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Research Article

Co-occurrence of temperate and tropical *Sinanodonta* lineages in Iraq suggests converging invasion pathways in the Middle East

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Abstract

Freshwater mussels of the genus *Sinanodonta*, native to East Asia, are among the most successful invasive bivalves globally, known for their rapid reproduction and growth, broad environmental tolerances, and ability to disrupt aquatic ecosystems. Their arrival and subsequent spread in parts of the Middle East remains poorly documented. Here, we present new DNA-based evidence that confirms the invasion of Iraq's freshwater ecosystems by two genetically distinct *Sinanodonta* lineages: *Sinanodonta woodiana* and *Sinanodonta pacifica*. Using COI DNA sequences, we confirm the co-occurrence of these lineages in southern Iraq, a pattern not previously reported in any Middle Eastern country. The two invasions appear to result from independent introduction pathways, both through their obligatory parasitic larvae on fish: aquaculture of East Asian carp (*S. woodiana*), and the ornamental fish trade or tilapia farming (*S. pacifica*). This discovery raises significant ecological concerns, as the dual invasion may further threaten Iraq's already declining native mussel fauna, particularly the endemic and potentially extirpated *Anodonta vescoiana*. Our findings highlight Iraq as an emerging hotspot for freshwater biological invasions, likely driven by its growing and largely unregulated fish farming industry. This underscores the urgent need for targeted genetic monitoring, risk assessments, and biosecurity measures to prevent further spread and ecological impact.

Key words: Aquatic bioinvasions, Invasive freshwater mussels, Molecular identification, *Sinanodonta woodiana*, *Sinanodonta pacifica*, Tigris–Euphrates Basin

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Introduction

Invasive bivalves are arguably one of the most disruptive biological forces in freshwater ecosystems worldwide (Lopes-Lima et al. 2025). Their ability to tolerate broad environmental conditions, rapidly increase population sizes, and disperse effectively allows them to colonize and thrive in new habitats, often at the expense of native biodiversity (Douda et al. 2025). Invasive freshwater bivalves can profoundly alter ecosystem functions, including water filtration, sediment dynamics and nutrient cycling, and disrupt interactions of native freshwater mussels (Bivalvia: Unionida) with their obligate host fish species (Sousa et al. 2014; Zieritz et al. 2018a, 2018b).

One of the most prolific invaders of the order Unionida is *Sinanodonta woodiana* (Lea, 1834), commonly known as the Chinese pond mussel. Initially described from the Yangtze River basin and surrounding East Asian waterways, *S. woodiana* rapidly expanded its range following unintentional introductions associated with the trade of Asian carp (*Cyprinus carpio*) and other East Asian cyprinids (Bolotov et al. 2016; Mehler et al. 2024; Douda et al. 2025). Once established, the species thrives in both natural and artificial lentic environments as well as river systems, attaining population densities of > 60 individuals m^{-2} and biomass of up to 25 kg m^{-2} (Kraszewski and Zdanowski 2007). In some cases, the species has been shown to progressively displace native unionids through host competition, habitat occupation, and shell-mediated habitat alteration (Donrovich et al. 2017; Urbańska and Andrzejewski 2019; Dobler et al. 2022). Now widespread across Europe, Asia, and North Africa, *S. woodiana* is regarded as a significant threat to native biodiversity and a growing concern in freshwater conservation and management (Bolotov et al. 2016; Lopes-Lima et al. 2017; Douda et al. 2025). Recent molecular studies have additionally demonstrated that morphologically similar *Sinanodonta* lineages may represent cryptic invasions, making DNA-based identification essential for reconstructing invasion pathways and accurately assessing species distributions (Bolotov et al. 2016; Douda et al. 2025). Situated at the crossroads of major transcontinental trade routes and traversed by the Tigris–Euphrates river system, Iraq represents a strategically significant yet understudied region in the context of freshwater biological invasions. Characterised by a hot (semi-)arid climate, discharge in this river system is highly seasonal, with values being up to 10-times higher during spring (March-May) compared to summer months (July-October) (Bozkurt and Sen 2013; Issa et al. 2013). Iraq's freshwater ecosystems face numerous anthropogenic pressures, including pollution, hydrological alterations, heating and drying (Bozkurt and Sen 2013; Issa et al. 2013; Yasser and Naser 2023; Yasser et al. 2024; Naser et al. 2025a; Boloorani et al. 2026). These pressures have resulted in a sharp decline in native mussel diversity, including the potential extirpation of the endemic freshwater mussel species *Anodonta vescoiana* Bourguignat, 1856 (Naser et al. 2025b). The *Sinanodonta* genus was first recorded in Iraq in 2021 in the Hilla River, a tributary of the Euphrates River (Bogan et al. 2021), and the mainstem of the Euphrates River near Najaf (Abdul Razak and Zwair 2021) (Fig. 1). Both these records were morphologically identified as *S. woodiana*, which is presumed native to the Yangtze River basin and has been designated as the "temperate invasive" lineage due to its widespread introduction across Europe and other temperate regions (Bolotov et al. 2016). No DNA sequences were published by Bogan et al. (2021), but four published cytochrome c oxidase subunit I (COI) DNA sequences (Genbank Accession Numbers LC651629, LC651630, LC656037, LC658986) appear to be associated with the Abdul Razak and Zwair (2021) record from the Euphrates River. Phylogenetic analyses of these sequences by Douda et al. (2025)

