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PERSPECTIVE

Paraphyletic classification and its consequences for the world's most endangered fishes

Thomas J. Near · Chase D. Brownstein

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Abstract Taxonomy is the organizing principle underlying how scientists, policymakers, and the public engage with biological diversity. Yet, the ongoing transition from Linnaean ranks to explicitly phylogenetic, rank-free taxonomy remains controversial. The tension between phylogenetic accuracy and nomenclatural stability is nowhere more consequential than in clades facing imminent extinction. In these cases, taxonomy directly shapes legal protections, conservation prioritization, and the identification of evolutionarily significant units. This means that taxonomic revisions carry consequences for the survival of lineages that extend well beyond their position in the catalog of biodiversity. Here, we argue that taxonomic revision using phylogenetic rank-free nomenclature provides a much-needed quantitative basis for conservation biology. We focus on the case of sturgeons (*Acipenseridae*), a clade of Holarctic ray-finned fishes in which all species are at risk of extinction. Recently, the IUCN Sturgeon Specialist Group (SSG) voted unanimously to reject a phylogenetic rank-free taxonomy of this clade published in 2025. A conservative alternative classification proposed by the SSG sustains a paraphyletic concept of *Acipenser* that fails on the group's stated terms of conserving names that reflect morphology and other aspects of natural history. We argue that the SSG rejection exemplifies a recurring response in which the practical costs of taxonomic change are invoked to resist classifications that are demonstrably more reflective of evolutionary history. This has direct consequences for conservation through the misrepresentation of evolutionary diversity, the distortion of conservation prioritization metrics, and the misidentification of evolutionarily significant units. Taxonomies based on empirically reconstructed evolutionary relationships do not inhibit conservation but inform the protection of Earth's biological heritage.

Keywords Sturgeons · *Acipenseridae* · *Acipenser* · *Huso* · Phylogeny

T. J. Near (✉)
Department of Ecology and Evolutionary Biology
and Peabody Museum of Natural History, Yale University,
New Haven, CT 06511, USA
e-mail: thomas.near@yale.edu

C. D. Brownstein
Department of Ecology and Evolutionary Biology,
New Haven, CT 06511, USA

C. D. Brownstein
Stamford Museum and Nature Center, Stamford, CT, USA

Introduction

Every decision in conservation biology, from species listings to the delineation of protected areas, depends on a prior decision about what counts as a distinct biological entity. When taxonomies accurately reflect evolutionary relationships, they convey information about common ancestry and the distribution of

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biological diversity that is directly useful for research and management; when they do not, taxonomies can misdirect basic research and result in the misallocation of conservation resources (Garnett and Christidis 2017; Padial et al. 2010). The stakes of getting classification right are therefore highest in lineages where conservation decisions are most urgent.

The transition from ranked classification toward explicitly phylogenetic, rank-free taxonomy is arguably the most important transformation in biological nomenclature since Linnaeus proposed a ranked system of classifying biodiversity (Cantino and de Queiroz 2020; de Queiroz and Gauthier 1994; Laurin 2023). This transition is driven by a persistent set of problems with the traditional Linnean system. Linnaean ranked categories are not biologically comparable across taxa, ranked classification produces redundant and uninformative group names, and the rank-based system creates nomenclatural conflicts rather than resolving them whenever phylogenetic hypotheses are modified (de Queiroz and Gauthier 1990, 1994; Laurin 2024). Recent work has begun to implement this framework across ray-finned fishes, applying PhyloCode-inspired phylogenetic definitions to actinopterygian clade names and revising the taxonomy of species-rich groups such as wrasses and parrotfishes (*Labridae*) to reflect consistent phylogenetic resolution of traditionally recognized but para- and polyphyletic taxa (Near et al. 2025; Near and Thacker 2024). In both cases, the argument is not only that taxa happen to be para- or polyphyletic when species are analyzed using phylogenetic methods, but also that the Linnaean ranked system is structurally incapable of stably representing natural groups as phylogenetic hypotheses improve (de Queiroz and Gauthier 1992, 1994).

