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# Molecular methods confirm the presence of the alien mussel *Perna viridis* Linnaeus, 1758 (Bivalvia, Mytilidae) in Southern Brazil

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Molecular methods confirm the presence of the alien mussel *Perna viridis* Linnaeus, 1758 (Bivalvia, Mytilidae) in Southern Brazil

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**Abstract**

The mussel *Perna viridis*, commonly known as the green mussel, is native from the Indo-Pacific region and has been introduced in various sites around the globe. In Brazil, the species has already been recorded in Rio de Janeiro and Ceará states. With the aim of assessing the presence of mussels in the southern region of the country, 14 individuals were collected in the Paranaguá Estuarine Complex, Paraná. The mussels were found attached at a depth of 2 meters on the artificial structure of Ponta do Poço Marina. The DNA was extracted using a commercial kit, the COI gene was amplified through PCR by the primers forward dgLCO-1490 and reverse dgHCO-2198, sequenced by the Sanger method, assembled in CLC Genomics Workbench, and the species was identified through the BOLD Systems. The phylogenetic tree was built on MEGA11 using 28 sequences from three species within the genus *Perna*. Therefore, the present study represents the first to confirm the occurrence of the exotic species *Perna viridis* in Brazil through molecular identification and characterizes the third Brazilian state where the mollusk has been recorded. This indicates that Brazilian coastline provides optimal environmental conditions for the establishment and development of the *P. viridis*.

**Keywords.** Alien species, green mussel, marine species, Paraná, molecular analysis

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## Introduction

Alien species are defined as those found outside their natural distribution area and that have the potential to spread in this new area, where they could not occur without anthropic introduction (Pyšek et al. 2020). When they harm the economy, environment or human health, these species are classified as “invasive” (IUCN 2021). The mytilids are one of the main invasive alien groups recognized for causing several impacts. Their success stems from their capability in adapting to new environments, becoming well-established and dominant in coastal areas (Micklem et al. 2016; Santos et al. 2023).

Once established, invasive mytilids demonstrate increased tolerance to environmental stress in comparison to taxonomically related native species (Lenz et al. 2011), consequently modifying ecosystem functioning and structure through competition, altering food chains and nutrient cycling (Pyšek et al. 2020). These species also affect human well-being by harming water systems in industrial complexes and marine transport, as well as causing human health problems through food poisoning. This is because their filter-feeding behavior concentrates heavy metals and other contaminants (Freire and Marafon 2018; Siriwardena 2022; Turbelin et al. 2022).

In Brazil, the occurrence of nine invasive species of marine/estuarine bivalves is documented, with seven recorded in the southern region of the country: the oysters *Isognomon bicolor* (C. B. Adams, 1845), *Crassostrea virginica* (Gmelin, 1791), *Saccostrea cucullata* (Born, 1778) and *Crassostrea gigas* (Thunberg, 1793); and the mussels *Mytilus galloprovincialis* Lamarck, 1819, *Leiosolenus aristatus* (Dillwyn, 1817) and *Perna perna* (Linnaeus, 1758) (Moura-Britto and Patrocínio 2005; Freire and Marafon 2018; Messano et al. 2019; Amaral et al. 2020; Belz et al. 2020; Teixeira and Creed 2020; Agudo-Padrón 2022; Stanski et al. 2022).

In relation to the species of mussels, the blue mussel *M. galloprovincialis* is an intertidal species, native to the Mediterranean and the Atlantic coasts of Europe and North Africa. This mollusk is widely distributed, occupying shores on every continent except Antarctica (McQuaid et al., 2015; Zardi et al., 2018). The small bivalve *L. aristatus* is an endolithic and wood-boring species that often causes damage and deformities in other mollusks. This mussel is native to the Caribbean Sea and having been identified in the Atlantic, Mediterranean, Caribbean, and Pacific

regions (Simone & Golçalves, 2006; Soriano & Salgado, 2019). Concerning the brown mussel *P. perna*, which is widely distributed around the world, and along the Brazilian coast it is particularly abundant from Espírito Santo to Santa Catarina, there has been extensive analysis and technical discussion about the species' origin in the country. According to Pierri et al. (2016), the presence of the species in Brazilian territory predates colonization in 1500, suggesting that *P. perna* is a native species. However, as demonstrated by Silva et al. (2018), the occurrence of the species along the Brazilian coast is attributed to invasion during the slave trade between Africa and Brazil from the 16th to the 19th centuries. Despite its origin, the species is naturalized in South America, with multiple introductions occurring over the past 500 years (Oliveira et al., 2017).

