicon abyssalis* at depth of more than 4 000 m are blind too. *Nicon*, one of the least species

rich genera of Nereididae, was described by Kinberg (1866) and including nine species. Those species have a wide distribution from intertidal to deep sea. Subfamily Gymnonereidinae, including *Ceratocephale* Malmgren, 1867, *Gymnonereis* Horst, 1919, *Micronereides* Day, 1963 and *Tambalagamia* Pillai, 1961, erected by Banse (1977) and characterised by bifid ventral cirri and chaetae forming dense bundles in the anterior 10–15 chaetigers. Fitzhugh (1987) presented the first cladistic analysis of Nereididae and expanded Gymnonereidinae to include all taxa with fully biramous parapodia and with either a smooth or papillate proboscis. Therefore *Nicon* was included within Gymnonereidinae. Santos et al. (2005) analyzed phylogenetic relationship within Nereididae, and restricted Gymnonereidinae to Banse's proposal.

In the present manuscript, a new species of eyeless *Nicon* (Nereididae) from the Northwest Pacific is described. The phylogenetic analysis was carried out to explore the relationship of *Nicon* inside Nereididae based on four molecular marker: mitochondrial 16S ribosomal RNA gene (16S rDNA) and cytochrome c oxidase subunit I (COI) gene; nuclear 18S ribosomal RNA gene (18S rDNA) and 28S ribosomal RNA gene (28S rDNA).

## 2 Materials and methods

The specimen was collected by *Hailong III* ROV (remotely-operated vehicle) during DY56 Cruise (the 56th China Ocean Scientific Research) in October 2019 and preserved in 95% ethanol

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solution then deposited in the Sample Repository of Second Institute of Oceanography (RSIO), Ministry of Natural Resources, Hangzhou, China. Specimen was examined under a stereomicroscope (Zeiss Discovery V20). To discern jaws and arrangement of the paragnaths, the withdrawn proboscis dissected. Details of the chaetae were observed using Scanning Electron Microscopy (SEM, HITACHI TM-1000).

The total genomic DNA was extracted from its muscle using DNeasy® Blood and Tissue Kit (QIAGEN, CA, USA) according to the manufacturer's protocol. DNA concentration used a NanoDrop 2000 Spectrophotometer and a Qubit fluorometer. The qualified DNA was stored in sterilized Milli-Q® water at -80°C before sequencing. The genome sequence was obtained by high-throughput sequencing (PE150) on HiSeq™ X-Ten platform (Illumina, CA, USA) at Zhejiang Tianke High Technology Development Co., Ltd. The *de novo* assembly was achieved by SPAdes genome assembler (Bankevich et al., 2012). The mitochondrial 16S rDNA and COI gene (*cox1*), and the nuclear 18S rDNA and 28S rDNA sequences were retrieved from the assembled contigs. The start and end position of the target sequences were checked by the reported universal PCR primer pairs (Norlinder et al., 2012). The 16S rDNA, COI gene, 18S rDNA and 28S rDNA sequences are deposited in GenBank with accession Nos MW525220, MW644966, MW525221 and MW525222, respectively.

The terminals consist of 28 nereidid species (Table 1). *Vrijenhoekia balaenophila* from family Hesionidae was chosen as the

outgroup species. The four marker genes were aligned using the ClustalW algorithm with default settings (15/6.66 as gap/gap length penalties) in Geneious prime software (Biomatters Ltd., New Zealand). The alignments of 16S rDNA, COI gene, 18S rDNA and 28S rDNA sequences were performed separately, and then concatenated into one file after manually trimming unalignable regions. The phylogenetic tree was performed with Maximum-Likelihood (ML) analysis via RAxML GUI v.1.5 software (Stamatakis, 2014; Silvestro and Michalak, 2012) and IQ-TREE package (Nguyen et al., 2015, Chernomor et al., 2016). A partitioned ML analysis was performed in RAxML, with 1 000 bootstrap replicates and the GTRGAMMA model (Lanave et al., 1984; Yang, 1994). The auto-selected best substitution model (-m MFP option) was used in IQ-TREE, also with 1 000 bootstrap replicates. The tree file was visualized and edited in Figtree 1.4.2 (<http://tree.bio.ed.ac.uk/software/figtree>).

