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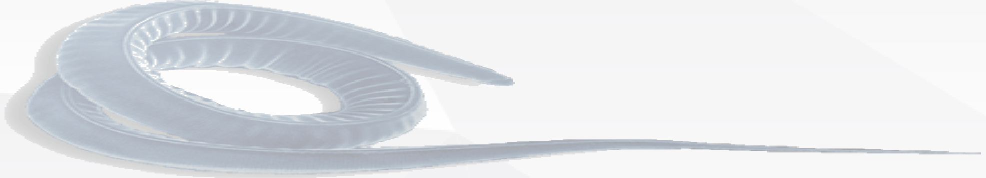


动物寄生线虫分子系统学与关键类群的演化

汇报人：李 亮

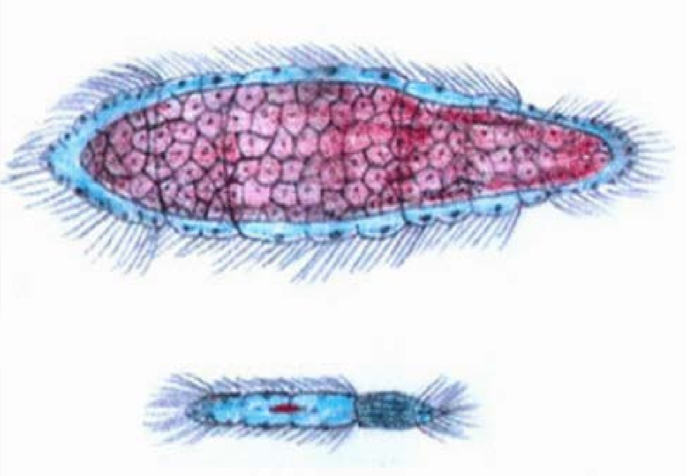
目录
CONTENTS

01

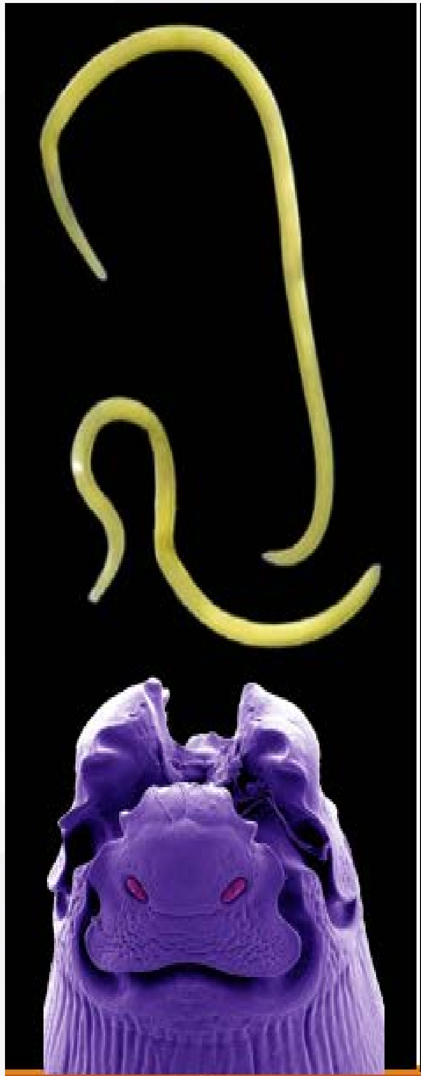
研究背景

寄生动物的主要类群

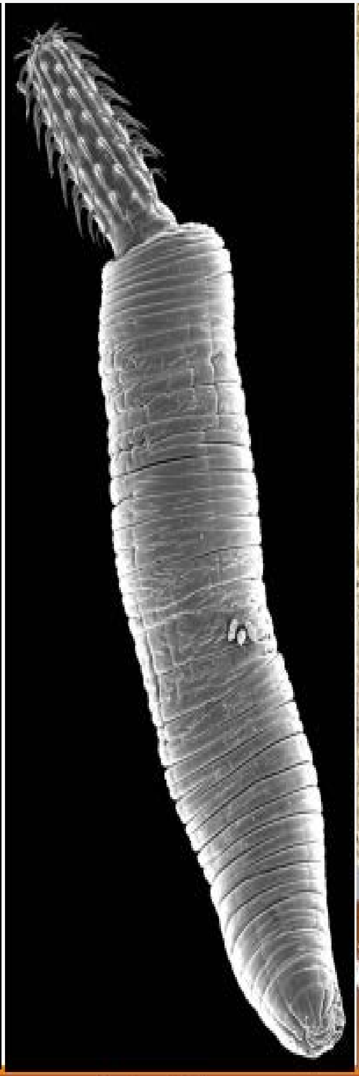
原生动物门



中生动物门



线虫动物门



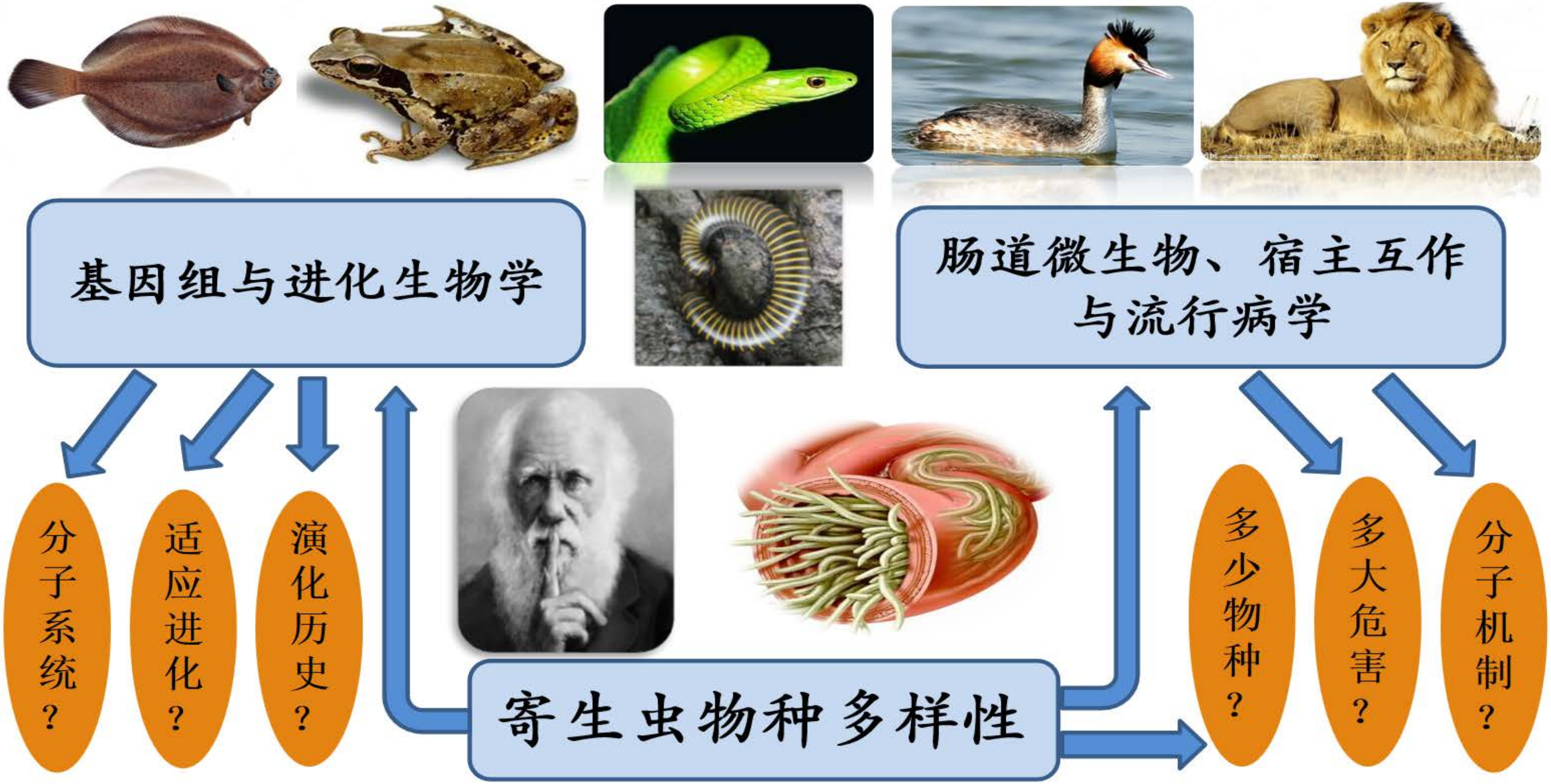
棘头动物门

线形动物门

扁形动物门

节肢动物门

主要研究方向



基因组与进化生物学

肠道微生物、宿主互作与流行病学

分子系统？

适应进化？

演化历史？

寄生虫物种多样性

多少物种？

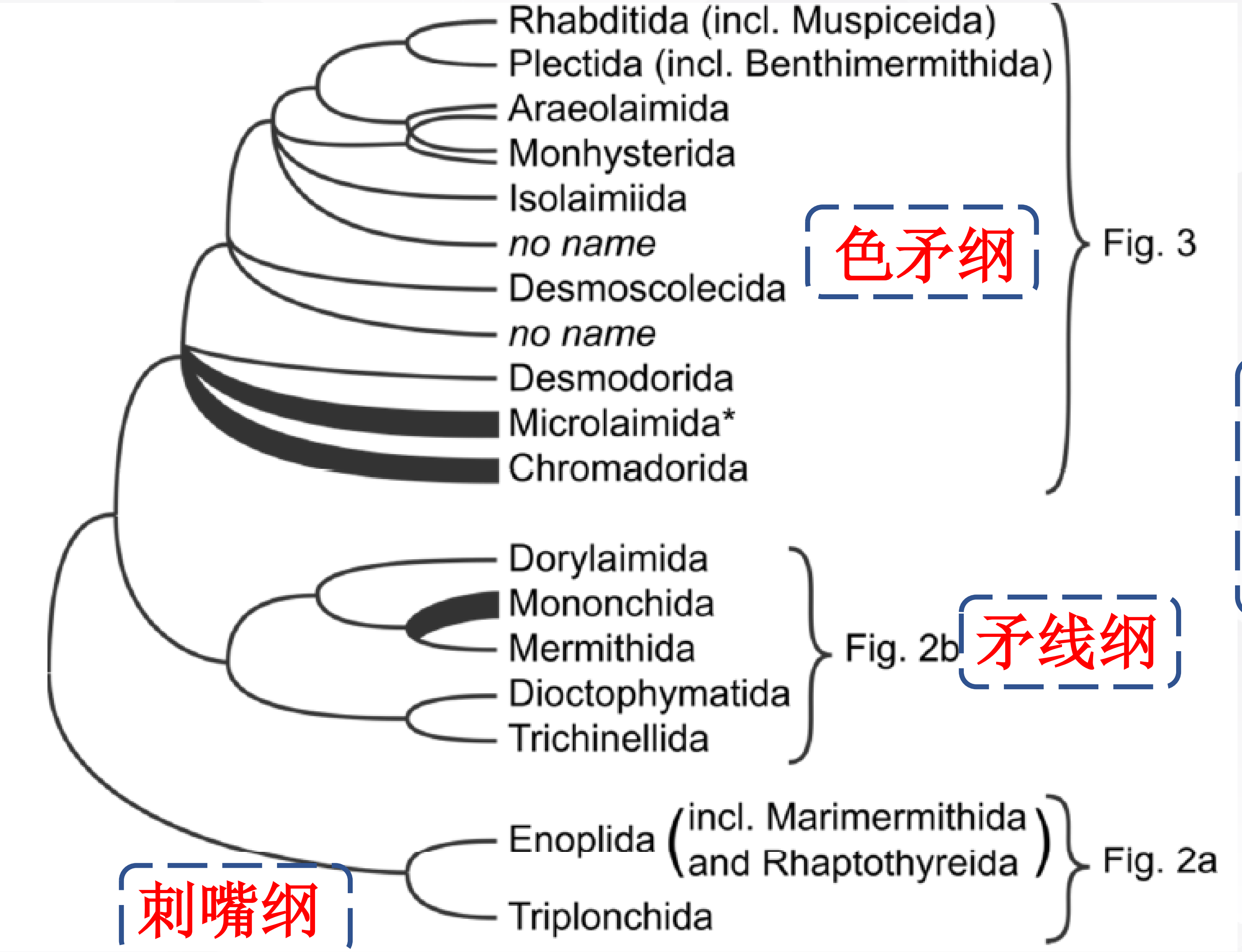
多大危害？

分子机制？

线虫动物门

3纲（刺嘴纲Enoplea、矛线纲Dorylaimea、色矛纲Chromadoria）8亚纲 超过30目 约30000种

线虫动物门分类系统

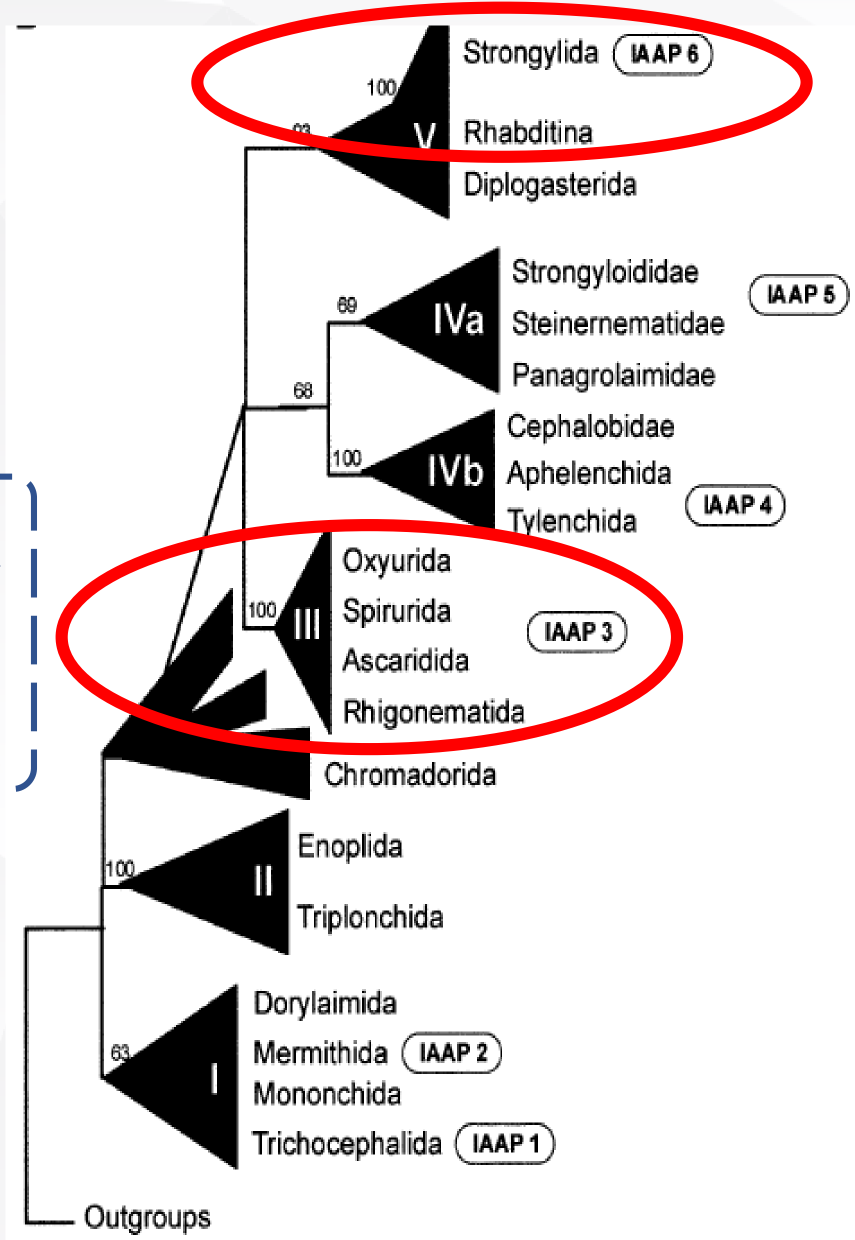


色矛纲

矛线纲

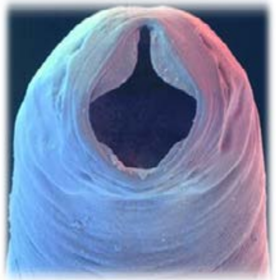
刺嘴纲

色矛纲

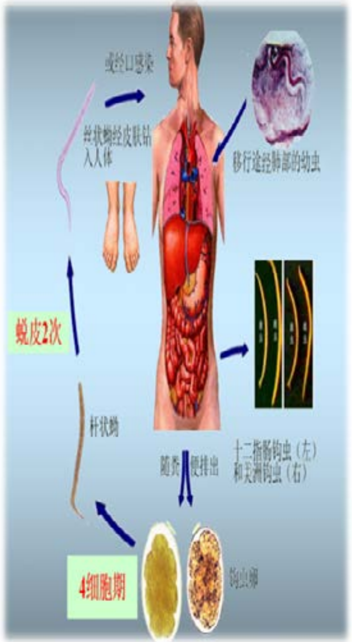


人体重要寄生线虫

Ancylostoma duodenale

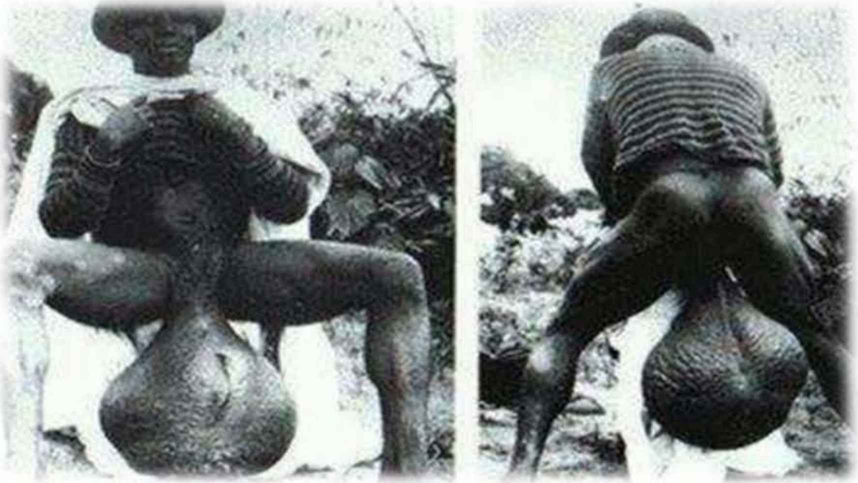


Necator americanus



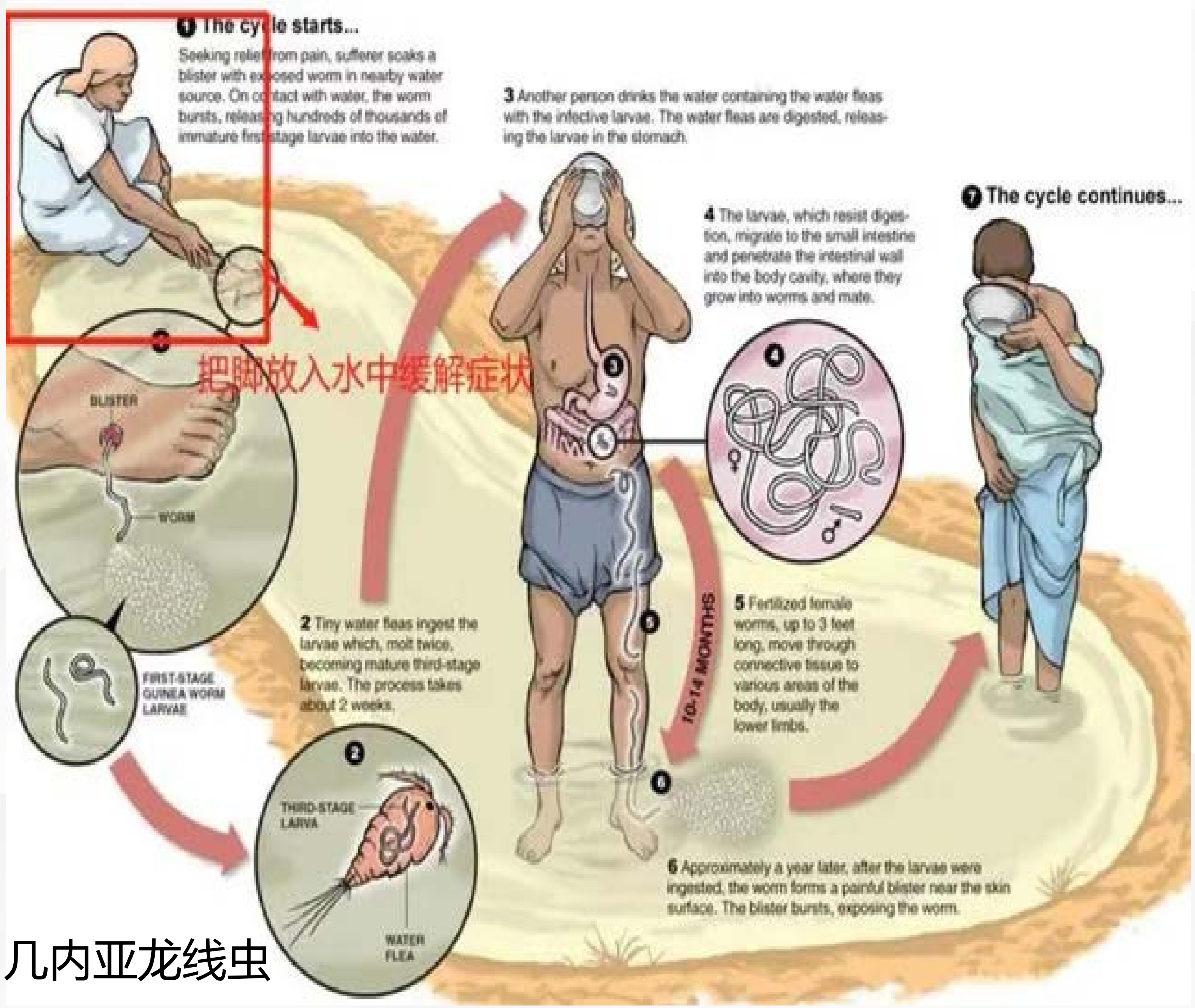
象皮肿

河盲症



巨睾症

人体重要寄生线虫



① The cycle starts...

