http://app.pan.pl/SOM/app67-Gardner_Wilson_SOM.pdf

SUPPLEMENTARY ONLINE MATERIAL FOR

The most complete bowfin amiid from the Coal Creek Member of the Kishenehn Formation (Eocene), Northwestern Montana

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Published in *Acta Palaeontologica Polonica* 2022 67 (2): 493-508.
https://doi.org/10.4202/app.00733.2020

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Morphological data matrix

Data matrix of characters used in USNM 618000 phylogenetic analysis. Character states defined by Grande and Bemis (1998).

39 69

Atractosteus_spatula

0100000101000100 00?0101001000-0-001000000-00010011??000000-0000-00000

Eurycormus_speciosus

000-0?000000000-0000000?-?000-0000?00000?000000000??00000000000000012

Dorsetichthys_bechei

000-?0000000?00-01000?0?-?00?-0000000000000000000000000000000000000112

Siemensichthys_macrocephalus

000-00000000?00--?000000-0000-0000000000000000000000000000000010112

Amiopsis_prisca

1?110000000?000??01???0??00000?0??00?000??0111?0???000???0011??0001?

Amiopsis_lepidota

1?110000000000000001001000000000000000000000111000??00011000110000011

Amiopsis_woodwardi

1?1100?000000000101?0100000000000000000?0111000?100011000110000011

Amiopsis_damoni

1?110000000000000101?0100000000000000000000111000??0001100011?000011

Amiopsis_dolloi

1?110?0000000000??01001?000000000000000000000111000??0001100011?000011

Solnhofenamia_elongata

1112100000000000010100100000000?00100000021111000?10001100011000011

Calamopleurus_cylindricus

1112111100000000001211211110000000000000000011100011000010001101000011

Pachyamia_latimaxillaris

1112??110000?010?0?2111?0?01111111111111110?????000?10001100011?00?011

Pachyamia_mexicana

1112?11100000010001211100001111111111111101?1111000??0001100011?000011

Vidalamia_catalunica

1?12??110000000000121110000111111111?000000111000 1?00011000110000011

Cyclurus_oligocenicus

1??2??111111121?1010?1?00000?000?00000000?0111000??0?0110?0?1?00101?

Cyclurus_macrocephalus

1?12??111111121?1010010?000000000000000000011100 0??0001100??1?001011

Cyclurus_ignotus

11122?1111111121110100100000000000000000000011100 0??00011000110001011

Cyclurus_valenciennesi

11122??111111121??0100100000000?000?00?00??0111000??0?0???00?1?001011

Cyclurus_fragosus

11122?11111111?1110100100000000000000000?00001110001?00011000110001011

Cyclurus_efremovi

11?22?1111111121110100100000000000000000000011100 0?10001100011000 1011

Cyclurus_gurleyi

11?22?111111112111010010000000000000000000011100011000110101100010 11

Cyclurus_kehreri

1112211111111121110100100000000000000000000111000110001100011000110001011

Amia_pattersoni

11122?1111111120000100 10?0000000000000010000111000110001100011000110001011

Amia_hesperia

11122?1111111120000100 10?0000000000000000?0?1??000??0??11??0110001011

Amia_scutata

1?122?1111111130000100100000000000000000100001110001100011000110001011

Amia_calva

11?2211111111130000100100000000000000000100001110001100011000110001011

Sinamia_zdanskyi

000?00?000000?00?-010110??00?0000000000000001??1111100011000110000011

Ikechaoamia_orientalis

0?000?00000?0?00?-01001???00000?00?000000?00111111??0001100011??0001?