placed them into *Sinanodonta pacifica* (Heude, 1878). This species is presumed to be native to eastern China and Taiwan and due to its widespread introduction across parts of tropical Asia, has been designated as the "tropical lineage" (Bolotov et al. 2016), although it has also been reported occasionally from other tropical and non-tropical regions (Douda et al. 2025).

More recently, additional records of *Sinanodonta* have been reported from several Iraqi localities, including the Euphrates River, Ptera Dam, Adua Marsh, Al-Majer, Al-Sweap River, Al-Gharraf River and Al-Ezz River (Naser et al. 2024, 2025b; Mashjel and Al-Taher 2025). However, because many of these records were based primarily on morphology, the identity and distribution of invasive *Sinanodonta* lineages in Iraq remain incompletely resolved.

Given Iraq's geographic position at the intersection of temperate and tropical *Sinanodonta* invasion pathways, accurate identification of invasive unionid species and mitochondrial lineages is essential to reconstruct introduction routes, assess lineage-specific ecological risks, and design effective conservation and management strategies for native mussel assemblages (Douda et al. 2025; Naser et al. 2025b). In this study, we aimed to (1) determine the identities and current distributions of genetically distinct *Sinanodonta* lineages in Iraq, (2) discuss their likely invasion pathways and vectors, and (3) provide recommendations for managing their spread and impacts. By generating new DNA sequence data and comparing them with previously published COI sequences, we clarify the occurrence and distribution of invasive *Sinanodonta* lineages in Iraq and highlight the Tigris–Euphrates Basin as a potential contact zone for cryptic co-invasion in Southwest Asia.

Materials and methods

The specimens analysed in this study originated from previously published Iraqi records of *Sinanodonta* from the Tigris and Euphrates river systems (Naser et al. 2024, 2025b). Specimens were collected during field surveys conducted in 2022 from the Tigris River at the Ptera Dam and from the lower Euphrates River (sites 3 and 4 in Fig. 1, respectively). Geographic coordinates and sampling localities are provided in Fig. 1 and associated references. The original Iraqi records from the Euphrates River near Najaf were morphologically identified as *S. woodiana* but were subsequently shown by molecular analyses to belong to *S. pacifica*; this issue is discussed further in the Discussion section. DNA sequences were obtained from two *Sinanodonta* specimens from each of the two sampled sites. The specimens were sampled in 2022 and preserved in 96% ethanol. A total of 16 specimens were processed for DNA extraction; however, only four yielded successful COI amplification, while the remaining samples failed to amplify, likely due to DNA degradation associated with poor preservation. DNA was extracted from foot tissue samples using the DNeasy® Blood and Tissue Kit following the manufacturer's protocol. A 658 base pair (bp) fragment of the COI region was amplified using standard primers LCO1490 and HCO2198 (Folmer et al. 1994) in 10 µl reactions containing 5.0 µL 10X Green Dye PCR Buffer, 0.5 µL 10 mmol L^{-1} of each primer, 1.0 µL DNA template and 3.0 µL nuclease free water. Polymerase chain reaction (PCR) cycle parameters were initial denaturation at 95 °C for 5 min, 35 cycles of denaturation at 95 °C (50 s), annealing at 52 °C (50 s) and extension at 72 °C (50 s), and a final extension at 72 °C for 5 min. Amplified and purified DNA fragments were sequenced by the commercial company Eurofins Genomics (Ebersberg, Germany) and deposited in the National Center for Biotechnology Information (NCBI) GenBank database under Accession Numbers [PZ392808, PZ392809, PZ392810 and PZ392811].