Seeking relief from pain, sufferer soaks a blister with exposed worm in nearby water source. On contact with water, the worm bursts, releasing hundreds of thousands of immature first-stage larvae into the water.

2 Tiny water fleas ingest the larvae which, molt twice, becoming mature third-stage larvae. The process takes about 2 weeks.

3 Another person drinks the water containing the water fleas with the infective larvae. The water fleas are digested, releasing the larvae in the stomach.

4 The larvae, which resist digestion, migrate to the small intestine and penetrate the intestinal wall into the body cavity, where they grow into worms and mate.

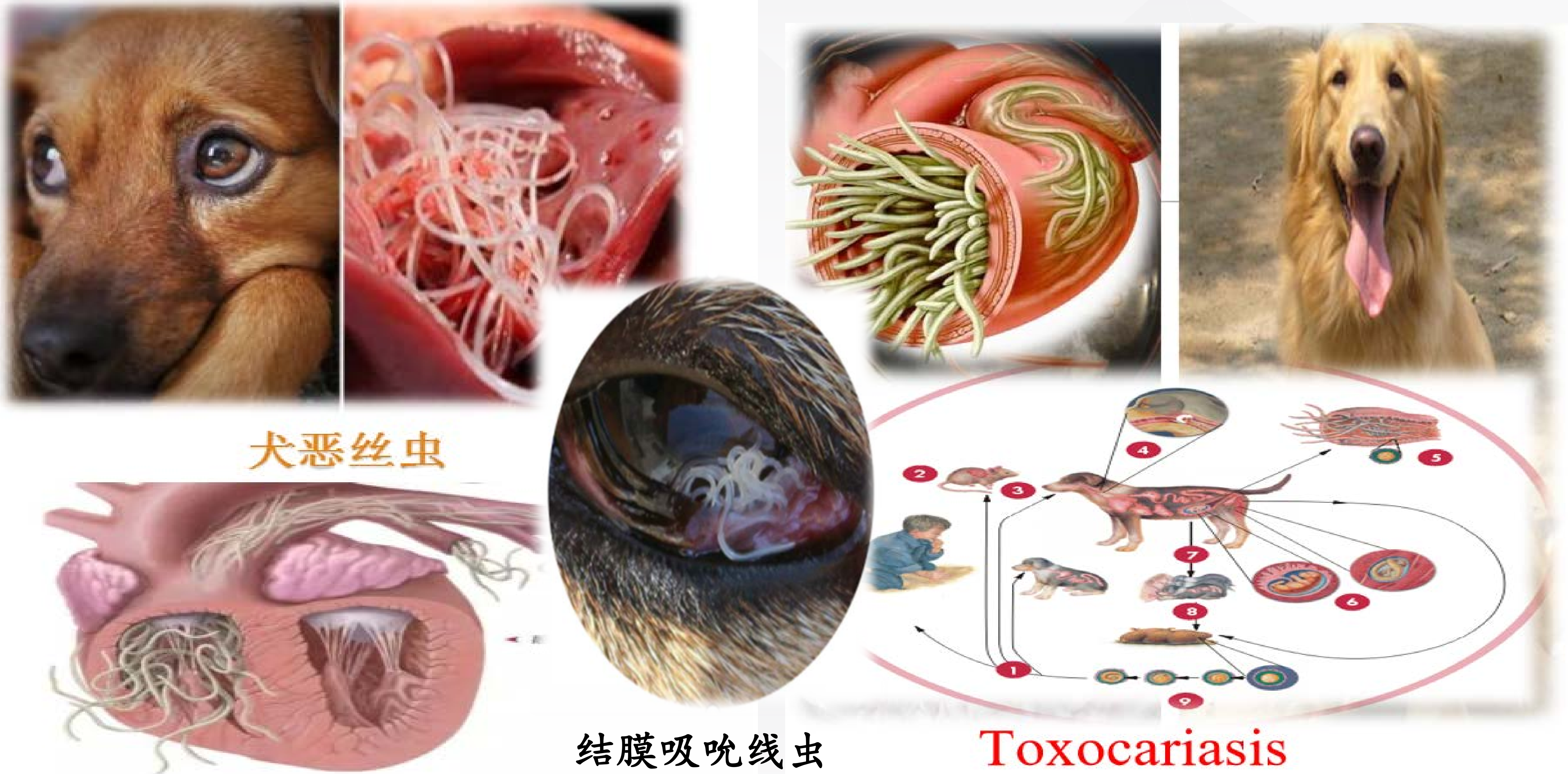
5 Fertilized female worms, up to 3 feet long, move through connective tissue to various areas of the body, usually the lower limbs.

6 Approximately a year later, after the larvae were ingested, the worm forms a painful blister near the skin surface. The blister bursts, exposing the worm.

⑦ The cycle continues...

几内亚龙线虫

家养动物重要寄生线虫



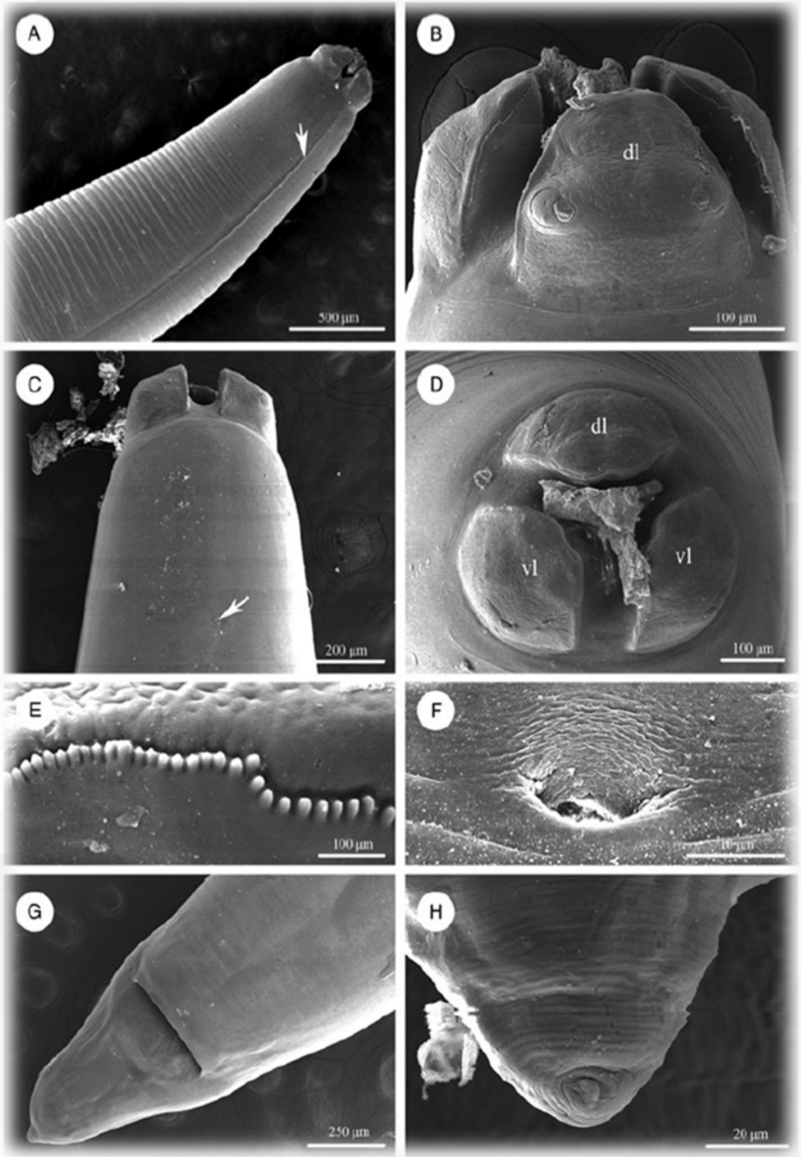
犬恶丝虫

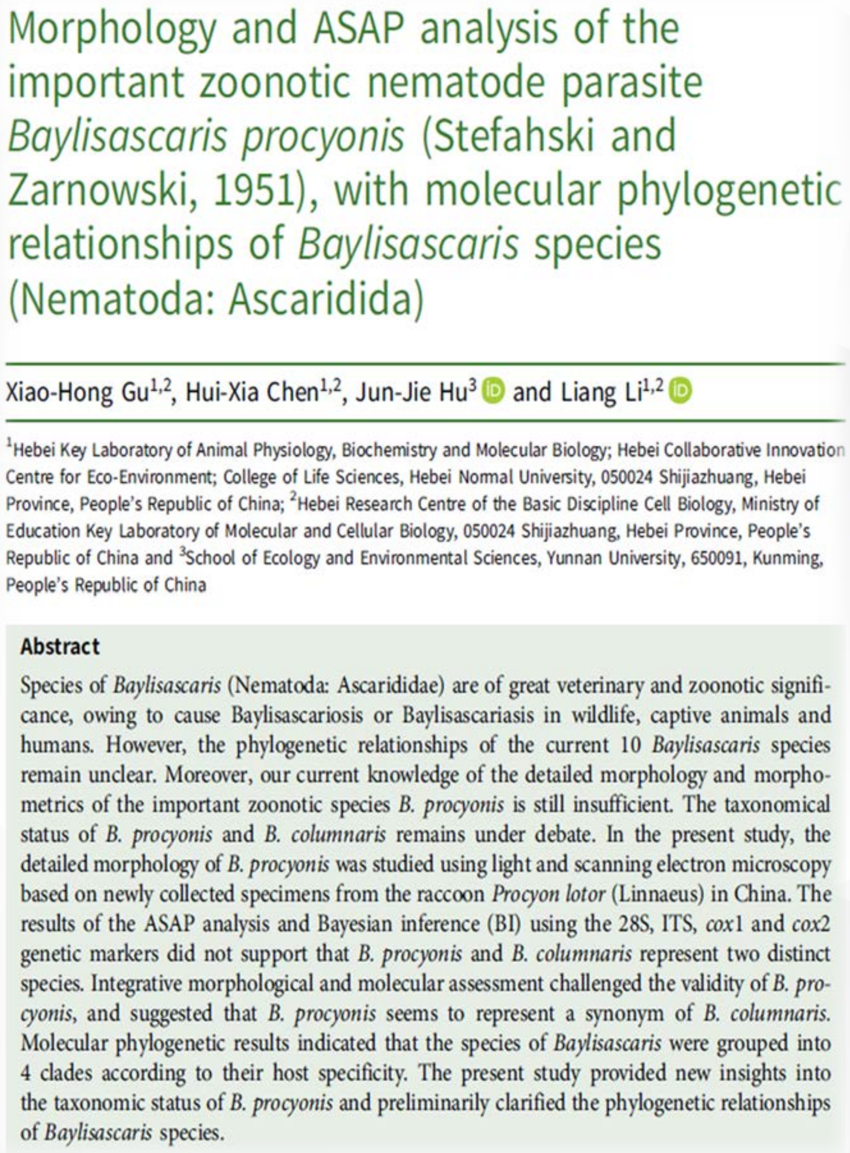
结膜吸吮线虫

Toxocariasis

动物园 养动物重要寄生线虫

浣熊贝蛔线虫





Morphology and ASAP analysis of the important zoonotic nematode parasite *Baylisascaris procyonis* (Stefahski and Zarnowski, 1951), with molecular phylogenetic relationships of *Baylisascaris* species (Nematoda: Ascaridida)

Xiao-Hong Gu[1,2], Hui-Xia Chen[1,2], Jun-Jie Hu[3] and Liang Li[1,2]

[1]Hebei Key Laboratory of Animal Physiology, Biochemistry and Molecular Biology; Hebei Collaborative Innovation Centre for Eco-Environment; College of Life Sciences, Hebei Normal University, 050024 Shijiazhuang, Hebei Province, People's Republic of China; [2]Hebei Research Centre of the Basic Discipline Cell Biology, Ministry of Education Key Laboratory of Molecular and Cellular Biology, 050024 Shijiazhuang, Hebei Province, People's Republic of China and [3]School of Ecology and Environmental Sciences, Yunnan University, 650091, Kunming, People's Republic of China

Abstract

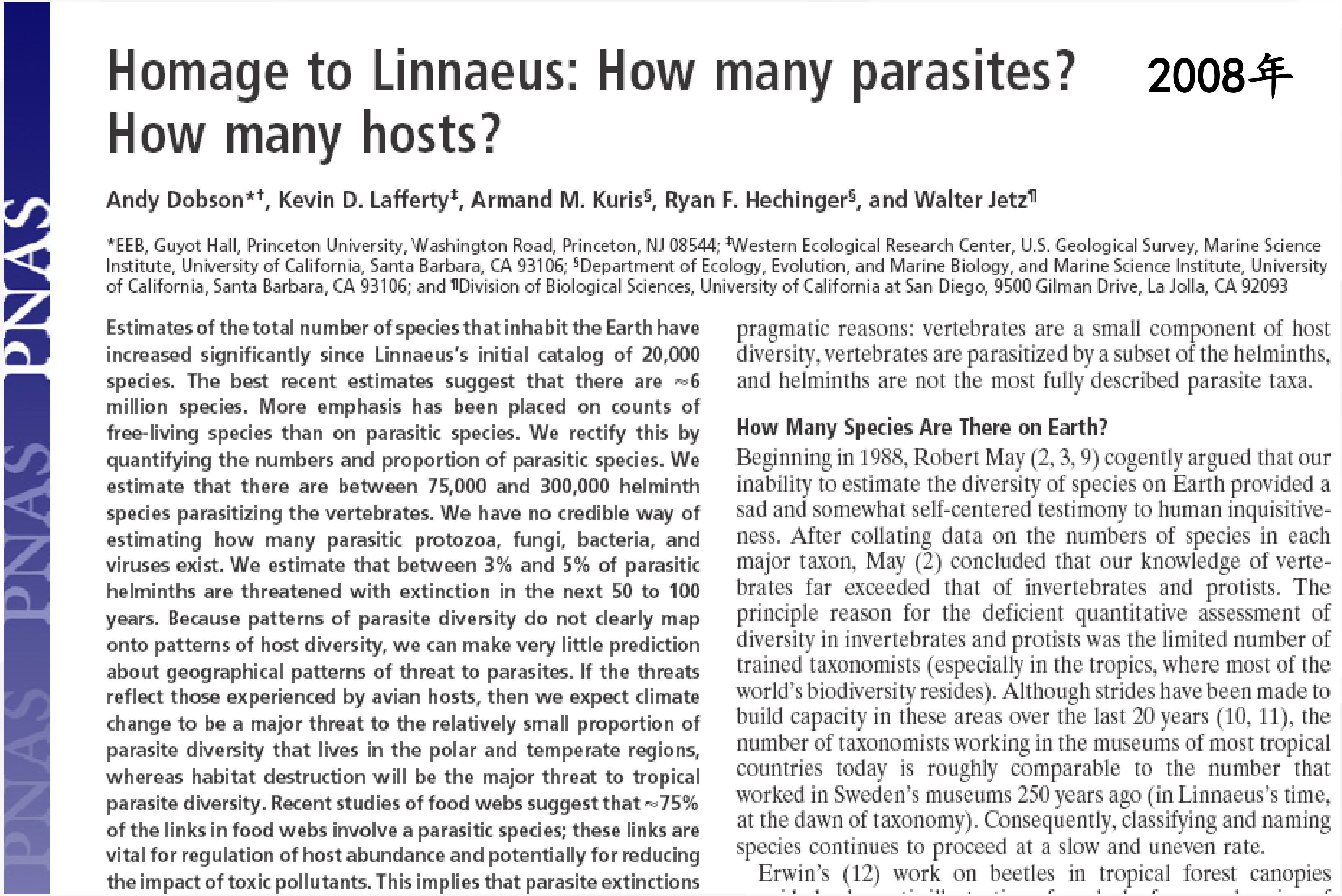
Species of *Baylisascaris* (Nematoda: Ascarididae) are of great veterinary and zoonotic significance, owing to cause Baylisascariosis or Baylisascariasis in wildlife, captive animals and humans. However, the phylogenetic relationships of the current 10 *Baylisascaris* species remain unclear. Moreover, our current knowledge of the detailed morphology and morphometrics of the important zoonotic species *B. procyonis* is still insufficient. The taxonomical status of *B. procyonis* and *B. columnaris* remains under debate. In the present study, the detailed morphology of *B. procyonis* was studied using light and scanning electron microscopy based on newly collected specimens from the raccoon *Procyon lotor* (Linnaeus) in China. The results of the ASAP analysis and Bayesian inference (BI) using the 28S, ITS, *cox*1 and *cox*2 genetic markers did not support that *B. procyonis* and *B. columnaris* represent two distinct species. Integrative morphological and molecular assessment challenged the validity of *B. procyonis*, and suggested that *B. procyonis* seems to represent a synonym of *B. columnaris*. Molecular phylogenetic results indicated that the species of *Baylisascaris* were grouped into 4 clades according to their host specificity. The present study provided new insights into the taxonomic status of *B. procyonis* and preliminarily clarified the phylogenetic relationships of *Baylisascaris* species.

02

动物寄生线虫物种多样性

动物寄生虫物种多样性研究

98. 地球上有多少物种?



Homage to Linnaeus: How many parasites? How many hosts?

2008年

Andy Dobson*†, Kevin D. Lafferty‡, Armand M. Kuris§, Ryan F. Hechinger§, and Walter Jetz¶

*EEB, Guyot Hall, Princeton University, Washington Road, Princeton, NJ 08544; ‡Western Ecological Research Center, U.S. Geological Survey, Marine Science Institute, University of California, Santa Barbara, CA 93106; §Department of Ecology, Evolution, and Marine Biology, and Marine Science Institute, University of California, Santa Barbara, CA 93106; and ¶Division of Biological Sciences, University of California at San Diego, 9500 Gilman Drive, La Jolla, CA 92093

Estimates of the total number of species that inhabit the Earth have increased significantly since Linnaeus's initial catalog of 20,000 species. The best recent estimates suggest that there are ≈6 million species. More emphasis has been placed on counts of free-living species than on parasitic species. We rectify this by quantifying the numbers and proportion of parasitic species. We estimate that there are between 75,000 and 300,000 helminth species parasitizing the vertebrates. We have no credible way of estimating how many parasitic protozoa, fungi, bacteria, and viruses exist. We estimate that between 3% and 5% of parasitic helminths are threatened with extinction in the next 50 to 100 years. Because patterns of parasite diversity do not clearly map onto patterns of host diversity, we can make very little prediction about geographical patterns of threat to parasites. If the threats reflect those experienced by avian hosts, then we expect climate change to be a major threat to the relatively small proportion of parasite diversity that lives in the polar and temperate regions, whereas habitat destruction will be the major threat to tropical parasite diversity. Recent studies of food webs suggest that ≈75% of the links in food webs involve a parasitic species; these links are vital for regulation of host abundance and potentially for reducing the impact of toxic pollutants. This implies that parasite extinctions

pragmatic reasons: vertebrates are a small component of host diversity, vertebrates are parasitized by a subset of the helminths, and helminths are not the most fully described parasite taxa.

How Many Species Are There on Earth?

Beginning in 1988, Robert May (2, 3, 9) cogently argued that our inability to estimate the diversity of species on Earth provided a sad and somewhat self-centered testimony to human inquisitiveness. After collating data on the numbers of species in each major taxon, May (2) concluded that our knowledge of vertebrates far exceeded that of invertebrates and protists. The principle reason for the deficient quantitative assessment of diversity in invertebrates and protists was the limited number of trained taxonomists (especially in the tropics, where most of the world's biodiversity resides). Although strides have been made to build capacity in these areas over the last 20 years (10, 11), the number of taxonomists working in the museums of most tropical countries today is roughly comparable to the number that worked in Sweden's museums 250 years ago (in Linnaeus's time, at the dawn of taxonomy). Consequently, classifying and naming species continues to proceed at a slow and uneven rate.