Ikechaoamia_meridionalis

0?000??000000?00?-010?1?0?0000000000000000?00111111??0001100011 0?00011

Caturus_furcatus

000-0000000000000101100 0?1000000000000000030000000111111100011001 0111

Amblysemius_pachyurus

0?0-0?0000000000010110000000 0-0000000000000000000??1111100010 0?10111

Liodesmus_gracilis

0?0-0?0000?00000?10110000?0000000000000000?0001000??11011000110010111

Liodesmus_sprattiformis

0?0-0?0000?00000?101100???000000000000000?0001000??11011000?10010111

Ionoscopus_cyprinoides

010000000000000000?100000100000000?000000000000000000000011000111000011

Ophiopsis_procera

10?21?000000000???0100000?0?000?000000000?1000?00???00011111?11000011

Macrepistius_arenatus

1002??01?0?0??1????1000?0?0????000?0000000100??00?0000?1?1111?1?00011

Oshunia_brevis

0000?000000?0?0000?1000?0000000000?000000?1?000000000001101111111000011

Watsonulus_eugnathoides

000-000000000000010300000000?000000000000000000?000000000000110000011

USNM_618000

1?12??1111?111?0??010?1?0?00???000??0001?000111?????0??1?0001?00010?1

Analyses

RaxML code for the phylogenetic analyses (each a single line separated by spaces). The first two lines of code are for the analyses without USNM 618000. The first analysis resulted in the best-supported parsimony and maximum likelihood trees seen in Fig. S4. The second line of code is for the rapid bootstrap analysis (Fig. S5). The third and fourth lines of code are for the analyses with USNM 618000. The third analysis resulted in the best-supported parsimony and maximum likelihood trees seen in Fig. S6. The fourth line of code is for the rapid bootstrap analysis (Fig. 6 in main text).

```
1. raxmlHPC -p 12345 -m MULTIGAMMA -K MK -o
Dorsetichthys_bechei,Siemensichthys_macrocephalus -s
GrandeBemisReanalysis.2021.phy -n GrandeBemis_MKTre -# 100

2. raxmlHPC -p 12345 -m MULTIGAMMA -K MK -o
Dorsetichthys_bechei,Siemensichthys_macrocephalus -s
GrandeBemisReanalysis.2021.phy -n GrandeBemis_MK.boot.Tre -f a -x 1234 -# 100

3. raxmlHPC -p 12345 -m MULTIGAMMA -K MK -o
Dorsetichthys_bechei,Siemensichthys_macrocephalus -s
USNM618000Analysis.2021.phy -n USNM618000_MKTre -# 100
```

4. raxmlHPC -p 12345 -m MULTIGAMMA -K MK -o Dorsetichthys_bechei,Siemensichthys_macrocephalus -s USNM618000Analysis.2021.phy -n USNM618000_MK.boot.Tre -f a -x 1234 -# 100

Results Summary

We ran all analyses for 100 runs in RaxML. The following is a brief summary of the results:

1. Grande and Bemis Reanalysis: Run 66 was the best tree with a likelihood of -631.486805; and final GAMMA-based score of the best tree was -631.486800.

2. USNM 618000 analysis: Run 34 was the best tree with a likelihood of -631.487350; final GAMMA-based score of the best tree was -631.487350.

Please refer to the main text for a more detailed description of the results, including the rapid bootstrap analysis.

