Bivalve Petitions 2021

B-2021-01 - *Lampsilis bergmanni* Inoue and Randklev 2020 in Inoue et al. 2020, recognition of a new species described from upstream reaches of the Guadalupe River basin, Texas.

B-2021-02 - *Lampsilis sietmani* Keogh and Simons 2019, recognition of a new species described from the Ohio, Upper Mississippi, and Sabine-Trinity biogeographic regions.

B-2021-03 - *Cambarunio* Watters, 2018, recognition of a new genus with *Unio iris* Lea, 1829 as the type species.

B-2021-04 - *Cambarunio hesperus* Watters, 2018, recognition of a new species described from south flowing streams of the Ozark Plateau in southern Missouri and northern Arkansas.

B-2021-05 - *Leaunio* Watters, 2018, recognition of a new genus with *Unio lienosa* Conrad, 1834 as the type species.

B-2021-06 - *Leaunio pataecus* Watters, 2018 n. sp., recognition of a new species restricted to the Little River of the Cumberland River system in Christian County, Kentucky.

B-2021-07 - *Paetulunio* Watters, 2018, recognition of a new genus with *Unio fabalis* Lea, 1831 as the type species.

B-2021-08 - *Sagittunio* Watters, 2018, recognition of a new genus with *Unio nasutus* Say, 1817 as the type species.

B-2021-09 - *Sagittunio aldermani* Watters, 2018, recognition of a new species described from Lake Marion, Cooper-Santee River Basin, South Carolina.

B-2021-10 - *Venustaconcha constricta* (Conrad, 1838) n. comb., recognition of a new combination for *Unio lienosus var. constrictus* Conrad, 1838.

B-2021-11 - *Theliderma johnsoni* Bogan and Lopes-Lima in Lopes-Lima and Bogan, 2019, recognition of a new species described from Mobile Bay Basin, Alabama, eastern Mississippi, and northwestern Georgia.

B-2021-12 - *Potamilus streckersoni* Smith, Johnson, Inoue, Doyle, and Randklev, 2019, n. sp. – A newly described species from the Brazos River in Texas.

B-2021-13 - *Atlanticoncha* Smith, Pfeiffer, and Johnson, 2020, n. gen. and *Atlanticoncha ochracea* (Say, 1817), n. comb. – A newly described monotypic genus from the Atlantic Slope of North America and associated new combination.

Bivalve Petitions 2021 (continued)

B-2021-14 - *Potamilus fragilis* (Rafinesque, 1820) and *Potamilus leptodon* (Rafinesque, 1820) – Taxonomic implications of considering *Leptodea* Rafinesque, 1820 a junior synonym of *Potamilus* Rafinesque, 1818.

B-2021-15 - Elevation of the junior synonym *Fusconaia iheringi* (Wright, 1898) based on the findings of Pfeiffer et al. (2016) and Smith et al. (2021).

B-2021-16 - Synonymy of *Cyclonaias asperata* (Lea, 1861) under *C. kieneriana* (Lea, 1852) based on the findings of Lopes-Lima et al. (2019).

B-2021-17 - Synonymy of *Quadrula apiculata* (Say, 1829) and *Quadrula rumphiana* (Lea, 1852) under *Quadrula quadrula* (Rafinesque, 1820) based on the analyses of Lopes-Lima et al. (2019).

B-2021-18 - Placement of *Quadrula nobilis* (Conrad, 1854) in the genus *Tritogonia* Agassiz, 1852 based on the findings of Lopes-Lima et al. (2019).

Title: *Lampsilis bergmanni* Inoue and Randklev 2020 in Inoue et al. 2020, recognition of a new species described from upstream reaches of the Guadalupe River basin, Texas.

Background: In western Gulf of Mexico coastal rivers, Lampsilis bracteata (Gould 1855) was thought to be endemic to the Colorado and Guadalupe River basins of the Edwards Plateau (Strecker 1931; Howells et al. 1996). This species was described from the Llano River, a tributary of the Colorado River (Gould 1855). The disjunct distribution of L. bracteata brings into question the taxonomic identity of the Guadalupe River population; however, the phylogenetics and population genetics of the Guadalupe River populations have not been assessed. Lampsilis hydiana (Lea 1838), thought to be a close congener of L. bracteata due to its similar conchology and distribution, occurs in downstream reaches of the Guadalupe River. This species occupies a wide geographical distribution ranging from tributaries of the lower Mississippi River (including the Ouachita and Red rivers in Arkansas, Louisiana, Oklahoma, and Texas) and Gulf of Mexico coastal rivers west of the Mississippi River to the Nueces River, except the Colorado River (Vidrine 1993, Howells et al. 1996). Although both L. hydiana and L. bracteata occur in the Guadalupe River basin, L. hydiana does not appear to be syntopic with L. bracteata and is restricted to lower reaches along the Gulf Coastal Plain downstream of the Edwards Plateau (Howells 2010). A distribution wide phylogenetic assessment was conducted to elucidate the taxonomic identity of the putative *Lampsilis* species in western Gulf coastal rivers.

Supplemental Information: Inoue et al. (2020) used mitochondrial (cox1 and nad1 genes) and nuclear (ITS1 locus and ANT gene) DNA sequences to delineate species boundaries within the three Lampsilis species by reconstructing phylogenies and estimating divergence time. Phylogenetic trees were reconstructed using Bayesian inference (BI), maximum-likelihood (ML), and maximum parsimony (MP) analyses based on a concatenated dataset (cox1, nad1, ITS1 and ANT). Secondly, Inoue et al. (2020) used three morphometric methods (traditional, geometric, and Fourier shape) to examine similarity in shell shapes among the species. Thirdly, Inoue et al. (2020) quantified differences in 11 anatomical soft tissue structures among the species. The BI, ML and MP phylogenies generated by Inoue et al. (2020) showed similar tree topologies and nodal supports. Colorado River basin L. bracteata and Guadalupe River basin L. bracteata formed separate monophyletic clades with strong nodal supports. Species delimitation analyses based on two Yule-coalescent methods recognized Guadalupe River basin L. bracteata as a distinct taxon. Based on the molecular, morphological and anatomical data, Inoue et al. (2020) described Lampsilis bergmanni from the upstream portion of the Guadalupe River and its tributaries of the Edwards Plateau, Texas, USA. Lampsilis bergmanni and L. bracteata are indistinguishable by conchological and soft anatomy morphologies; however, these species are not sympatric as each occurs within different river basins of the Edwards Plateau region. Lampsilis bergmanni may resemble L. hydiana, but L. bergmanni is more vividly rayed and has a thinner shell. Both species occur within the Guadalupe River basin; however, they are not syntopic. Lampsilis bergmanni is restricted to the upstream portion of the Guadalupe River and its tributaries of the Edwards Plateau, whereas L. hydiana ranges throughout the downstream portion of the Guadalupe River and adjacent tributaries of the Gulf Coastal Plain.

Specific Recommendation: We recommend recognition of *Lampsilis bergmanni*, common name Guadalupe Fatmucket, as provided with the original description.