Erwin's (12) work on beetles in tropical forest canopies

动物寄生虫物种多样性研究

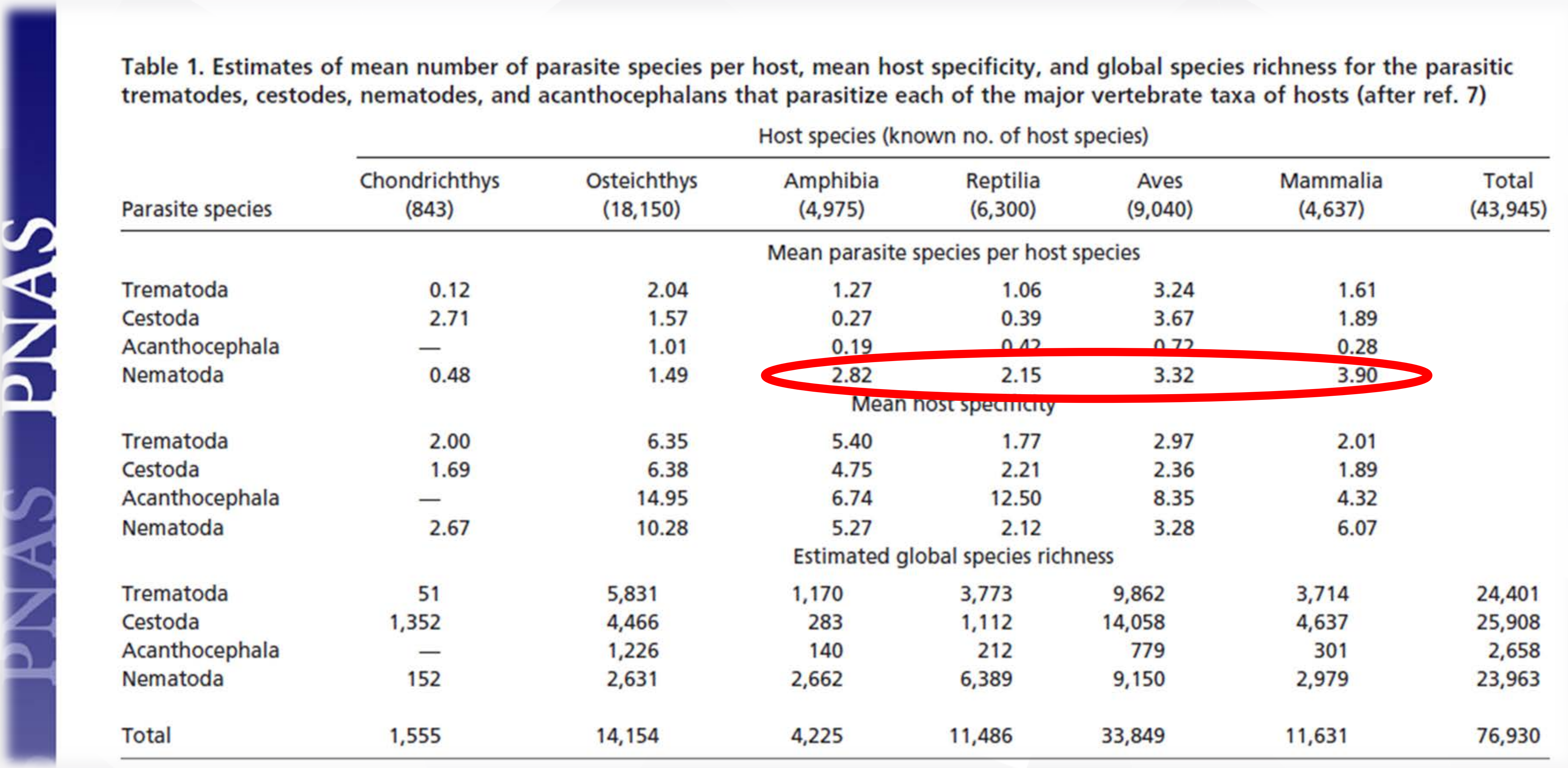


Table 1. Estimates of mean number of parasite species per host, mean host specificity, and global species richness for the parasitic trematodes, cestodes, nematodes, and acanthocephalans that parasitize each of the major vertebrate taxa of hosts (after ref. 7)

	Host species (known no. of host species)						
Parasite species	Chondrichthys (843)	Osteichthys (18,150)	Amphibia (4,975)	Reptilia (6,300)	Aves (9,040)	Mammalia (4,637)	Total (43,945)
			Mean parasite species per host species				
Trematoda	0.12	2.04	1.27	1.06	3.24	1.61	
Cestoda	2.71	1.57	0.27	0.39	3.67	1.89	
Acanthocephala	—	1.01	0.19	0.42	0.72	0.28	
Nematoda	0.48	1.49	2.82	2.15	3.32	3.90	
			Mean host specificity				
Trematoda	2.00	6.35	5.40	1.77	2.97	2.01	
Cestoda	1.69	6.38	4.75	2.21	2.36	1.89	
Acanthocephala	—	14.95	6.74	12.50	8.35	4.32	
Nematoda	2.67	10.28	5.27	2.12	3.28	6.07	
			Estimated global species richness				
Trematoda	51	5,831	1,170	3,773	9,862	3,714	24,401
Cestoda	1,352	4,466	283	1,112	14,058	4,637	25,908
Acanthocephala	—	1,226	140	212	779	301	2,658
Nematoda	152	2,631	2,662	6,389	9,150	2,979	23,963
Total	1,555	14,154	4,225	11,486	33,849	11,631	76,930

动物寄生虫物种多样性研究


Xie *et al. Parasites & Vectors* (2017) 10:277
DOI 10.1186/s13071-017-2209-2

Parasites & Vectors

RESEARCH Open Access

Ancylostoma ailuropodae n. sp. (Nematoda: Ancylostomatidae), a new hookworm parasite isolated from wild giant pandas in Southwest China

Yue Xie[1,2], Eric P. Hoberg[3], Zijiang Yang[4], Joseph F. Urban Jr[2] and Guangyou Yang[1*]

Abstract

Background: Hookworms belonging to the genus *Ancylostoma* (Dubini, 1843) cause ancylostomiasis, a disease of considerable concern in humans and domestic and wild animals. Molecular and epidemiological data support evidence for the zoonotic potential among species of *Ancylostoma* where transmission to humans is facilitated by rapid urbanization and increased human-wildlife interactions. It is important to assess and describe these potential zoonotic parasite species in wildlife, especially in hosts that have physiological similarities to humans and share their habitat. Moreover, defining species diversity within parasite groups that can circulate among free-ranging host species and humans also provides a pathway to understanding the distribution of infection and disease. In this study, we describe a previously unrecognized species of hookworm in the genus *Ancylostoma* in the giant panda, including criteria for morphological and molecular characterization.

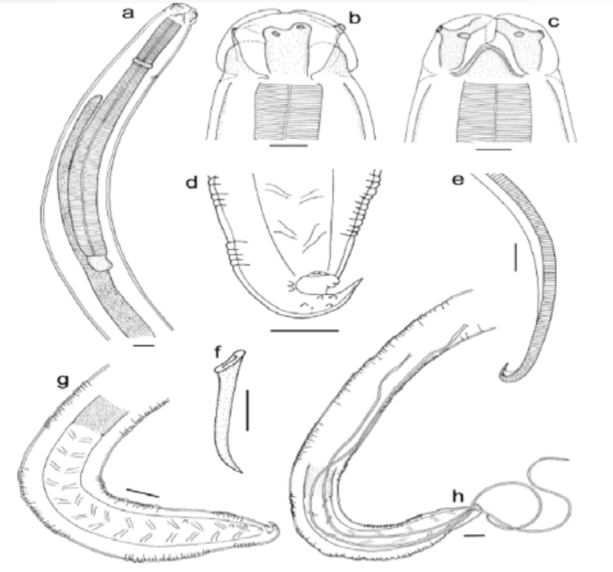
Methods: The hookworm specimens were obtained from a wild giant panda that died in the Fengtongzai Natural Reserve in Sichuan Province of China in November 2013. They were microscopically examined and then genetically analyzed by sequencing the nuclear internal transcribed spacer (ITS, ITS1-5.8S-ITS2) and mitochondrial cytochrome *c* oxidase subunit 1 (*cox*1) genes in two representative specimens (one female and one male, FTZ1 and FTZ2, respectively).

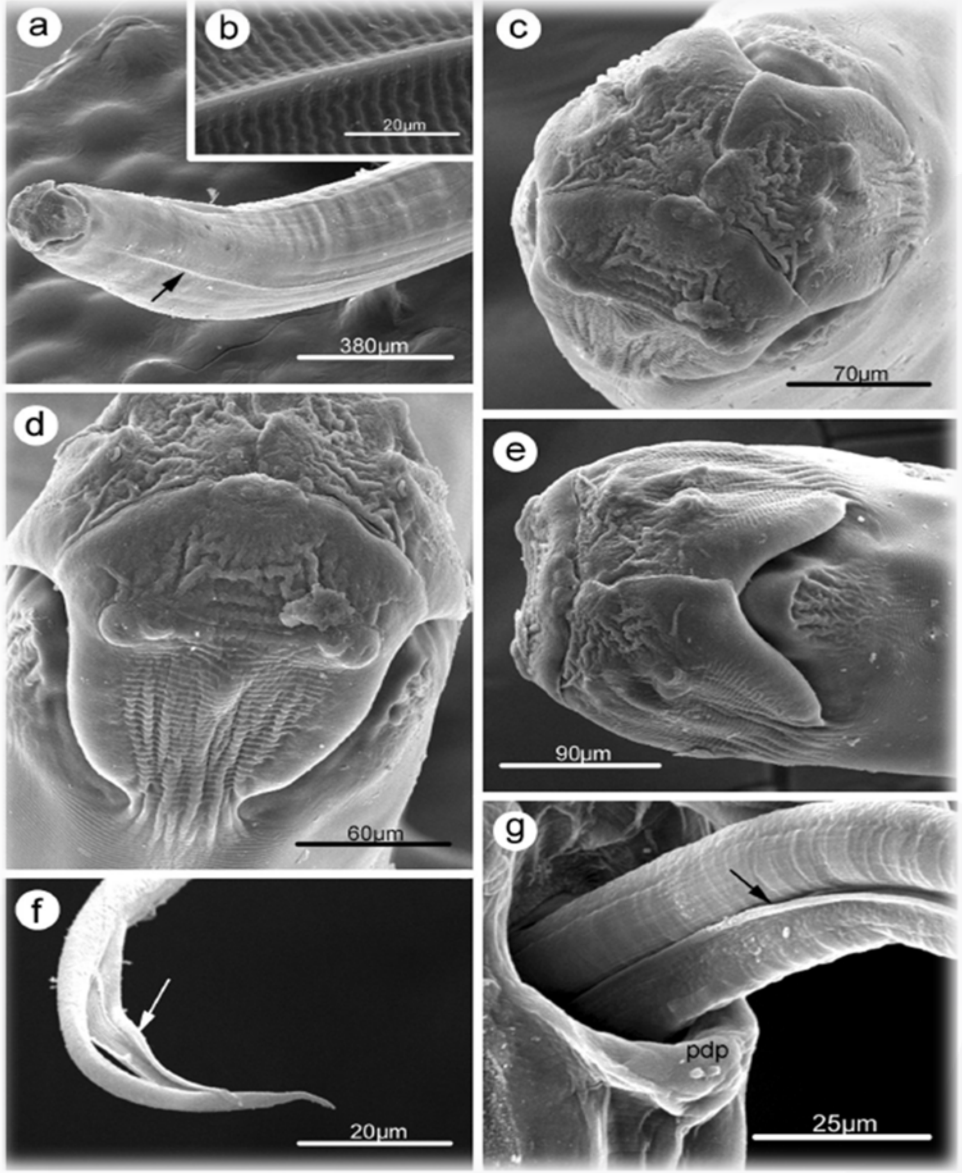
Results: *Ancylostoma ailuropodae* n. sp. is proposed for these hookworms. Morphologically the hookworm specimens differ from other congeneric species primarily based on the structure of the buccal capsule in males and females, characterized by 2 pairs of ventrolateral and 2 pairs of dorsolateral teeth; males differ in the structure and shape of the copulatory bursa, where the dorsal ray possesses 2 digitations. Pairwise nuclear and mitochondrial DNA comparisons, genetic distance analysis, and phylogenetic data strongly indicate that *A. ailuropodae* from giant pandas is a separate species which shared a most recent common ancestor with *A. ceylanicum* Looss, 1911 in the genus *Ancylostoma* (family Ancylostomatidae).

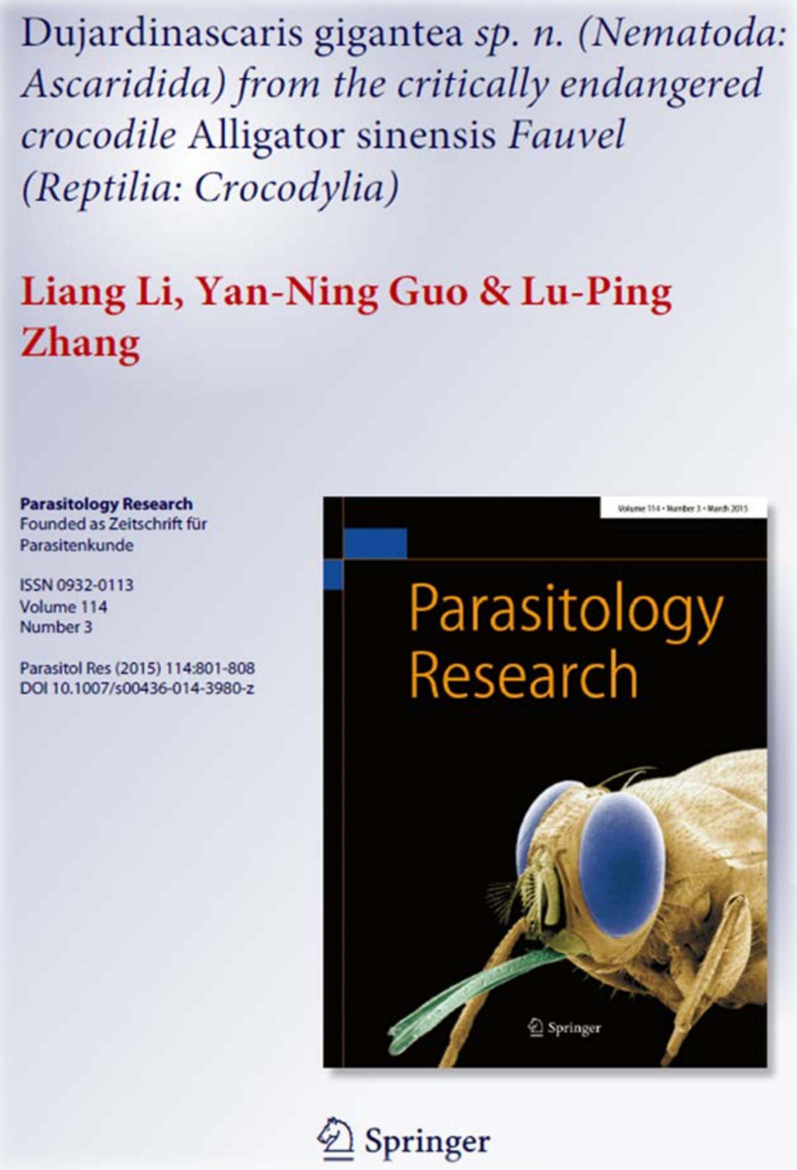
(Continued on next page)

动物寄生虫物种多样性研究

扬子鳄*Alligator sinensis*







Dujardinascaris gigantea *sp. n. (Nematoda: Ascaridida) from the critically endangered crocodile* Alligator sinensis *Fauvel (Reptilia: Crocodylia)*

Liang Li, Yan-Ning Guo & Lu-Ping Zhang

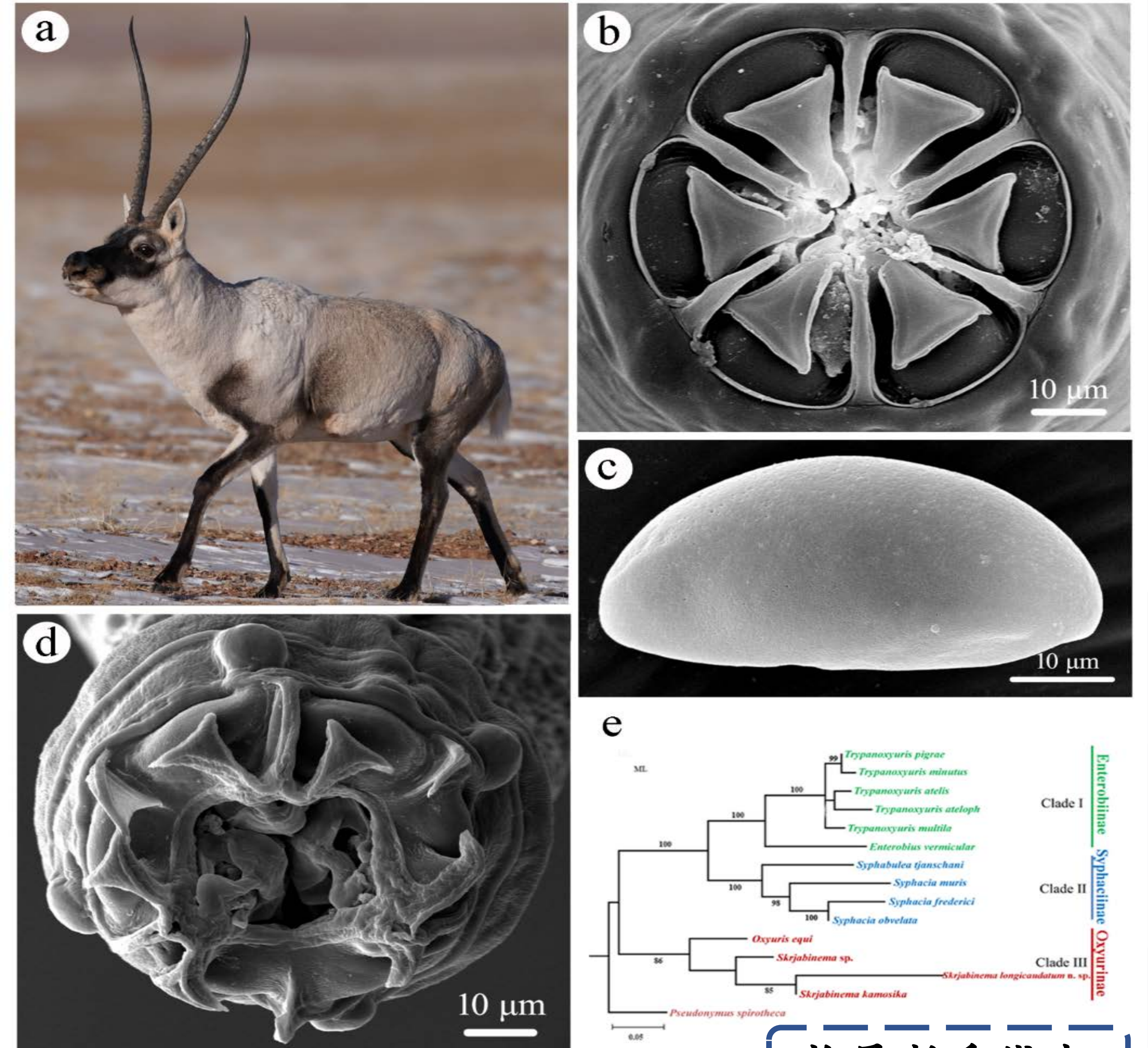
Parasitology Research
Founded as Zeitschrift für
Parasitenkunde

ISSN 0932-0113
Volume 114
Number 3

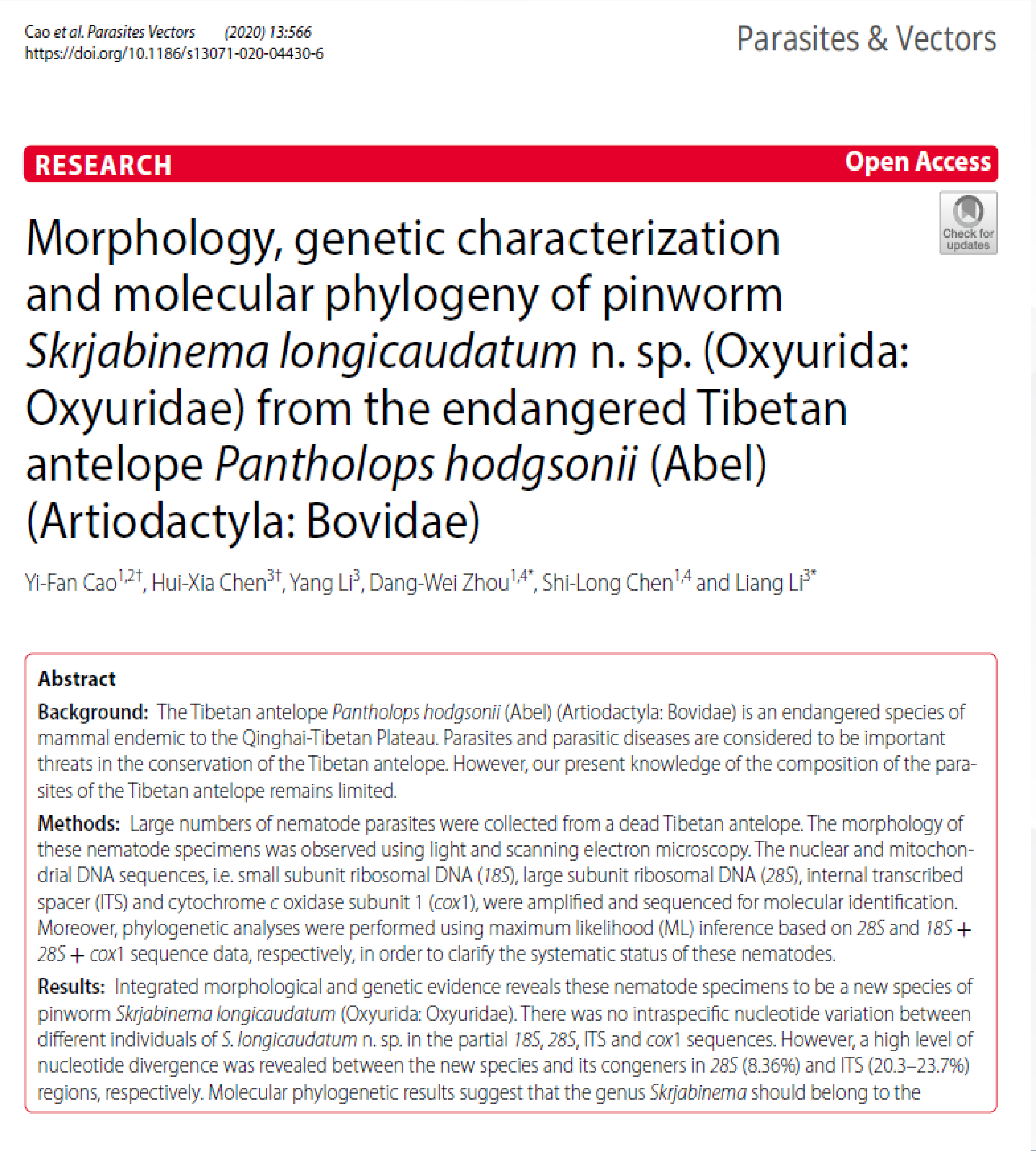
Parasitol Res (2015) 114:801-808
DOI 10.1007/s00436-014-3980-z

Springer

动物寄生虫物种多样性研究



长尾斯氏线虫


Cao *et al. Parasites Vectors* (2020) 13:566
https://doi.org/10.1186/s13071-020-04430-6

Parasites & Vectors

RESEARCH **Open Access**

Morphology, genetic characterization and molecular phylogeny of pinworm *Skrjabinema longicaudatum* n. sp. (Oxyurida: Oxyuridae) from the endangered Tibetan antelope *Pantholops hodgsonii* (Abel) (Artiodactyla: Bovidae)

Yi-Fan Cao[1,2†], Hui-Xia Chen[3†], Yang Li[3], Dang-Wei Zhou[1,4*], Shi-Long Chen[1,4] and Liang Li[3*]

Abstract

Background: The Tibetan antelope *Pantholops hodgsonii* (Abel) (Artiodactyla: Bovidae) is an endangered species of mammal endemic to the Qinghai-Tibetan Plateau. Parasites and parasitic diseases are considered to be important threats in the conservation of the Tibetan antelope. However, our present knowledge of the composition of the parasites of the Tibetan antelope remains limited.