Sturgeons comprise the clade *Acipenseridae*, a lineage of 27 living species distributed across the Northern Hemisphere in marine coastal waters, large rivers, and lakes from the Atlantic and Pacific coasts of North America to Europe, the Black and Caspian seas, Siberian rivers, and the river systems of East Asia (Bemis et al. 1997; Bemis and Kynard 1997; Choudhury and Dick 1998). Sturgeons and their sister group, the paddlefishes (*Polyodontidae*), are classified in *Acipenseriformes* and are characterized as living fossils based on their morphological conservatism, with body plans of living species closely resembling those of extinct forms from the Late Cretaceous (Hilton and Grande 2023), and their dramatically reduced molecular evolutionary rates relative to other ray-finned fishes (Brownstein et al. 2024; Krieger and Fuerst 2002). *Acipenseriformes* originated in the Jurassic, with crown *Acipenseridae* diverging approximately 100 million years ago, meaning that the genera of living sturgeons represent lineages with deep and independent evolutionary histories that diverged from one another in the Cretaceous and early Paleogene (Brownstein and Near 2025). Sturgeons have long been economically important, particularly for the international trade in black caviar, but the twentieth century saw a rapid expansion of this trade that drove severe population declines across the family, a trajectory now compounded by the growth of captive aquaculture (Rueness et al. 2025).

All 27 living species of sturgeons are threatened with extinction: 17 are currently assessed as Critically Endangered, three are Endangered, four are Vulnerable, and one is Extinct in the Wild (IUCN 2026). Sturgeons are protected by a dense network of conservation measures, from CITES (Rueness et al. 2025) and IUCN Red List assessments (IUCN 2026) to the EU Habitats Directive (Strat and Gheorghe 2023), HELCOM, the Bern Convention (Congiu et al. 2023a; Gessner et al. 2019), and the U.S. Endangered Species Act. Because these instruments are tied to specific genus and species names, taxonomy changes carry policy consequences. Researchers have recognized for decades that the traditional classification of *Acipenseridae* conflicts with its phylogeny (Fig. 1) (Brownstein and Near 2025). Both *Acipenser* and *Huso*, which together include 21 of the 27 species of sturgeons, are resolved as paraphyletic in every molecular and morphological analysis published since the late 1990s (Birstein and DeSalle 1998; Birstein et al. 2002; Dadkhah et al. 2023; Dillman et al. 2007; Hilton et al. 2011; Krieger et al. 2008; Luo et al. 2019; Peng et al. 2007; Shedko 2022; Shen et al. 2020). This makes sturgeons an unusually high-stakes test case for how the scientific community navigates the conflict between taxonomic stability and phylogenetic accuracy (Brownstein and Near 2026; Kottelat and Freyhof 2025).

In 2025, we applied the principles of *PhyloCode* and a well-resolved phylogeny to revise the taxonomy of sturgeons (*Acipenseridae*) using a rank-free, phylogeny-based framework (Brownstein and Near 2025). Our rank-free taxonomy of *Acipenseridae*

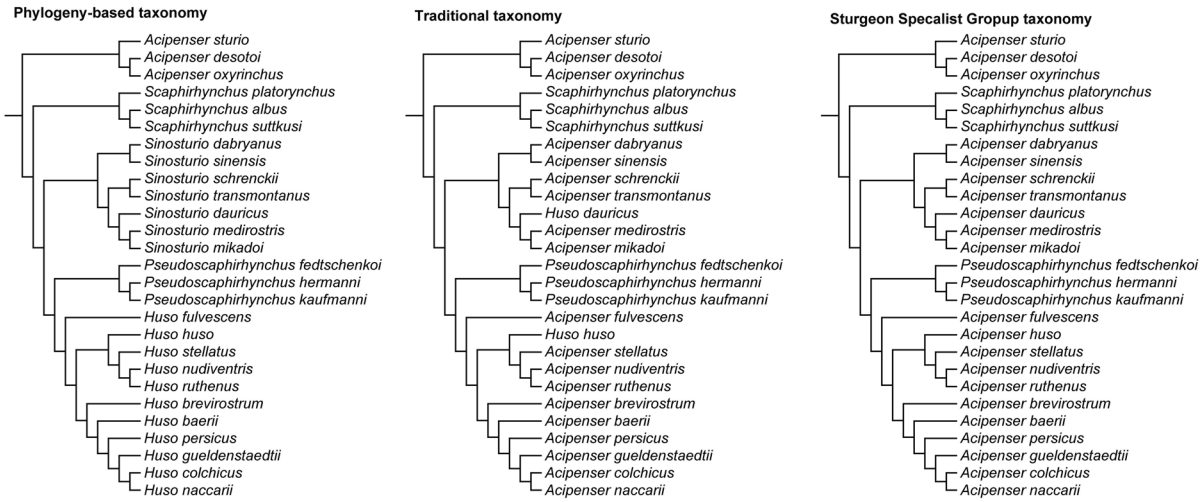

Fig. 1 Three alternative taxonomies of sturgeons shown on a phylogeny of *Acipenseridae* presented in Brownstein and Near (2025)

