

SUPPORTING INFORMATION

Parallel evolution of jugal structures in Devonian athyridide brachiopods

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Appendix S1. Character descriptions (after Alvarez *et al.* 1998; Alvarez and Rong 2002). No new characters were added, but character 36 have been amended.

1. size: small (0); moderate (1); large (2); very large (3).
2. lateral profile: biconvex (0); plano or concavoconvex (1).
3. radial ornament: smooth (0); plica (1); ribs (2); fine lines (3); delayed costation (4).
4. spines: absent (0); rounded (1); tabular (2); hollow (3); fimbriae (4).
5. growth lines: absent (0); weak (1); strong (2).
6. frills: absent (0); short (1); long (2).(ordered)
7. fold and sulcus: absent (0); weak (1); strong (2); fold both valves (3); sulcus both valves (4).
8. adult folding: alternate (0); opposite (1); mixed (2).
9. palintrope: reduced (0); moderate (1); extensive (2).
10. palintrope orientation: catacline-apsacline (0); apsacline (1); apsacline-orthocline

- (2); orthocline (3).
11. hinge line: strophic (0); almost strophic (1); astrophic (2).
 12. hinge line width: short (0); medium (1); long (= greatest shell width) (2).
 13. pedicle opening: hypothyriddid (0); meso-permesothyridid (1); permeso-epithyriddid (2); epithyriddid (3).
 14. delthyrium: open (0); partially covered (1); completely covered (2).
 15. pedicle supports: absent (0); pedicle collar (1); delthyrial plate (2).
 16. dental plates: absent (0); short (1); medium (2); long, not extending as ridges anteriorly along muscle scars (3); long extending (4); indistinct (5).
 17. mystrochial plates: absent (0); present (1).
 18. ventral shoe-lifter: absent (0); present (1).
 19. spondylial structure: absent (0); present (1).
 20. ventral median septum: absent (0); short (1); long, supporting spondylium (2); long, not related to spondylium (3).
 21. ventral muscle field: deeply impressed (0); moderately (1); weakly (2).
 22. cardinal plate: absent (0); without inner hinge plate (1); disjunct (2); apically perforate (3); not perforate and thick (4); not perforate, inner hinge plates short, supported by high septum (5); not perforate, inner hinge plates very short or absent, low dorsal median septum or myophragm present (6). (ordered)
 23. cardinal process: absent (0); moderate (1); strong (2). (ordered)
 24. myophragm: absent (0); present (1).
 25. dorsal median septum: absent (0); short, moderately high (1); short, very high (2); long, moderately high (3); long, very high (4).

26. septalium: absent (0); deep, narrow, and partially covered (1); shallow and partially covered (2); deep, narrow, and uncovered (3); shallow and uncovered (4); wide and uncovered (5). (ordered)
27. cruralium: absent (0); present (1).
28. dorsal shoe-lifter: absent (0); present (1).
29. brachidium: absent (0); present, tips directed laterally (1); ventrally (2); medially (3) (State 3 is added for Cyclospiridae).
30. primary lamellae: absent (0); curving posterodorsally from crura (1); curving laterally from crura (2).
31. jugum: absent (0); present between spiral cones (1).
32. lateral branches of jugum: absent (0); vertical (1); inclined anteriorly (2); posteriorly (3); strong posteriorly (4); almost parallel to commissural plane (5).
33. jugal saddle: absent (0); directed anteriorly (1); directed posteriorly (2).
34. jugal stem: absent (0); short (1); long (2).
35. arms of the jugum: absent (0); present (1).
36. accessory jugal lamellae: absent (0); free and short (1); reunite with stem (2); reunite with lateral branches of jugum (3); free, ending near lateral branches of jugum (4); arising by bifurcation from jugal stem, free, intercalated with spiralia to apex (5); arising from jugal arch, free, intercalated with spiralia to apex (6); secondarily connected with spiralia (7). (states 5 and 6 are modified from the old state 5 to distinguish the origination of accessory jugal lamellae among the double spiraliu-bearing groups. New state 5 represent for Diplospirellinae, Hungarispirinae and *Sinathyris* and new state 6 for Helenathyridinae and

Koninckinoidea).

37. shell structure: impunctate (0); punctate (1).

Appendix S2. Data matrix used in the phylogenetic analyses based on Alvarez *et al.* (1998) and Alvarez and Rong (2002). Coding of character 33 for Didymothyridinae were amended and characters number 29 and 36 were modified. Cyclospiridae and two generic taxa *Sinathyris* and *Sphaerathyris* were added.