FIGURES

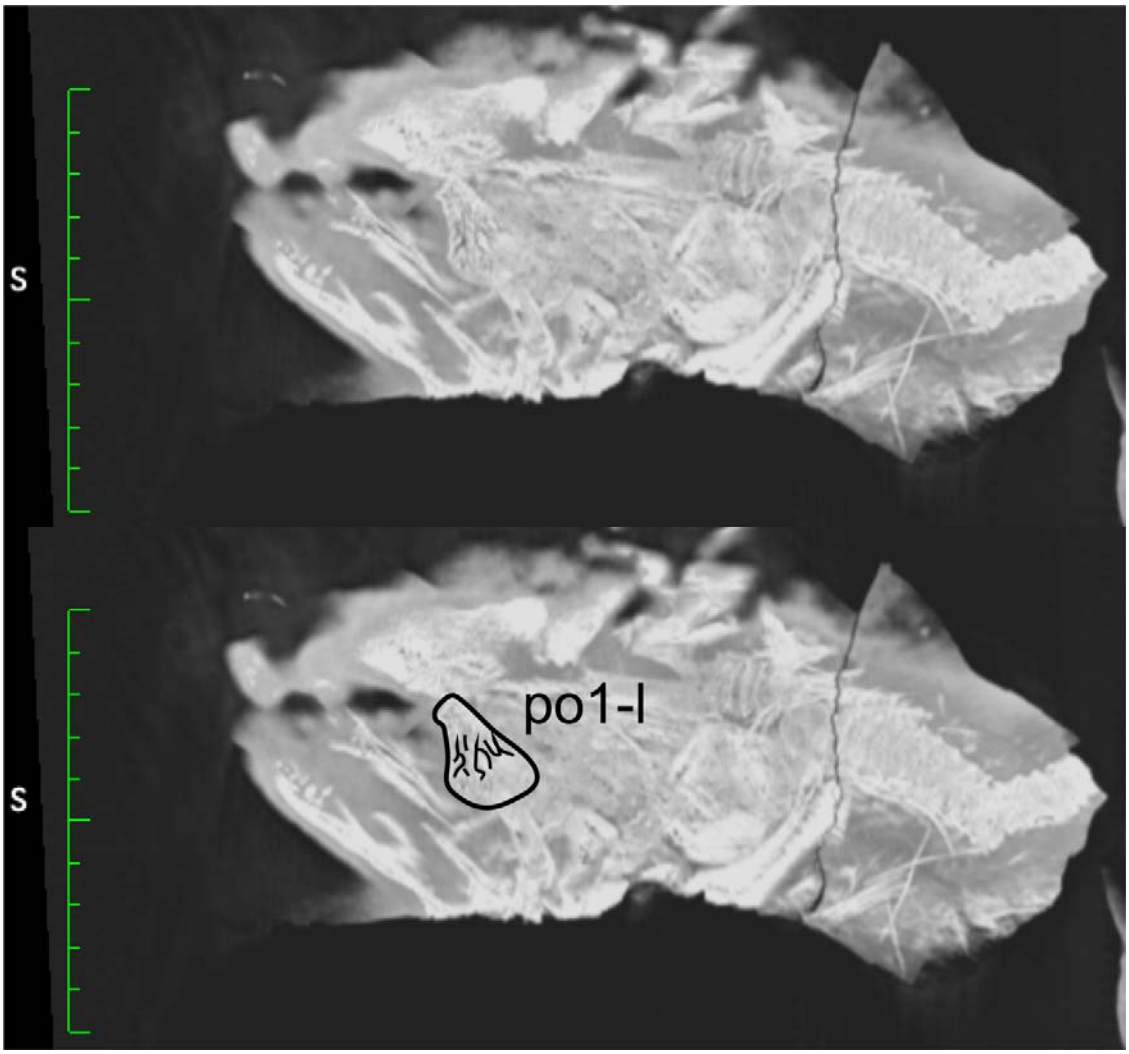


FIGURE S1: CT slice image showing the presence of dermal ornamentation on the first postinfraorbital (po1) in USNM 618000.

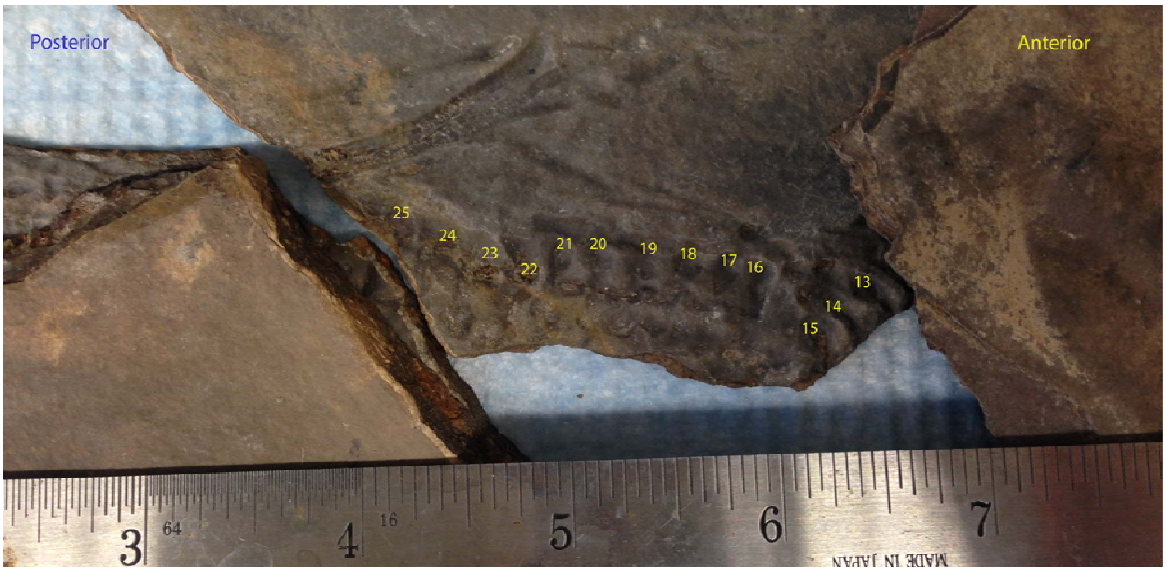
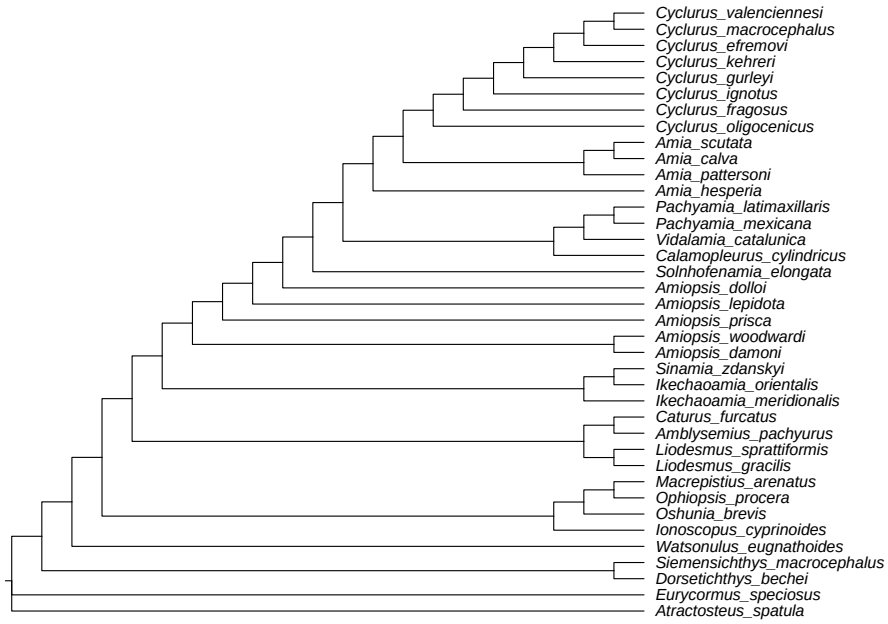