drew on analyses of mitochondrial DNA (cytochrome *b*), 30 single-copy nuclear orthologs, discretely coded morphological characters, and combined molecular and morphological datasets (Brownstein and Near 2025). The new rank-free taxonomy identified five monophyletic groups treated as genera under the ICZN: *Acipenser* sensu stricto (comprising *A. sturio*, *A. oxyrinchus*, and *A. desotoi*), the resurrected genus *Sinosturio* (seven species mostly distributed in and around the Pacific Ocean), an expanded *Huso* (eleven species distributed in the Atlantic and Eurasia), and the unaltered delimitations of *Scaphirhynchus* and *Pseudoscaphirhynchus* (Fig. 1). In this taxonomy, all acipenserid genera are monophyletic (Brownstein and Near 2025), resolving the paraphyly of *Acipenser* and *Huso* that has characterized the taxonomy of *Acipenseridae* for decades (Birstein and DeSalle 1998; Brownstein and Near 2025; Hilton et al. 2011; Kottelat and Freyhof 2025; Luo et al. 2019).

In October 2025, during the 10th International Sturgeon Symposium in Yichang, China, the IUCN SSG convened a workshop that voted unanimously to reject the revised taxonomy of sturgeons presented in Brownstein and Near (2025) (North American Sturgeon and Paddlefish Society, 2025, https://nasps-sturgeon.org/acipenseridae-taxonomy/). The SSG statement cited weak statistical support for the phylogenies that provide the basis of the taxonomy, missing data in DNA sequence alignments, incompatibility with the evolution of polyploidy in sturgeons, potential for hybridization to confound the resolution of phylogenetic relationships, a lack of morphological synapomorphies for a newly defined *Acipenser*, and concerns about negative conservation consequences stemming from the change of genera for many species of *Acipenseridae*.

The SSG (North American Sturgeon and Paddlefish Society, 2025) also cites Kottelat and Freyhof (2025), who suggested that some nomenclatural acts in Brownstein and Near (2025) were erroneous, but this misrepresents the nature of that contribution. Kottelat and Freyhof (2025) accepted the phylogenetic taxonomy of *Acipenseridae* and agree that all genera recognized by Brownstein and Near (2025) are monophyletic; their sole objection is the opinion that *Sterletus* Rafinesque, 1820 is a senior synonym of *Huso* Lovetzky, 1834. Brownstein and Near (2026) argue that *Sterletus* qualifies as a *nomen oblitum* and *Huso* as a *nomen protectum* under the ICZN, resolving the dispute. The SSG's invocation of Kottelat and Freyhof (2025) as evidence against the revised taxonomy conflates a limited nomenclatural disagreement among scientists who share the same phylogenetic conclusions with a substantive rejection of those conclusions.

These criticisms, taken together, raise questions that extend beyond the specific case of sturgeons. Here, we use the case of sturgeons to illuminate this view. The argument that policy impacts on conservation necessitate the retention of taxonomies that do

not reflect phylogeny is pragmatically motivated but inverts the causal relationship between systematic biology and conservation policy. Allowing policy frameworks to constrain the taxonomy that informs them does not protect conservation outcomes but undermines them by preserving classifications that misrepresent the evolutionary diversity those frameworks are designed to protect. To illustrate why we hold this view, we first show that the proposed retention of *Acipenser* paraphyly settled on by the SSG (North American Sturgeon and Paddlefish Society, 2025) fails to meet their own stated goal of having taxonomy that reflects natural history and organismal biology. The nature of the SSG's argument exemplifies a pattern in which concerns about the practical costs of taxonomic change are used to resist classifications that more accurately reflect phylogeny.

The claim of weak statistical support

The SSG (North American Sturgeon and Paddlefish Society, 2025) places particular emphasis on bootstrap support values as a basis for rejecting the phylogenies presented in Brownstein and Near (2025), stating that the revision reflects "weak statistical support for many of the clades presented." Bootstrap support values are continuous measures of support provided by the data for a particular clade, not threshold criteria for the existence of clades. The convention of treating bootstrap values above 70% as indicative of meaningful support is long established in the phylogenetic literature (Alfaro et al. 2003; Hillis and Bull 1993). The only genera of sturgeons in the taxonomy of Brownstein and Near (2025) supported by bootstrap values of less than 93% in some analyses are *Sinosturio* in the mtDNA gene tree and the phylogeny inferred from the combined mtDNA and nuclear gene dataset and *Huso* in the phylogenies inferred from the 30 nuclear genes and the combined mtDNA and nuclear gene dataset. However, *Sinosturio* is supported with a bootstrap score of 100% in the phylogeny inferred from 30 nuclear genes and *Huso* is resolved as a clade in 93–99% of the bootstrap trees in analysis of mtDNA (Brownstein and Near 2025).