Ancistrorhynchidae	1020001002 2000020000 2100000000 0000000
Athyridinae	2000211001 2010020000 2311000011 1112140
Athyrisininae	2020222002 2110020000 23--000011 1212110
Camarophorellinae	1000100103 2010031012 -000440111 12-2130
Clavigerinae	3010114123 0220020001 0421000011 12-2110
Cleiothyridininae	2002221002 2010010000 1311000011 1112140
Comelicaninae	3010111012 1200010000 2320000011 1----40
Didymothyridinae	1000101002 20---10000 2301000011 1-{01}2140
Diplospirellinae	0000100103 2020010000 2421000011 1202150
Helenathyridinae	0004110102 20--010000 2300000011 12?2160
Hungarispirinae	0010104123 1222000000 2620400011 1002151
Hustedinae	1010101013 1112100000 2620100011 1202001
Hyattidinidae	10001-2002 20-0010000 22-0000011 1-00000

Koninckinoidea	1100001002 02--020000 20-0000022 150-160
Lochengiinae	3000210103 2110000000 2311000011 1112140
Meristellinae	2000101002 2011050000 0000340011 1302120
Meristinae	2000101002 2010041100 -000440011 1302130
Misoliinae	2020100103 202-010000 2421000011 120--40
Mongolospiroidea	1000000103 2012010000 ---0400011 1200001
Neoretziinae	201010--13 1122100000 2620400011 1202171
Nucleospiroidea	1001101001 1102200003 2021000011 1102000
Ochotathyridinae	3000101002 2020250000 2421000011 1212140
Parazygidae	1023211001 2112120000 2511000011 1220001
Plectospirinae	0010101012 1112000000 26-0300011 1102001
Plicathyridinae	2010222213 1110020000 2311000011 1212140
Pradoiinae	20411-4113 2010020000 2311000011 1212110
Retzielloidea	1020101012 2010010000 2000320011 11-0000
Retziidae	2020101012 2022100000 2620000011 1202101
Rhynchospirinidae	1020201001 2112--0000 2510100011 1120001

Rowleyellinae	0000100103 2010031012 -0004511-- -----0
Septathyridinae	2030102002 2112030000 2000340011 1302120
Spirigerellinae	2000111002 2010020000 2320000011 1112140
Tetractinellinae	1010211113 1120220000 2421000011 1112140
Triathyridinae	2030103102 2031010000 2000340011 1302120
Trigonirhynchiidae	1020001002 2001020000 2000310000 0000000
Whitfieldellinae	2000100102 2010010000 2000210011 1101000
Xenosariinae	1000104102 1000000000 2300000011 1-----0
<i>Sinathyris</i>	1000101012 200?000000 0301000011 1102150
<i>Sphaerathyris</i>	0000000113 20?1?10000 ?300000011 1102150
Cyclospiridae	0000002003 2012000000 1000300032 0000000

Appendix S3. Data matrix used in the phylogenetic analyses based on Alvarez *et al.* (1998) and Alvarez and Rong (2002). Coding of character 33 for Didymothyridinae was amended and a new state was added in character 29 only. Cyclospiridae and two generic taxa *Sinathyris* and *Sphaerathyris* were added.

Ancistrorhynchidae	1020001002 2000020000 2100000000 0000000
Athyridinae	2000211001 2010020000 2311000011 1112140
Athyrisininae	2020222002 2110020000 23--000011 1212110
Camarophorellinae	1000100103 2010031012 -000440111 12-2130
Clavigerinae	3010114123 0220020001 0421000011 12-2110
Cleiothyridininae	2002221002 2010010000 1311000011 1112140
Comelicianiinae	3010111012 1200010000 2320000011 1----40
Didymothyridinae	1000101002 20---10000 2301000011 1-{01}2140
Diplospirellinae	0000100103 2020010000 2421000011 1202150
Helenathyridinae	0004110102 20--010000 2300000011 12?2150
Hungarispirinae	0010104123 1222000000 2620400011 1002151
Hustedinae	1010101013 1112100000 2620100011 1202001
Hyattidinidae	10001-2002 20-0010000 22-0000011 1-00000

Koninckinoidea	1100001002 02--020000 20-0000022 150-150
Lochengiinae	3000210103 2110000000 2311000011 1112140
Meristellinae	2000101002 2011050000 0000340011 1302120
Meristinae	2000101002 2010041100 -000440011 1302130
Misoliinae	2020100103 202-010000 2421000011 120--40
Mongolospiroidea	1000000103 2012010000 ---0400011 1200001
Neoretziinae	201010--13 1122100000 2620400011 1202161
Nucleospiroidea	1001101001 1102200003 2021000011 1102000
Ochotathyridinae	3000101002 2020250000 2421000011 1212140
Parazygidae	1023211001 2112120000 2511000011 1220001
Plectospirinae	0010101012 1112000000 26-0300011 1102001
Plicathyridinae	2010222213 1110020000 2311000011 1212140
Pradoiinae	20411-4113 2010020000 2311000011 1212110
Retzielloidea	1020101012 2010010000 2000320011 11-0000
Retziidae	2020101012 2022100000 2620000011 1202101
Rhynchospirinidae	1020201001 2112--0000 2510100011 1120001