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Submitted By: John L. Harris and Arthur E. Bogan

Proposal Date: 15 January 2021

Petition Number: B-2021-01

Subcommittee Member Voting:

 \Box I support the petition

 \Box I do not support the petition

Title: *Lampsilis sietmani* Keogh and Simons 2019, recognition of a new species described from the Ohio, Upper Mississippi, and Sabine-Trinity biogeographic regions.

Background: Lampsilis teres (Rafinesque 1820) is a taxon with a wide distribution, a high degree of conchological variation, and a complex taxonomic history (see Keogh and Simons 2019, Table 1). The names teres, anodontoides, floridensis, and fallaciosa have all been inconsistently applied to morphological variants of the same species complex. The lack of type specimens and vague descriptions that accompany these names, make application difficult. Williams et al. (2008), using molecular and conchological data, concluded that populations in the isolated Eastern Gulf region represented a species distinct from L. teres and resurrected Lampsilis floridensis (Lea 1852) for this species, restricting L. teres to the form(s) occupying the rest of the range. Keogh and Simons (2019) argued that anodontoides and fallaciosa are synonyms with a single widespread morphotype they identified as Lampsilis teres sensu stricto. Since 1988, L. teres has been considered a monotypic species with two morphological variants (Turgeon et al. 1988). Keogh and Simons (2019) referred to the more widespread phenotypic variant (cylindrical shell outline, periostracum coloration varying from bronze to yellow, sometimes with green rays, typically smaller in size) as Lampsilis teres sensu stricto. The less common phenotypic variant (more circular shell outline, thick, robust shell, periostracum typically uniformly bright yellow, lacking green rays although sometimes present on juveniles) was described by Keogh and Simons (2019) as Lampsilis sietmani.

Supplemental Information: Keogh and Simons (2019) used molecular data in phylogenetic analyses of Lampsilis to determine whether morphological variants of L. teres sensu lato were monophyletic and whether they were each other's closest living relatives. They used morphological data to determine whether morphological variation is continuous or whether the variants represent distinct morphologies and identified conchological characters useful for diagnosis and field identification. Finally, they integrated data from species descriptions including quantifiable shell morphology (either reported shell dimensions or diagrams) into morphological datasets to track the historical taxonomic treatment of morphological variants and address the proper taxonomic treatment of diagnosable forms in the Lampsilis teres species complex. Keogh and Simons (2019) tested for genetic structure among morphological variants of L. teres sensu lato that have historically been classified as subspecies or distinct species. Sampling of the known distribution of morphological variants, multi-locus molecular phylogenetics, and two morphometric approaches revealed two divergent lineages living in sympatry across multiple biogeographic zones. Quantitative morphological approaches discriminated between the two morphotypes with 97% accuracy. Keogh and Simons concluded that Lampsilis teres sensu lato contained two species, Lampsilis teres sensu stricto and the new species Lampsilis sietmani.

Specific Recommendation: We recommend recognition of *Lampsilis sietmani*, common name Canary Kingshell, as provided with the original description.

Literature Cited

- Keogh, S.M. and A.M. Simons. 2019. Molecules and morphology reveal 'new' widespread North American freshwater mussel species (Bivalvia: Unionidae). Molecular Phylogenetics and Evolution 138 (2019) 182-192.
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Submitted By: John L. Harris and Arthur E. Bogan

Proposal Date: 15 January 2021

Petition Number: B-2021-02

Subcommittee	Member	Voting:
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 \Box I support the petition

 \Box I do not support the petition

Title: *Cambarunio* Watters, 2018, recognition of a new genus with *Unio iris* Lea, 1829 as the type species.

Background: *Cambarunio* Watters, 2018 with *Unio iris* as the type species, included six new combinations: *Cambarunio dactylus* (Lea, 1840), *Cambarunio iris* (Lea, 1829), *Cambarunio jonesii* (Lea, 1859), *Cambarunio nebulosus* (Conrad, 1834), *Cambarunio simus* (Lea, 1838), *Cambarunio taeniat*us (Conrad, 1834), and a newly described species *Cambarunio hesperus* Watters, 2018 [see separate petition for this species]. Watters (2018) introduced two new subspecies combinations: *Cambarunio taeniatus pictus* (Lea, 1834), *Cambarunio taeniatus punctatus* (Lea, 1865), and two new subspecies: *Cambarunio dactylus anatinensis* Watters, 2018, *Cambarunio dactylus viridensis* Watters, 2018, but they are not discussed/considered beyond this listing.

Supplemental Information: Kuehnl (2009: figs. 2.2-2.4, 3.1-3.3) analyzed Villosa iris sensu lato which in his results contained Vi. taeniata and Venustaconcha sima along with seven wellsupported clades. The Vi. iris clade was found to be separate from the Villosa type species, Villosa villosa (Wright, 1898). Campbell et al. (2005) and Zanatta and Murphy (2006) (with only three different Villosa species) recovered a polyphyletic Villosa. Watters (2018: 15) observed "In Villosa the marsupium is bean-shaped and largely limited to the distal portion of the water tube. In Cambarunio the entire length of the water tube is charged with glochidia, resulting in a less beanlike appearance." Watters (2018: 15) noted that Cambarunio has a "mantle lure modified into long tentacular processes anterior to the incurrent siphon in at least some species." Watters (2018: 33) stated "morphologically the female mantle of *Cambarunio* has a single long flap from which tentacular processes arise on the inner side; Leaunio has two flaps, the outer smooth, the inner produced into tentacles or digitations."Watters (2018) stated the genus name is based on the crayfish genus Cambarus and that "C. iris and other members of the genus have an elaborate mantle display and movement that mimic crayfish for the purpose of parasitizing fish lured to the mussel." MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat the genus Cambarunio as valid and recognize Cambarunio iris as the type species. Both databases recognize the seven species included in this new genus as valid.

Specific Recommendation: We recommend recognition of the genus *Cambarunio* Watters, 2018 and its type species *Cambarunio iris* (Lea, 1829) provided with the original description. The common name of *C. iris* is Rainbow (Williams et al. 2017). We also recommend recognition of the five additional new combinations: *Cambarunio dactylus* (Lea, 1840), common name Cumberland River Rainbow (Watters 2018: 17); *Cambarunio jonesii* (Lea, 1859), common name Yellow Rainbow (Watters 2018: 25); *Cambarunio nebulosus* (Conrad, 1834), common name Alabama Rainbow (Williams et al., 2017); *Cambarunio simus* (Lea, 1838), common name Caney Fork Rainbow (Williams et al., 2017); and *Cambarunio taeniat*us (Conrad, 1834), common name Painted Creekshell (Williams et al., 2017).

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- Kuehnl, K.F. 2009. Exploring levels of genetic variation in the freshwater mussel genus *Villosa* (Bivalvia: Unionidae) at different spatial and systematic scales: implications for biogeography, taxonomy, and conservation. Unpublished Ph.D. Dissertation, Ohio State University, Columbus. 261 pages.
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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 15 January 2021

Petition Number: B-2021-03

Subcommittee Member Voting:

 I support recognizing <i>Cambarunio</i> Watters 2018 n. gen. I do not support recognizing <i>Cambarunio</i> Watters 2018 n. gen.
 I support recognizing <i>Cambarunio iris</i> (Lea, 1829) n. comb. I do not support recognizing <i>Cambarunio iris</i> (Lea, 1829) n. comb.
 □ I support recognizing <i>Cambarunio dactylus</i> (Lea, 1840) n. comb. □ I do not support recognizing <i>Cambarunio dactylus</i> (Lea, 1840) n. comb.