Methods: Large numbers of nematode parasites were collected from a dead Tibetan antelope. The morphology of these nematode specimens was observed using light and scanning electron microscopy. The nuclear and mitochondrial DNA sequences, i.e. small subunit ribosomal DNA (*18S*), large subunit ribosomal DNA (*28S*), internal transcribed spacer (ITS) and cytochrome *c* oxidase subunit 1 (*cox*1), were amplified and sequenced for molecular identification. Moreover, phylogenetic analyses were performed using maximum likelihood (ML) inference based on *28S* and *18S* + *28S* + *cox*1 sequence data, respectively, in order to clarify the systematic status of these nematodes.

Results: Integrated morphological and genetic evidence reveals these nematode specimens to be a new species of pinworm *Skrjabinema longicaudatum* (Oxyurida: Oxyuridae). There was no intraspecific nucleotide variation between different individuals of *S. longicaudatum* n. sp. in the partial *18S*, *28S*, ITS and *cox*1 sequences. However, a high level of nucleotide divergence was revealed between the new species and its congeners in *28S* (8.36%) and ITS (20.3–23.7%) regions, respectively. Molecular phylogenetic results suggest that the genus *Skrjabinema* should belong to the

动物寄生虫物种多样性研究

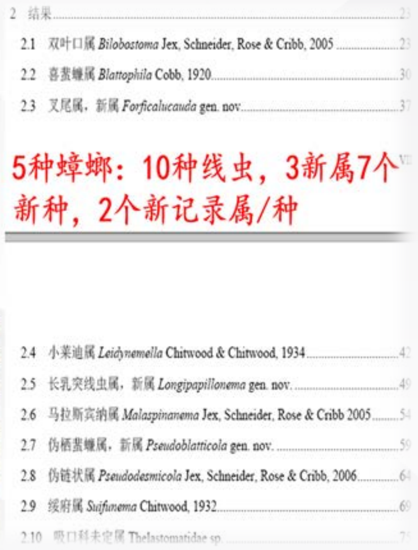
河北师范大学

硕士学位论文

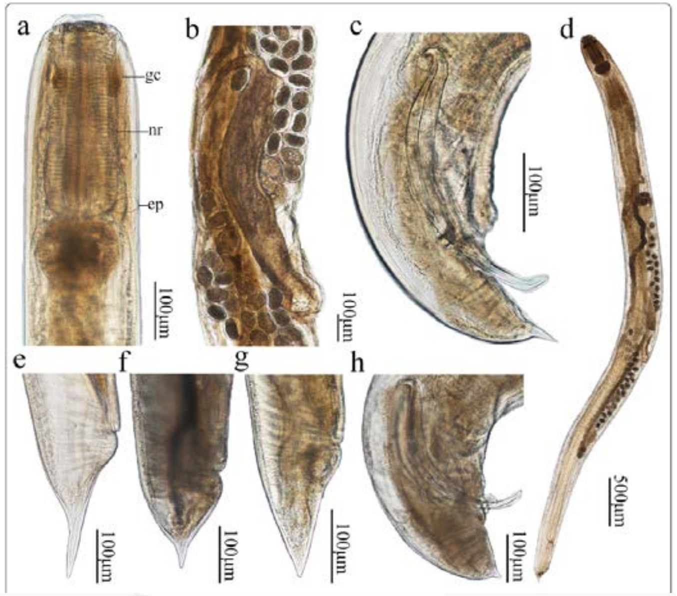
（学历硕士）

云南地区蜚蠊目昆虫寄生吸口类线虫分类学研究及尖尾次目系统发育关系的分析

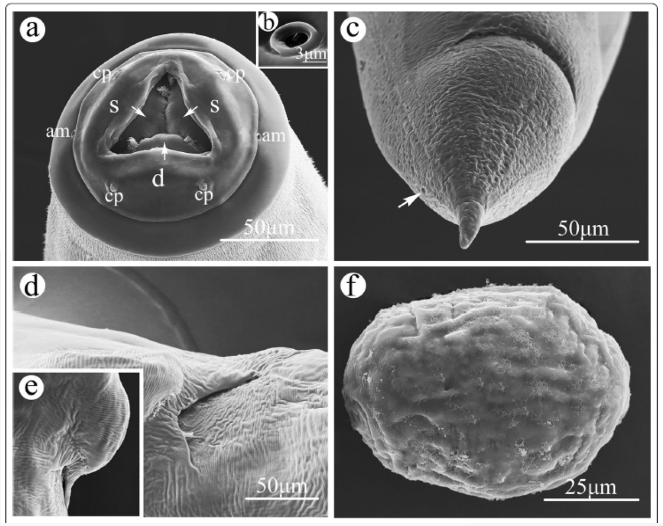
Taxonomy of thelastomatoid nematodes from cockroaches in Yunnan Province and phylogenetic analysis of Oxyuridomorpha



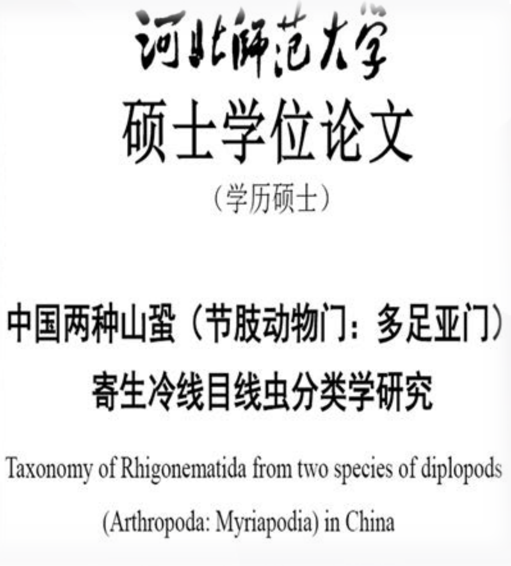
5种蟑螂：10种线虫，3新属7个新种，2个新记录属/种



Rhigonema sinense



6种山蛩：4科7属14种线虫，10个新种、2中国新纪录科、6新记录属。



河北师范大学

硕士学位论文

（学历硕士）

中国两种山蛩（节肢动物门：多足亚门）寄生冷线目线虫分类学研究

Taxonomy of Rhigonematida from two species of diplopods (Arthropoda: Myriapodia) in China

Zhang et al. Parasites & Vectors (2022) 15:427
https://doi.org/10.1186/s13071-022-05544-9

Parasites & Vectors

RESEARCH **Open Access**

Molecular identification of a new species of *Rhigonema* (Nematoda: Rhigonematidae) and phylogenetic relationships within the infraorder Rhigonematomorpha

Yu Zhang[1,2,3], Lian-Di Wang[1,2,3], Koichi Hasegawa[4], Seiya Nagae[4], Hui-Xia Chen[1,2,3], Lin-Wei Li[1,2,3] and Liang Li[1,2,3*]

Abstract

Background: The infraorder Rhigonematomorpha comprises a group of obligate parasitic nematodes of millipedes (Arthropoda: Diplopoda). The current species identification of Rhigonematomorpha nematodes remains mainly based on morphological features, with molecular-based identification still in its infancy. Also, current knowledge of the phylogeny of Rhigonematomorpha is far from comprehensive.

Methods: The morphology of Rhigonematomorpha nematodes belonging to the genus *Rhigonema*, collected from the millipede *Spirobolus bungii* Brandt (Diplopoda: Spirobolida) in China, was studied in detail using light and scanning electron microscopy. Five different genetic markers, including the nuclear small ribosomal subunit (18S), internal transcribed spacer (ITS) and large ribosomal subunit (28S) regions and the mitochondrial *cox*1 and *cox*2 genes of these Rhigonematomorpha nematodes collected from China and *Rhigonema naylae* collected from Japan were sequenced and analyzed using Bayesian inference (BI) and Assemble Species by Automatic Partitioning (ASAP) methods. Phylogenetic analyses that included the most comprehensive taxa sampling of Rhigonematomorpha to date were also performed based on the 18S + 28S genes using maximum likelihood (ML) and BI methods.

Results: The specimens of *Rhigonema* collected from *S. bungii* in China were identified as a new species, *Rhigonema sinense* n. sp. Striking variability in tail morphology was observed among individuals of *R. sinense* n. sp. ASAP analyses based on the 28S, ITS, *cox*1 and *cox*2 sequences supported the species partition of *R. sinense* n. sp. and *R. naylae*, but showed no evidence that the different morphotypes of *R. sinense* n. sp. represent distinct genetic lineages. BI analyses also indicated that *R. sinense* n. sp. represents a separated species from *R. naylae* based on the *cox*1 and *cox*2 genes, but showed that *R. naylae* nested in samples of *R. sinense* n. sp. based on the ITS and 28S data. Phylogenetic results showed that the representatives of Rhigonematomorpha formed two large clades. The monophyly of the families Carnoyidae and Ichthyocephalidae and the genus *Rhigonema* was rejected. The representatives of the family Ransomnematidae clustered together with the family Hethidae with strong support.

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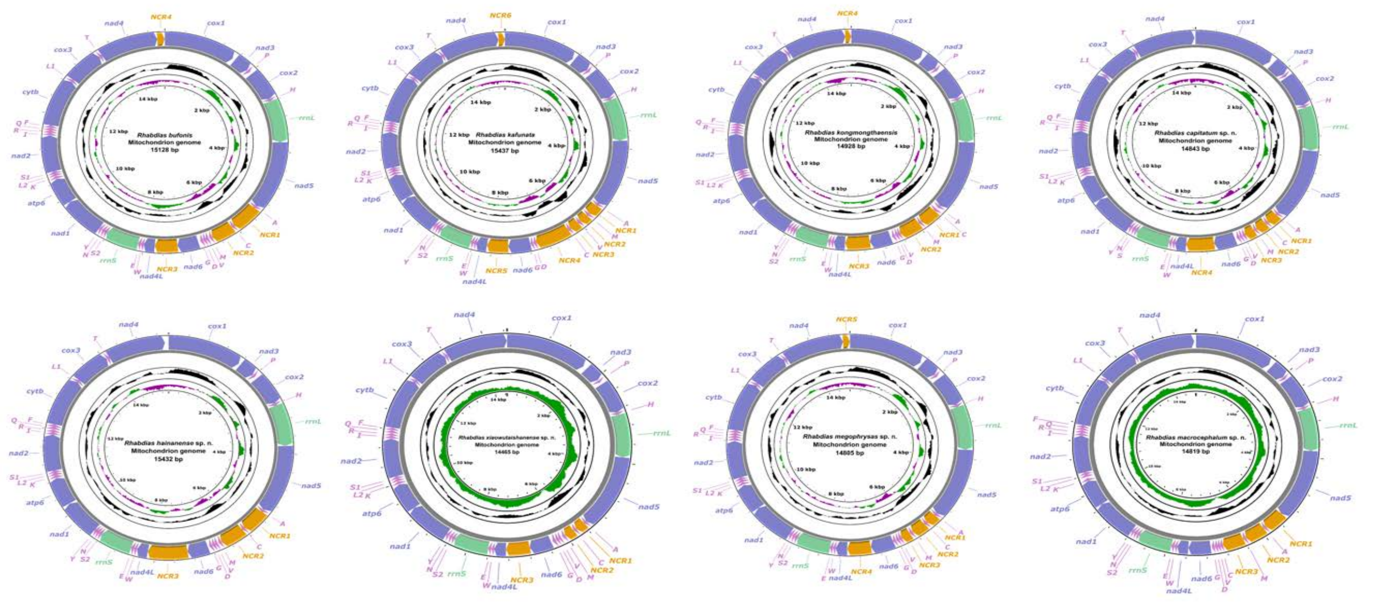
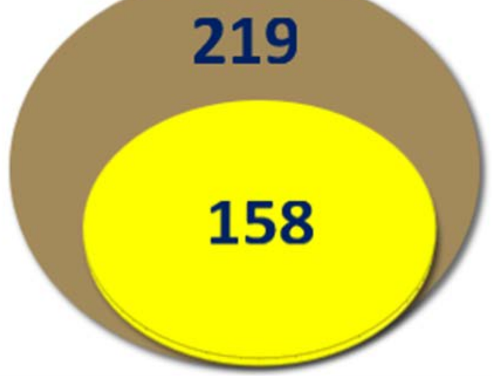
Full list of author information is available at the end of the article

动物寄生线虫物种多样性

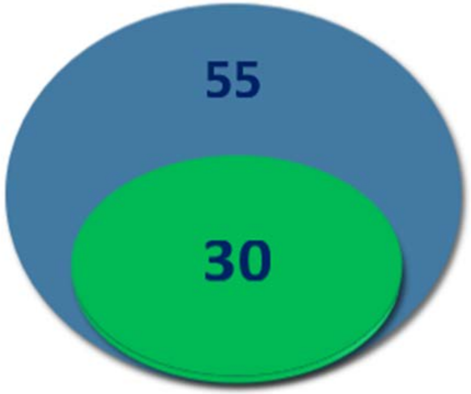
- 建立动物寄生线虫新科1个、报道中国新纪录科6个。
- 发现描述动物寄生线虫新物种93种、报道中国新纪录种56种。
- 首次测序组装了超过42个科、亚科或属级阶元的线粒体基因组。