Rowleyellinae	0000100103 2010031012 -0004511-- -----0
Septathyridinae	2030102002 2112030000 2000340011 1302120
Spirigerellinae	2000111002 2010020000 2320000011 1112140
Tetractinellinae	1010211113 1120220000 2421000011 1112140
Triathyridinae	2030103102 2031010000 2000340011 1302120
Trigonirhynchiidae	1020001002 2001020000 2000310000 0000000
Whitfieldellinae	2000100102 2010010000 2000210011 1101000
Xenosariinae	1000104102 1000000000 2300000011 1-----0
<i>Sinathyris</i>	1000101012 200?000000 0301000011 1102150
<i>Sphaerathyris</i>	0000000113 20?1?10000 ?300000011 1102150
Cyclospiridae	0000002003 2012000000 1000300032 0000000

Appendix S4 Experimental results of cladistic analyses.

A new data-matrix (Appendix S2) was constructed on the basis of the data of Alvarez *et al.* (1998) and Alvarez and Rong (2002), with only minor changes in the coding of their character 33 (jugal saddle) for Didymothyridinae and character 36 (accessory jugal lamellae), as well as a new state introduced in character 29 for the new selected outgroup Cyclospiridae (see section *Phylogenetic position of Sinathyris among athyridides*). The coding of *Sinathyris* gen. nov., is based on our new study and observation and that of *Sphaerathyris* is based on the description and serial sections of Baranov (1994). The coding of Cyclospiridae is based on Copper (2002). Two series of analyses were performed under different character weighting strategy for comparing the results related to character weighting and taxon-addition.

The first series of analyses adopted the character weighting strategy strictly after Alvarez *et al.* (1998) and Alvarez and Rong (2002): four characters (numbers 3, 5, 6, and 25) were weighted three times greater than the others; three characters (numbers 22, 23, and 26) five times greater; and the character (punctate or impunctate) of the shell structure (number 37) 13 times. In the second series of analyses all characters were equally weighted. The character ordering is the same in two series to that used by Alvarez *et al.* (1998) and Alvarez and Rong (2002): four characters (numbers 6, 22, 23 and 26) were ordered and all others unordered. Cyclospiridae is selected as an outgroup if it is included in the analysis besides the two rhynchonellide taxa adopted by Alvarez *et al.* (1998) and Alvarez and Rong (2002).

We made four sets of experiments by using the data-matrixes in Appendixes S2 and S3 for each series: (1) deleting Cyclospiridae and *Sphaerathyris* from each

data-matrix to keep *Sinathyris* gen. nov. with the 37 suprageneric taxa used by Alvarez *et al.* (1998) and Alvarez and Rong (2002); (2) by adding *Sphaerathyris* as an ingroup to experiment (1); (3) by adding Cyclospiridae as an outgroup to experiment (1); (4) by adding Cyclospiridae as an outgroup to experiment (2).

The experimental results of the first series are shown in Figures 1–2. Under the condition of weighting on the selected characters, the number of obtained most parsimonious trees and topology of the cladograms are exactly the same between the two data-matrixes in each experiment, indicate that modification of character 36 does not affect the search result of each experiment except value of consistency index (CI) and the tree length (if *Sphaerathyris* added). We obtained three equally most parsimonious trees from experiments (1) and (2). The resulted cladograms are highly in agreement to those of Alvarez *et al.* (1998), with the phylogenetic relationship of most ingroups resolved in the consensus tree of each analysis except Nucleospiroidea (Fig. 1A, C). Four equally most parsimonious trees were obtained from experiments (3) and (4), one tree more than that from experiments (1) and (2). Among the four resulted cladograms, three are in agreement to those from experiments (1) and (2) and Alvarez *et al.* (1998) and one does not. In the latter cladogram, Koninckinoidea is placed below Cyclospiridae (Fig. 2C) and the phylogenetic relationship of Koninckinoidea becomes unresolvable from Cyclospiridae in the strict consensus tree (Fig. 2A–B). Anyway, in all cases of the first series of analyses, the new genus *Sinathyris* is always resolved as a sister group of Didymothyridinae in a position more primitive than Xenosariinae and more derived than Hyattidinidae at the base of the superfamily Athyrdoidea (Figs. 1 and 2), and *Sphaerathyris*, if added, is resolved as

an independent lineage below Helenathyridinae (Figs. 1C, 2B, 2C).