Congruence across independent datasets with different evolutionary histories and different sources of systematic error is itself powerful evidence for a phylogenetic hypothesis. A cytochrome *b* gene tree, a phylogeny inferred from DNA sequences of 30 nuclear genes, a phylogeny inferred from concatenated nuclear and mitochondrial genes, and a phylogeny inferred from 62 discretely coded morphological characters all infer the traditional delimitation of *Acipenser* and *Huso* as not monophyletic (Fig. 1). Most critically, much of the diversity of sturgeons remains classified in paraphyletic groups regardless of which data type is analyzed.

The missing data objection

The SSG (North American Sturgeon and Paddlefish Society, 2025) raises concerns about missing data in the molecular matrix, noting that the "entire systematic [sic] is based upon a data set that contains substantial missing data." This objection conflates a general methodological concern with a specific claim about the Brownstein and Near (2025) analysis.

The 30 single-copy nuclear orthologs were drawn from a curated dataset in which paralogs had been explicitly filtered out prior to publication (Luo et al. 2019). The concern about missing data is legitimate as a general methodological consideration, but modern phylogenetic methods, including the maximum likelihood and Bayesian approaches used by Brownstein and Near (2025), handle missing data by estimating likelihoods conditional on observed data. Extensive simulation studies have demonstrated that phylogenies with substantial missing data can be highly accurate when the available data are informative (Roure et al. 2013; Wiens 2003; Wiens and Morrill 2011). Missing data are only a problem if they are distributed in a way that systematically misleads the analysis. The SSG does not demonstrate that the pattern of missing data in the Brownstein and Near (2025) matrix produces biased results.

The introgression and hybridization argument

The SSG (North American Sturgeon and Paddlefish Society, 2025) argues that introgression of mitochondrial and nuclear loci among sturgeon species can confound molecular phylogenetic results, which undermines their confidence in the phylogenies

presented in Brownstein and Near (2025). Sturgeons are known to hybridize both in nature and in aquaculture (Birstein et al. 1997; Havelka and Arai 2018; Ludwig et al. 2009; Schrey et al. 2011, 2007; Tranah et al. 2004; Vasilyeva et al. 2019), and hybridization has been documented among species across multiple genera in aquacultural settings (Zhang et al. 2013). Hybridization is a potential complication in sturgeon systematics, as historical introgression confounds phylogenetic inference across vertebrates (Luo et al. 2026; Rancilhac et al. 2024; Santos et al. 2025). However, the species complexes most extensively documented as involved in hybridization and introgression are all placed in the same genera in the new phylogenetic taxonomy (Brownstein and Near 2025). Hybridization between species is not likely to lead to error in reconstructing phylogenetic relationships among more inclusive clades. The historical introgression problem would be most damaging to the revised taxonomy if hybridizing species were in different genera; the opposite is true. The intergeneric hybridization documented in the literature occurs between lineages whose separation at the generic level is precisely what the revised taxonomy reflects.

Brownstein and Near (2025) directly address one case where introgression appears to have influenced the topology: the incongruence between the mitochondrial and nuclear phylogenies for *Pseudoscaphirhynchus*. The mtDNA gene tree infers that species of *Pseudoscaphirhynchus* are nested within *Huso* as the sister clade to *H. stellatus*, whereas nuclear gene phylogenies and concatenated analyses resolve *Pseudoscaphirhynchus* as sister to *Huso*. Brownstein and Near (2025) interpret this incongruence as likely reflecting ancient mitochondrial introgression from a *Huso* lineage into the ancestor of *Pseudoscaphirhynchus* and treat the nuclear gene inferred phylogeny as the primary signal for genus-level delimitation. Dillman et al. (2007) also highlighted the conflict between morphological and molecular datasets for *Scaphirhynchinae*, concluding that "at least one of these two data sets does not reflect the true history of these species." This acknowledgment, which comes from the paper the SSG cites as a primary methodological authority, establishes that incongruence between data types is a known and expected feature of sturgeon phylogenetics.