### 3 Systematics

Family Nereididae Lamarck, 1818

Genus *Nicon* Kinberg, 1866

*Nicon ablepsia* sp. nov.

Material examined: Holotype, catalog number B6416500072, KIOST seamount (according to MarineRegions.org <https://www.marinerregions.org>) in the Northwest Pacific Ocean (Fig. 1), 13.391 5°N, 149.884 7°E, 2 763 m, 5 October 2019.

Description: The holotype specimen incomplete, 39 chaetigers, 17.0 mm in length, 1.5 mm wide at chaetiger 1 excluding

**Table 1.** Information and GenBank accession No. of marker genes used in the phylogenetic analysis

Subfamily/family	Taxa	16S rDNA, length/bp	COI gene, length/bp	18S rDNA, length/bp	28S rDNA, length/bp
<b>Nereidinae</b>	<i>Alitta succinea</i>	MN823959, 352	MN823952, 1 515	AY210447, 1 891	AY210464, 3 504
	<i>Ceratonereis longiceratophora</i>	–	AY583701, 400	AB106251, 1 642	AF185189, 533
	<i>Hediste japonica</i>	LC323064, 416	LC323029, 570	–	LC380658, 804
	<i>Hediste diadroma</i>	KX499500, 1 196	KX499500, 1 535	LC323646, 1 698	LC380656, 804
	<i>Nectoneanthes oxypoda</i>	–	MN256616, 658	KX290701, 1 793	LC168841, 527
	<i>Nereis heterocirrata</i>	KC833492, 462	MN256591, 658	KC840697, 790	–
	<i>Nereis pelagica</i>	AY340470, 465	HQ024126, 660	AY340438, 1 795	–
	<i>Nereis vexillosa</i>	GU362677, 442	MF121661, 658	DQ790083, 1 829	DQ790043, 3 087
	<i>Nereis</i> sp.	MF960765, 1 182	MF960765, 1 534	–	–
	<i>Paraleonnates uschakovi</i>	KX462988, 1 191	KX462988, 1 533	–	–
	<i>Perinereis wilsoni</i>	LC482173, 422	MN256542, 658	KC840691, 779	–
	<i>Perinereis aibuhitensis</i>	KF611806, 1 197	KF611806, 1 534	–	–
	<i>Perinereis cultrifera</i>	MN812983, 1 016	MN812983, 1 534	–	–
	<i>Perinereis nuntia</i>	JX644015, 1 199	JX644015, 1 537	–	–
	<i>Perinereis</i> sp.	MN823971, 1 138	MN823962, 1 536	–	–
	<i>Platynereis cf. australis</i>	MN830369, 1 196	MN830369, 1 534	–	–
	<i>Platynereis bicanaliculata</i>	MN812984, 1 170	MN812984, 1 534	–	–
	<i>Platynereis dumerilii</i>	AF178678, 1 172	AF178678, 1 534	AY894303, 1 805	–
	<i>Pseudonereis variegata</i>	MN855213, 613	MN855134, 1 308	KC840693, 779	–
	<b>Gymnonereidinae</b>	<i>Ceratocephale abyssorum</i>	GQ426618, 493	GQ426683, 421	GQ426585, 1 709
<i>Gymnonereis</i> sp.		KY704332, 472	KY805814, 633	–	–
<i>Laeonereis culveri</i>		KU992689, 1 007	KU992689, 1 536	–	–
<i>Tylorrhynchus heterochaetus</i>		KM111507, 1 236	KM111507, 1 534	–	–
	<b><i>Nicon ablepsia</i> sp. nov.</b>	<b>MW525220, 513</b>	<b>MW644966, 1 534</b>	<b>MW525221, 1 820</b>	<b>MW525222, 1 059</b>
<b>Namanereidinae</b>	<i>Namalycastis abiuma</i>	KU351089, 1 019	KU351089, 1 534	–	–
	<i>Namalycastis hawaiiensis</i>	LC213728, 521	MN125542, 658	LC213729, 1 781	LC213727, 816
	<i>Namalycastis indica</i>	MF959005, 482	MF958995, 660	–	MF959019, 766
	<i>Namalycastis jaya</i>	JX483870, 462	JN790067, 699	JX483866, 1 744	–
<b>Hesionidae</b>	<i>Vrijenhoekia balaenophila</i>	JN571884, 512	JN571831, 658	JN571895, 1 777	JN571904, 781

Note: – means the sequence was not reported. The text in bold indicates the measurement results in this paper.

parapodia (Fig. 2a). Prostomium slightly wider than long with one pair of frontal antennae and one pair of palps (Figs 2b–d).