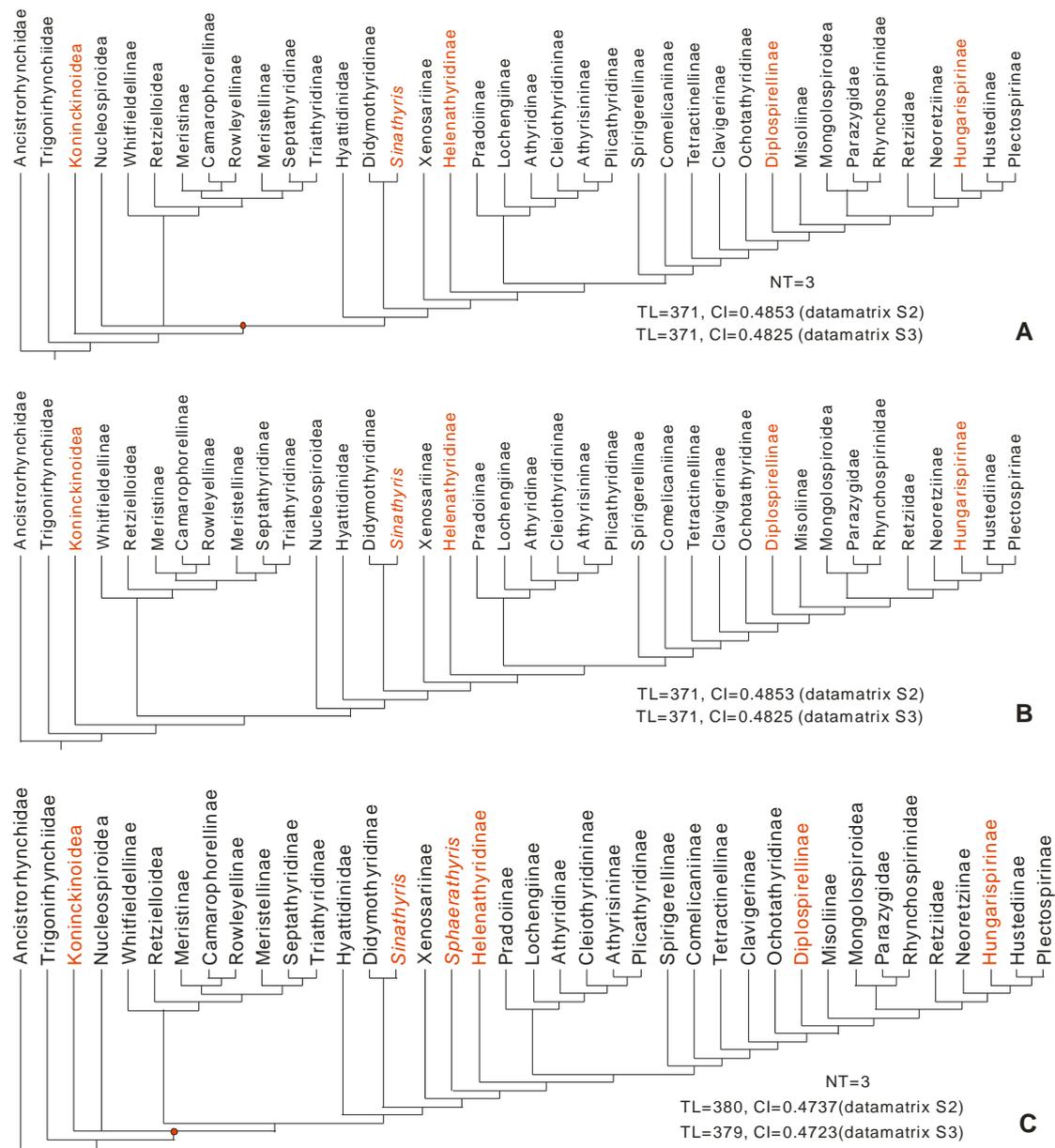


Fig. 1 Cladograms obtained from the first series of experimental analyses (with selected characters weighting as Alvarez *et al.* (1998) and Alvarez and Rong (2002) suggested). A–B, the strict consensus and one preferred tree of the three equally most parsimonious trees obtained from experiment (1); C, the strict consensus tree of the three equally most parsimonious trees obtained from experiment (2). Emendation on character 36 does not affect the search results except the tree length (if *Sphaerathyris* included) and CI value. Double spiralia-bearing taxa

marked with red colour. Unresolved node indicated by red heavy dot. NT, number of trees;

TL, tree length; CI, Consistency index.