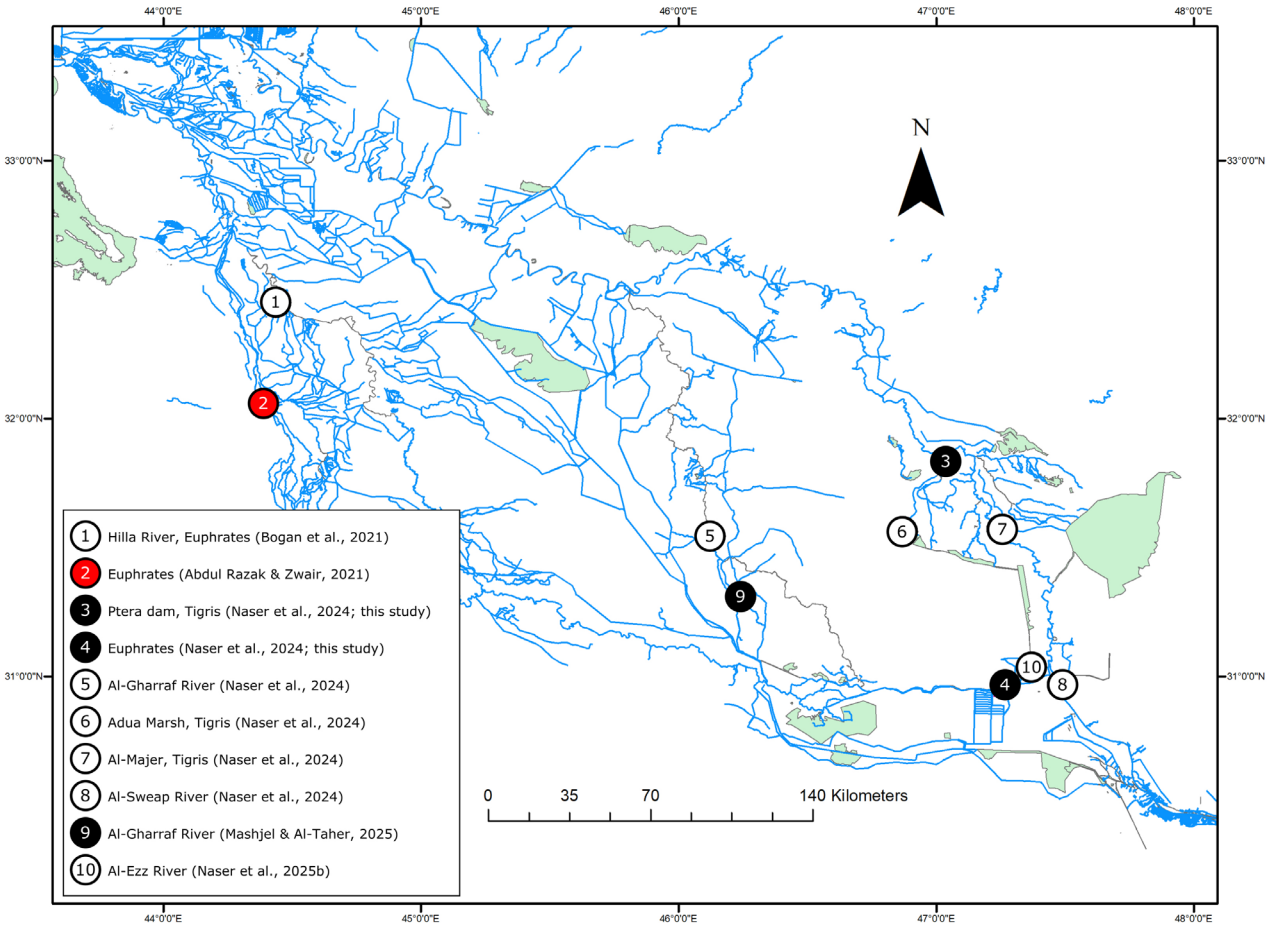

Figure 1. Verified occurrences of *Sinanodonta* spp. in the Tigris–Euphrates Basin of Iraq. Records for which species have been identified by DNA barcoding in red (*S. pacifica*) and black (*S. woodiana*), respectively; white records are not DNA barcoded and are considered *Sinanodonta* sp. For each record, the name of the water body and the reference of the relevant publication are provided.