The polyploidy objection

The SSG (North American Sturgeon and Paddlefish Society, 2025) states that the Brownstein and Near (2025) revision "does not align with the phylogeny, especially the polyploidy events in the family," implying that the history of whole-genome duplication in *Acipenseridae* is inconsistent with the inferred phylogenies. Chromosome counts alone are insufficient to reconstruct the history of polyploidization in a group as complex as sturgeons, where ploidy levels vary across and within species and where the correspondence between chromosome number and ploidy history is not straightforward (Ludwig et al. 2001; Vasil'ev 1999, 2009). The claim that polyploidy conflicts with the Brownstein and Near (2025) topology cannot be evaluated without specifying what topology the history of polyploidization predicts and why, something the SSG statement does not provide. The SSG acknowledges that whole genome sequencing data were presented at ISS 10 and that these data provide higher taxonomic resolution but does not state whether these unpublished data conflict with the published phylogenetic taxonomy. Those data have not been published or incorporated into a competing phylogenetic analysis. Importantly, a published phylogenomic analysis of sturgeons that includes only eight species resolves the traditional delimitation of *Acipenser* as paraphyletic and relationships among the sampled species are similar to those in the phylogeny we used to construct the rank-free taxonomy (Brownstein and Near 2025; Liu et al. 2022). Critically, the mitochondrial genome is not subject to nuclear whole-genome duplication events, so the concern about polyploidy does not apply to the mitochondrial component of the Brownstein and Near (2025) analysis. The polyploidy objection as currently stated by the SSG does not constitute a specific falsification of the phylogeny of sturgeons.

The morphological synapomorphies objection

The SSG (North American Sturgeon and Paddlefish Society, 2025) states that the Brownstein and Near (2025) taxonomy "is not supported by synapomorphies in morphological characters" and that "those morphological features named are not defined and therefore not readily applicable." Brownstein and

Near (2025) explicitly acknowledge the absence of known morphological synapomorphies for *Acipenser* sensu stricto. The absence of recognized morphological synapomorphies for a clade does not mean the clade does not exist, but only that morphological synapomorphies have not yet been identified or described. The monophyly of many major lineages of ray-finned fishes was validated only after the application of molecular data and these clades lack substantive morphological synapomorphies (Betancur-R et al. 2014; Dornburg and Near 2021; Miya et al. 2003; Near et al. 2025; Near and Thacker 2024), so the SSG criterion would require rejecting the results of phylogenomic analyses conducted across the globe over several decades. That morphological synapomorphies are unknown for some clades is expected rather than exceptional, and perhaps especially so in sturgeons, which are among the most morphologically conservative of all vertebrates (Bemis et al. 1997; Hilton and Grande 2023; Hilton et al. 2011; Vasil'eva, 1999, 2009).

More fundamentally, this objection applies with equal force to the classification the SSG proposes to maintain. The traditionally recognized, broadly defined *Acipenser*, paraphyletic in every published analysis, has no morphological synapomorphies either, because it is not a natural group. Demanding morphological synapomorphies as a precondition for accepting a molecularly supported clade sets a standard that the existing classification does not meet and that the SSG does not apply to itself. Dillman et al. (2007) themselves noted a fundamental conflict between morphological and molecular datasets in *Scaphirhynchinae*, a traditional taxonomic group that includes species of *Pseudoscaphirhynchus* and *Scaphirhynchus*. Phylogenetic analysis of morphological characters supports monophyly of *Scaphirhynchinae,* but molecular data consistently reject it. The shovel-nosed body form with a flat and spade-like snout, smaller body size, absence of a spiracle, subopercle not covering all of the gill chamber, and small transverse mouth shape shared by species of *Scaphirhynchus* and *Pseudoscaphirhynchus* (Mayden and Kuhajda 1996) are likely adaptations to fast-flowing riverine environments, and their distribution across what molecular data recover as a non-monophyletic assemblage is consistent with convergent evolution rather than shared ancestry. This conflict illustrates that morphological characters in sturgeons can mislead as readily as they can clarify.

The internal contradiction of the proposed alternative

Specifically, the SSG (North American Sturgeon and Paddlefish Society, 2025) proposes dissolving both *Huso* and *Sinosturio* and transferring all their species into a broadly defined *Acipenser*, yielding three genera: *Acipenser*, *Scaphirhynchus*, and *Pseudoscaphirhynchus*. Paradoxically, this proposed classification maintains a paraphyletic *Acipenser*. Dillman et al. (2007), the paper the SSG treats as its primary methodological authority, presented molecular phylogenies where *Acipenser* is resolved as paraphyletic, dispersed among three separate clades. Thus, the argument presented by the SSG is not that the results presented in Brownstein and Near (2025) are wrong, but rather that nomenclatural stability should be prioritized over phylogenetic accuracy. This outcome is an almost inevitable consequence of Linnaean ranked classification: when a ranked taxon is demonstrated to be paraphyletic, the Linnaean framework provides no principled mechanism for resolving the conflict between nomenclatural priority and phylogenetic accuracy. The result is exactly what the SSG proposes: expanding a paraphyletic group to absorb a formerly recognized taxon, producing a familiar name with an even less accurate phylogenetic content. The SSG's position acknowledges that *Acipenser* sensu lato is paraphyletic while insisting that the paraphyly be preserved in the name of stability.