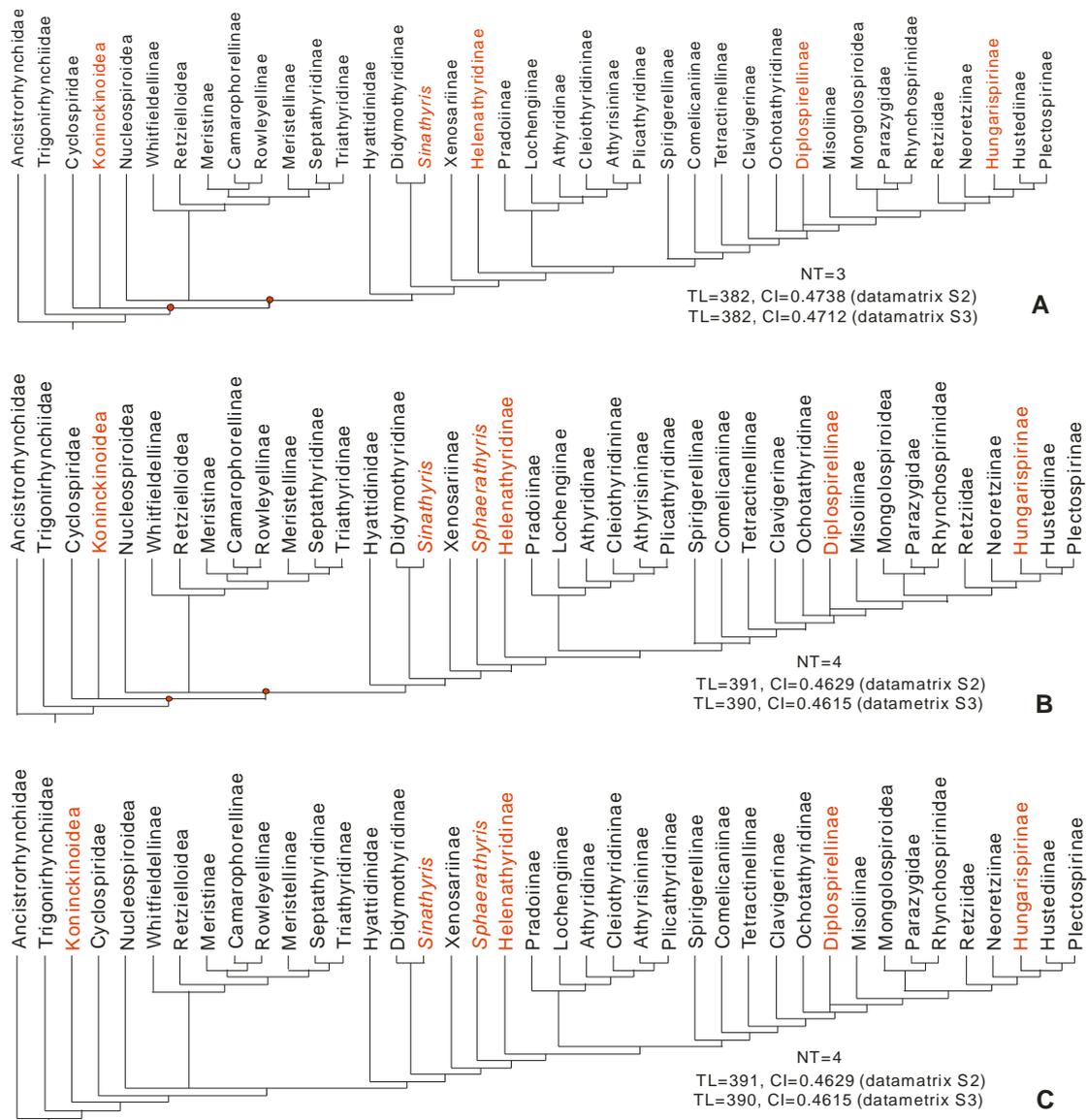


Fig. 2 Cladograms obtained from the first series of experimental analyses (with selected characters

weighting as Alvarez *et al.* (1998) and Alvarez and Rong (2002) suggested). A, the strict consensus tree of the four equally most parsimonious trees obtained from experiment (3).

B–C, the strict consensus and one un-preferred tree of the four equally most parsimonious

trees obtained from experiment (4). Emendation on character 36 does not affect the search results except the tree length (if *Sphaerathyris* included) and CI value. For explanations see

Fig. 1.