Antennae digitate, same length as palps. Palpostyles sub-conical (Fig. 2d). Eyes absent. Peristomium isometric to chaetiger 1, with

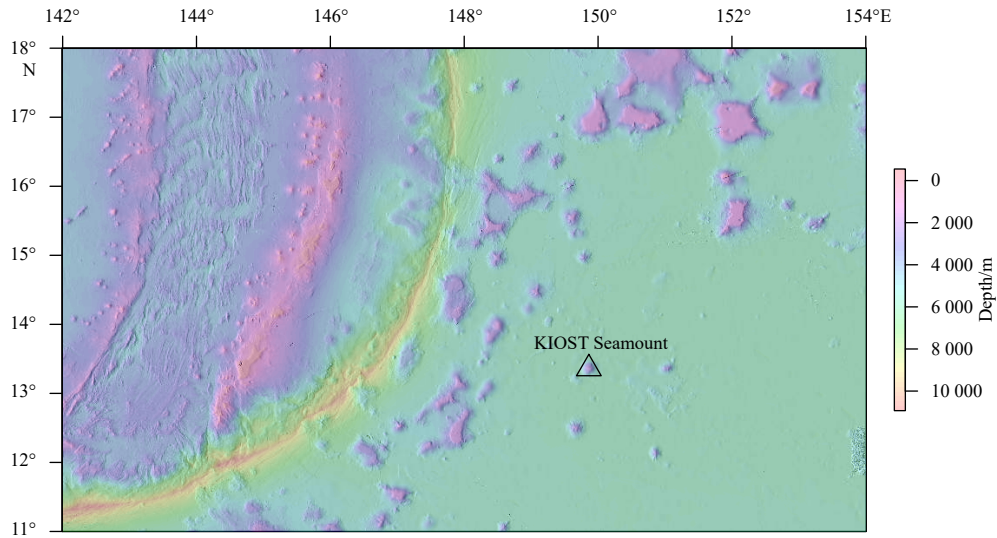


Fig. 1. Sampling site, KIOST seamount where the sample was collected.