- □ I support recognizing *Cambarunio jonesii* (Lea, 1859) n. comb.
- □ I do not support recognizing *Cambarunio jonesii* (Lea, 1859) n. comb.
- □ I support recognizing *Cambarunio nebulosus* (Conrad, 1834) n. comb.
- □ I do not support recognizing *Cambarunio nebulosus* (Conrad, 1834) n. comb.
- □ I support recognizing *Cambarunio simus* (Lea, 1838) n. comb.
- □ I do not support recognizing *Cambarunio simus* (Lea, 1838) n. comb.
- □ I support recognizing *Cambarunio taeniat*us (Conrad, 1834) n. comb.
- □ I do not support recognizing *Cambarunio taeniat*us (Conrad, 1834) n. comb.

Title: *Cambarunio hesperus* Watters, 2018, recognition of a new species described from south flowing streams of the Ozark Plateau in southern Missouri and northern Arkansas.

Background: Watters (2018) described the genus *Cambarunio* with *Unio iris* as the type species and included five additional new combinations: *Cambarunio dactylus* (Lea, 1840), *Cambarunio jonesii* (Lea, 1859), *Cambarunio nebulosus* (Conrad, 1834), *Cambarunio simus* (Lea, 1838), and *Cambarunio taeniat*us (Conrad, 1834). He also described the new species, *Cambarunio hesperus* Watters, 2018.

Supplemental Information: Kuehnl (2009) utilized partial gene sequences of the mitochondrially encoded cytochrome oxidase 1 (CO1) and NADH dehydrogenase 1 (ND1) genes to determine the monophyly and phylogeographic structure of the widely distributed species Villosa iris. Several authors (e.g. Gordon 1995, Parmalee and Bogan 1998) suggested V. iris likely consisted of a species complex rather than a single taxon. Molecular analysis of 116 specimens representing approximately 35 localities sampled across its range of revealed V. iris as a polyphyletic composite of at least seven well-supported clades (Kuehnl 2009). Phylogenetic analysis results of mitochondrial CO1 and ND1 sequences and of the combined data set (Kuehnl 2009: figs. 2.2-2.4) suggest that V. iris described by Lea (1829) should be restricted to Clade G, since this clade includes multiple individuals from the type drainage basin which encompasses the type locality "Ohio River" near Cincinnati. Geographic distribution of individuals within Clade G was exceptionally broad (AL to MI) including individuals collected from the lower Tennessee River drainage, upper Tennessee River drainage, Ohio River drainages, and Great Lakes drainages. Clade B consisted solely of specimens from west of the Mississippi River localities in Missouri and Arkansas including St. Francis River, MO (1), Eleven Point River, AR (2), Spring River, AR (2), Buffalo River, AR (1), Beaver Creek, MO (3) and James River, MO (1). The average sequence divergence between clade B and other clades of V. iris was 3.8% for CO1 and 5.7% for ND1 (Kuehnl 2009: Table 2.2). Kuehnl (2009) stated that some conchological characters (e.g. coloration and ray shape and pattern) may separate this lineage (Clade B) from others. Kuehnl (2009) also noted that Clade B variation in mantle flap pigment and papillae patterns may be of further use in delineating lineages with western populations having mantle flaps more closely resembling a crayfish in appearance and behavior than populations east of the Mississippi River. Watters 2018) described the shell and mantle and marsupial morphology but only mentioned that C. hesperus "is generally smaller than C. dactylus or C. iris and lacks the posterior smudging of C. dactylus" in the comparison with other species. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat Cambarunio *hesperus* as valid.

Recommendation: We recommend recognition of *Cambarunio hesperus*, common name Western Rainbow, as provided with the original description.

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Submitted By: John L. Harris and Arthur E. Bogan

Proposal Date: 25 January 2021

Petition Number: B-2021-04

Subcommittee Member Voting:

 \Box I support the petition \Box I do not support the petition

Title: *Leaunio* Watters, 2018, recognition of a new genus with *Unio lienosa* Conrad, 1834 as the type species.

Background: Leaunio Watters, 2018 with Unio lienosa as the type species included four new combinations: Leaunio lienosus (Conrad, 1834) n. comb., Leaunio ortmanni (Walker, 1925) n. comb., Leaunio umbrans (Lea, 1857) n. comb., Leaunio vanuxemensis (Lea, 1838) n. comb. and a newly described species Leaunio pataecus Watters, 2018 n. sp. [see separate petition for this species]. Watters (2018) introduced three new subspecies combinations Leaunio lienosus lienosus (Conrad, 1834) n. comb., Leaunio lienosus (Lea, 1845) n. comb., and Leaunio lienosus unicostatus (Wright, 1899) n. comb., and two new subspecies Leaunio lienosus aquilonius Watters, 2018 n. ssp., and Leaunio lienosus ouachitaensis Watters, 2018 n. ssp. The subspecies are not discussed/considered beyond this listing.

Supplemental Information: Graf and Ó Foighil (2000) included *Villosa iris* and *V. vanuxemensis* which were shown to be in separate clades. Campbell et al. (2005) included *Villosa vanuxemensis*, *V. iris* and *V. villosa* in their analyses and concluded that *Villosa* was polyphyletic. Zanatta and Murphy (2006) included three species of *Villosa*, and their analyses documented that *Villosa* was a polyphyletic group, and *V. vaunexmensis* was widely separated from *V. iris* and *V. fabalis*. Kuehnl (2009: 87, 104) analyzed the clade of *Villosa vanuxemensis*, *V. umbrans*, *V. lienosa and V. ortmanni* and reported it was a separate complex from the *V. iris* complex.

Watters (2018: 11) listed the range of *Leaunio* as the "Mississippi River system including Ohio, Duck, Cumberland, and Tennessee river systems. Gulf of Mexico drainages but absent from peninsular Florida. Absent from the Atlantic Coastal Plain and the Great Lakes drainages." *Leaunio* shells are sexually dimorphic and often with greatly different shapes. The marsupium is restricted to the posterior most or central 8-30 water tubes and the entire length of the water tube is used for brooding. The marsupium is often pigmented on the distal margin (Watters: 2018: 33). Female *Leaunio* have two flaps in gravid specimens. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat the genus *Leaunio* as valid and recognize *Leaunio lienosus* as the type species. Both databases recognize the five species included in this new genus as valid.

Specific Recommendation: We recommend recognition of the genus *Leaunio* Watters, 2018, and its type species *Leaunio lienosus* (Conrad, 1834) and four new combinations: *Leaunio lienosus* (Conrad, 1834) n. comb., common name Little Spectaclecase (Williams et al., 2017); *Leaunio ortmanni* (Walker, 1925) n. comb., common name Kentucky Creekshell (Williams, et al., 2017); *Leaunio umbrans* (Lea, 1857) n. comb., common name Coosa Creekshell (Williams, et al., 2017); *Leaunio vanuxemensis* (Lea, 1838) n. comb., common name Mountain Creekshell (Williams, et al., 2017); *Leaunio vanuxemensis* (Lea, 1838) n. comb., common name Mountain Creekshell (Williams, et al., 2017); *Leaunio vanuxemensis* (Lea, 1838) n. comb., common name Mountain Creekshell (Williams, et al., 2017).