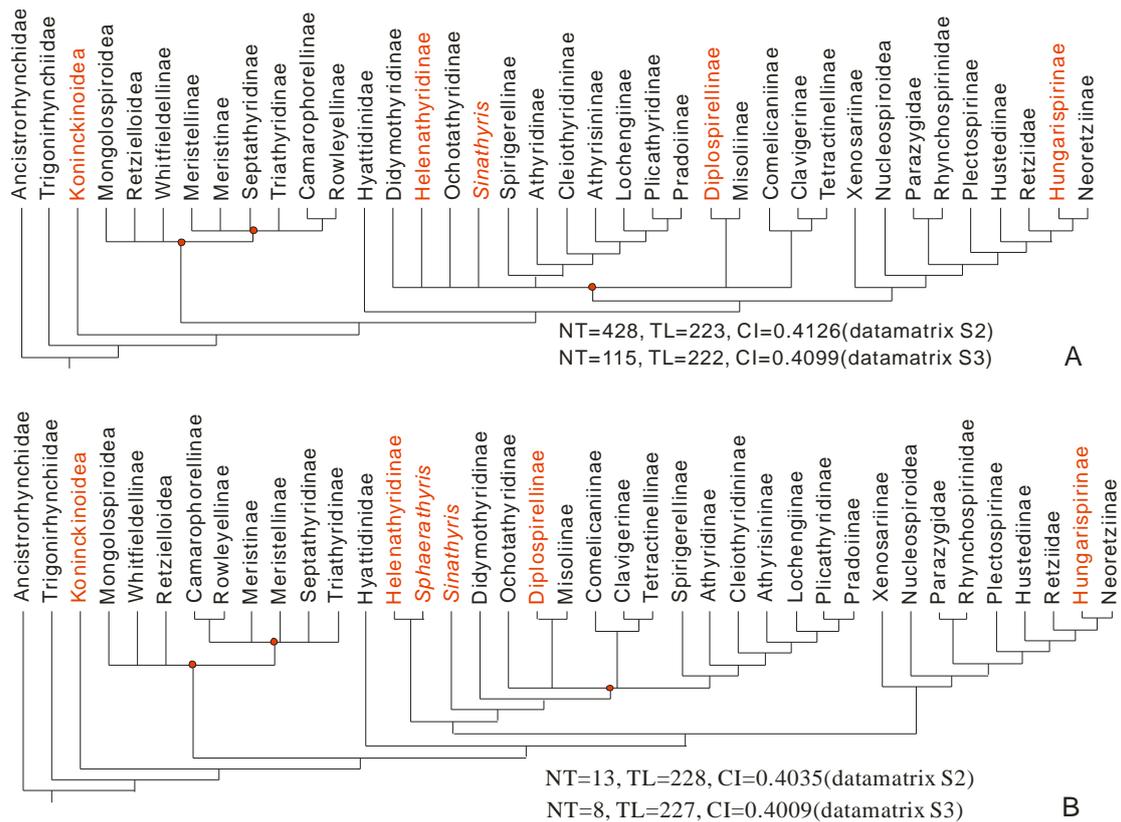


Fig. 3 Cladograms obtained from the second series of experimental analyses (all characters equally weighted). A–B, the strict consensus trees obtained from experiments (1) and (2), respectively. The pattern of the strict consensus trees obtained from the two data-matrixes in each experiment is the same but the number of trees, tree length and CI value is varied. For explanations see Fig. 1.

The experimental results of the second series are shown in Figures 3 and 4. Under the condition of all characters equally weighted, the obtained most parsimonious trees are highly unstable and contain multiple polytomies. In contrast to the first series of experiments, phylogenetic relationship of *Sinathyris* gen. nov. is resolved only in the experiments (2) and (4) as an independent lineage more primitive than Didymothyridinae and more derived than the clad including Helenathyridinae and *Sphaerathyris* (when *Sphaerathyris* is added) (Figs. 3B, 4C). Adding Cyclospiridae as an outgroup does not affect the search result under condition of all characters equally

weighted. The result of these experiments reveals that the topology of cladograms is variable, whether or not modifying character 36 and whether or not adding new taxa, and that in the strict consensus tree of each experiment, the relationship of many taxa remains not resolved.