A broader argument sometimes advanced in defense of paraphyletic classifications is that they serve a useful placeholder function, retaining informative names while phylogenetic resolution remains incomplete, much as the vernacular term "fish" remains widely used despite being paraphyletic. There is an important distinction between informal vernacular terms used for communicative convenience and formal genus names embedded in legal instruments, conservation assessments, and international treaties. The term "fish" carries no legal or regulatory consequences; the genus name *Acipenser* does. When a paraphyletic formal genus name is embedded in CITES appendices, ESA listings, and IUCN assessments, the failure of that name to correspond to a

natural group is not a harmless placeholder but a classification that actively misrepresents the evolutionary relationships it purports to summarize, and those misrepresentations propagate into every downstream application of the name. A pragmatic version of the placeholder argument does not rest on phylogenetic uncertainty but on a deliberate decision to maintain a known inaccuracy for practical and legal reasons until a definitive genomic analysis resolves the matter beyond dispute. We understand and respect the motivation behind this position, and we agree that a phylogenomic analysis of all sturgeon species is both needed and within reach (Li et al. 2026). However, a pragmatic placeholder argument of this kind carries its own burden of justification: it must weigh the costs of interim inaccuracy against the costs of taxonomic change and demonstrate that the former are low enough to make waiting the better option. The SSG statement does not perform this weighing. The costs identified in The Conservation Argument section, including the distortion of evolutionary distinctiveness metrics, the provision of misleading guidance for captive breeding programs, and the creation of identification ambiguity in CITES enforcement contexts, are precisely the costs that accrue during the period in which a paraphyletic classification is retained as a placeholder. A placeholder is only costless if nothing consequential depends on it during the interim period. In the case of sturgeons, a great deal does.

Dillman et al. (2007) The citation in context

The SSG (North American Sturgeon and Paddlefish Society, 2025) explicitly invokes Dillman et al. (2007) as a justification for resisting taxonomic change, quoting the statement that "the taxonomy of sturgeon species should not be altered on the basis of any single data set…[and] we do not feel that the data sets assembled to date provide sufficient resolving power to alter any currently recognized genera." The SSG asserts that this conclusion "remains true today."

The SSG's invocation of Dillman et al. (2007) requires careful examination. That paper was written before the 30-gene nuclear dataset used by Brownstein and Near (2025) existed. The caution it expressed was explicitly directed at analyses based on limited mitochondrial data subject to the dramatically reduced substitution rates that Dillman et al. (2007) themselves documented. The concern that any single dataset might be insufficient is addressed directly by the multi-dataset approach of Brownstein and Near (2025), which integrates congruent signal across the mitochondrial gene cytochrome *b*, 30 single-copy nuclear orthologs, morphological characters, and combined analyses.

The conservation argument

The SSG (North American Sturgeon and Paddlefish Society, 2025) argues that the revised taxonomy could negatively impact the conservation of sturgeons by disrupting species names embedded in CITES listings, IUCN Red List assessments, the EU Habitats Directive, regional instruments such as HELCOM and the Bern Convention, and domestic legislation such as the U.S. Endangered Species Act. We acknowledge that regulatory frameworks are built around names, and that changes to those names create administrative burdens that are not trivial when the organisms in question are critically endangered and subject to active enforcement actions at international borders. However, the conservation argument for maintaining an inaccurate classification rests on a premise that does not survive scrutiny: that an inaccurate taxonomy is a neutral baseline whose costs are zero, while a revised taxonomy carries costs that must be weighed against its benefits (Morrison et al. 2009). An inaccurate taxonomy is not a neutral baseline (Thomson et al. 2018), but an active source of conservation risk (Clavero et al. 2024).

The costs of paraphyletic classification for conservation are not abstract. Three concrete mechanisms connect taxonomic inaccuracy to conservation harm. First, conservation funding prioritization frameworks that incorporate evolutionary distinctiveness are directly sensitive to the accuracy of phylogenetic classification (Pizzardo et al. 2024; Yang and Pavoine 2023). EDGE (Evolutionarily Distinct and Globally Endangered) scores, used by the Zoological Society of London and by international funding bodies to direct resources toward the most irreplaceable lineages, are calculated from branch lengths on a time-calibrated phylogeny (Gumbs et al. 2023). When deeply divergent lineages are subsumed within a single paraphyletic genus, their individual evolutionary distinctiveness is obscured, and resources