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 2 February 2021

Petition Number: B-2021-05

Subcommittee Member Voting:

□ I support recognizing *Leaunio* Watters 2018 n. gen.

I do not support recognizing <i>Leaunic</i>	Watters 2018 n. gen.
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□ I support recognizing *Leaunio lienosus* (Conrad, 1834) n. comb.

□ I do not support recognizing *Leaunio lienosus* (Conrad, 1834) n. comb.

□ I support recognizing *Leaunio ortmanni* (Walker, 1925) n. comb.

□ I do not support recognizing *Leaunio ortmanni* (Walker, 1925) n. comb.

□ I support recognizing *Leaunio umbrans* (Lea, 1857) n. comb.

□ I do not support recognizing *Leaunio umbrans* (Lea, 1857) n. comb.

□ I support recognizing *Leaunio vanuxemensis* (Lea, 1838) n. comb.

□ I do not support recognizing *Leaunio vanuxemensis* (Lea, 1838) n. comb.

Title: *Leaunio pataecus* Watters, 2018 n. sp., recognition of a new species restricted to the Little River of the Cumberland River system in Christian County, Kentucky.

Background: Watters (2018) described the genus *Leaunio* with *Unio lienosa* Conrad, 1834 as the type species and included four additional new combinations: *Leaunio lienosus* (Conrad, 1834), *Leaunio ortmanni* (Walker, 1925), *Leaunio umbrans* (Lea, 1857) and *Leaunio vanuxemensis* (Lea, 1838). He also described the new species, *Leaunio pataecus* Watters, 2018.

Supplemental Information: Kuehnl (2009) did not use any specimens from the Little River in the Cumberland River basin in Christian County, Kentucky. Watters (2018:43) based his species description on 35 specimens but did not have any gravid females. He noted that this species is "immediately recognized by its very small size, wedge-shaped females and pale, green-rayed shells with purple nacre." Watters (2018:45) remarked that females of *L. umbrans* but rarely *L. lienosa* as well as *L. ortmanni* and *L. pataecus* often have a peculiar posterio-dorsal projection. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat *Leaunio pataecus* Watters, 2018 as valid.

Recommendation: We recommend recognition of *Leaunio pataecus* Watters, 2018 n. sp., common name Dwarf Rainbow, as provided with the original description.

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 5 February 2021

Petition Number: B-2021-06

Subcommittee Member Voting:

 \Box I support the petition \Box I do not support the petition

Title: *Paetulunio* Watters, 2018, recognition of a new genus with *Unio fabalis* Lea, 1831 as the type species.

Background: *Paetulunio* Watters, 2018 with *Unio fabalis* as the type species and the sole species placed in the genus "occurs in the Ohio, Duck, and Tennessee river systems and the western basin of Lake Erie and tributaries. Its current distribution appears discontinuous with large gaps in the lower Ohio and lower Tennessee rivers and an absence in the intervening Cumberland and Green rivers." (Watters 2018:14). *Paetulunio* was formerly part of the polyphyletic genus *Villosa* Frierson, 1927. Early authors including Agassiz (1852), Simpson (1900, 1914) and Ortmann (1912) did not consider *fabalis* related to other "*Villosa*" and this conclusion was supported by the molecular data and phylogenetic analyses presented by Kuehnl (2009). The new combination is *Paetulunio fabalis*.

Supplemental Information: Kuehnl (2009: 101, 107) reported *fabalis* clustered with *Toxolasma*, *Obliquaria* and *Cyrtonaias* and not with other "*Villosa*" species, and this result was consistent with the results of Zanatta and Murphy (2006). Campbell et al. 2005:140, 146) reported that *Villosa* included taxa only distantly related but included just three species of *Villosa* [*iris, villosa* and *vanuxemensis*, but not *V. fabalis*] in the analysis. Campbell and Lydeard (2012) included *V. fabalis* in their analyses, and it was sister to *Toxolasma* but included no other *Villosa* species. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat the genus *Paetulunio* as valid and recognize *P. fabalis* as the type species.

Specific Recommendation: We recommend recognition of the genus *Paetulunio* Watters, 2018 and its single contained species *Paetulunio fabalis* (Lea, 1831) provided with the original description. The common name of *P. fabalis* is Rayed Bean (Williams et al. 2017).

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 15 January 2021

Petition Number: B-2021-07

Subcommittee Member Voting:

 \Box I support the petition \Box I do not support the petition

Title: *Sagittunio* Watters, 2018, recognition of a new genus with *Unio nasutus* Say, 1817 as the type species.

Background: Sagittunio Watters, 2018 with Unio nasutus as the type species included Sagittunio subrostratus (Say, 1831) and Sagittunio vaughanianus (Lea, 1838). All are new combinations. Watters (2018: 55) also described a new species, Sagittunio aldermani Watters, 2018 (Watters, 2018:55) [see separate petition for this species]. Sagittunio was formerly part of the polyphyletic genus Villosa Frierson, 1927 and the genus Ligumia Swainson, 1840.

Supplemental Information: Kuehnl (2009: 104) noted the separation of *Ligumia nasuta*, *L. subrostrata* and *Villosa vaughaniana* as a distinct undescribed genus, and it was likely the primary basis for Watters 2018 interpretation. Zanatta and Murphy (2006) noted *Ligumia recta*, type species of *Ligumia*, was not associated with the other species assigned to the genus. Raley et al. (2007) in a poster, also confirmed the placement of *L. nasuta*, *L. subrostrata* and *V. vaughaniana* as a clade separate from *Villosa* and *Ligumia*. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat the genus *Sagittunio* as valid and recognize *S. nasutus* as the type species. Both databases recognize the four species included in this new genus as valid.

Specific Recommendation: We recommend recognition of the genus *Sagittunio* Watters, 2018 and its type species *Sagittunio nasutus* (Say, 1817) provided with the original description. The common name of *S. nasutus* is Eastern Pondmussel (Williams et al. 2017). We also recommend recognition of the two other new combinations, *Sagittunio subrostratus* (Say, 1831), common name Pondmussel (Williams et al. 2017) and *Sagittunio vaughanianus* (Lea, 1838), common name Carolina Creekshell (Williams et al., 2017).

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 18 January 2021

Petition Number: B-2021-08

Subcommittee Member Voting:

- □ I support recognizing *Sagittunio* Watters, 2018 n. gen.
- □ I do not support recognizing *Sagittunio* Watters, 2018 n. gen.
- □ I support recognizing *Sagittunio nasutus* (Say, 1817) n. comb.
- ☐ I do not support recognizing *Sagittunio nasutus* (Say, 1817) n. comb.
- □ I support recognizing *Sagittunio subrostratus* (Say, 1831) n. comb.
- □ I do not support recognizing *Sagittunio subrostratus* (Say, 1831) n. comb.
- □ I support recognizing *Sagittunio vaughanianus* (Lea, 1838) n. comb.
- □ I do not support recognizing *Sagittunio vaughanianus* (Lea, 1838) n. comb.

Title: *Sagittunio aldermani* Watters, 2018, recognition of a new species described from Lake Marion, Cooper-Santee River Basin, South Carolina.