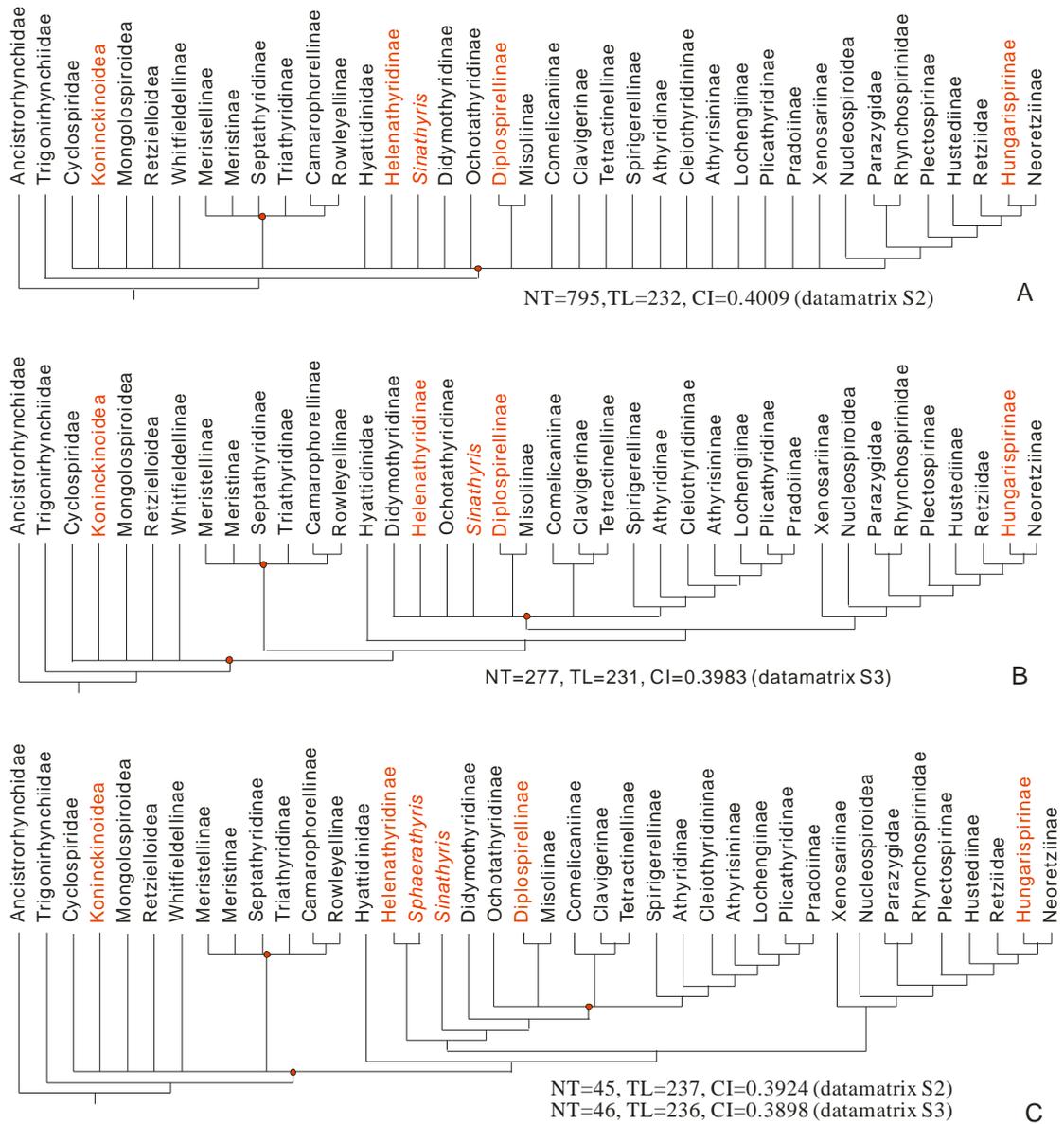


Fig. 4 Cladograms obtained from the second series of experimental analyses (all characters equally weighted). A–B, the strict consensus trees obtained from experiment (3) by using the data-matrixes in Appendixes S2 and S3, respectively. C, the strict consensus trees obtained from experiment (4) of the second series. Note the pattern of the strict consensus trees from

the two data-matrixes is different in experiment (3). For explanations see Fig. 1.

Considering the phylogenetic relationship of Koninckinoidea becomes unresolvable after adding Cyclospiridae as an outgroup in the experiments (3) and (4) of the first series (Fig. 2), we carried further experimental analyses on the base of the experiments of the first series by deleting Koninckinoidea from the datasets. The results are shown in Figure 5 and 6. We obtained only single most parsimonious tree from each experiment. The result shows that the phylogenetic relationship of Nucleospiroidea is significantly affected by adding Cyclospiridae as an outgroup, while the phylogenetic relationship of other ingroups keeps consistent pattern as that of the experimental analyses of the first series.