MAFFT v7.304 (Katoh and Standley 2013) was used to assemble the COI dataset, which included the four sequences produced in this study, plus all previously published *Sinanodonta* COI sequences (n = 553), including those in the recent review by Douda et al. (2025) and additional sequences published since then (i.e. Mashjel and Al-Taher 2025; LC833751, LC833752) (see Suppl. material 1). To ensure that there was minimal or no bias in phylogenetic inference, third-party COI sequences were examined for potential diagnostic terminal artefacts (clusters of end-confined substitutions and/or deletions). This included sequences LC833751 and LC833752 (Mashjel and Al-Taher 2025). Publicly available sequences of the freshwater mussels *Margaritifera laevis* (F. Haas, 1910), *Beringiana japonica* (Clessin, 1874), and *Beringiana beringiana* (Middendorff, 1851) were included as outgroup taxa (Suppl. material 1).

The COI dataset was collapsed into unique haplotypes (see Suppl. material 1 for haplotype codes) and analysed using Maximum Likelihood (ML) and Bayesian Inference (BI). ML analyses were performed in IQ-TREE v2.2.0 (Minh et al. 2020), and BI analyses were conducted in MrBayes v3.2.7a (Ronquist et al. 2012). PartitionFinder 2 (Lanfear et al. 2016) was used to determine the best-fit substitution models and partitioning schemes under the Bayesian Information Criterion for BI analyses. Bayesian analyses were initiated from random trees using four Markov chains with default incremental heating. Two independent runs of 20 × 10^6 generations were performed, sampling every 1,000 generations to produce 20,000 trees.

Convergence and burn-in were assessed using Tracer v1.7.1 (Rambaut et al. 2018). For ML analyses, the best-fit models and partitioning schemes were identified with ModelFinder (Kalyaanamoorthy et al. 2017). Phylogenetic inference was then performed in IQ-TREE with an initial tree search followed by 10 independent runs and 10,000 ultrafast bootstrap replicates.

Results

Our data provide new DNA-based confirmation of the presence of *S. woodiana* in the lower Tigris–Euphrates Basin, specifically from the Tigris River at Ptera Dam and the lower reaches of the Euphrates River. This complements a previous DNA-based record of *S. pacifica* from the middle Euphrates River (Fig. 1), confirming that both of the invasive *Sinanodonta* lineages occur in Iraq but currently exhibit apparently distinct distributions. Together, these findings support the presence of cryptic co-invasion by two genetically distinct *Sinanodonta* lineages within the Tigris–Euphrates Basin.

Our analyses additionally revealed that the two previously published DNA sequences from the Al-Gharraf River (LC833751, LC833752) contained terminal sequencing artefacts. After conservative end-trimming, both sequences matched the invasive *S. woodiana* haplotype SWA01 exactly; they were therefore included in the haplotype dataset but excluded from phylogenetic reconstruction. Both ML and BI analyses of the *Sinanodonta* COI dataset produced congruent topologies, recovering eleven clades corresponding to the species delimitations previously reported by Douda et al. (2025) (Fig. 2). The four newly sequenced specimens from Iraq (haplotype SWA01) clustered within the *Sinanodonta woodiana sensu stricto* clade, and were identical to the widespread invasive haplotype recorded across Europe and Central Asia (Fig. 2, Suppl. material 1). In contrast, the Iraqi sequences already available in GenBank (haplotype SWB02) grouped within the *Sinanodonta pacifica* clade and were identical to sequences from Peninsular Malaysia (Fig. 2; Suppl. material 1). Representative shell morphology of the two lineages is shown in Fig. 3.

Discussion

Cryptic co-invasion of two genetic lineages of *Sinanodonta*

Our molecular analyses confirm the occurrence of two genetically distinct invasive *Sinanodonta* lineages in Iraq, namely *Sinanodonta woodiana* and *S. pacifica*. The newly generated Iraqi COI sequences clustered within the *S. woodiana sensu stricto* clade and were identical to haplotype SWA01, the dominant invasive haplotype widely distributed across introduced populations in Europe and Central Asia (Douda et al. 2025). In contrast, the previously published Iraqi sequences associated with the Euphrates River near Najaf (LC651629, LC651630, LC656037, LC658986) grouped within the *S. pacifica* clade and matched haplotype SWB02, previously reported from Peninsular Malaysia. These findings demonstrate that morphologically similar *Sinanodonta* populations in Iraq represent two genetically distinct invasive lineages and provide the first molecular evidence for cryptic co-invasion within the Tigris–Euphrates Basin.

The Iraqi *S. pacifica* sequences are particularly important because the original records were morphologically identified as *S. woodiana* (Abdul Razak and Zwair 2021). However, phylogenetic analyses by Douda et al. (2025), confirmed by our results, clearly place these sequences within *S. pacifica*. This inconsistency highlights the constraint of shell morphology for recognizing invasive *Sinanodonta* lineages.