Background: Sagittunio Watters, 2018 with Unio nasutus as the type species included Sagittunio subrostratus (Say, 1831) and Sagittunio vaughanianus (Lea, 1838). All are new combinations. Watters (2018: 55) also described a new species, Sagittunio aldermani Watters, 2018 (Watters, 2018:55). Sagittunio was formerly part of the polyphyletic genus Villosa Frierson, 1927 and the genus Ligumia Swainson, 1840.

Supplemental Information: Watters (2018) states that *Sagittunio aldermani* is geographically isolated from the other *Sagittunio* species, and in the comparison with other species it was separated by being the largest member of the genus with a more central umbo and the marsupial portion of the shell not as expanded. We found no available genetic data or phylogenetic analyses for this new species. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat *Sagittunio aldermani* as valid.

Recommendation: We recommend recognition of *Sagittunio aldermani* and its common name Santee Pondmussel as provided with the original description.

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 25 January 2021

Petition Number: B-2021-09

Subcommittee Member Voting:

 \Box I support the petition \Box I do not support the petition

Title: *Venustaconcha constricta* (Conrad, 1838) n. comb., recognition of a new combination for *Unio lienosus var. constrictus* Conrad, 1838.

Background: Watters (2018) documented that *Unio constricta* Conrad, 1838 did not fall into *Villosa* Frierson, 1927, *Cambarunio* Watters, 2018, *Leaunio* Watters, 2018, *Paetulunio* Watters, 2018 or *Sagittunio* Watters, 2018, but clustered with *Venustaconcha ellipsiformis* (Conrad, 1836), *Venustaconcha trabalis* (Conrad, 1834) and *Venustaconcha perpurpurea* (Lea, 1861) [now a synonym of *V. trabalis* fide Lane et al. (2016)].

Supplemental Information: Frierson (1927: 81) recognized a group of species including Unio venustus Lea, 1838 [=U. ellipsiformis Conrad, 1834], U. pleasii Marsh, 1891, U. ellipsiformis Conrad, 1836, U. arkansasensis Lea, 1862, U. constrictus Conrad, 1838 and U. trabalis Conrad, 1834 and named this subgenus Lampsilis (Venusta) Frierson, 1927. Unio venustus Lea, 1838 is the type species by tautonymy and original designation. Lampsilis (Venusta) Frierson, 1927 non Boettger, 1877 was preoccupied and a replacement name, Venustaconcha, was supplied in the errata for Frierson, 1927. Thiele (1934) later supplied a replacement name Venustaconcha Thiele, 1934, unaware that Frierson (1927: errata) had earlier proposed the same name (Article 60.3 ICZN Code). Kuehnl (2009: 102, 103) recognized that Villosa constricta clustered with Vi. perpurpurea (Lea, 1861), Vi. trabalis and Venustaconcha ellipsiformis. Lane et al. (2016) subsequently revised the placement of Vi. trabalis reassigning it to Venustaconcha, moved U. perpurpurea to the synonymy of Ve. trabalis, and recognized Ve. troostensis (Lea, 1834) as a valid species. Watters (2018) noted Ve. constricta was restricted to the Atlantic Slope rivers from the Rappahannock River south to the Cooper-Santee River basin. The species has marked sexually dimorphic shells. He noted the early recognition of the placement by Frierson (1927) but did not cite supporting evidence from Kuehnl (2009). MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) recognized Venustaconcha constricta as valid.

Recommendation: We recommend recognition of the assignment of *Venustaconcha constricta* (Conrad, 1838) n. comb.

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 2 February 2021

Petition Number: B-2021-10

Subcommittee Member Voting:

 \Box I support the petition

 \Box I do not support the petition

Title: *Theliderma johnsoni* Bogan and Lopes-Lima in Lopes-Lima and Bogan, 2019, recognition of a new species described from Mobile Bay Basin, Alabama, eastern Mississippi, and northwestern Georgia.

Background: Lopes-Lima et al. (2019) evaluated the polyphyletic *Quadrula* Rafinesque, 1820 and recognized *Cyclonaias* Pilsbry in Ortmann and Walker, 1922, *Quadrula* Rafinesque, 1820, *Theliderma* Swainson, 1840 and *Tritogonia* Agassiz, 1852 as valid. Lopes-Lima et al. (2019) recognized *Theliderma* Swainson, 1840 with *Obliquaria* (*Quadrula*) *metanevra* Rafinesque, 1820 as the subsequently designated type species. In the genus, they included *Theliderma cylindrica* (Say, 1817) n. comb., *Theliderma intermedia* (Conrad, 1836) n. comb., *Theliderma sparsa* (Lea, 1841) n. comb. and *Theliderma stapes* (Lea, 1831) n. comb. (Lopes-Lima et al. 2019).

Supplemental Information: Lopes-Lima et al. (2019) listed *Theliderma johnsoni* Bogan and Lopes-Lima as a new species but failed to register the electronic journal paper and new species with ZooBank, so it was not available (ICZN Code; Zhang, 2012). *Theliderma johnsoni* Bogan and Lopes-Lima, 2019 was validated by publication of an errata for the paper (Lopes-Lima and Bogan, 2019) and was registered with ZooBank. *Theliderma johnsoni* n. sp. is geographically isolated from its sister species *Theliderma metanevra*. Lopes-Lima et al. (2019) combined DNA sequence data and Fourier Shape analyses of morphological data with geographical distribution information in an integrative approach. The genera were validated by combining molecular, morphological, anatomical, and ecological data. This integrative approach showed the Mobile Bay Basin populations of *Quadrula metanevra* belonged to a separate new species, *Theliderma johnsoni* Bogan and Lope-Lima, 2019. MolluscaBase (2021) and MUSSELp (Graf and Cummings, 2021) treat *Theliderma johnsoni* Bogan and Lopes-Lima, 2019 as valid.

Recommendation: We recommend recognition of *Theliderma johnsoni* Bogan and Lopes-Lima, 2019, common name Southern Monkeyface, as provided with the original description.

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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 5 February 2021

Petition Number: B-2021-11

Subcommittee Member Voting:

 \Box I support the petition

 \Box I do not support the petition

Title: *Potamilus streckersoni* Smith, Johnson, Inoue, Doyle, and Randklev, 2019, n. sp. – A newly described species from the Brazos River in Texas.

Overview and Supporting Information: *Potamilus ohiensis* occurs throughout much of the Mississippi River Basin with a disjunct population in the Brazos River drainage in Texas. This biogeographic pattern is unique within unionids and the shell morphology of *P. ohiensis* from the Brazos River resembles that of *P. amphichaenus*, a congener endemic to the Sabine, Neches, and Trinity rivers in eastern Texas. The disjunct distribution and morphological similarity of *P. amphichaenus* and *P. ohiensis* from the Brazos River has led to speculation that *P. ohiensis* had been introduced into the Trinity River drainage (Howells et al., 1996).