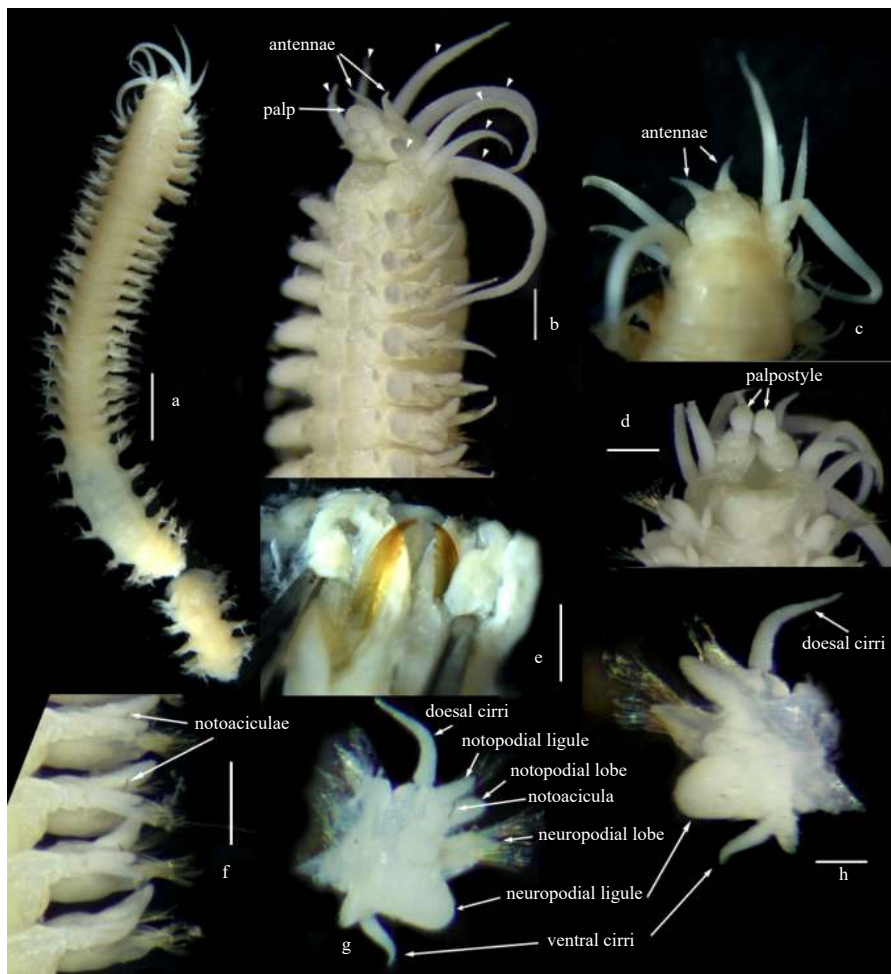


Fig. 2. *Nicon ablepsia* sp. nov.: a. dorsal view of the holotype; b. lateral view of the holotype, white triangles mark tentacular cirri; c. dorsal view of head; d. ventral view of head; e. jaws; f. chaetigers 8–17, dorsal view; g. chaetiger 7, end view; and h. chaetiger 7, frontal view. Scale bars: 2.0 mm (a), 0.5 mm (e), 0.05 mm (b, d, f, h).

four pairs of tentacular cirri; postero-dorsal pair the longest, extending back to posterior margin of 6th chaetiger. Jaws brown, dentate cutting edge with five teeth (Fig. 2e). Oral and maxillary rings without paragnaths and papillae.

First two chaetigers only with neuropodia. Biramous chaetigers present from chaetiger 3. Notopodia with dorsal cirri twice as long as notopodial ligule; dorsal cirri inserted in middle of ligule (Figs 2f–h; Fig. 3a). Notopodial ligule and notopodial lobe sub-conical; ligule slightly shorter than lobe. Neuropodial ligule conical, stouter than lobe. Ventral cirri inserted at base of ligule, slightly shorter than it. Notochaetae present from chaetiger 3, homogomph spinigers (Fig. 3d). Homogomph spinigers and heterogomph falcigers present in neurochaetae dorsal and ventral fascicle (Figs 3e and f). Acicular chaetae black in color. Notoaciculae visible on epidermis of notopodial lobe with curved distal ends on middorsal side of notopodial lobe (Figs 2f and 3b). Neoroaciculae straight with curved tips (Fig. 3e).

Total segmental number and pygidium unknown as the specimen incomplete.

Etymology: The specific name *ablepsia* come from Latin and refers to the eyeless character of this new species.

Distribution: Known only for type locality.