FIGURE S2: Image of the first vertebral column section represented only by impressions (anterior-most vertebral column section missing from Fig. 2c in the main text).

FIGURE S3: Image of the second vertebral column section only represented by impressions (posterior-most vertebral column section missing from Fig. 2c in the main text).

A



B

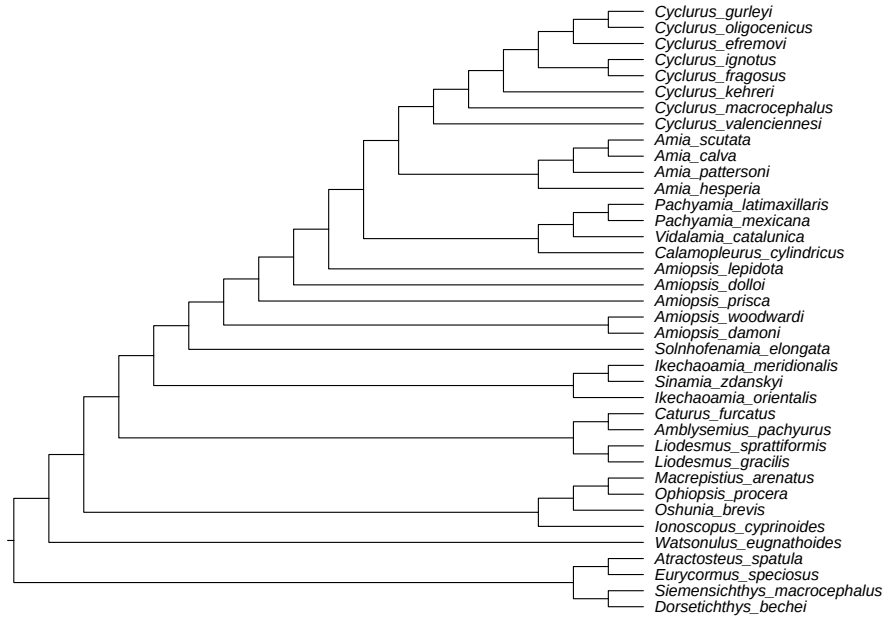


FIGURE S4: Resulting cladograms from the analysis without USNM 618000. **A,** parsimony tree from best-scoring run; **B,** maximum likelihood tree from best-scoring run.