Smith et al (2019) implemented an integrative approach to resolve species boundaries and distributional patterns in the *P. ohiensis* species complex (*P. amphichaenus*, *P. ohiensis* from the Brazos River, and *P. ohiensis* from the Mississippi River Basin). Multiple lines of evidence were collected and analyzed, all of which support the recognition of three evolutionarily divergent groups within the *P. ohiensis* species complex: *P. amphichaenus* (Sabine, Neches, and Trinity rivers), *P. ohiensis* (Mississippi River Basin), and *P. cf. ohiensis* endemic to the Brazos River. The molecular, morphological, and biogeographic evidence presented by Smith et al. (2019) provide overwhelming support that species-level diversity in this group was previously underestimated and the recognition of *Potamilus streckersoni* sp. nov., which is endemic to the Brazos River drainage in Texas, is warranted.

Specific Recommendation: We recommend recognition of *Potamilus streckersoni* Smith, Johnson, Inoue, Doyle, and Randklev, 2019, n. sp. and its common name Brazos Heelsplitter as provided in the original description.

Literature Cited

Howells, R.G., R.W. Neck, & H.D. Murray. 1996. Freshwater mussels of Texas. Texas Parks and Wildlife Press, Austin.

Smith, C.H., N.A. Johnson, K. Inoue, R.D. Doyle & C.R. Randklev. 2019. Integrative taxonomy reveals a new species of freshwater mussel, *Potamilus streckersoni* sp. nov. (Bivalvia: Unionidae): implications for conservation and management. Systematics and Biodiversity 17(4): 331-348.

Submitted By: Nathan A. Johnson, Chase H. Smith, and Charles R. Randklev

Proposal Date: 8 February 2021

 Petition Number: B-2021-12

 Subcommittee Member Voting:

 I support the petition

 I do not support the petition

Title: *Atlanticoncha* Smith, Pfeiffer, and Johnson, 2020, n. gen. and *Atlanticoncha ochracea* (Say, 1817), n. comb. – A newly described monotypic genus from the Atlantic Slope of North America and associated new combination

Overview: Previous generic placements of *Unio ochraceus* Say, 1817 include the genera *Lampsilis* (Simpson, 1900), *Leptodea* (Williams et al., 2017), and *Ligumia* (Smith, 2000). The works of Smith et al. (2019; 2020) showed *U. ochraceus* to be distinct from *Leptodea s.s.* and *Potamilus s.s.* and described a new genus, *Atlanticoncha*, to better reflect the evolutionary relationship and systematic position of this taxon.

Supplemental Information: Smith et al. (2019; 2020) reconstructed the origin and patterns of life history diversification within *Aplodinotus grunniens* specialists using a combination of phylogenetic analyses of molecular data and ancestral character reconstruction (ACR) of life history characters. Molecular data included mitochondrial (mtDNA: CO1 and ND1) and nuclear (nDNA: ITS1 and 28S) DNA sequences along with 626 probe and 1247 flanking regions from the Unioverse anchored hybrid enrichment probe set developed by Pfeiffer et al. (2019). The ACR dataset included host fish use, growth during encapsulation, axe-head shaped glochidia, larval surface area, and average annual fecundity.

Bayesian inference of the concatenated DNA sequence dataset recovered *U. ochraceus* sister to the *A. grunniens* group. Phylogenetic position across all analyses, however, was incongruent and lacked strong nodal support and further work was recommended (Smith et al., 2019). The Bayesian topology and ACR resolved a non-monophyletic *Leptodea* and placed *U. ochraceus* as sister to *Leptodea* s.s. and *Potamilus* s.s. (Smith et al., 2020). Due to the non-monophyly of *Leptodea*, the distinct larval morphology, host use, geographic isolation, and divergent anatomical characters in *U. ochraceus*, Smith et al. (2020) formally described the new genus, *Atlanticoncha* to more accurately reflect the evolutionary history of the species.

Specific Recommendation: We recommend recognition of *Atlanticoncha* Smith, Pfeiffer, and Johnson, 2020, n. gen. and *Atlanticoncha ochracea* (Say, 1817), n. comb. along with retention of its common name Tidewater Mucket.

Literature Cited

Pfeiffer, J.M., Breinholt, J.W. and Page, L.M., 2019. Unioverse: phylogenomic resources for reconstructing the evolution of freshwater mussels (Unionoida). Molecular Phylogenetics and Evolution 137, 114–126.

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Simpson, C.T. 1900. Synopsis of the naiades, or pearly fresh-water mussels. Proceedings of the United States National Museum 22: 501-1044.

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Smith, C.H., J.M. Pfeiffer & N.A. Johnson. 2020. Comparative phylogenomics reveal complex evolution of life history strategies in a clade of bivalves with parasitic larvae (Bivalvia: Unionoida: Ambleminae). Cladistics 36: 505-520.

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Williams, J. D., Bogan, A. E., Butler, R. S., Cummings, K. S., Garner, J. T., Harris, J. L., Johnson, N. A., & Watters, G. T. 2017. A Revised List of the Freshwater Mussels (Mollusca: Bivalvia: Unionida) of the United States and Canada. Freshwater Mollusk Biology and Conservation, 20(2), 33-58

Submitted By: Nathan A. Johnson, Chase H. Smith, and John M. Pfeiffer

Proposal Date: 8 February 2021

Petition Number: B-2021-13

Subcommittee Member Voting:

 \Box I support the petition

 \Box I do not support the petition

Title: *Potamilus fragilis* (Rafinesque, 1820) and *Potamilus leptodon* (Rafinesque, 1820) – Taxonomic implications of considering *Leptodea* Rafinesque, 1820 a junior synonym of *Potamilus* Rafinesque, 1818.

Overview and supporting information: Molecular data have consistently resolved *Leptodea* and *Potamilus* as non-monophyletic (Roe and Lydeard, 1998; Smith et al., 2019), primarily due to the placement of *Unio ochraceus*, which is now in the new genus *Atlanticoncha* (see Smith et al., 2020). The foundation of *Potamilus*, and therefore separation from *L. fragilis* and *L. leptodon*, has long been based on the unique axe-head larval morphology (Ortmann, 1912; Frierson, 1927). Smith et al. (2020) resolved axe-head shaped glochidia as the ancestral state of *L. fragilis*, *L. leptodon*, and *Potamilus* (see Fig. 5); however, their results suggest that the trait is an adaptation to reduce larval size and reduction has been further accentuated in *L. fragilis* and *L. leptodon* (see Fig. 6a). Based on the phylogenetic relationships resolved in Smith et al. (2020 – see Figs. 1 and 2) and larval morphological characters, brooding morphology, brooding phenology, host attraction, and host use (Ortmann, 1912; Frierson, 1927; Williams et al., 2008; Haag, 2012; Sietman et al., 2018), Smith et al. (2020) formally recognize *Leptodea* as a junior synonym of *Potamilus*.

Specific Recommendation: We recommend recognizing *Leptodea* Rafinesque, 1820 a junior synonym of *Potamilus* Rafinesque, 1818 and the resulting new combinations *Potamilus fragilis* and *Potamilus leptodon*.

Literature Cited

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Smith, C.H., N.A. Johnson, K. Inoue, R.D. Doyle & C.R. Randklev. 2019. Integrative taxonomy reveals a new species of freshwater mussel, *Potamilus streckersoni* sp. nov. (Bivalvia: Unionidae): implications for conservation and management. Systematics and Biodiversity 17(4): 331-348.