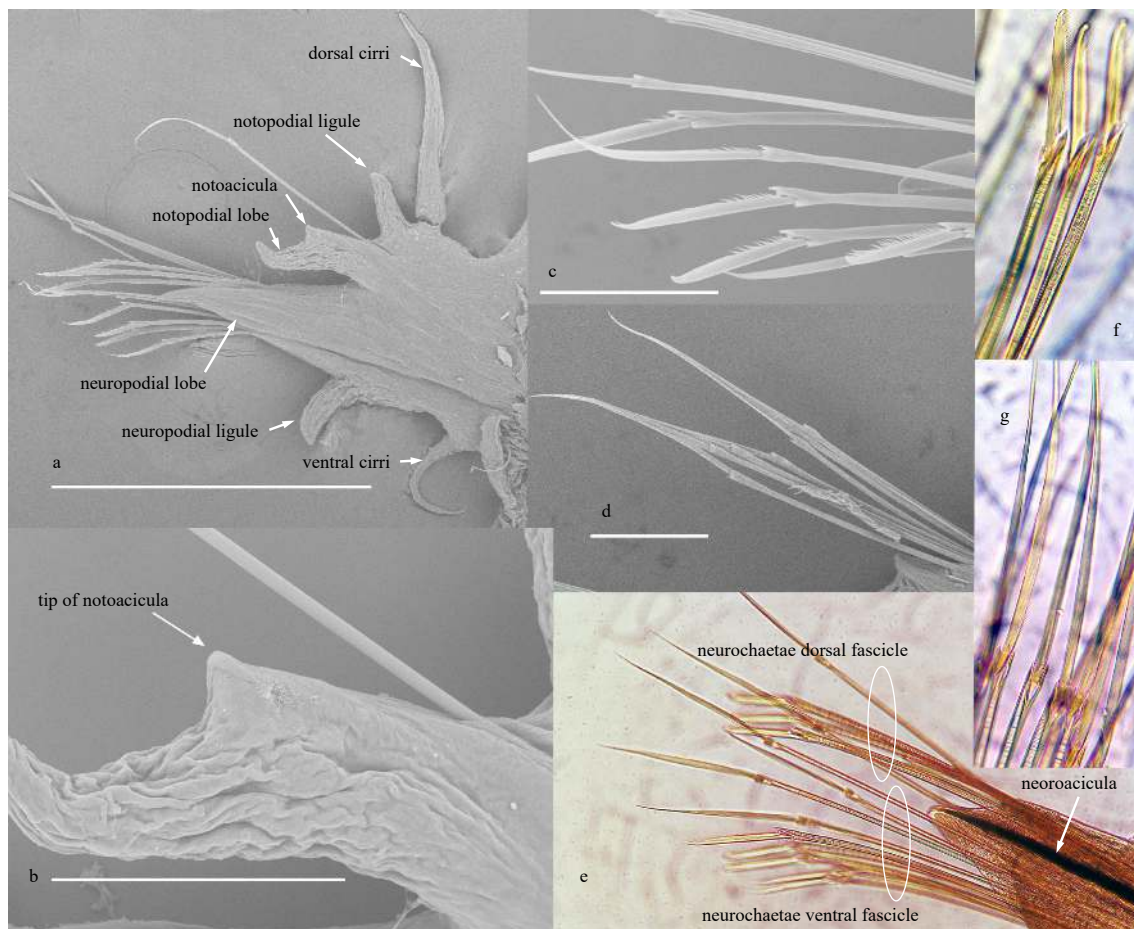
Molecular analysis: The length of 16S rDNA, COI gene, 18S rDNA and 28S rDNA sequences were confirmed by respective se-

quence of PCR primers (Norlinder et al., 2012). The primer-sequence alignments of PCR primers located in relevant position of marker genes correctly. The partial 16S rDNA, the complete COI gene, the partial 18S rDNA and 28S rDNA sequences of *N. ablepsia* sp. nov. (voucher B6416500072) contained 1 820 bp, 1 059 bp, 513 bp and 1 534 bp length, respectively.

Genera *Namalycastis* and *Tylorrhynchus* formed a well-supported clade, which was sister to the group of Nereidinae + *Nicon* + *Laeonereis* clade. Neither the Gymnonereidinae sensu Fitzhugh (1987) nor Nereidinae were recovered as monophyletic as *Nicon* and *Laeonereis* being clustered with genera from Nereidinae. The *Nicon ablepsia* sp. nov. and *Alitta succinea* showed different topological cluster in the RaxML tree (Fig. 4) and IQ-tree (Fig. A1 in Appendix) with very low support value.

#### 4 Discussion

The genus *Nicon* is characterized by having all notochaetae homogomph spinigers and neurochaetae falcigers, lacking paragnaths or papillae on oral and maxillary ring. de León-González and Trovant (2013) recognized eleven *Nicon* species. Later, *N. polaris* was transferred to *Kainonereis* since it bears elytriform structures (Conde-Vela et al., 2018). *Nicon sinica* Wu & Sun, 1979 was transferred to *Sinonereis* because it is a junior synonym of *Sinonereis heteropoda* based on affinities in chaetal and parapo-



**Fig. 3.** Parapodia and chaetae (a–d, SEM; e–g, optical picture). a. Parapodium; b. notopodial lobe, arrow shows curved tip of notoacicula; c. neurochaetae, homogomph spinigers and heterogomph falcigers; d. notochaetae, homogomph spinigers; e. neuropodium with neurochaetae; f. heterogomph falcigers; and g. notochaetae, homogomph spinigers. Scale bars: 0.5 mm (a), 0.1 mm (b–d).