➢ 首次测序组装了 棒线科线虫的线粒体基因组8种



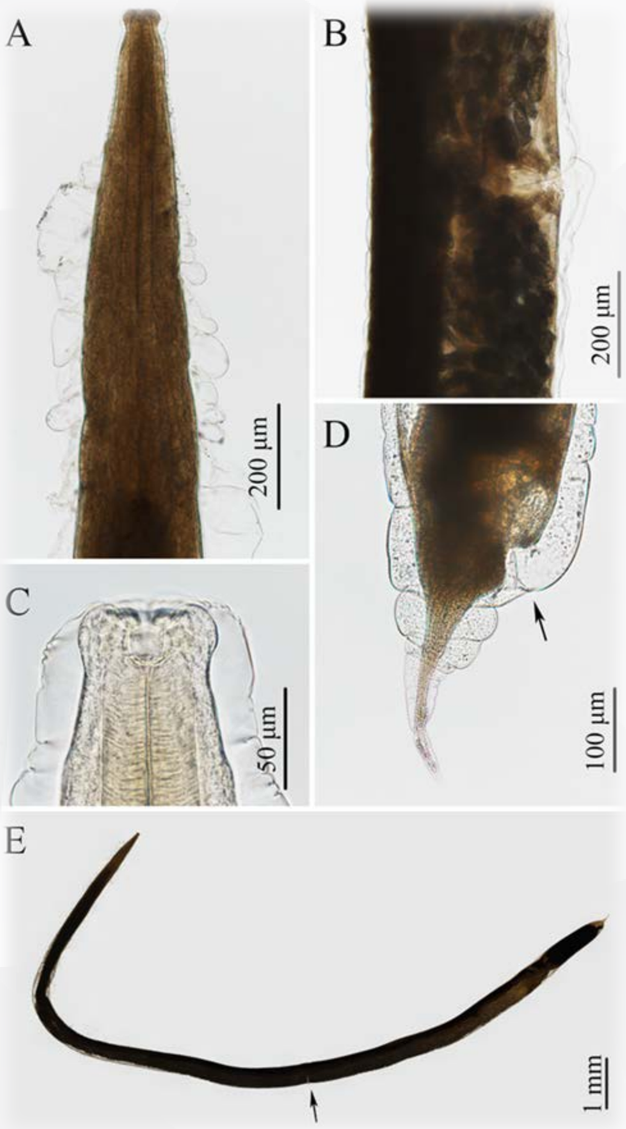


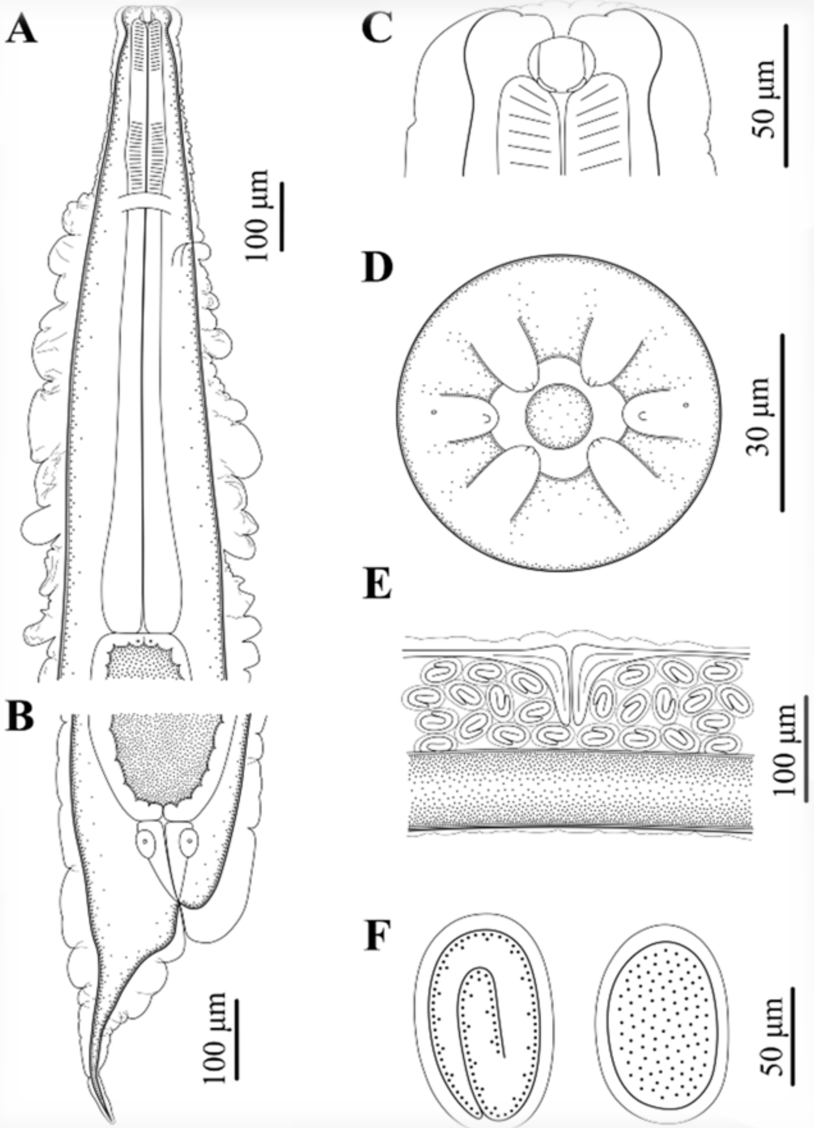
中国蛔目线虫物种数量增加38.6%

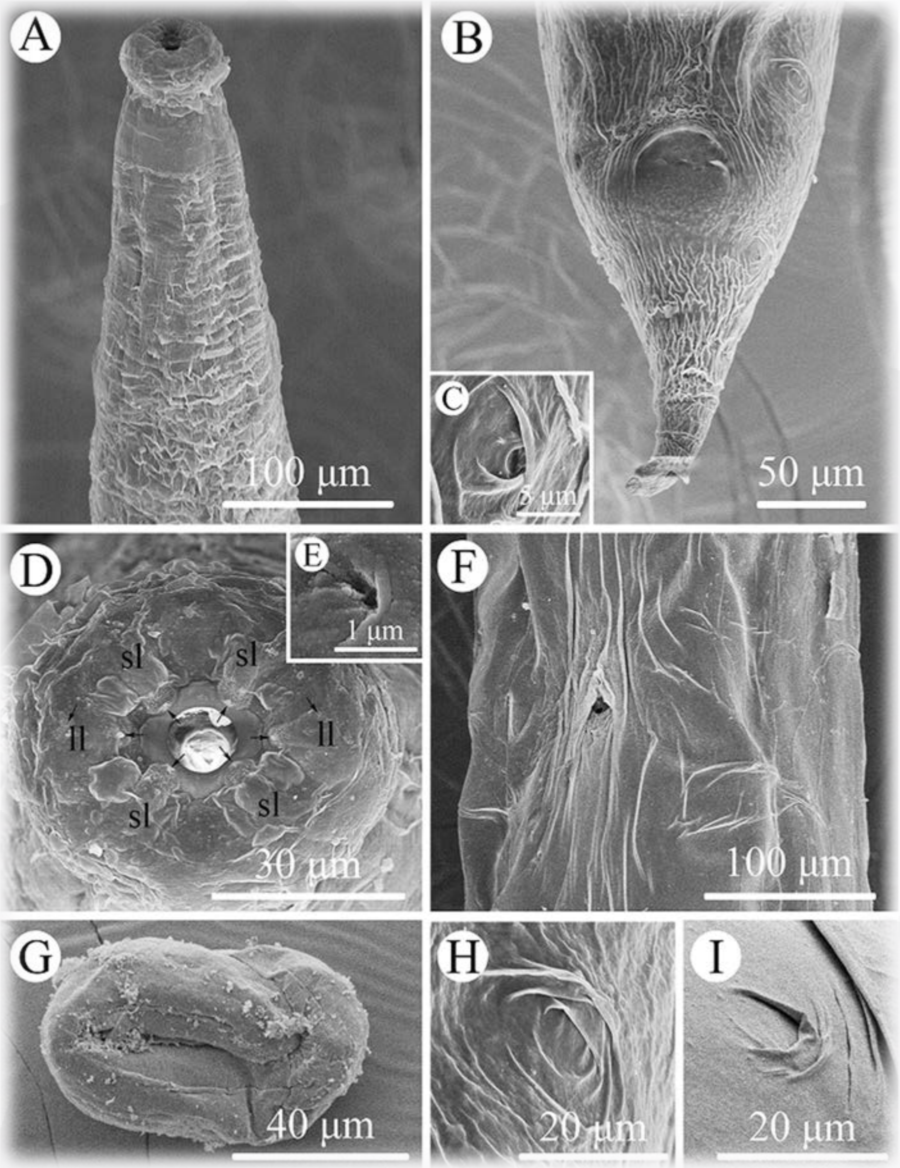


世界蛔目线粒体基因组数量增加83.3%

动物寄生线虫物种鉴定范式的建立

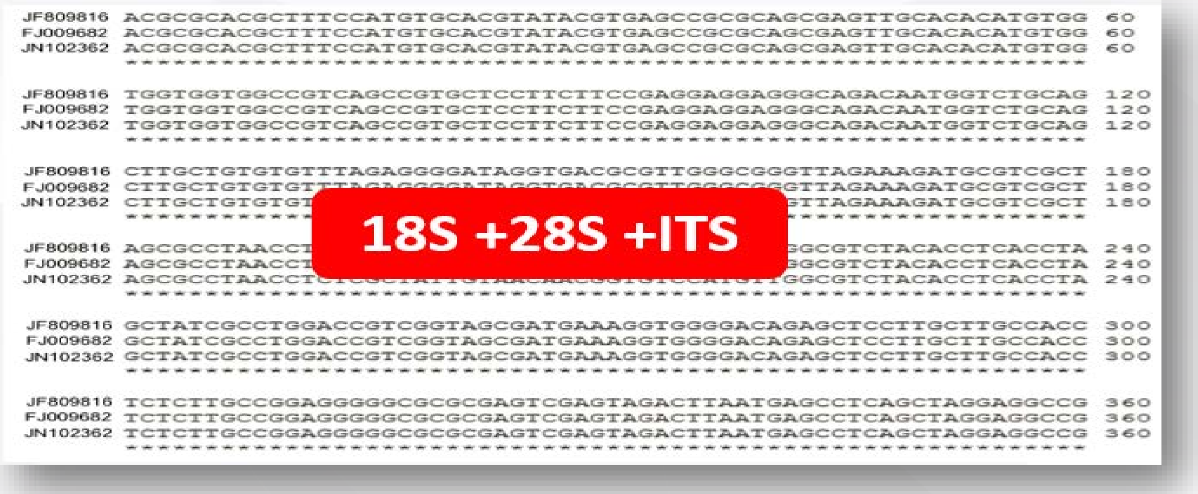






Rhabdias macrocephalum **sp. n.**

棒线科线虫物种鉴定范式的建立



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FJ009682 ACGCGCACGCTTTCCATGTGCACGTATACGTGAGCCGCGCAGCGAGTTGCACACATGTGG 60
JN102362 ACGCGCACGCTTTCCATGTGCACGTATACGTGAGCCGCGCAGCGAGTTGCACACATGTGG 60
         ************************************************************

JF809816 TGGTGGTGGCCGTCAGCCGTGCTCCTTCTTCCGAGGAGGAGGGCAGACAATGGTCTGCAG 120
FJ009682 TGGTGGTGGCCGTCAGCCGTGCTCCTTCTTCCGAGGAGGAGGGCAGACAATGGTCTGCAG 120
JN102362 TGGTGGTGGCCGTCAGCCGTGCTCCTTCTTCCGAGGAGGAGGGCAGACAATGGTCTGCAG 120
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JF809816 CTTGCTGTGTGTTTAGAGGGGATAGGTGACGCGTTGGGCGGGTTAGAAAGATGCGTCGCT 180
FJ009682 CTTGCTGTGTGT[illegible]GTTAGAAAGATGCGTCGCT 180
JN102362 CTTGCTGTGTGT[illegible]GTTAGAAAGATGCGTCGCT 180
         ************[illegible]******************

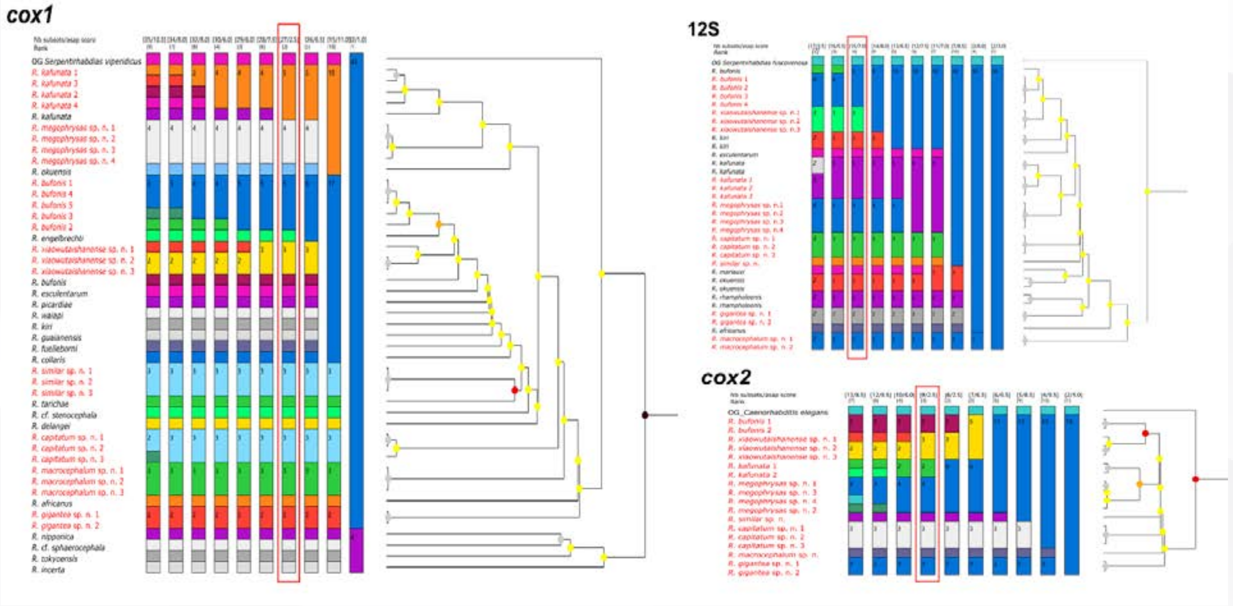
JF809816 AGCGCCTAACCT[illegible]GGCGTCTACACCTCACCTA 240
FJ009682 AGCGCCTAACCT[illegible]GGCGTCTACACCTCACCTA 240
JN102362 AGCGCCTAACCT[illegible]GGCGTCTACACCTCACCTA 240
         ************************************************************

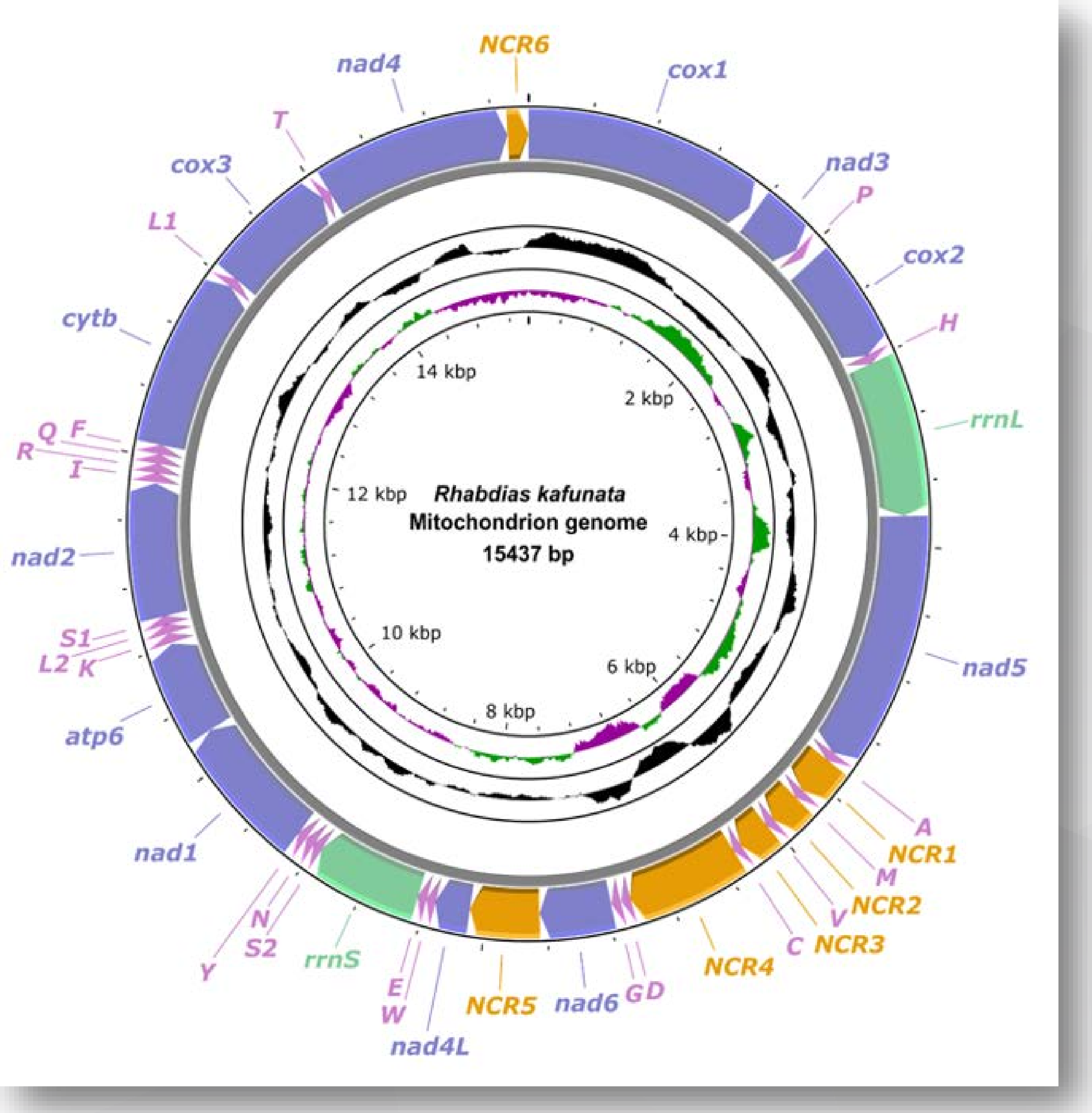
JF809816 GCTATCGCCTGGACCGTCGGTAGCGATGAAAGGTGGGGACAGAGCTCCTTGCTTGCCACC 300
FJ009682 GCTATCGCCTGGACCGTCGGTAGCGATGAAAGGTGGGGACAGAGCTCCTTGCTTGCCACC 300
JN102362 GCTATCGCCTGGACCGTCGGTAGCGATGAAAGGTGGGGACAGAGCTCCTTGCTTGCCACC 300
         ************************************************************