Smith, C.H., J.M. Pfeiffer & N.A. Johnson. 2020. Comparative phylogenomics reveal complex evolution of life history strategies in a clade of bivalves with parasitic larvae (Bivalvia: Unionoida: Ambleminae). Cladistics 36: 505-520.

Williams, J.D., A.E. Bogan, and J.T. Garner. 2008. Freshwater Mussels of Alabama and the Mobile Basin in Georgia. University of Alabama Press, Tuscaloosa, AL.

Submitted By: Nathan A. Johnson and Chase H. Smith

Proposal Date: 8 February 2021

Petition Number: B-2021-14

Subcommittee Member Voting:

□ I support recognition of *Potamilus fragilis* (Rafinesque, 1820) n. comb.

□ I do not support recognition of *Potamilus fragilis* (Rafinesque, 1820) n. comb.

□ I support recognition of *Potamilus leptodon* (Rafinesque, 1820) n. comb.

□ I do not support recognition of *Potamilus leptodon* (Rafinesque, 1820) n. comb.

Title: Elevation of the junior synonym *Fusconaia iheringi* (Wright, 1898) based on the findings of Pfeiffer et al. (2016) and Smith et al. (2021).

Overview and Supporting Information: *Fusconaia mitchelli* (Simpson in Dall, 1895) has long been considered endemic to three river basins in central Texas (Brazos, Colorado, and Guadalupe drainages). Pfeiffer et al. (2016) revealed significant intraspecific genetic variation between geographically separated populations of *F. mitchelli*, however, small sample sizes for several of the populations precluded formal taxonomic revision. Smith et al. (2021) increased taxon sampling and used multilocus DNA sequence data and traditional morphometrics to re-evaluate species boundaries in *F. mitchelli*. Phylogenetic analyses depicted deep genetic divergence between *F. mitchelli* in the Guadalupe and those in the Brazos and Colorado drainages, which was further supported by available biogeographic information. Morphometric analyses and coalescent-based species delimitation models integrating both DNA sequence and morphological data provided strong support for the divergence observed between the two geographically isolated clades of *F. mitchelli*. Based on these results, Smith et al. (2021) revised taxonomy by elevating the junior synonym *Fusconaia iheringi* (Wright, 1898) to represent the Brazos and Colorado populations and restricted the distribution of *F. mitchelli* to the Guadalupe River drainage.

Specific Recommendation: We recommend recognition of *Fusconaia iheringi* and its common name, Balcones Spike, which was given by Smith et al. (2021).

Literature Cited

Dall, W.H. 1895. Diagnosis of new mollusks from the survey of the Mexican boundary. Proceedings of the United States National Museum, 18, 1–6.

Pfeiffer, J.M., N.A. Johnson, C.R. Randklev, R.G. Howells, & J.D. Williams. 2016. Generic reclassification and species boundaries in the rediscovered freshwater mussel '*Quadrula*' *mitchelli* (Simpson in Dall, 1896). Conservation Genetics, 17(2), 279–292.

Smith, C.H., N.A. Johnson, K. Havlik, R.D. Doyle, & C.R. Randklev. 2021. Resolving species boundaries in the critically imperiled freshwater mussel species, *Fusconaia mitchelli* (Bivalvia: Unionidae). Journal of Zoological Systematics and Evolutionary Research, 59(1), 60–77.

Wright, B.H. (1898). A new Unio from Texas. Nautilus, 12, 93.

Submitted By: Nathan A. Johnson, Chase H. Smith, and Charles R. Randklev

Proposal Date: 8 February 2021

Petition Number: B-2021-15

Subcommittee Member Voting:

 \Box I support the petition \Box I do not support the petition

Title: Synonymy of *Cyclonaias asperata* (Lea, 1861) under *C. kieneriana* (Lea, 1852) based on the findings of Lopes-Lima et al. (2019).

Background: *Unio asperatus* Lea, 1861 was described from the Alabama River, Claiborne [Monroe County], Alabama (Williams et al. 2008) and *Unio kieneriana* Lea, 1852 was described from the Coosawattee River, Murray County, Georgia (Williams et al. 2008). Williams et al. (2017) listed *Cyclonaias asperata* (Lea, 1861) and *Cyclonaias kieneriana* (Lea, 1852) as valid species. Lopes-Lima et al. (2019), using F-type mtDNA COI and ND1 sequence data with (BI and ML) analyses, were unable to separate the two species indicating that *C. asperata* should be synonymized under *C. kieneriana*.

Supplemental Information: Williams et al. (2017) recognized *Cyclonaias asperata* and *C. kieneriana* based on their morphological distinctiveness and the fact that molecular evidence for synonymy was based on only one marker (ND1) from a single specimen (Serb et al. 2003). Johnson et al. (2018) recognized nine of the 14 *Cyclonaias* species listed by Williams et al. (2017) as valid; however, *C. kieneriana* was not included in their study.

Morphological analyses supported the distinct morphology of the two nominal species but very few *C. kieneriana* shells (n = 4) were available, preventing a comprehensive analysis (Lopes-Lima et al. (2019). Using only the nominal species *C. kieneriana* and *C. asperata*, Fourier coefficients differed significantly between *C. kieneriana* and *C. asperata* (MANOVA: *F*18,82 = 2.094, p = 0.013), and 95% of specimens were classified correctly based on shell shape through linear discriminant analysis. Although *C. asperata* has been reported from a much wider geographic range than *C. kieneriana*, both species are sympatric in the whole range of *C. kieneriana* suggesting that specimens previously described as *C. kieneriana* are particularly smooth forms of the same species (Lopes-Lima et al. 2019).

Genetic divergence between *C. asperata* and *C. kieneriana* sequences was extremely low. As a result, both COI and ND1 (BI and ML) analyses were unable to resolve both species' phylogenies, and all ND1 species delineation methods were unable to separate the two species, indicating that *C. asperata* should be synonymized under *C. kieneriana* (Lopes-Lima et al., 2019).

Lopes-Lima et al. (2019) considered *C. asperata* a synonym of *C. kieneriana* due to the residual genetic divergence between these two taxa (COI *p*-distance = 1.2% and ND1 *p*-distance <1%) and the fact that *C. kieneriana* (Lea, 1852) has priority over *C. asperata* (Lea, 1861). Graf and Cummings (2021) and MolluscaBase (2021) recognized the synonymy.

Specific Recommendation: We recommend synonymizing *Cyclonaias asperata* (Lea, 1861), Alabama Orb under *Cyclonaias kieneriana* (Lea, 1852), Coosa Orb. Considering the range of the combined species is not restricted to the Coosa River, we suggest using the common name Alabama Orb for *Cyclonaias kieneriana*.