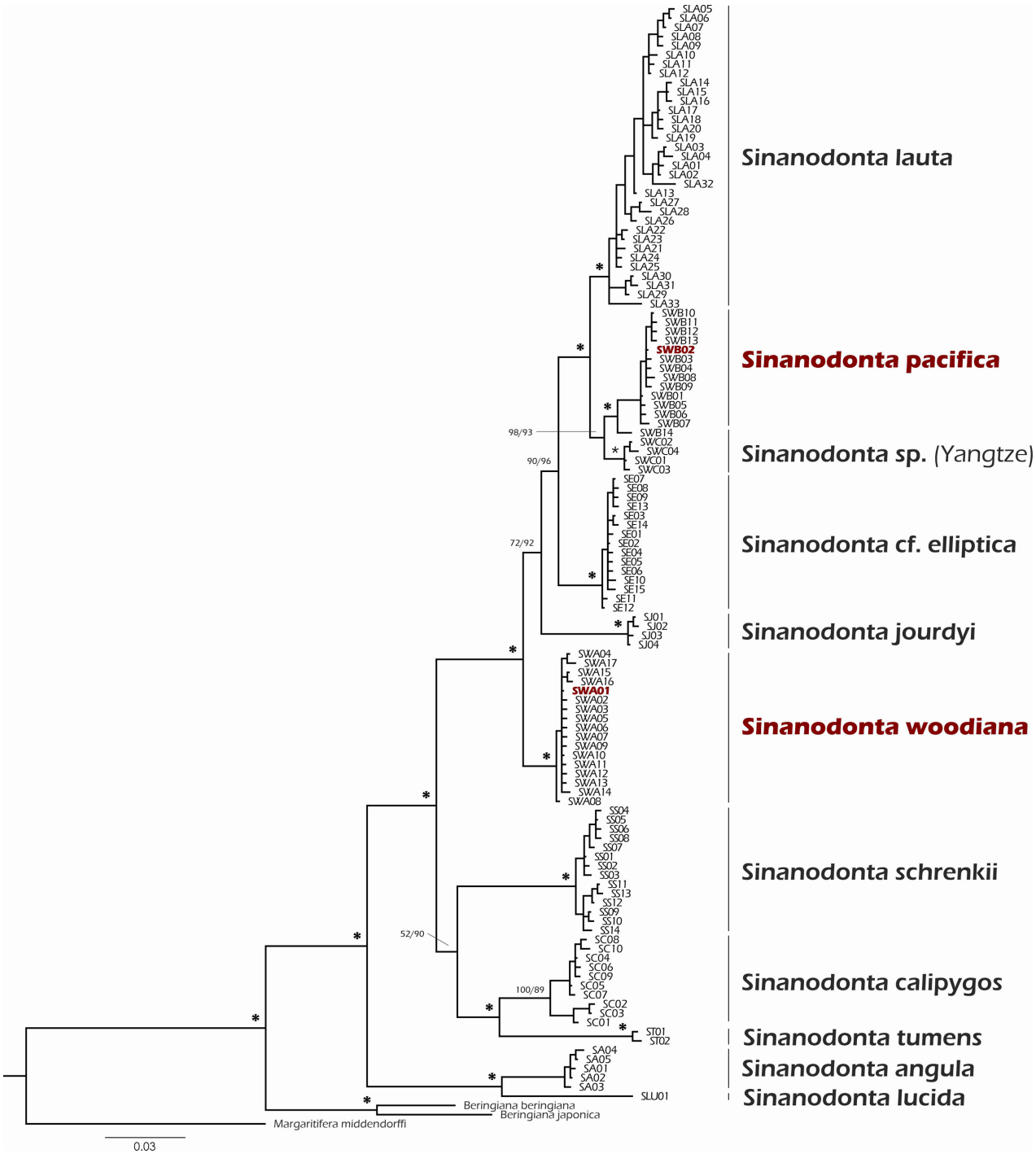

Figure 2. Bayesian Inference (BI) and Maximum Likelihood (ML) phylogenetic tree inferred from the cytochrome c oxidase subunit I (COI) gene of *Sinanodonta* species. Support values above the branches are percent posterior probabilities/ultrafast bootstraps. Support values > 95% for both phylogenetic analyses are represented by an asterisk; support values within each species clade were erased for clarity. Haplotypes including Iraqi sequences were highlighted in red.