JF809816 TCTCTTGCCGGAGGGGGCGCGCGAGTCGAGTAGACTTAATGAGCCTCAGCTAGGAGGCCG 360
FJ009682 TCTCTTGCCGGAGGGGGCGCGCGAGTCGAGTAGACTTAATGAGCCTCAGCTAGGAGGCCG 360
JN102362 TCTCTTGCCGGAGGGGGCGCGCGAGTCGAGTAGACTTAATGAGCCTCAGCTAGGAGGCCG 360
         ************************************************************
```

18S +28S +ITS

ASAP+BI分析（物种界定）

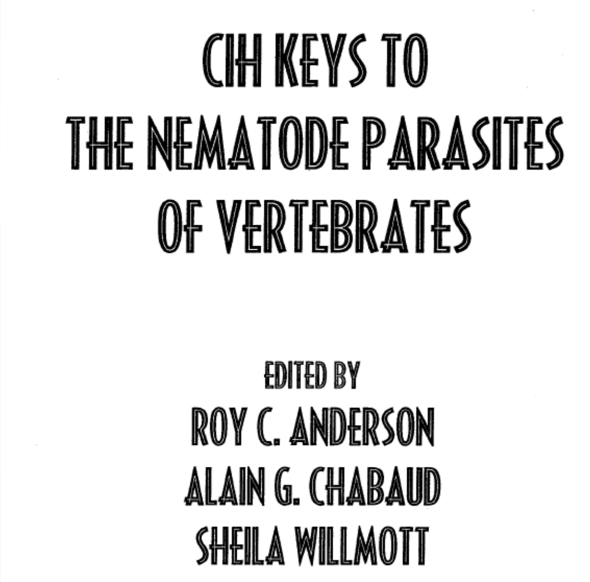




03

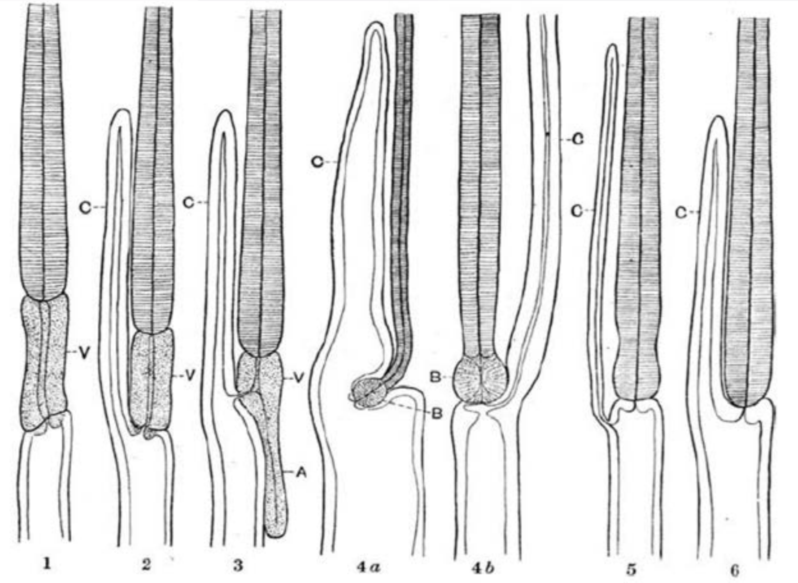
动物寄生线虫分子系统学

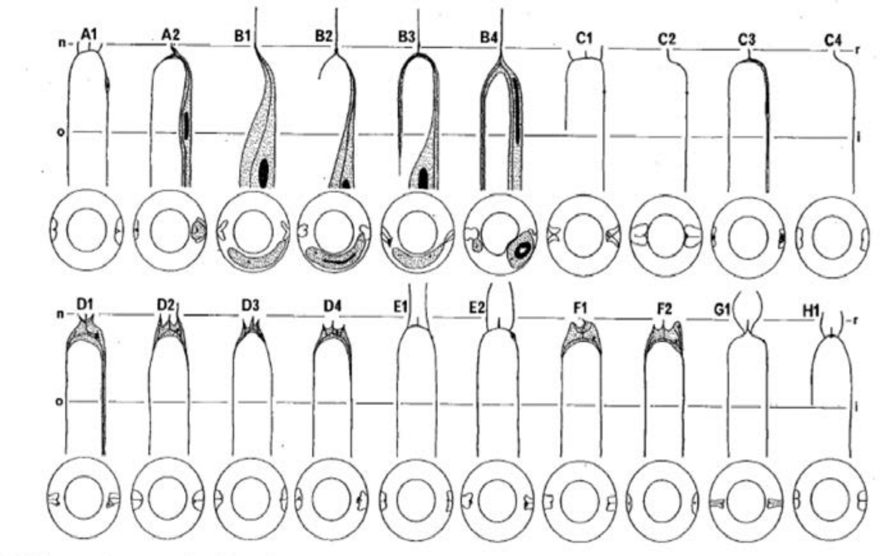
动物寄生线虫经典分类系统学



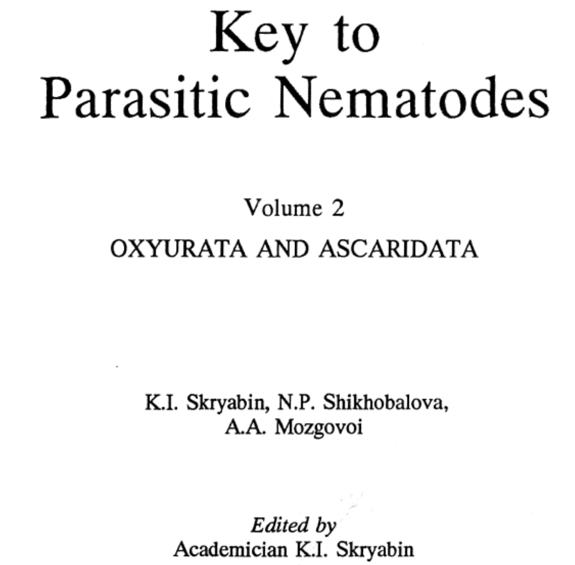
CIH KEYS TO
THE NEMATODE PARASITES
OF VERTEBRATES

EDITED BY
ROY C. ANDERSON
ALAIN G. CHABAUD
SHEILA WILLMOTT





. 1. A diagrammatic representation of the configuration of the excretory system in certain ascaridoids. A, Acanthocheilidae; B, Anisakinae; C, Goe



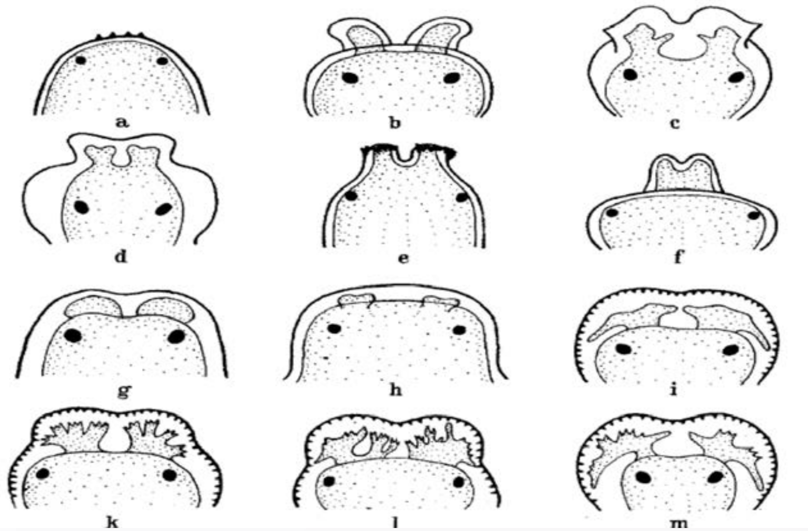
Key to
Parasitic Nematodes

Volume 2
OXYURATA AND ASCARIDATA

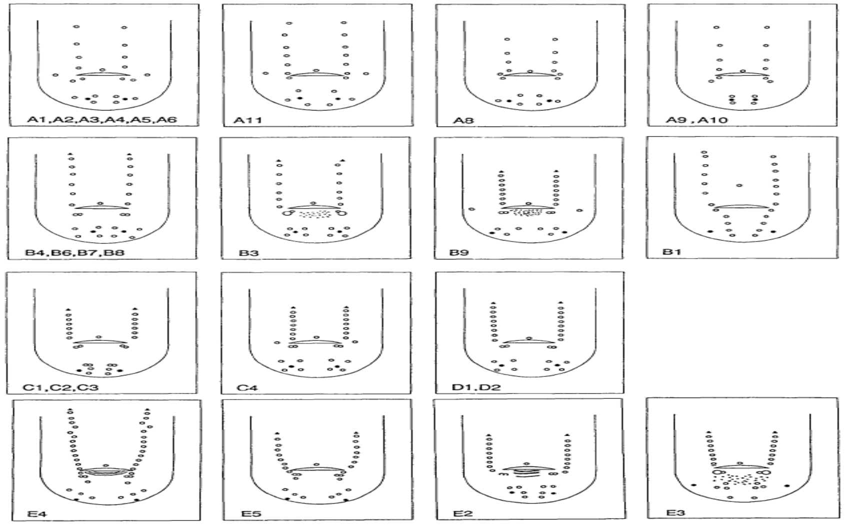
K.I. Skryabin, N.P. Shikhobalova,
A.A. Mozgovoi

Edited by
Academician K.I. Skryabin

Beiträge zur Morphologie, Ökologie und Phylogenie der Ascaridoidea 499



Systematics of ascaridoid nematodes 221



动物寄生线虫分子系统学研究

A molecular evolutionary framework for the phylum Nematoda

Mark L. Blaxter[*], Paul De Ley[†‡], James R. Garey[§],
Leo X. Liu[‖¶], Patsy Scheldeman[†], Andy Vierstraete[†],
Jacques R. Vanfleteren[†], Laura Y. Mackey[#], Mark Dorris[*],
Linda M. Frisse[⋆], J. T. Vida[⋆] & W. Kelley Thomas[⋆]

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[‖] Harvard-Thorndike Laboratory, Department of Medicine, Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, Massachusetts 02215, USA
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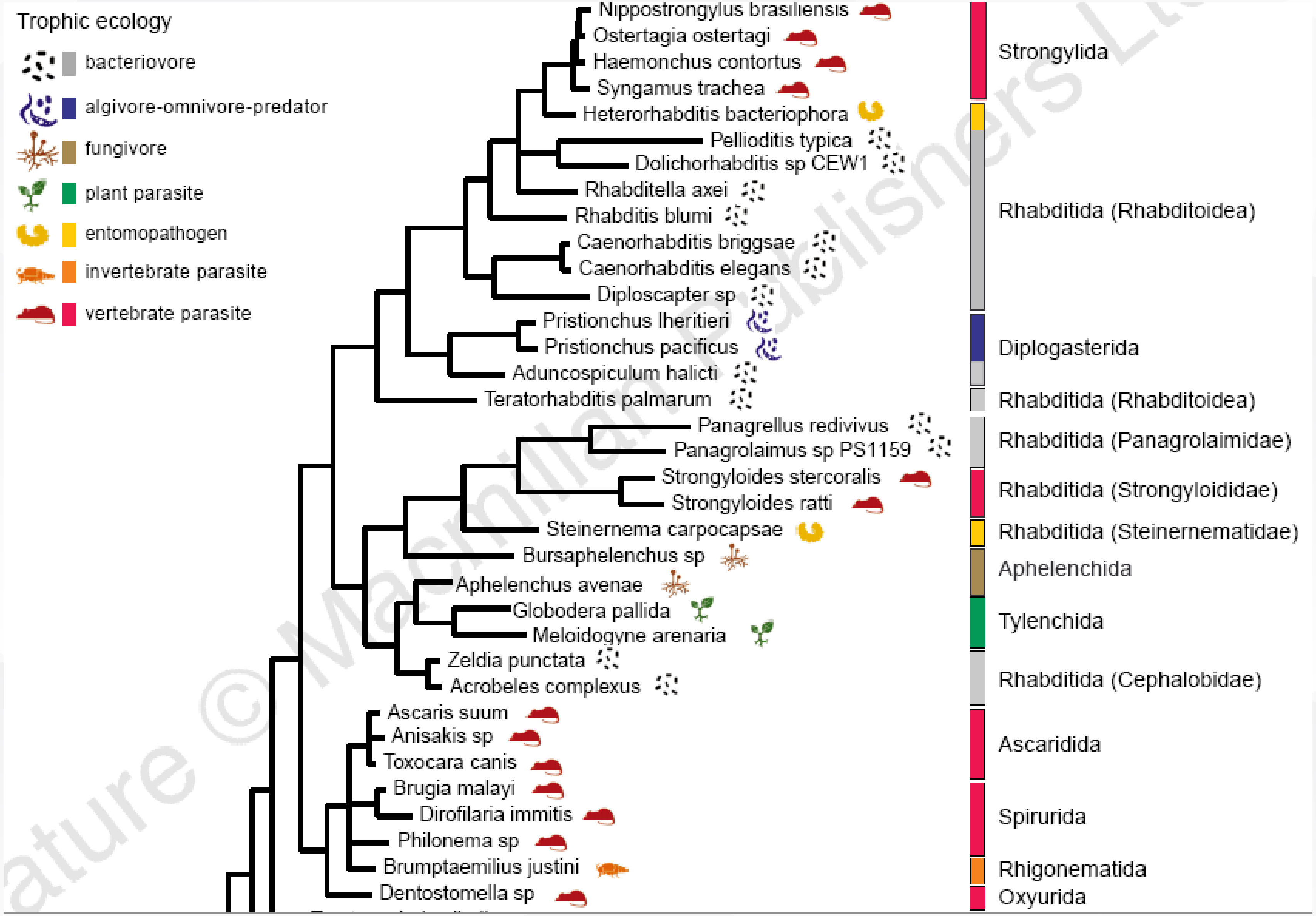
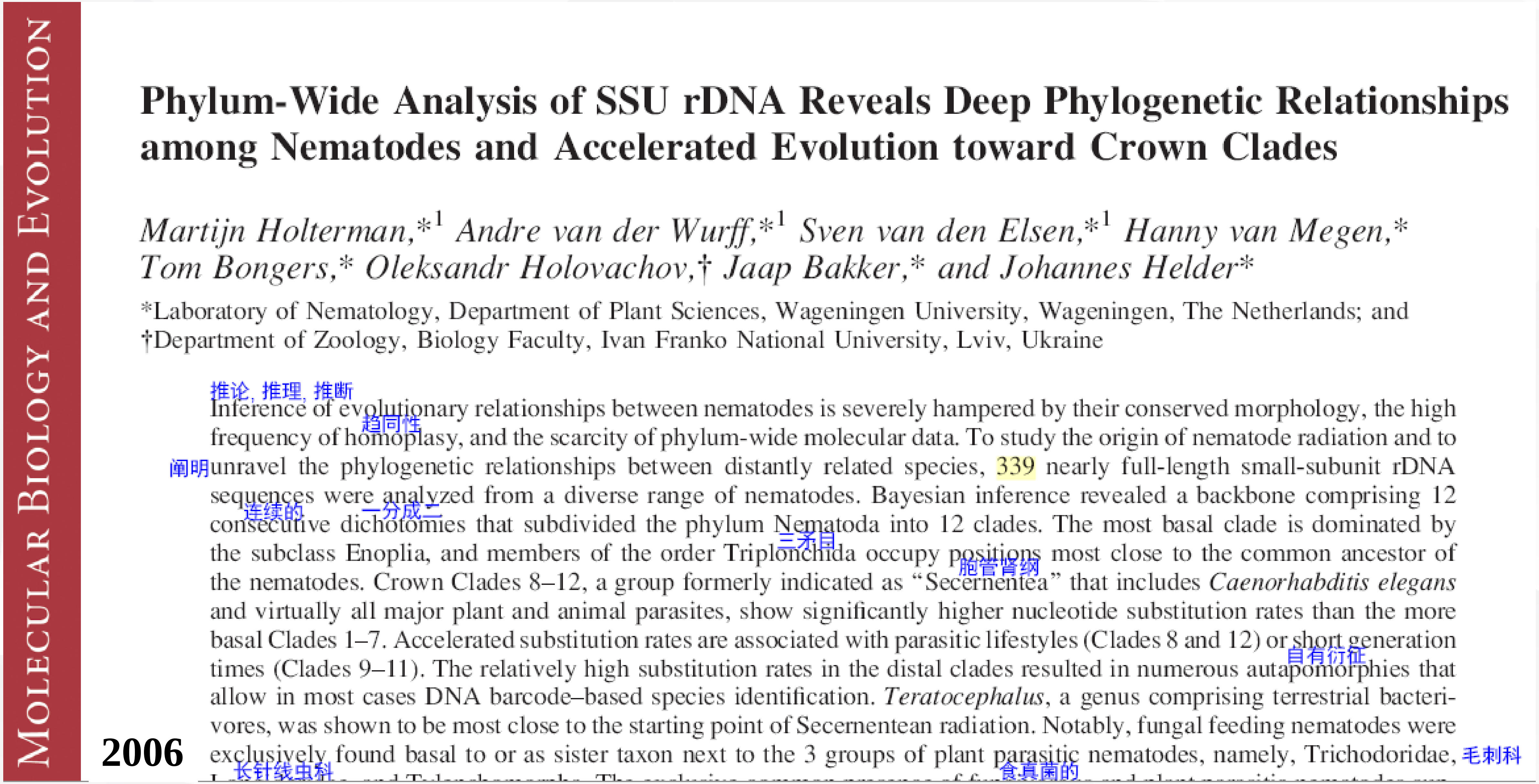
[#] Department of Molecular Physiology and Biophysics, Baylor College of Medicine, Houston, Texas 77030, USA
[⋆] Division of Molecular Biology and Biochemistry, School of Biological Sciences, University of Missouri, Kansas City, Missouri 64110, USA



动物寄生线虫分子系统学研究



MOLECULAR BIOLOGY AND EVOLUTION

Phylum-Wide Analysis of SSU rDNA Reveals Deep Phylogenetic Relationships among Nematodes and Accelerated Evolution toward Crown Clades

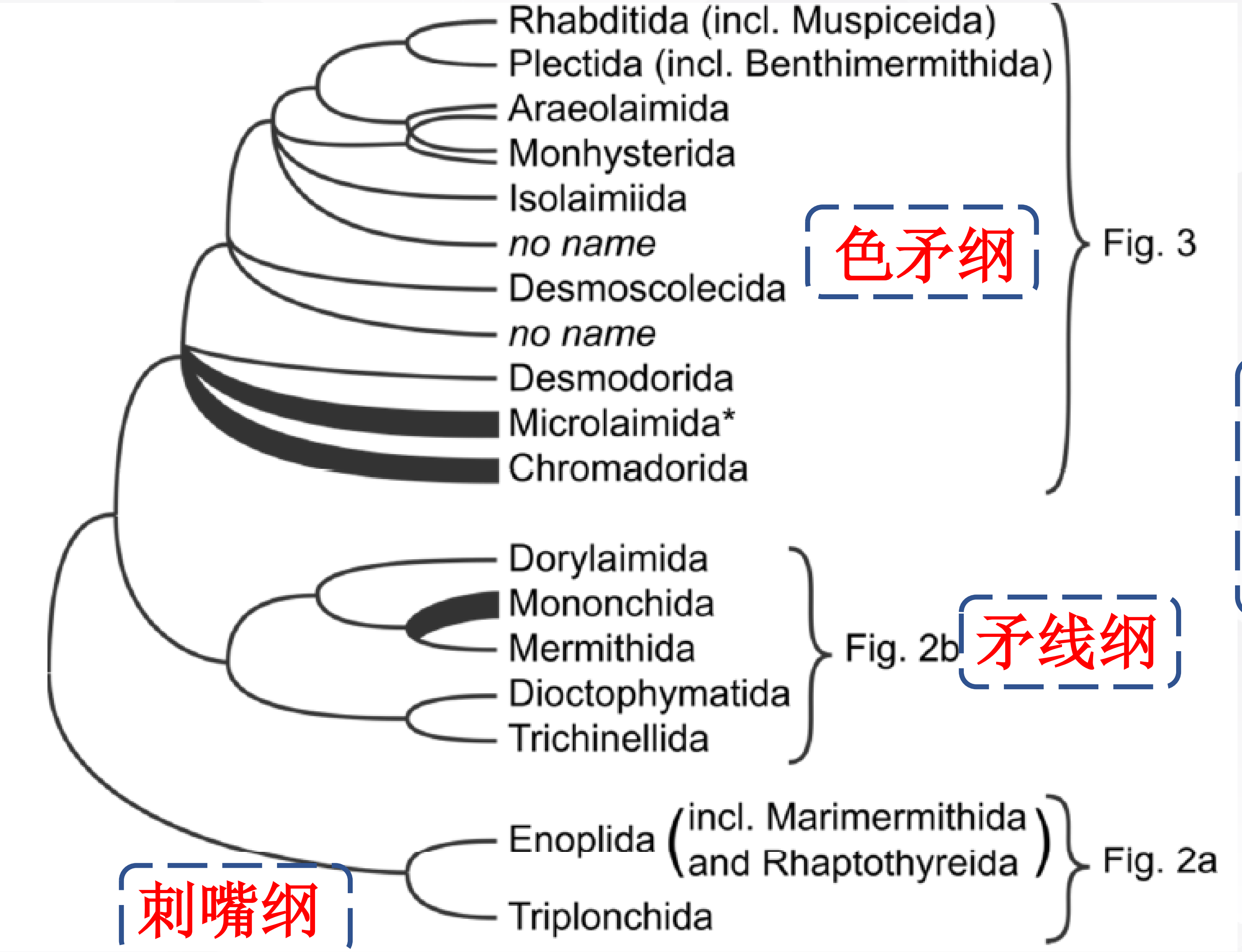
Martijn Holterman,[1] Andre van der Wurff,*[1] Sven van den Elsen,*[1] Hanny van Megen,* Tom Bongers,* Oleksandr Holovachov,† Jaap Bakker,* and Johannes Helder**