Literature Cited

- Graf, D.L. and K.S. Cummings. 2021. A 'big data' approach to global freshwater mussel diversity (Bivalvia: Unionoida), with an updated checklist of genera and species. Journal of Molluscan Studies 87(1): [1-36].
- Lea, I. 1852. Descriptions of new species of the family Unionidæ [New fresh water and land shells]. Transactions of the American Philosophical Society 10 [O. 5]: 253-294, pls. 12-29.
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- Lopes-Lima, M., L. Burlakova, A. Karatayev, A. Gomes-dos-Santos, A. Zieritz, E. Froufe, and A.E. Bogan. 2019. Revisiting the North American freshwater mussel genus *Quadrula* sensu lato (Bivalvia Unionidae): Phylogeny, taxonomy and species delineation. Zoologica Scripta 48(11): 1-24.
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Submitted By: Arthur E. Bogan and John L. Harris

Proposal Date: 17 March 2021

Petition Number: B-2021-16

Subcommittee Member Voting:

- □ I support the synonymy of *Cyclonaias asperata* under *Cyclonaias kieneriana*.
- □ I do not support the synonymy of *Cyclonaias asperata* under *Cyclonaias kieneriana*.
- □ I support the common name Alabama Orb for *Cyclonaias kieneriana*.
- □ I do not support the common name Alabama Orb for *Cyclonaias kieneriana*.

Title: Synonymy of *Quadrula apiculata* (Say, 1829) and *Quadrula rumphiana* (Lea, 1852) under *Quadrula quadrula* (Rafinesque, 1820) based on the analyses of Lopes-Lima et al. (2019).

Background: *Unio apiculatus* Say, 1829 was described from New Orleans, Louisiana (Williams et al., 2008) and *Unio rumphianus* Lea, 1852 was described from West Georgia [Coosa River drainage] (Williams et al. 2008). *Obliquaria (Quadrula) quadrula* Rafinesque, 1820 was described from the Ohio River, and the neotype (ANSP 20224) designated by (Johnson and Baker, 1973) is from Salt River, Kentucky. Williams et al. (2017) listed *Quadrula apiculata* (Say, 1829), *Q. quadrula* (Rafinesque, 1820), and *Q. rumphiana* (Lea, 1852) as valid species. Lopes-Lima et al. (2019) recommended synonymizing of *Q. apiculata* and *Q. rumphiana* under *Q. quadrula* based on the low level of divergence among the three nominal species for the markers COI and ND1.

Supplemental Information: Lopes-Lima et al. (2019) found all sequences from the nominal species *Quadrula quadrula*, *Quadrula apiculata* and *Quadrula rumphiana* clustered within the *Q. quadrula* clade in all phylogenies. Although only a small number of sequences were available for *Q. apiculata* and *Q. rumphiana*, the level of divergence among the three nominal species was low for both markers, and both nominal species *Q. apiculata* and *Q. rumphiana* were found to be nested within *Q. quadrula* (Lopes-Lima et al., 2019). The level of divergence between the three nominal taxa was lower than the divergence between the distinct clades based on analyses of COI within *Q. quadrula* sensu stricto identified by Mathias et al. (2018). A specific rank for each of these divergent clades was rejected in Mathias et al. (2018) due to the existence of gene-flow among them as shown by their microsatellite dataset. The COI and ND1 95% threshold haplotype networks of the *Q. quadrula* clade revealed a low number of mutations among the nominal taxa *Q. quadrula*, *Q. apiculata* and *Q. rumphiana* (Lopes-Lima et al., 2019).

In morphological comparisons, Fourier coefficients differed significantly between the three nominal species of *Quadrula* (MANOVA, pairwise Hotelling's tests p < 0.05). The nominal species *Q. apiculata*, *Q. rumphiana* and *Q. quadrula* sensu stricto presented distinct shell shapes but only 76% of specimens were assigned to the correct nominal species with 21% and 11% of misidentifications between *Q. apiculata* versus *Q. quadrula* and *Q. rumphiana*, respectively (Lopes-Lima et al., 2019). The slightly distinct shell morphology again suggests that distinct nominal species were assigned to regional shell forms despite the relative overlap in distribution range of *Q. apiculata* with both *Q. quadrula* and *Q. rumphiana* that may also be related to the considerable overlap among shell shape forms (Lopes-Lima et al., 2019).

Lopes-Lima et al. (2019) recommended synonymy of *Q. apiculata* and *Q. rumphiana* under *Q. quadrula*. That said, subtler potential genetic differences between populations originally assigned to these species are likely to be revealed in future studies applying faster evolving markers. Graf and Cummings (2021) and MolluscaBase (2021) followed the recommendation of Lopes-Lima et al. (2019) in synonymizing *Q. apiculata* and *Q. rumphiana* under *Q. quadrula*.

Specific Recommendation: We recommend synonymizing *Quadrula apiculata* (Say, 1829), Southern Mapleleaf and *Q. rumphiana* (Lea, 1852), Ridged Mapleleaf under *Quadrula quadrula* (Rafinesque, 1820), Mapleleaf.

Literature Cited

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Submitted By: Arthur E. Bogan and John L. Harris

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Subcommittee Member Voting:

 \Box I support the petition \Box I do not support the petition

Title: Placement of *Quadrula nobilis* (Conrad, 1854) in the genus *Tritogonia* Agassiz, 1852 based on the findings of Lopes-Lima et al. (2019).

Background: Unio nobilis Conrad, 1854 was described from Bayou Teche, Louisiana and a lectotype (ANSP 43019a) was designated by Johnson and Baker (1973). Until the end of the 20th century, *Quadrula nobilis* was not recognized by most authors as a separate species from *Q. quadrula* (Williams et al., 2008); however, its placement under *Tritogonia* is not new (Simpson 1914). Williams et al. (2017) listed it as *Quadrula nobilis* (Conrad, 1854). Lopes-Lima et al. (2019) found their phylogenies revealed a well-supported clade comprising *Q. nobilis* and *T. verrucosa* and recommended moving the nominal species *Q. nobilis* into *Tritogonia* as *T. nobilis*.

Supplemental Information: A molecular phylogeny by Serb et al. (2003) recovered four clades: *Quadrula* sensu strictu, the *pustulosa* species group, the *metanevra* species group and a fourth clade including *Tritogonia verrucosa* and *Quadrula nobilis*. The position of *Q. nobilis* could not be resolved in a previous single marker approach (Serb et al., 2003), but in Lopes-Lima et al. (2019), all phylogenies revealed a well-supported clade comprising *Q. nobilis* and *T. verrucosa*. Lopes-Lima et al. (2019) analyses revealed a complete consensus of two individual molecular operational taxonomic units (MOTUs) within *Tritogonia*. The two recognized MOTUs *T. verrucosa* and *Tritogonia nobilis* exhibited high interspecific p-distance divergence, 8.5% (COI)/9.3% (ND1), and low intraspecific p-distance <0.9% for COI and <1.1% ND1.

Tritogonia verrucosa and *Q. nobilis* are sexually dimorphic in shell shape, a trait that is unique within the Quadrulini and therefore diagnostic of the genus. In addition, the mantle display mechanism of *T. verrucosa*, which involves the mantle completely covering both the incurrent and excurrent aperture, is distinct from all other *Quadrula* s.l. species. This trait needs to be verified for *T. nobilis*.

Graf and Cummings (2021) followed the recommendation of Lopes-Lima et al. (2019) in moving *Quadrula nobilis* to *Tritogonia*. MolluscaBase (2021) also followed Lopes-Lima et al. (2019) in recognizing *Tritogonia nobilis* and included *Quadrula nobilis* as a synonym.

Specific Recommendation: Place *Quadrula nobilis* (Conrad, 1854) in the genus *Tritogonia* as *Tritogonia nobilis* (Conrad, 1854), Gulf Mapleleaf.

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