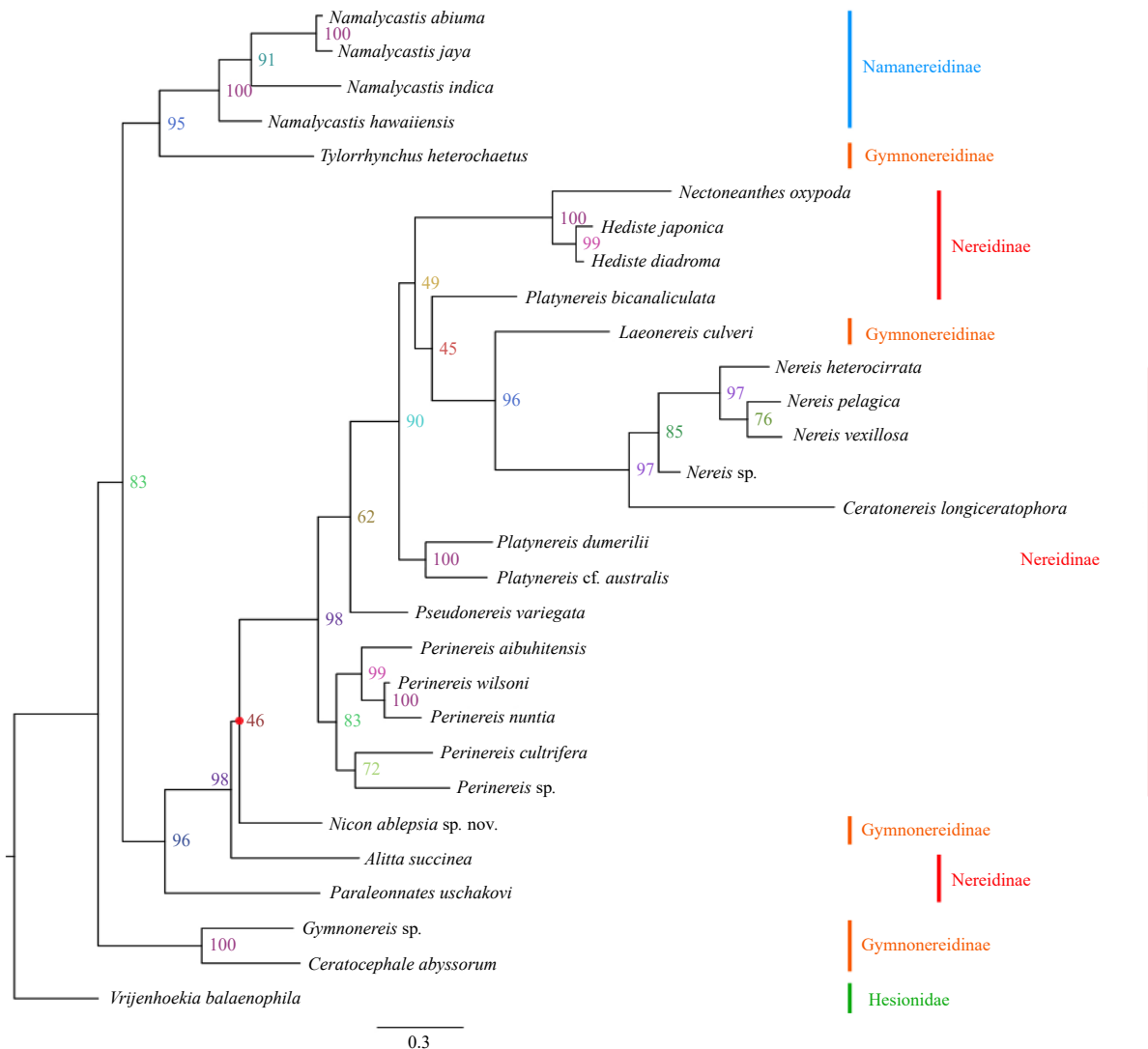
dial features (Conde-Vela and Wu, 2019). The new species lacks eyes, therefore, is easily distinguished from other species of *Nicon*. *Nicon ablepsia* sp. nov. is similar to *N. abyssalis* by absence of eyes but differs from the latter in the position of the antennae, length of tentacular cirri and relative length between peristomium and chaetiger 1. The antennae of *N. abyssalis* are inserted closely together in the frontal margin of the prostomium, and the bases of the antennae are in contact (Hartman, 1967). The antennae of *N. ablepsia* sp. nov. are separate from each other. Tentacular cirri are short in *N. abyssalis* (reaching chaetiger 2), but long in *N. ablepsia* sp. nov., reaching chaetiger 6. The peristomium of *N. abyssalis* is prolonged and nearly twice as long as chaetiger 1, while equal to the length of chaetiger 1 in *N. ablepsia* sp. nov.