*Laboratory of Nematology, Department of Plant Sciences, Wageningen University, Wageningen, The Netherlands; and †Department of Zoology, Biology Faculty, Ivan Franko National University, Lviv, Ukraine

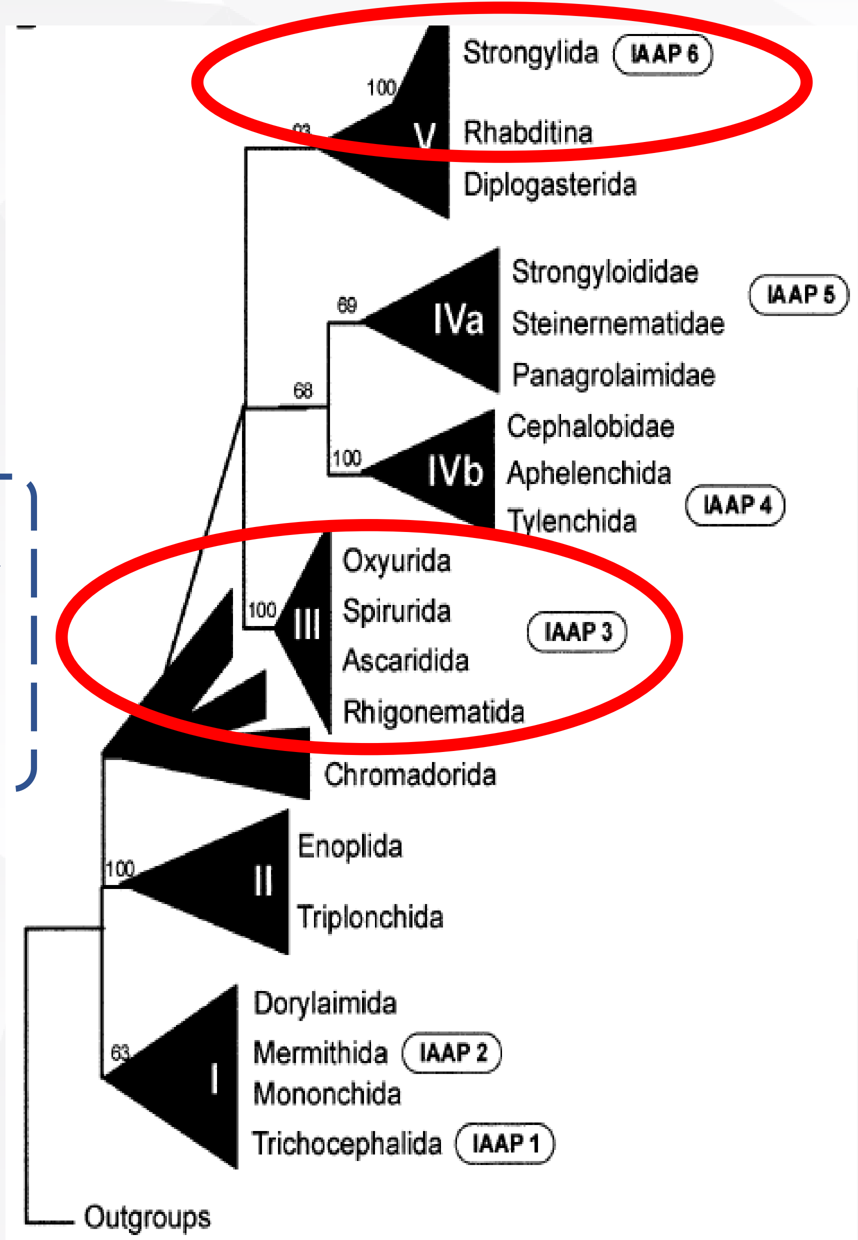
Inference of evolutionary relationships between nematodes is severely hampered by their conserved morphology, the high frequency of homoplasy, and the scarcity of phylum-wide molecular data. To study the origin of nematode radiation and to unravel the phylogenetic relationships between distantly related species, 339 nearly full-length small-subunit rDNA sequences were analyzed from a diverse range of nematodes. Bayesian inference revealed a backbone comprising 12 consecutive dichotomies that subdivided the phylum Nematoda into 12 clades. The most basal clade is dominated by the subclass Enoplia, and members of the order Triplonchida occupy positions most close to the common ancestor of the nematodes. Crown Clades 8–12, a group formerly indicated as "Secernentea" that includes *Caenorhabditis elegans* and virtually all major plant and animal parasites, show significantly higher nucleotide substitution rates than the more basal Clades 1–7. Accelerated substitution rates are associated with parasitic lifestyles (Clades 8 and 12) or short generation times (Clades 9–11). The relatively high substitution rates in the distal clades resulted in numerous autapomorphies that allow in most cases DNA barcode–based species identification. *Teratocephalus*, a genus comprising terrestrial bacterivores, was shown to be most close to the starting point of Secernentean radiation. Notably, fungal feeding nematodes were exclusively found basal to or as sister taxon next to the 3 groups of plant parasitic nematodes, namely, Trichodoridae,

2006

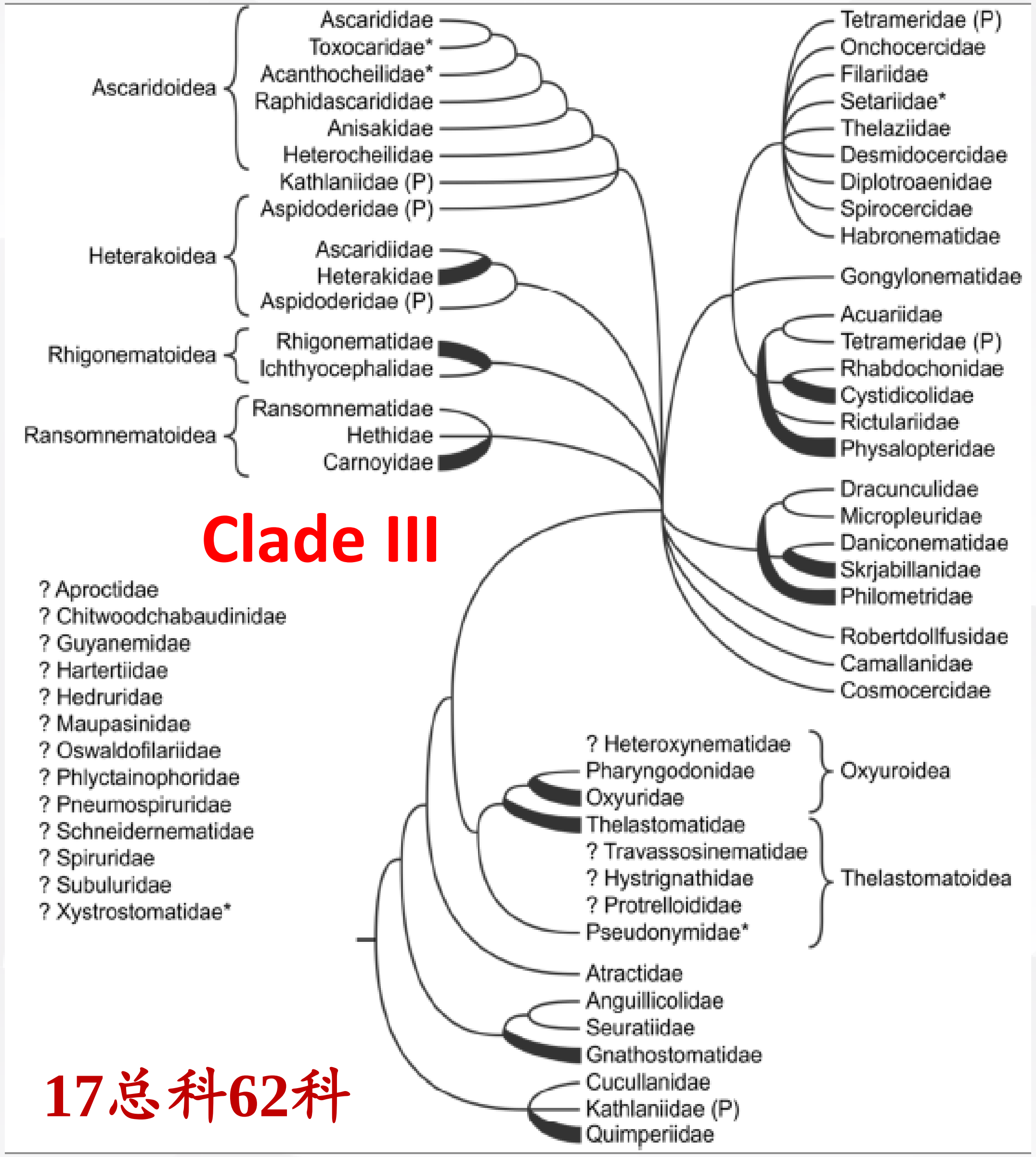
线虫动物门分类系统



色矛纲

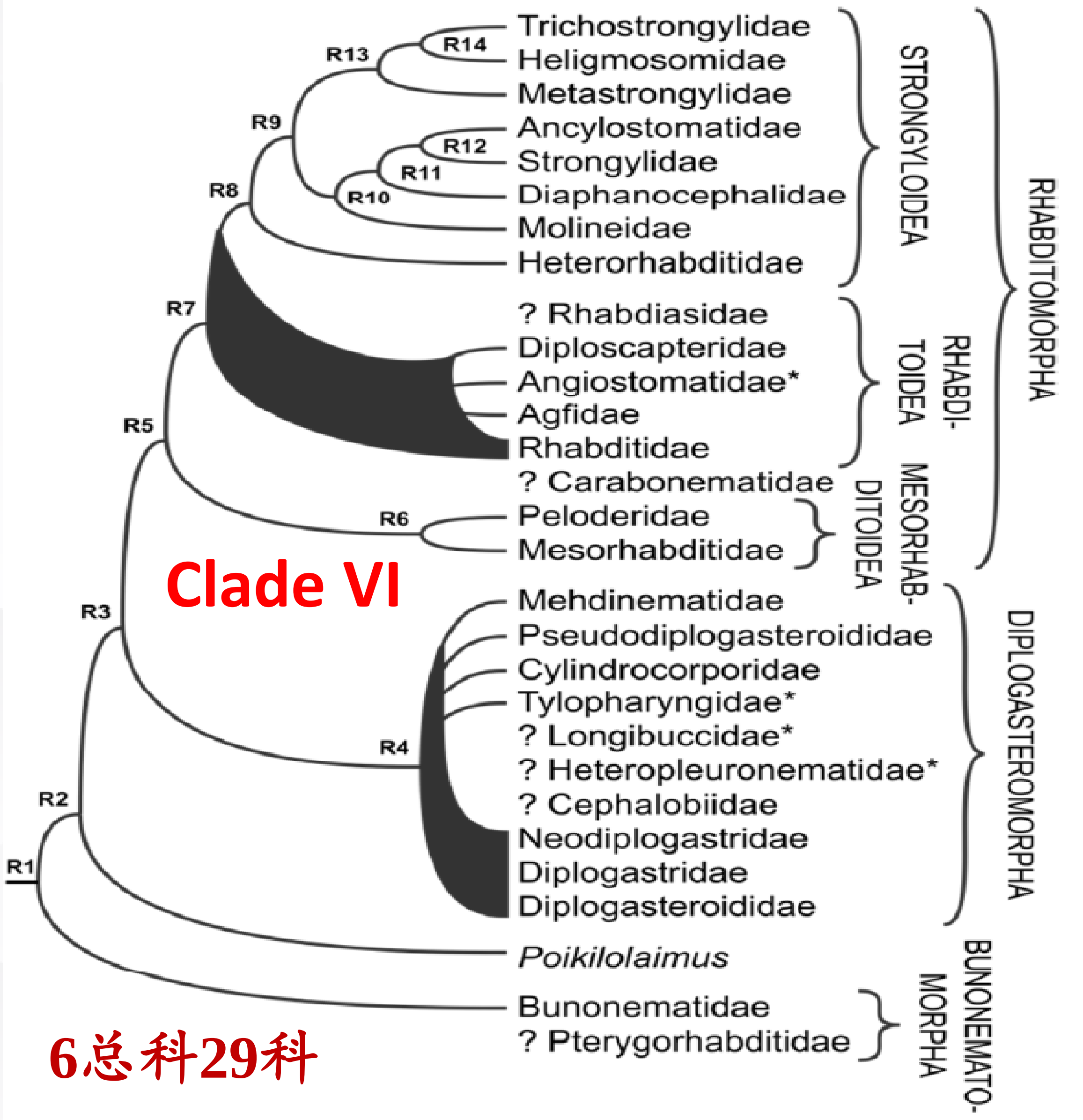


线虫动物门CladeIII、VI各类群进化关系



Clade III

17总科62科



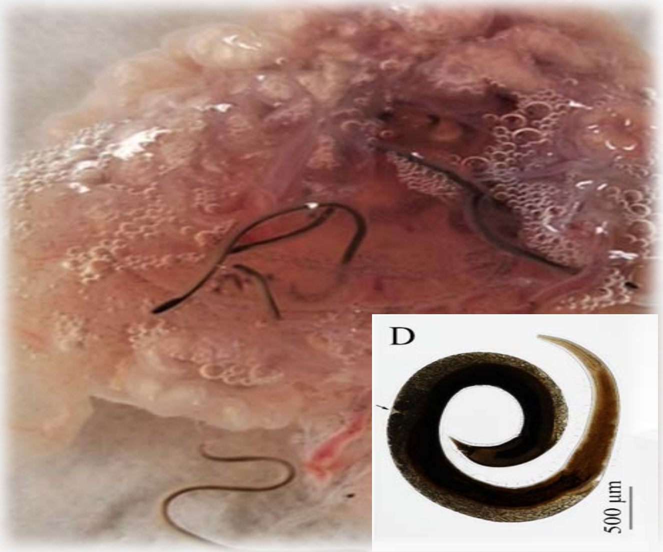
Clade VI

6总科29科

03

动物寄生线虫分子系统学

杆形目分子系统学研究



棒线科 110种
Rhabdiasidae

- **夏比属** *Chabirenia*
- **棘棒线属** *Acanthorhabdias*

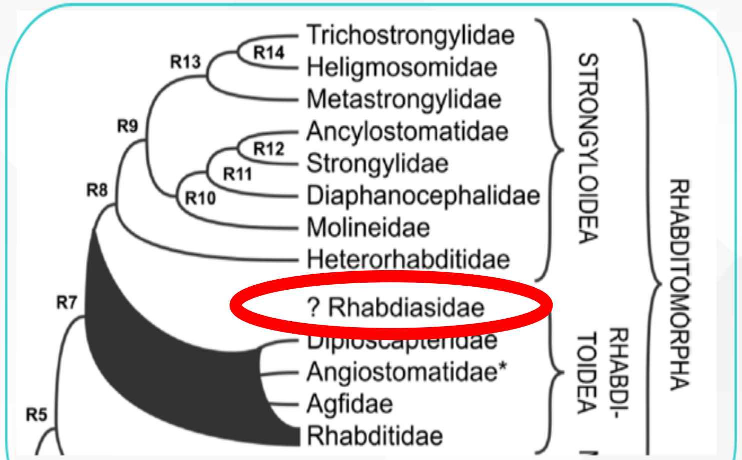
无分子数据

- **曲线属** *Kurilonema*
- **球囊属** *Entomelas*
- **肺线属** *Pneumonema*
- **新球囊属** *Neoentomelas*
- **棒线属** *Rhabdias* 96种
- **蛇棒线属** *Serpentirhabdias*

中国仅报道8种