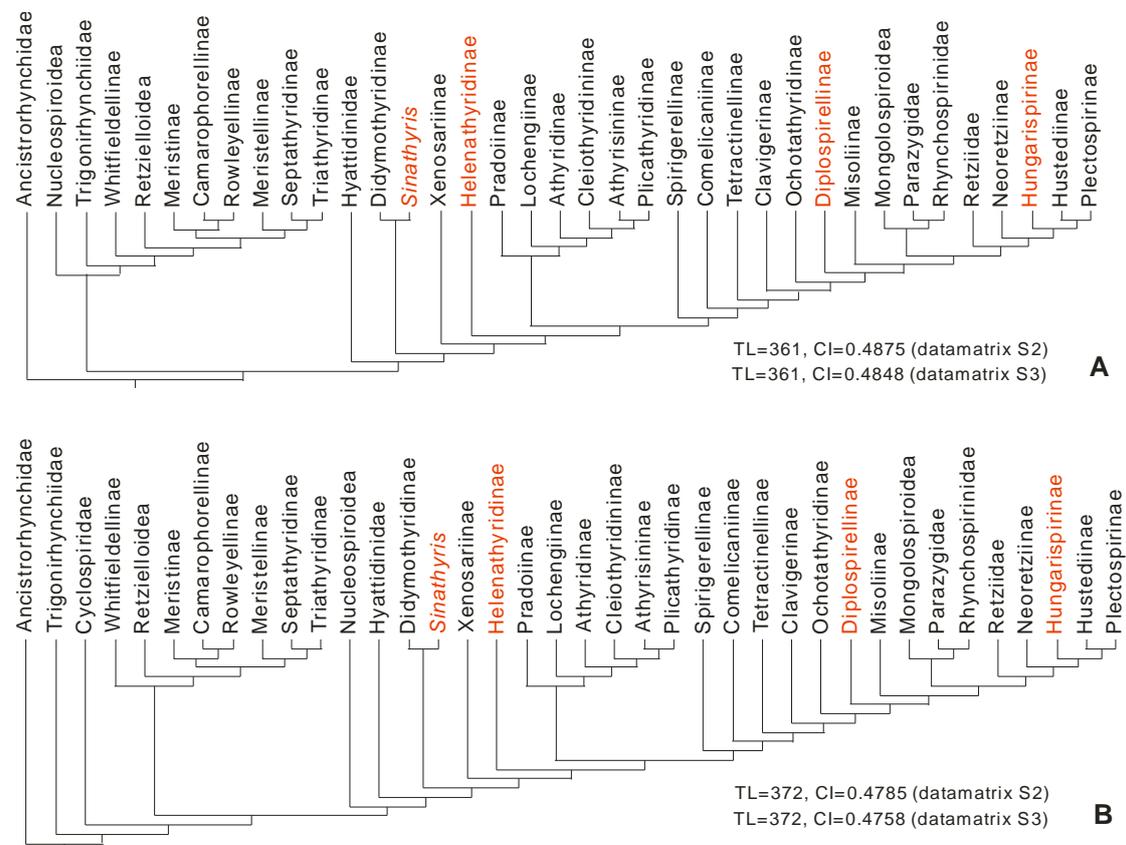


Fig. 5 Cladograms obtained from the experimental analyses by deleting Koninckinoidea (with selected characters weighting as Alvarez *et al.* (1998) and Alvarez and Rong (2002)

suggested). A, the single most parsimonious tree obtained from experiment (1) (both Cyclospiridae and *Sphaerathyris* excluded); B, the single most parsimonious tree obtained from experiment (3) (Cyclospiridae included but *Sphaerathyris* excluded). For explanations see Fig. 1.

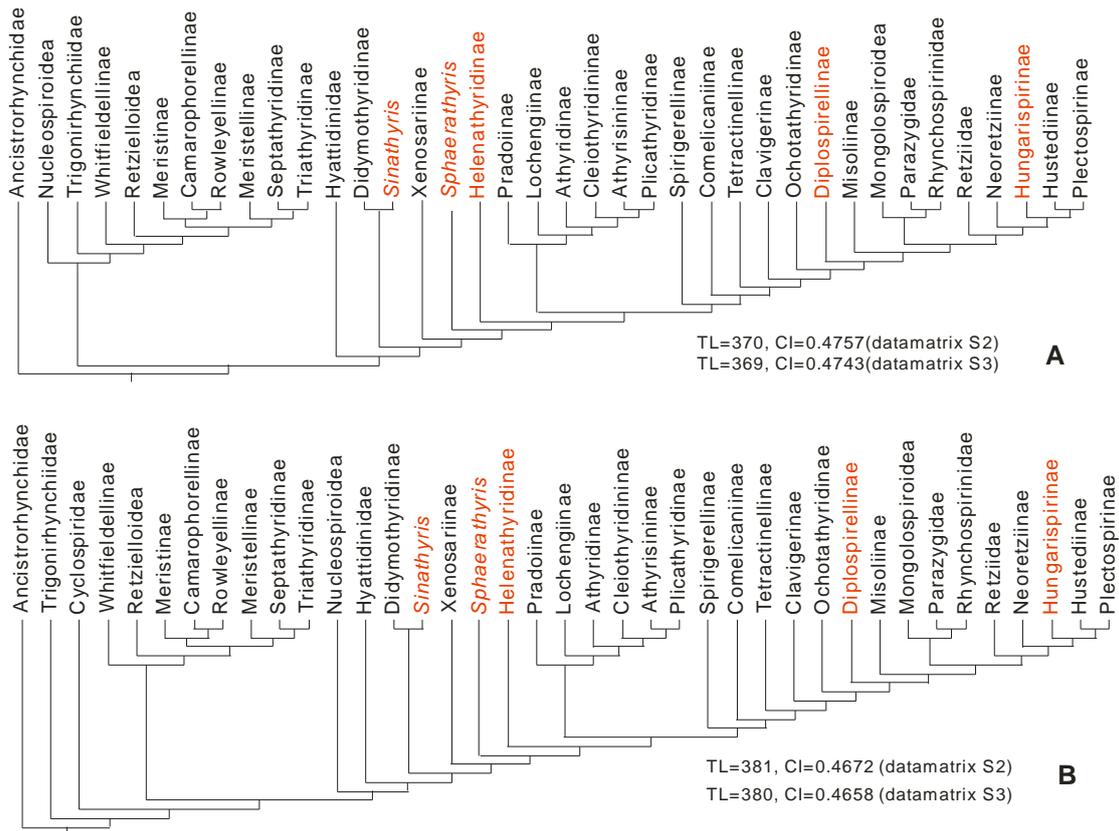


Fig. 6 Cladograms obtained from the experimental analyses by deleting Koninckinoidea (with selected characters weighting as Alvarez *et al.* (1998) and Alvarez and Rong (2002) suggested). A, the single most parsimonious tree obtained from experiment (2) (Cyclospiridae excluded); B, the single most parsimonious tree obtained from experiment (4) (Cyclospiridae included). For explanations see Fig. 1.

References

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