may be directed toward lineages whose distinctiveness is overestimated at the expense of those whose distinctiveness is underestimated. The five genera recognized by Brownstein and Near (2025) represent lineages that diverged in the Cretaceous and early Paleogene; treating them as a single genus erases those divergences from the quantitative frameworks used to allocate conservation investment. Second, captive breeding, assisted reproduction programs, and restocking of captive-bred individuals are among the most important active conservation tools for critically endangered sturgeons (Barca et al. 2022; Chandra and Fopp-Bayat 2021; Dudu et al. 2022). These programs depend on accurate species identification to avoid inadvertent hybridization between lineages (Barca et al. 2022; Kozlova et al. 2024). When taxonomic frameworks misrepresent relationships, they provide misleading guidance about which combinations of individuals represent intraspecific versus interspecific crosses, with direct consequences for the genetic integrity of captive populations (Barca et al. 2022; Huang et al. 2026). Third, wildlife inspectors and forensic scientists rely on morphological identification guides and reference databases organized by genus to distinguish legal from illegal caviar and sturgeon products (Ludwig 2008). All species of *Acipenseriformes* are listed as a single unit under CITES Appendix II, meaning that genus and species-level taxonomy provides the primary framework by which enforcement agencies disaggregate the lineage into identifiable units. Within this framework, a paraphyletic *Acipenser* that encompasses lineages of very different geographic origins, sizes, and caviar characteristics creates identification ambiguity that can be exploited to launder products from the most endangered species behind the names of less endangered ones (Zhang et al. 2022). An accurate genus-level classification that reflects phylogenetic and geographic structure directly reduces this ambiguity by ensuring that the genus names used in enforcement correspond to natural groups with coherent geographic and morphological signatures, rather than to assemblages of distantly related lineages whose products are difficult to distinguish (Congiu et al. 2023b).

We contend that paraphyletic genera misrepresent the scope and structure of evolutionary diversity in ways that mislead conservation decision-making. When species from deeply divergent lineages are subsumed under a single familiar genus name, conservation managers, policymakers, and the public may perceive them as variations on a theme rather than as representatives of independently evolved lineages with distinct evolutionary histories, ecologies, and conservation needs. The five lineages formalized as genera by Brownstein and Near (2025) diverged from one another in the Cretaceous and early Paleogene. Treating them as a single genus obscures the evolutionary history of sturgeon diversity, especially when a stated goal in conservation biology is to preserve evolutionary history (Stein et al. 2018). This is the concern that motivates the shift towards phylogenetic rank-free classification (Near et al. 2025; Near and Thacker 2024): taxonomies that fail to represent natural groups are not merely misleading for academic researchers but carry practical consequences for conservation planning and management.

The appropriate response to the practical challenges of taxonomic change in regulatory contexts is not to freeze taxonomy in an inaccurate state but to develop better mechanisms for updating legal and regulatory frameworks when taxonomy improves. Other groups of conservation concern have navigated genus-level taxonomic revisions without catastrophic consequences for their legal protection (Dulvy et al. 2021; Kitchener et al. 2017; Morrison et al. 2009). The argument that sturgeons are uniquely unable to survive a taxonomic revision is not supported by evidence and sets a damaging precedent: that conservation regulatory frameworks can veto scientific progress in systematics.

The procedural problem

The scientific objections raised by the SSG (North American Sturgeon and Paddlefish Society, 2025) have been addressed in the preceding sections and do not withstand scrutiny on their own terms. We raise the following procedural concern not as a substitute for that scientific rebuttal, but because the mechanism by which the rejection was produced has direct consequences for how its conclusions will be received and acted upon in regulatory and legal contexts. The question of whether a revised taxonomy is adequately supported by phylogenetic evidence is not one that a workshop vote is structured to resolve. Conservation practitioners, regulatory officials, aquaculturists, and ecologists are exactly the right people to evaluate the

policy and management consequences of taxonomic change, as that is a question on which their expertise is directly relevant and essential. But these are two distinct questions, and a workshop vote conflates them in a way that does not serve either.

Unanimity in a vote on a scientific question is not the same as scientific consensus, particularly when the question is a technical one about phylogenetic evidence. Scientific consensus on a phylogenetic question is established through peer-reviewed publication, replication, and the accumulation of congruent evidence across independent datasets. A unanimous vote establishes that the SSG membership shares strong concerns about the consequences of taxonomic change for conservation and regulatory frameworks. It does not establish that the phylogenetic evidence presented in Brownstein and Near (2025) is flawed.

The SSG statement carries institutional weight that its scientific content does not support. There is a real risk that its conclusions will be incorporated into regulatory and legal frameworks before a thorough peer-reviewed response exists in the literature, which is precisely why we are writing this paper. We encourage the broader systematics and conservation biology communities to evaluate the competing taxonomic hypotheses on their scientific merits, in the peer-reviewed literature, with the rigor these conservation stakes require.