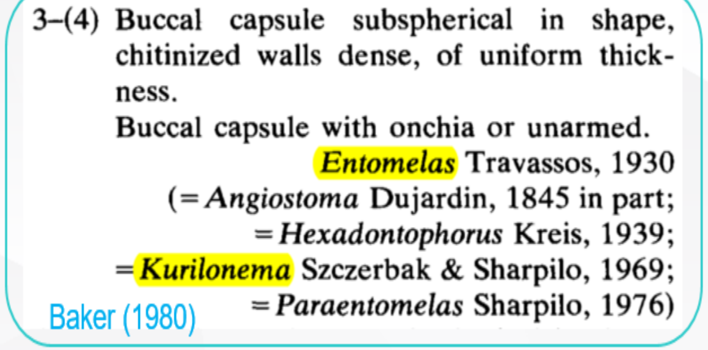
Kuzmin (2013)

棒线科的系统地位?



Ahmed & Holovachov (2021)

棒线科各属的系统发育关系?

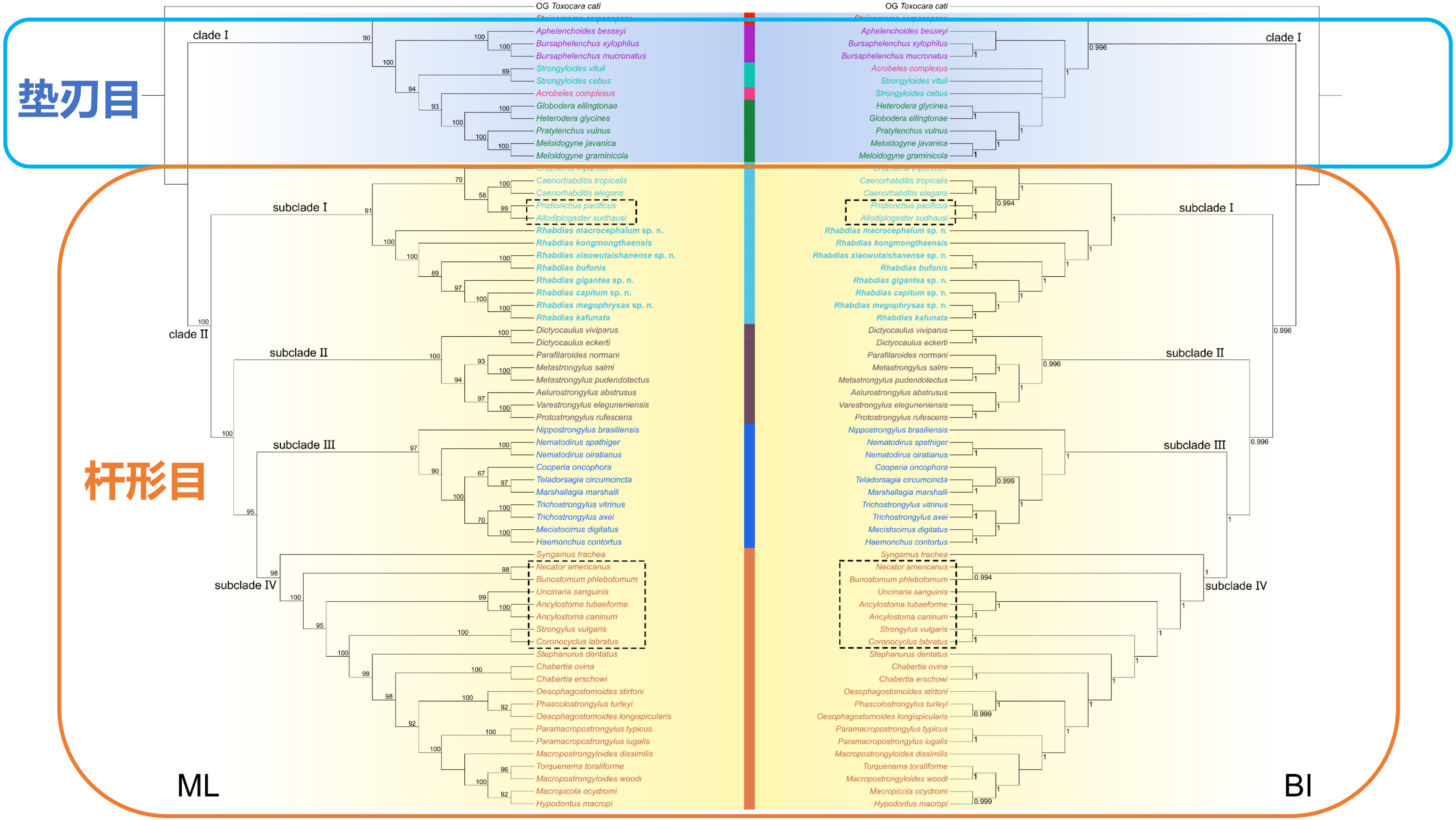


3–(4) Buccal capsule subspherical in shape, chitinized walls dense, of uniform thickness.
Buccal capsule with onchia or unarmed.
Entomelas Travassos, 1930
(= *Angiostoma* Dujardin, 1845 in part;
= *Hexadontophorus* Kreis, 1939;
= *Kurilonema* Szczerbak & Sharpilo, 1969;
= *Paraentomelas* Sharpilo, 1976)

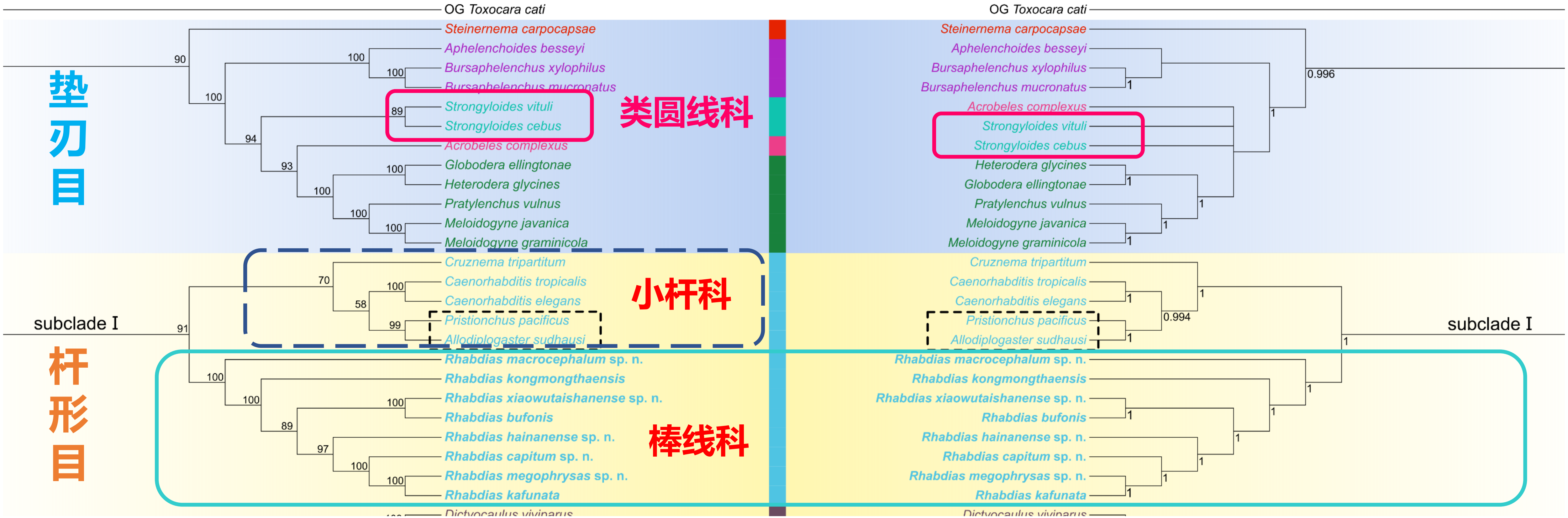
Baker (1980)

棒线科的系统地位研究

基于 12PCGs氨基酸序列构建的 **ML+BI**树



棒线科的系统地位研究



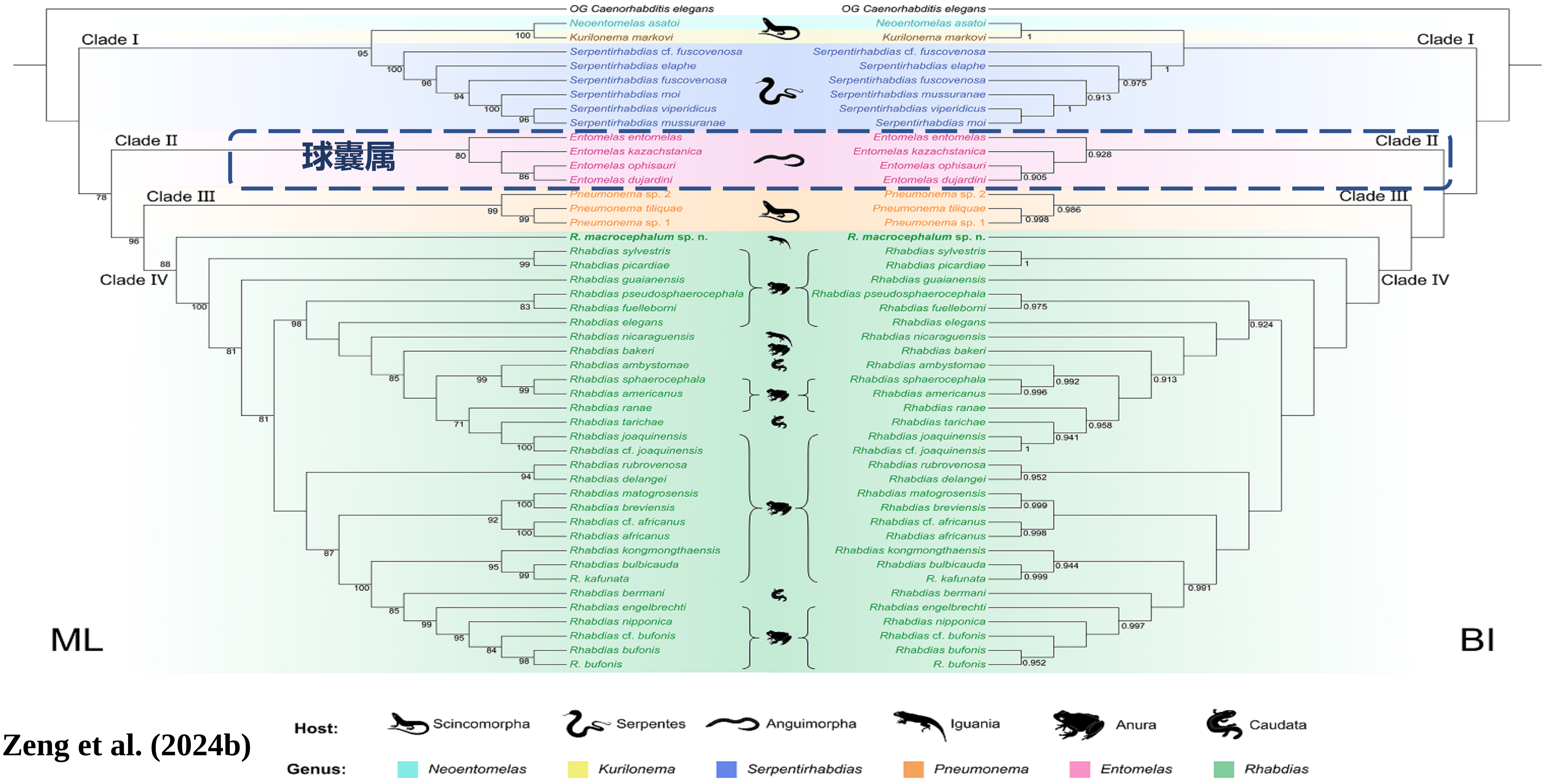
- 棒线科属于杆形目杆形总科，与小杆科构成姊妹群。

Zeng et al. (2024a)

棒线科不同属间进化关系

基于 ITS+28S序列构建的 **ML+BI**树

棒线科祖先由爬行动物向两栖动物辐射进化

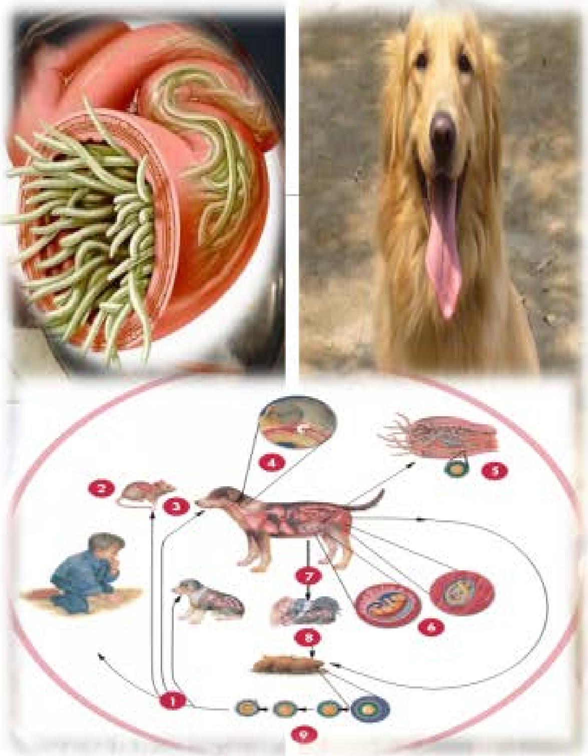


Zeng et al. (2024b)

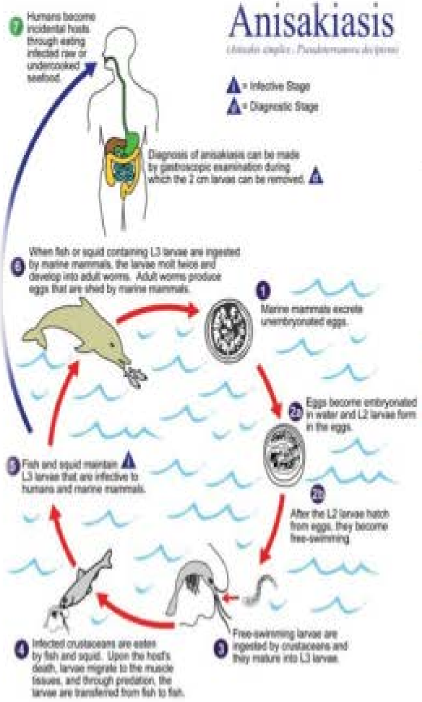
04

动物寄生线虫早期演化

蛔总科线虫的早期演化研究



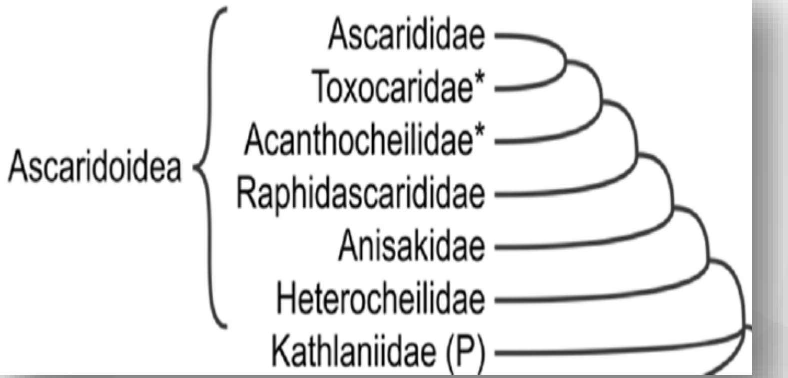
Toxocariasis



Anisakiasis

吃鱼需谨慎

Qin et al. (2013)



Ascaridoidea
- Ascarididae
- Toxocaridae*
- Acanthocheilidae*
- Raphidascarididae
- Anisakidae
- Heterocheilidae
- Kathlaniidae (P)

锥尾总科Subuluroidea
仅寄生鸟类+哺乳类

异刺总科Heterakoidea
寄生爬行类+鸟类+哺乳类
偶见两栖类（无鱼类）

蛔总科Ascaridoidea
寄生鱼类+爬行类+鸟类+哺乳类
偶见两栖类

色带总科Seuratoidea
鱼类+两栖类+爬行类+鸟类
+哺乳类均寄生

丽尾总科Cosmocercoidea
主要寄生两栖类+其次寄生爬行类
偶见鱼类+哺乳类（无鸟类）

蛔目线虫演化关系

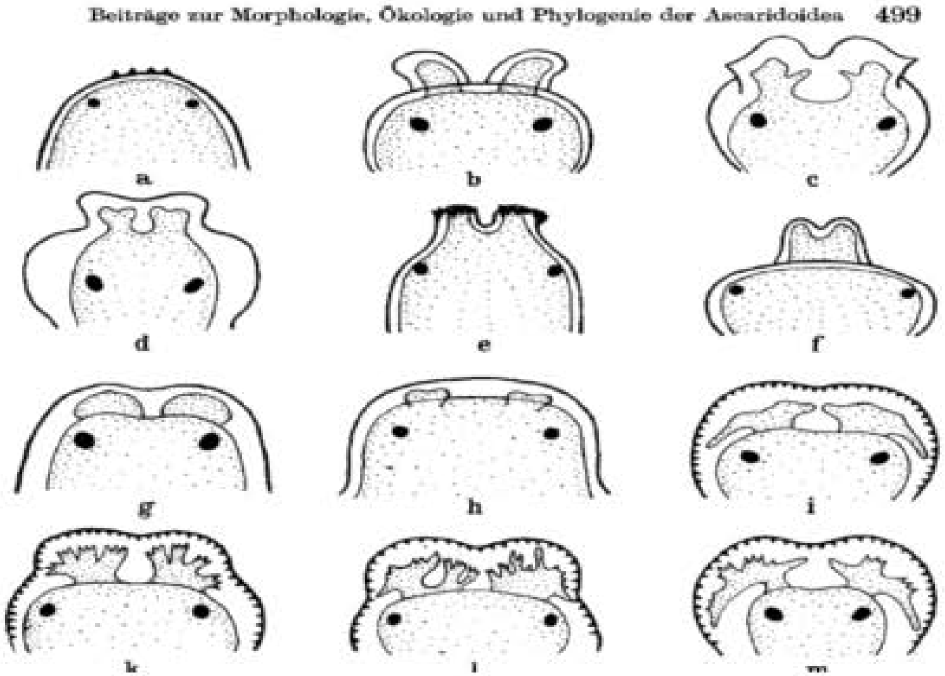
蛔总科线虫的早期演化研究

Osche (1958)

When?

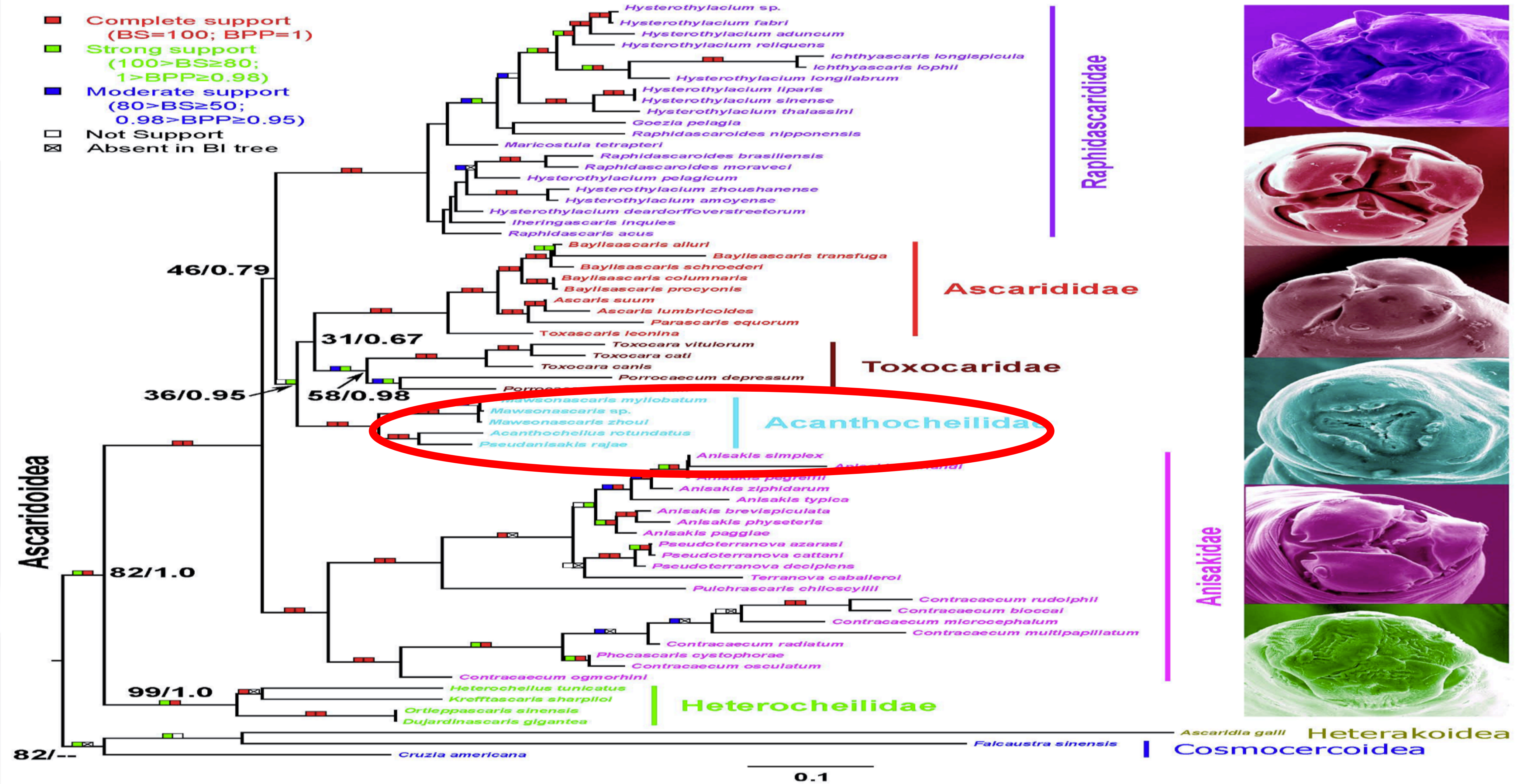
Where?

What?

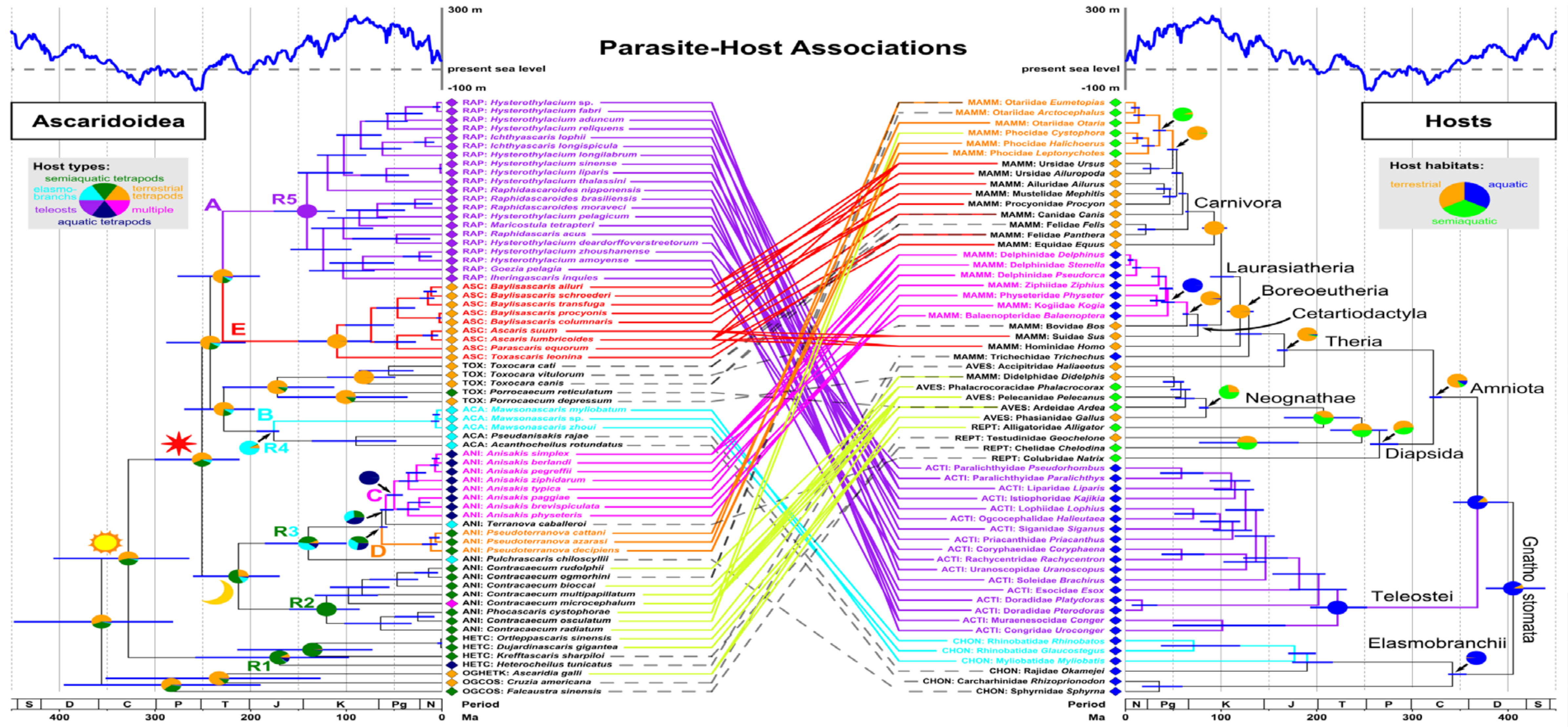


Beiträge zur Morphologie, Ökologie und Phylogenie der Ascaridoidea 499

蛔总科线虫分子系统学研究

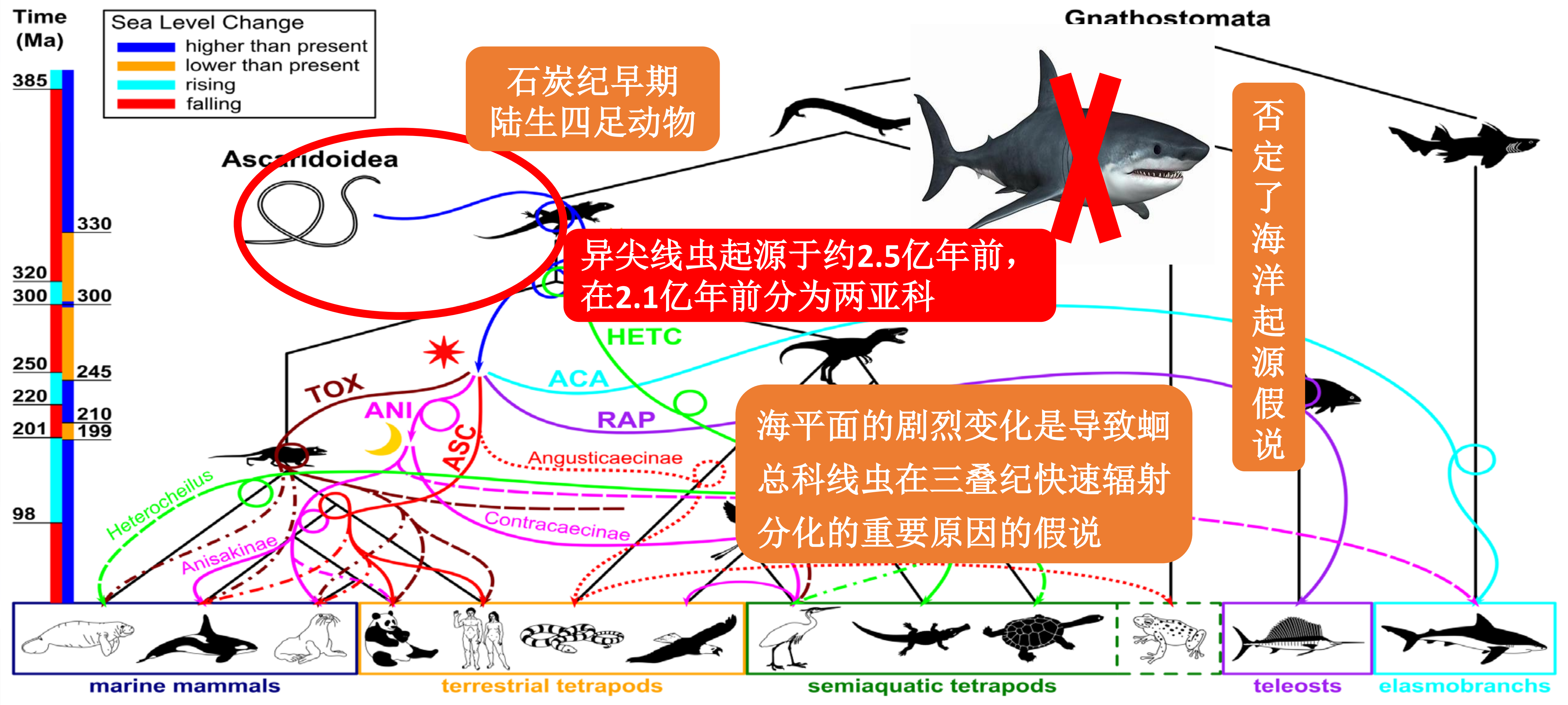


蛔总科线虫的早期演化研究



Time tree of the Ascaridoidea and their hosts (Li et al. 2018, Syst Biol)

蛔总科线虫的早期演化研究



石炭纪早期
陆生四足动物

异尖线虫起源于约2.5亿年前，
在2.1亿年前分为两亚科

否定了海洋起源假说

海平面的剧烈变化是导致蛔总科线虫在三叠纪快速辐射分化的重要原因的假说

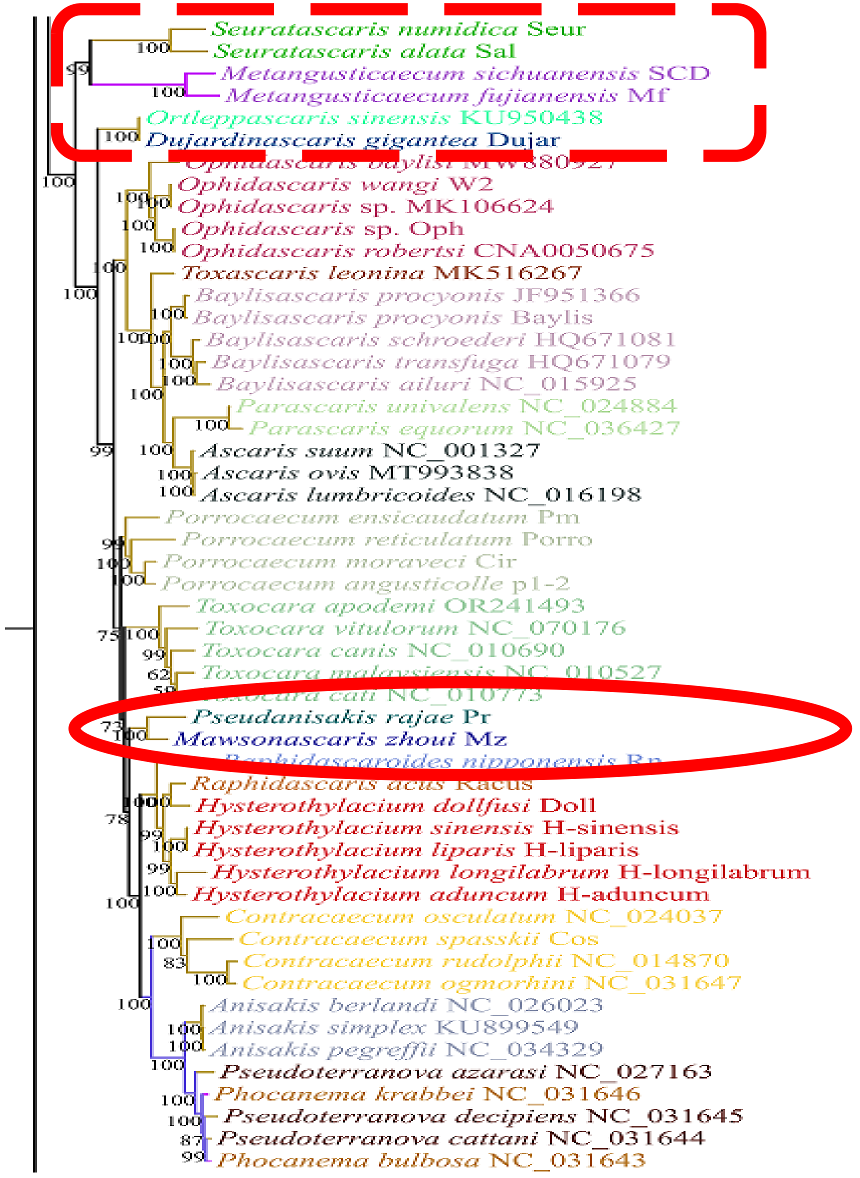
Scheme of the main host switches of high-level ascaridoids (Li et al. 2018, Syst Biol)

蛔总科线虫的早期演化研究

Phylogeny of the Ascaridoidea based on AAs of 12PCGs (unpublished data)

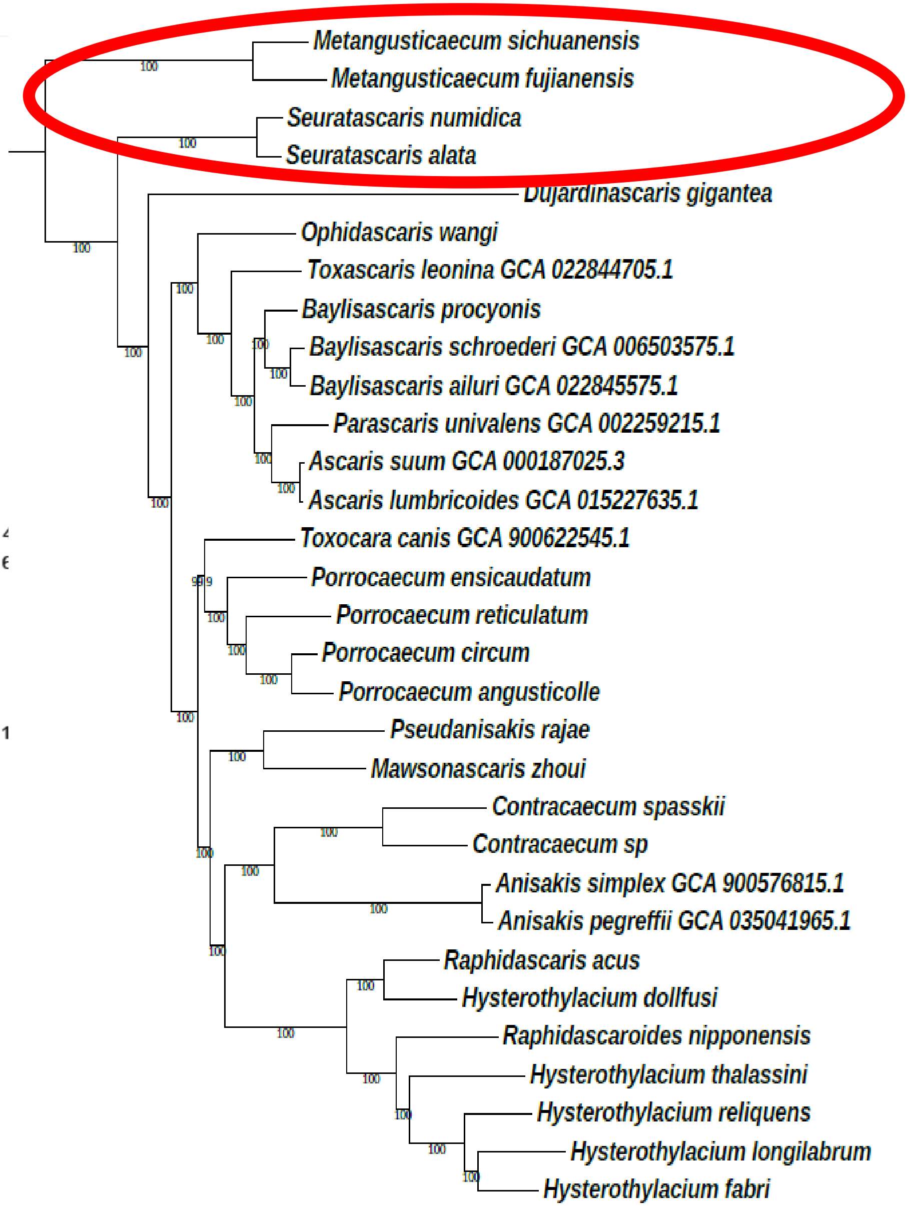
蛔总科进化关系

基于不同分子数据构建的 ML+BI树



线粒体基因组数据

线粒体基因组数据+3核基因



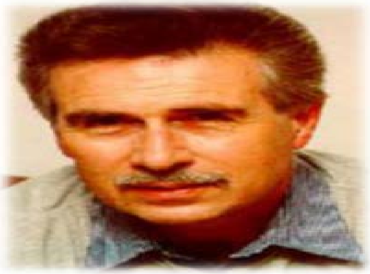
简化基因组数据

致 谢

Tomas Scholz

František Moravec

Aneta Kostadinova



David Gibson

致 谢

- 国家高层次人才特殊支持计划（2022-2024）。
- 国家自然科学基金（Nos 32170442、32170442、31872197、31750002、31572231、31101615）。
- 河北省杰出青年基金、中国博士后基金特别资助等项目。