Previous studies have shown that shell shape in *S. woodiana* is highly plastic and affected by external factors, which may mask species limits and hinder identification based on morphological traits (Guarneri et al. 2014). More broadly, recent molecular studies demonstrated that invasive populations formerly treated as a single widespread species comprise several cryptic lineages, including *S. woodiana sensu stricto*, *S. pacifica*, and *S. lauta* (Bolotov et al. 2016; Douda et al. 2025). This research points to the significance of genetic identification in tracing the origins of

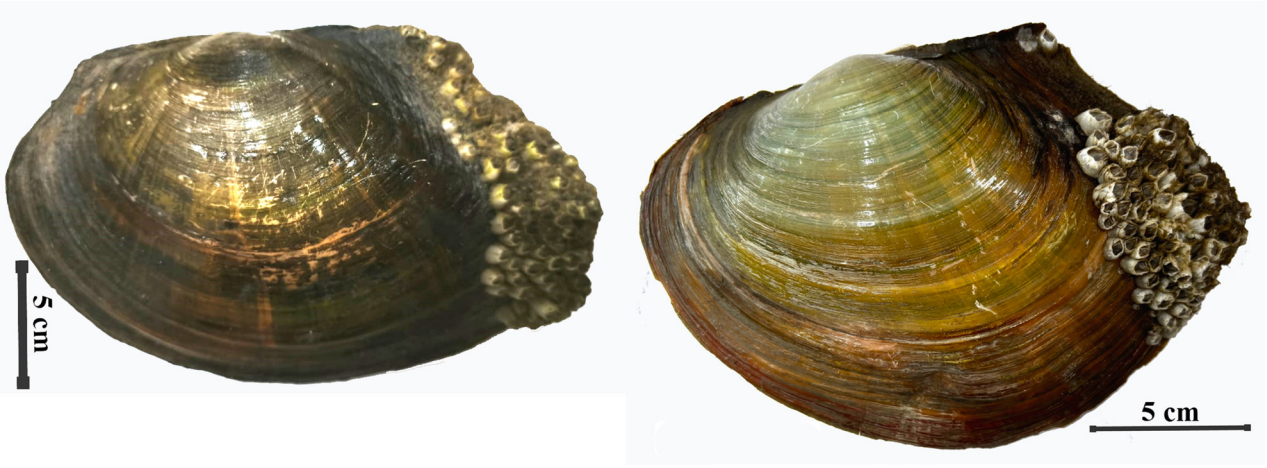

Figure 3. Shell morphology of invasive *Sinanodonta* species recorded in Iraq. **A.** *Sinanodonta woodiana* from the Tigris River (Ptera Dam); **B.** *Sinanodonta pacifica* from the Euphrates River. Photo Murtada Naser.

invasions and getting an exact picture of species distribution. Our results further indicate that the two invasive lineages currently occupy different sectors of the Tigris–Euphrates river system. *Sinanodonta woodiana* has so far been confirmed from the southeastern lowlands of the Al-Gharraf River and associated marsh systems, whereas *S. pacifica* has been recorded farther northwest in the middle Euphrates River system. The closest confirmed records of the two lineages remain separated by approximately 200 km in straight-line distance or roughly 360 km following river-course connectivity. Despite the lack of documented local sympatry, comprehensive surveys might uncover zones of contact or overlapping ranges for the two invasive lineages in this basin. The Iraqi records are biogeographically notable because co-invasion by multiple *Sinanodonta* lineages within the same country or river basin remains relatively uncommon. Outside Iraq, simultaneous occurrence of *S. woodiana* and *S. pacifica* has only rarely been documented, including in the Irrawaddy Basin of Myanmar (Vikhrev et al. 2017; Bolotov et al. 2022). Comparable cases involving other invasive *Sinanodonta* lineages have also been reported from the Volga Basin and Kazakhstan (*S. woodiana* and *S. lauta*) and from Malaysian Borneo (*S. pacifica* and *S. lauta*) (Kondakov et al. 2020a; Zieritz et al. 2024; Douda et al. 2025). The convergence of unique invasive *Sinanodonta* lineages in the Tigris–Euphrates Basin suggests that multiple, distinct introduction events occurred through fish trade and aquaculture practices.