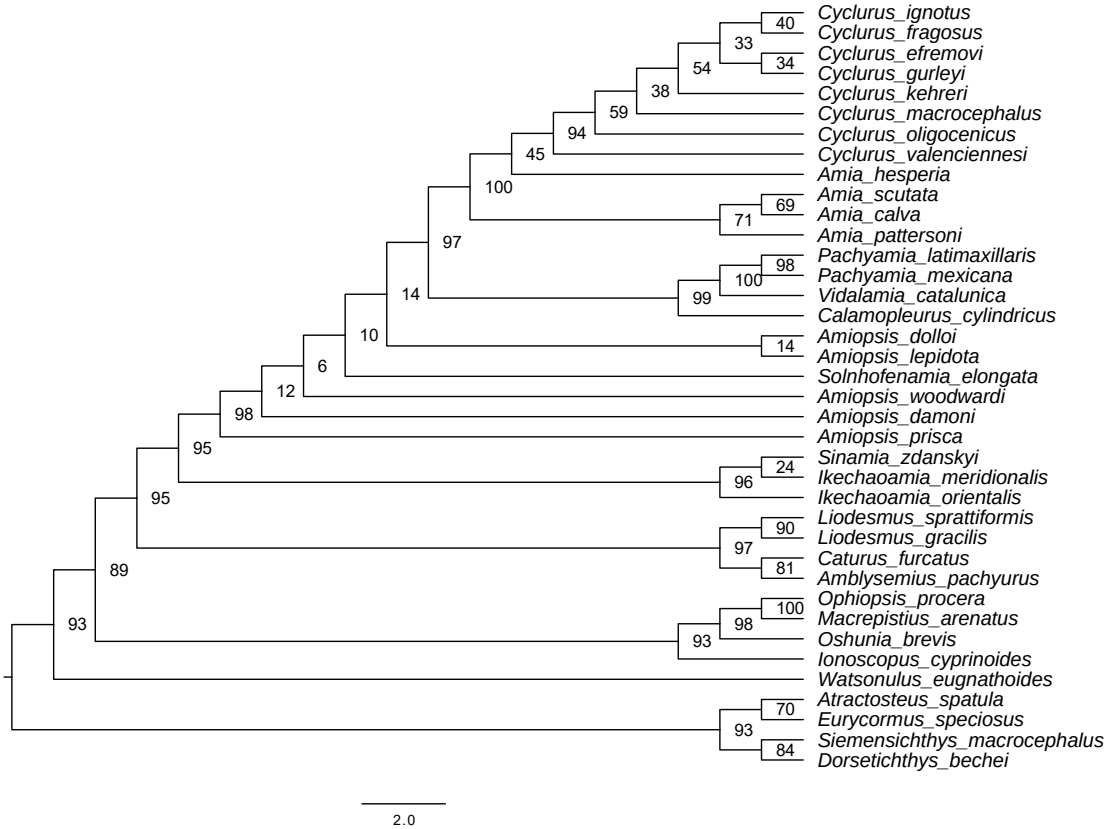
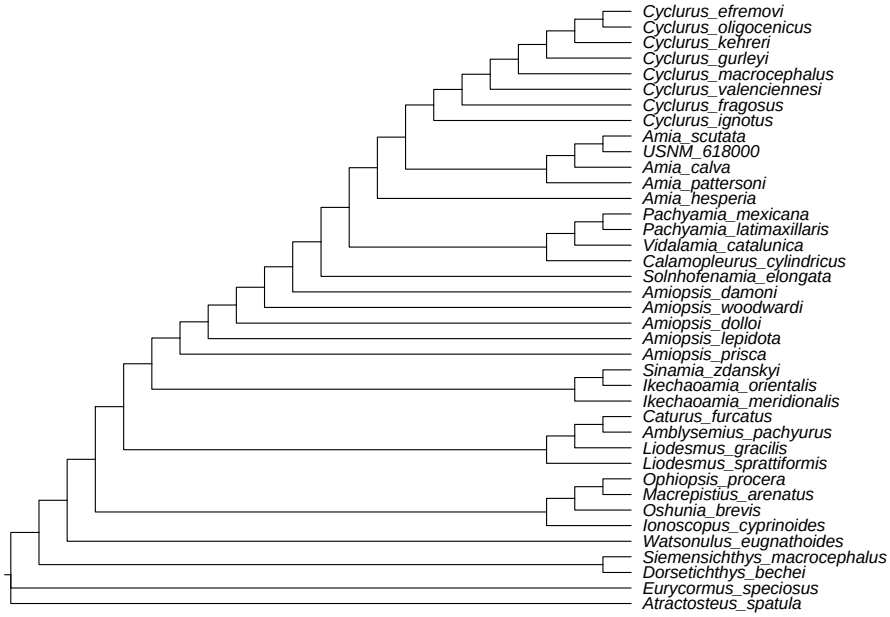


FIGURE S5: Cladogram from the maximum likelihood rapid bootstrap analysis, excluding USNM 618000, with bootstrap support values for each node.