Conclusions

The SSG (North American Sturgeon and Paddlefish Society, 2025) rejection of Brownstein and Near (2025) exemplifies a problem that extends far beyond sturgeons. As molecular and genomic data continue to reveal the extent to which Linnaean ranked classifications misrepresent the tree of life, the transition toward explicitly phylogenetic rank-free frameworks will increasingly intersect with conservation regulatory systems built around familiar names. The response of those systems, and of the specialist communities that advise them, will determine whether the improvements in biological classification that phylogenetics makes possible are translated into better conservation outcomes or are resisted in the name of stability.

The scientific objections raised by the SSG against Brownstein and Near (2025) do not withstand scrutiny. The bootstrap support objection ignores the fact that the phylogenies presented in Brownstein and Near (2025) are quite strongly supported. The missing data objection invokes a general methodological concern without demonstrating that it applies specifically to the Brownstein and Near (2025) dataset in a way that biases the results. The introgression objection misidentifies the taxonomic level at which hybridization occurs and is addressed transparently in the original paper. The polyploidy objection is asserted without an explicit competing model and is not applicable to the mitochondrial component of the analysis. The morphological synapomorphies objection demands a standard of evidence that the existing classification does not meet and that is not applied symmetrically to the SSG's own proposed alternative.

Most fundamentally, the SSG's proposed alternative, a broadly defined paraphyletic *Acipenser*, fails on the very terms the SSG invokes. Every published analysis, including Dillman et al. (2007), the paper the SSG treats as its primary methodological authority, resolves *Acipenser* as paraphyletic. The SSG acknowledges this paraphyly and proposes to preserve it anyway. This is not a scientifically defensible position; it is a preference for familiarity over phylogenetic accuracy.

The conservation argument for maintaining the existing classification, while pragmatically motivated, inverts the actual relationship between accurate taxonomy and effective conservation. Paraphyletic classifications misrepresent evolutionary diversity and distort ESU delineation in ways that have real consequences for the allocation of conservation resources. The short-term administrative costs of taxonomic change are real but manageable; the long-term conservation costs of maintaining an inaccurate classification compound silently and are borne by the organisms themselves.

The Brownstein and Near (2025) revision of *Acipenseridae* is part of a coherent and explicitly articulated research program aimed at constructing fish classifications that directly reflect evolutionary relationships and are free of the structural limitations of Linnaean ranked hierarchy. Near and Thacker (2024) demonstrated across the full breadth of ray-finned fish diversity that Linnaean ranked taxa are not biologically comparable to one another in any evolutionarily meaningful sense, that ranked classification produces redundant and uninformative names at a striking rate,

and that a *PhyloCode*-based rank-free framework provides names with explicit, testable phylogenetic content that remain stable as phylogenetic hypotheses are refined. Near et al. (2025) showed in *Labridae* that the practical consequences of this problem are not abstract: polyphyletic and paraphyletic Linnaean genera actively confound both biological research and conservation management, and that a blended approach, using *PhyloCode* definitions that retain ICZN conventions at the genus and species level, provides a pragmatic and scientifically rigorous path forward. Brownstein and Near (2025) brought this same framework to *Acipenseridae* and for the first time produced a classification in which all genera are monophyletic.

This research program is not iconoclastic; it follows directly from the phylogenetic revolution in systematics applied to groups where the need for accurate taxonomy is most urgent. The most endangered vertebrate lineage on Earth is exactly the kind of group for which getting taxonomy right matters most. We recognize that the sturgeon community, including the SSG, is united by a genuine and deep commitment to the conservation of these animals, and that the disagreement examined here is one about means rather than ends. The scientific objections to the Brownstein and Near (2025) revision do not withstand scrutiny, but the conservation concerns that motivated the SSG response are real, and the most productive path forward is one that takes both seriously.

We close with a call for a coordinated phylogenomic analysis that would put sturgeon systematics on the most secure possible foundation. An in-progress whole-genome phylogenomic study sampling all 27 living species (Li et al. 2026), integrated with a comprehensive morphological dataset and the fossil record, will provide the kind of evidence that all parties in this discussion have identified as the appropriate basis for a definitive classification. The consistent recovery of paraphyletic *Acipenser* and *Huso* across mtDNA gene trees, phylogenetic analysis of 30 nuclear genes, phylogenies inferred from morphology, and combined analyses spanning more than two decades of independent investigation makes it highly likely that a genome-scale analysis will corroborate the classification proposed by Brownstein and Near (2025) rather than overturn it. We urge the sturgeon systematics and conservation communities to undertake this work collaboratively, bringing together the expertise in genomics, morphology, paleontology, taxonomic nomenclature, and conservation law that a durable and broadly accepted solution will require. The goal is to build the empirical foundation for the protection and conservation of the world's most endangered fishes.

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Declarations

Conflict of interest The authors declare no conflict of interest.

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