Genetic lineages, invasion pathways and co-invasion dynamics

Although both *Sinanodonta* lineages recorded in Iraq were most likely introduced unintentionally during their parasitic glochidial stage via fish hosts, the available molecular evidence suggests that their invasion pathways differ. Earlier genetic investigations showed that invasive populations of *Sinanodonta* are organized into multiple primary lineages linked to various geographical sources and aquaculture systems (Bolotov et al. 2016; Douda et al. 2025). The widespread temperate invasive lineage of *S. woodiana sensu stricto* occurring throughout Europe and Central Asia is characterised by a dominant COI haplotype originating from the Yangtze River basin in China (Konečný et al. 2018; Kondakov et al. 2018; Urbańska et al. 2021). The Iraqi *S. woodiana* sequences we identified are part of this identical invasive haplotype, which reinforces the theory that populations in Iraq emerged via the same broad introduction route responsible for invasions across Europe and

Central Asia. The most likely vector for introduction of the temperate *S. woodiana* lineage into Iraq is aquaculture-mediated translocation of East Asian cyprinids. In Europe and temperate Asia, *S. woodiana* spread repeatedly with silver carp (*Hypophthalmichthys molitrix*) and grass carp (*Ctenopharyngodon idella*) imported from China for aquaculture and stocking programmes (Konečný et al. 2018; Urbańska et al. 2021; Douda et al. 2025). In Iraq, Asian carp (*Cyprinus carpio*) aquaculture is widespread across the Tigris–Euphrates Basin and includes hatcheries, fish farms, and floating-cage operations (Al-Khafaji and Al-Amary 2016; Khudair and Fahd 2024). Therefore, the existence of the same invasive COI haplotype in Iraq strongly suggests that it was introduced through aquaculture routes related to carp. By contrast, the Iraqi *S. pacifica* sequences matched haplotype SWB02 previously reported from Peninsular Malaysia, indicating a potentially different invasion history associated with tropical aquaculture networks. Tropical invasive *Sinanodonta* lineages have frequently been linked to fish hatcheries and warm-water aquaculture systems in Southeast Asia and Central America (Bauer et al. 2021; Douda et al. 2025). Since the late 1990s, tilapia aquaculture has grown significantly in Iraq. *Oreochromis* species and red belly tilapia (*Coptodon zillii*) are now commonly cultivated and naturalized in a number of freshwater systems in Iraq (Jawad et al. 2018; Mohamed and Al-Wan 2020, 2023; Jawad and Abdulsamad 2021). Continuous propagation and movement of cultured fish stocks may therefore have facilitated introduction of *S. pacifica* into Iraqi inland waters.

The ornamental fish trade may represent an additional secondary introduction pathway. In Germany, ornamental-shop *S. woodiana* populations were shown to be genetically similar to wild invasive populations, demonstrating that the aquarium trade can contribute to regional spread of invasive *Sinanodonta* (Benedict et al. 2024). Since the early 2000s, importation and sale of tropical ornamental fishes have increased considerably in several Iraqi cities, with many traded species originating from Southeast Asia (Jawad et al. 2021). This introduction pathway cannot currently be ruled out, even though there is currently no concrete evidence connecting ornamental fish imports to *Sinanodonta* introductions in Iraq. Therefore, it is possible that the Tigris–Euphrates Basin serves as a secondary contact zone where various invasive *Sinanodonta* lineages brought in via various aquaculture routes come together within a single fluvial network. Similar cases of cryptic co-invasion involving multiple *Sinanodonta* lineages have been documented elsewhere, including the Yenisei River in Siberia, the Volga Basin, Kazakhstan, and the Irrawaddy Basin of Myanmar (Bespalaya et al. 2017; Kondakov et al. 2020a; Bolotov et al. 2022; Douda et al. 2025). Such systems are biogeographically important because they reflect multiple independent introduction events rather than local diversification.

Variations in climatic affinities may also have an impact on future expansion and establishment success. The temperate *S. woodiana* lineage has demonstrated a remarkable ability to establish populations in colder environments far beyond its native climatic range, whereas *S. pacifica* appears more strongly associated with tropical and subtropical regions (Urbańska et al. 2019; Yermoshyna and Pavliuchenko 2021; Douda et al. 2025). These ecological distinctions imply that the two invasive lineages might react differently to the Middle East's ongoing hydrological change and climate change.

Although the proposed invasion pathways remain partly hypothetical, the available molecular and biogeographic evidence strongly supports the interpretation that Iraqi populations of *S. woodiana* and *S. pacifica* originated through separate introduction histories linked to different fish-translocation networks. Additional studies using higher-resolution genetic markers combined with detailed analysis of aquaculture trade pathways will be required to reconstruct the chronology and directionality of these invasion events more precisely.