A


Cyclurus_efremovi
Cyclurus_oligocenicus
Cyclurus_kehreri
Cyclurus_gurleyi
Cyclurus_macrocephalus
Cyclurus_valenciennesi
Cyclurus_fragosus
Cyclurus_ignotus
Amia_scutata
USNM_618000
Amia_calva
Amia_pattersoni
Amia_hesperia
Pachyamia_mexicana
Pachyamia_latimaxillaris
Vidalamia_catalunica
Calamopleurus_cylindricus
Solnhofenamia_elongata
Amiopsis_damoni
Amiopsis_woodwardi
Amiopsis_dolloi
Amiopsis_lepidota
Amiopsis_prisca
Sinamia_zdanskyi
Ikechaoamia_orientalis
Ikechaoamia_meridionalis
Caturus_furcatus
Amblysemius_pachyurus
Liodesmus_gracilis
Liodesmus_sprattiformis
Ophiopsis_procera
Macrepistius_arenatus
Oshunia_brevis
Ionoscopus_cyprinoides
Watsonulus_eugnathoides
Siemensichthys_macrocephalus
Dorsetichthys_bechei
Eurycormus_speciosus
Atractosteus_spatula

B

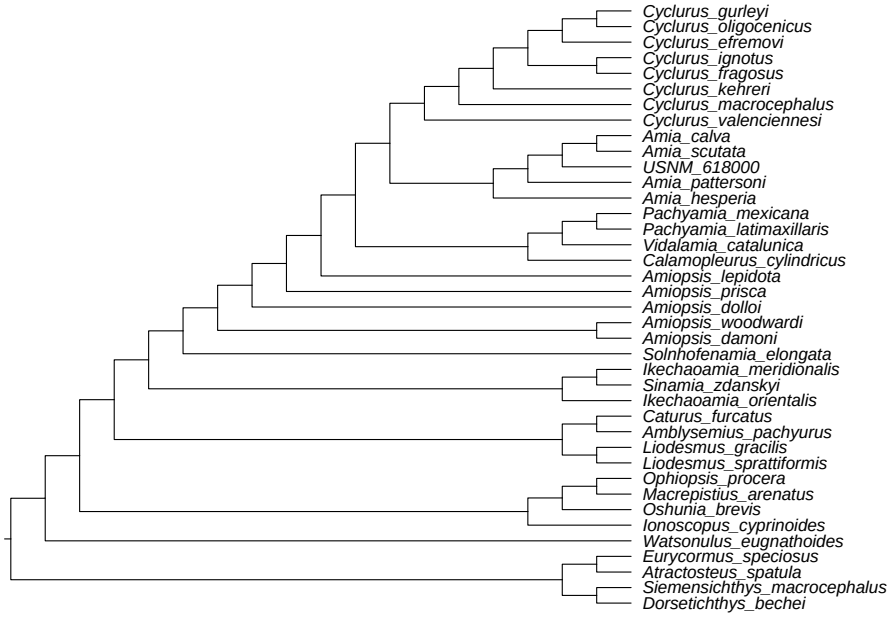

Cyclurus_gurleyi
Cyclurus_oligocenicus
Cyclurus_efremovi
Cyclurus_ignotus
Cyclurus_fragosus
Cyclurus_kehreri
Cyclurus_macrocephalus
Cyclurus_valenciennesi
Amia_calva
Amia_scutata
USNM_618000
Amia_pattersoni
Amia_hesperia
Pachyamia_mexicana
Pachyamia_latimaxillaris
Vidalamia_catalunica
Calamopleurus_cylindricus
Amiopsis_lepidota
Amiopsis_prisca
Amiopsis_dolloi
Amiopsis_woodwardi
Amiopsis_damoni
Solnhofenamia_elongata
Ikechaoamia_meridionalis
Sinamia_zdanskyi
Ikechaoamia_orientalis
Caturus_furcatus
Amblysemius_pachyurus
Liodesmus_gracilis
Liodesmus_sprattiformis
Ophiopsis_procera
Macrepistius_arenatus
Oshunia_brevis
Ionoscopus_cyprinoides
Watsonulus_eugnathoides
Eurycormus_speciosus
Atractosteus_spatula
Siemensichthys_macrocephalus
Dorsetichthys_bechei

FIGURE S6: Resulting cladograms from the analysis with USNM 618000. **A,** parsimony tree from best-scoring run; **B,** maximum likelihood tree from best-scoring run.