The phylogeny of the Nereididae and the higher taxonomic relationships within it has been explored through molecular approaches recently (Alves et al., 2020). However, the molecular phylogenetic relationship between *Nicon* and other Nereidid

genera has not been investigated yet. Santos et al. (2005) assessed relationships of nereidids in a morphology-based parsimony analysis of 41 terminal taxa. Gymnonereidinae was restricted to *Ceratocephale*, *Gymnonereis*, *Tambalagamia* and *Micronereides*. Systematic status of *Nicon* was not resolved in Santos's results. In our tree, *Nicon ablepsia* sp. nov. is closely to *Alitta succinea* with low support. *Alitta* is characterized by conical paragnaths on maxillary and oral ring, and dorsal cirrus mid-dorsally to subterminally attached to dorsal notopodial ligule on posterior chaetigers (Bakken and Wilson, 2005). *Nicon ablepsia* sp. nov. has no paragnaths and dorsal cirrus attached to base of notopodium.

The explicit systematic status of *Nicon* is still undetermined due to the type species of *Nicon*, and some of its closely related genera are not included in the present analysis. Therefore, more extensive taxon coverage are required in further studies to elucidate the systematic status of *Nicon*.

The sequence data reported can provide base information for molecular phylogenetic research of Family Nereididae in the fu-



**Fig. 4.** The Maximum-Likelihood phylogenetic tree of 29 species based on the concatenated dataset of 16S rDNA, COI gene, 18S rDNA and 28S rDNA sequences with 1 000 bootstrap replicates. Bootstrap support values (calculated by RAxML software) are indicated adjacent to each node. The red solid dot shows the inconsistent topology cluster between the tree constructed by RAxML and IQ-TREE. All the other nodes were identical.

ture, and can also supply the basic information for designing primers. A taxonomic key to species of *Nicon* is provided here.

**Key to *Nicon* species** (emended from de León-González and Trovant, 2013)

1. Superior notopodial lobe present..... 2
  - Superior notopodial lobe absent..... 5
2. Tentacular cirri short, reaching chaetiger 2..... 3
  - Tentacular cirri reaching chaetiger 5..... *N. aestuarensis*
3. Heterogomph falcigers present on supra- and subacicular fascicle, dorsal ligule subtriangular..... 4
  - Heterogomph falcigers absent, with sesquigomph falcigers in infracicular position, dorsal ligule long and thin on median and posterior parapodia..... *N. orensanzii*
4. With homogomph falcigers in neuropodial subacicular position..... *N. rotunda*
  - Homogomph falcigers lacking..... *N. japonica*
5. Tentacular cirri short, reaching chaetiger 2..... 6
  - Tentacular cirri reaching chaetiger 5..... 7
6. Dorsal ligule cirriform, reduced in posterior chaetigers; falcigers with prolonged blade..... *N. abysssalis*
  - Dorsal ligule subtriangular, similar in size throughout; falcigers with long, anteriorly blunt blade distinctly serrated along inner margin..... *N. yaquinae*
7. Eyes present; tentacular cirri reaching chaetiger 5; supra and infracicular sesquigomph falcigers present..... *N. pettibonae*
  - Eyes absent; tentacular cirri reaching chaetiger 6; supra and infracicular sesquigomph falcigers absent.. *N. ablespia* sp. nov.
  - Tentacular cirri reaching chaetiger 9–10..... 8
8. Longest pair of tentacular cirri partially annulated on distal end; falcigers with long blade, denticulate along inner margin..... *N. maculate*
  - All tentacular cirri annulated, with cylindrical articles; falcigers with short blades, denticles on proximal inner margin..... *N. moniloceras*