Ecological implications of co-invasion

Although ecological impacts are much better documented for *Sinanodonta woodiana* than for *S. pacifica*, the occurrence of two invasive *Sinanodonta* lineages within the Tigris–Euphrates Basin raises important ecological concerns. Invasive *Sinanodonta* species share several life-history characteristics associated with invasion success, including rapid growth, high fecundity, broad environmental tolerances, extended reproductive periods, and use of a wide range of fish hosts during the parasitic glochidial stage (Konečný et al. 2018; Urbańska et al. 2019, 2021; Douda et al. 2025). Experimental and field studies from Europe further demonstrated that *S. woodiana* can establish dense populations with high reproductive output and successful recruitment even under suboptimal climatic conditions (Dobler et al. 2022; Urbańska et al. 2021). Similar reproductive patterns have also been reported for *S. pacifica* in tropical Southeast Asia, suggesting strong dispersal and establishment potential for both invasive lineages (Sahidin et al. 2024).

Once established, invasive *Sinanodonta* populations may negatively affect native unionids through several mechanisms. Previous studies showed that *S. woodiana* glochidia successfully develop on a broad range of fish hosts and may even exhibit higher metamorphosis success than native unionids (Douda et al. 2011; Huber and Geist 2019). Experimental evidence additionally demonstrated that prior infestation of host fish by *S. woodiana* glochidia can significantly reduce metamorphosis success of native mussel larvae through host-mediated immune responses and competition for suitable hosts (Donrovich et al. 2017; Dobler et al. 2022). Other studies reported negative physiological effects on infested fish, including reduced body condition, altered blood chemistry, impaired swimming performance, and increased mortality under some conditions (Douda et al. 2017; Anil et al. 2025). In addition, invasive *Sinanodonta* may alter benthic habitats and ecosystem processes through intensive filter feeding, biodeposition, and competition for substrate and food resources (Douda and Čadková 2018; Poznańska-Kakareko et al. 2021).

In Iraq, establishment of *S. woodiana* coincides with the probable extirpation of the endemic freshwater mussel *Anodonta vescoiana* from large parts of its historical range (Naser et al. 2025b). Although direct causation cannot yet be demonstrated, the spread of invasive *Sinanodonta* together with hydrological alteration, salinisation, habitat fragmentation, and pollution may collectively have contributed to the decline of native unionid assemblages in the southern marshes and rivers of Iraq.

Potential future sympatry between *S. woodiana* and *S. pacifica* may further increase ecological risks. Co-invasion by multiple *Sinanodonta* lineages has previously been documented in several Eurasian river systems, including the Yenisei River, Kazakhstan, and the Irrawaddy Basin (Bespalaya et al. 2017; Kondakov et al. 2020b; Bolotov et al. 2022; Douda et al. 2025). Where multiple invasive lineages occur together, additive or synergistic ecological impacts may arise through increased propagule pressure, broader exploitation of host-fish assemblages, intensified competition for habitat and food resources, and cumulative effects on ecosystem functioning. There have also been reports of hybridization and complex lineage interactions within *Sinanodonta*, indicating further ecological and evolutionary complexity where invasive lineages come into secondary contact. (Kondakov et al. 2018; Douda et al. 2025).

Despite increasing knowledge of invasive *Sinanodonta* elsewhere, virtually no information is available regarding comparative ecology, host use, filtration impacts, or competitive interactions between *S. woodiana* and *S. pacifica* under semi-arid riverine conditions such as those characterising the Tigris–Euphrates Basin.

To better understand their effects on native freshwater biodiversity in Iraq and the surrounding areas, targeted ecological and experimental studies addressing population dynamics, host associations, ecological interactions, and potential hybridization between the two lineages are therefore desperately needed.

Author contribution

Sample collections: MN, AY. Sample design and methodology: MN, AY, AZ, ML. Data analysis and interpretation: MN, AY, ML, AZ. writing: original draft: MN, AZ, AY, ML, JS, B AG, JD. DB, FE. writing - review & editing: MN, AZ, AY, ML, JS, BAG, JD. DB, FE.

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Artificial Intelligence (AI) use

Regarding the use of AI in the preparation of this manuscript, the authors declare the following: GPT
Used for: Language, style and writing.

Data availability

All of the data that support the findings of this study are available in the main text or Supplementary material.

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Supplementary material 1

List of sequences used of *Sinanodonta* sp. for the phylogenetic analysis

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Data type: docx

Explanation note: List of sequences with corresponding, GenBank reference, haplotype number, species, country, origin and bibliographic reference. Iraqi sequences in dark red in bold.

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