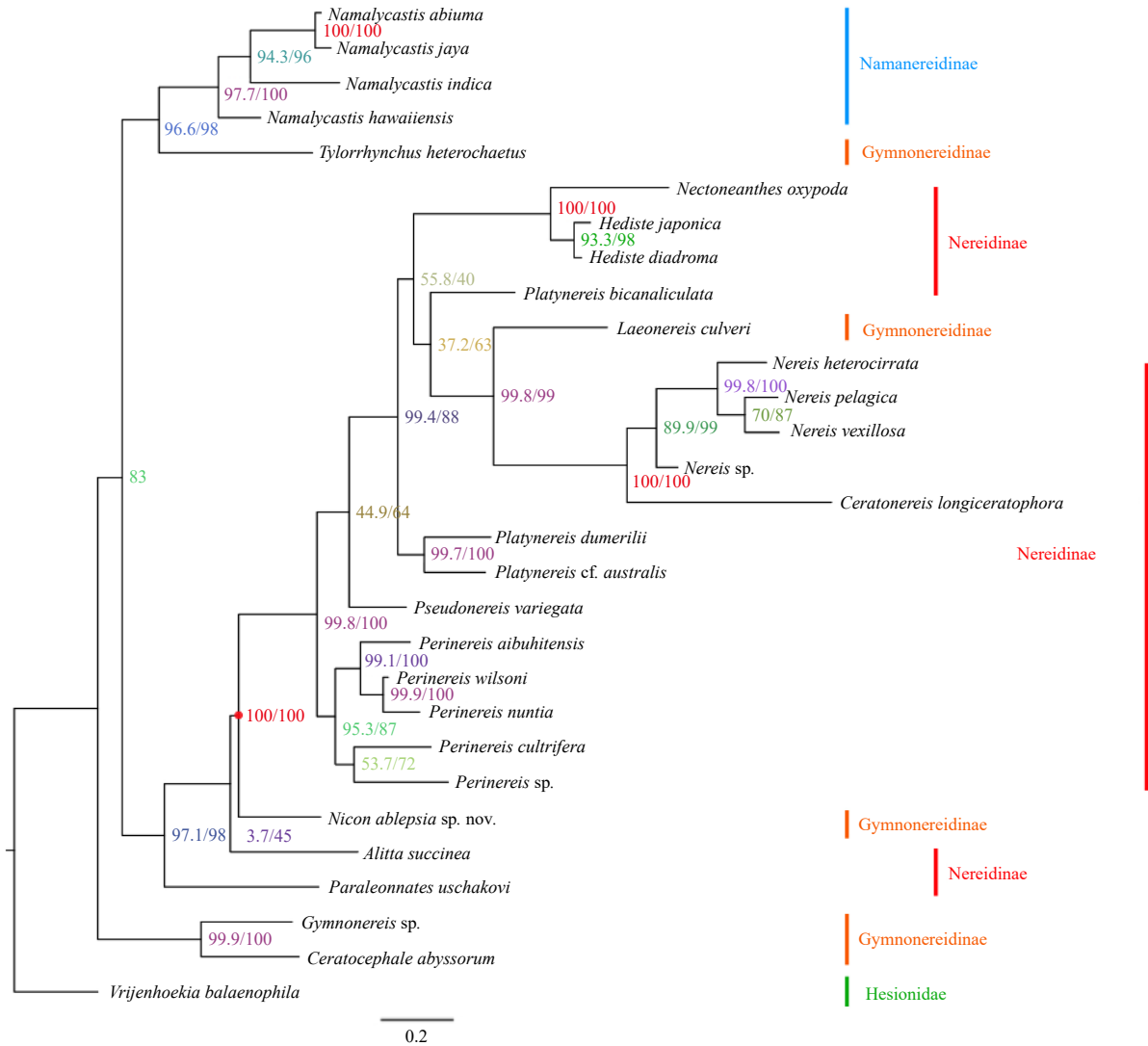
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## Appendix:



**Fig. A1.** The Maximum-Likelihood tree constructed by IQ-TREE. Numbers near the branch nodes refer to SH-aLRT/UFBoot support values (all based on 1 000 replicates). The red solid dot showed the inconsistent topology cluster between the tree constructed by RAxML and IQ-TREE. The partitioned scheme and best model information was auto selected by IQ-TREE as follows: Part 1 (1–1 158 nt, 16S rDNA), GTR+F+I+G4 model; Part 2 (1 159–2 697 nt, COI gene), TIM2+F+R4 model; Part 3 (2 698–4 600 nt, 18S rDNA), TIM2e+FQ+I+G4 model; and Part 4 (4 601–5 559 nt, 28S rDNA), TN+F model.