Regarding the mussel *Perna viridis*, although the presence of the species has not yet been confirmed by molecular methods in Brazil, based on specimens sampled in May 2018, Messano et al. (2019) reported the first occurrence in the Southwest Atlantic. The bivalve was found attached to experimental plates installed to test anti-fouling systems at Guanabara Bay, Rio de Janeiro, on the southeastern Brazilian coast. Recently, Soares et al. (2022) reported the species settled near the port of Mucuripe (Fortaleza, Ceará), located in northeast Brazil, also in settlement plates. Subsequently, Santos et al. (2023) reported *P. viridis* in lantern nets within the Marine Extractive Reserve, from Arraial do Cabo (Rio de Janeiro). It is suggested that all these introductions of the mussel on the Brazilian coast were accidental, probably via fouling or ballast water (Santos et al. 2023).

The mollusk bivalve *Perna viridis* (Linnaeus, 1758), synonymous with *Mytilus viridis* Linnaeus, 1758, *Mytilus smaragdinus* Gmelin, 1791 and *Mytilus opalus* Lamarck, 1819, (MolluscaBase 2024), inhabits the midlittoral and sublittoral zones of marine and estuarine ecosystems, where it is usually found forming dense colonies attached to a variety of structures or substrates via byssus threads (Rajagopal et al. 2006). Over the years, it has been reported in polluted and anthropogenic areas (Rajagopal et al. 1997; Micklem et al. 2016), but also in pristine and protected systems (Gracia and Rangel-Buitrago 2020; Santos et al. 2023).

The species is native to the Indo-Pacific region, extending from the Persian Gulf to the Philippines, and in adjacent areas, such as China and Japan (Baker et al. 2007). The mussel *P. viridis* has been introduced in different regions around the globe, mainly through ship hull fouling,

and its occurrence has been documented in the Northwest and Northeast Pacific, Oceania, South Africa, Gulf of Mexico, Caribbean, and Northwest Atlantic (Santos et al. 2023). In the early 1990s, the first records of the species introduction in South America were made in Trinidad and Tobago and, subsequently, it dispersed to Jamaica, Venezuela, Colombia, and the United States by the end of the decade (Baker et al. 2007). In the introduced areas, this species can cause significant negative impacts, including competition for space leading to displacement of native species and alterations in community structure. Additionally, there is a risk of transmitting diseases and parasites to local species, as well as harming other aquaculture species, such as crabs and mussels, by obstructing traps and cultivation bags (Gracia et al. 2011).

The exceptional invasive skills of *P. viridis* is primarily attributed to their physiology, characterized by a high rate of dispersion, phenotypic plasticity, rapid growth and recruitment, the competence to detach and re-attach with byssus, and the capacity to form dense clusters that alter the native ecosystem (Gobin et al. 2013). In addition to these characteristics, one of the main reasons for the competitive superiority of *P. viridis* is its high resistance to environmental stress. A study conducted by Lenz et al. (2011), comparing *Brachidontes exustus*, a native species from Caribbean, with the related non-indigenous species *P. viridis*, concluded that under stressful conditions, the non-native species exhibits a wider tolerance range. The mussel *P. viridis* tolerates a high level of particulate matter, a temperature range of 15°C to 32.5°C, and can even survive at a temperature of 39°C for about 200 minutes (Rajagopal et al. 2006).

Although *P. viridis* is recognized in the literature as a green-shelled mussel, with the color being one of the taxonomic characteristics used for its identification, it is not a reliable character. Micklem et al. (2016) concluded that specimens genetically identified as the variants of indigenous *P. perna* in South Africa displayed a wide range of shell colors, including blue-green. This finding indicates that the designations *P. viridis* as 'green mussel' and *P. perna* as 'brown mussel' are unsuitable for discerning these species. The only morphological differences found to separate the taxa in the study were the poorly developed mantle papillae and the wavy pallial line in *P. viridis*. Thus, the exclusive reliance on morphological characteristics can present challenges in identification. In certain cases, species are indistinguishable based on morphology alone, therefore, the use of DNA assumes significant relevance as a tool to confirm the species identification (Smith et al. 2022). In this context, this study aimed to confirm the presence of a new non-indigenous

mussel using molecular methods in southern Brazil with the purpose of compiling information about the species' expansion in the South Atlantic Ocean.

## Methods

The subtropical Paranaguá Bay Estuarine Complex, located in the extreme east of Paraná State, spans an area of 612 km<sup>2</sup>, making it the primary estuarine system in the state (Lana et al. 2001). The region, bordered by mangroves, marshes and extensive tidal flats, exhibits seasonal variation patterns of water circulation and stratification (Knoppers et al. 1987; Egres et al. 2012; Moreira-González et al. 2020). The estuary has an average depth of 5.4 meters and water residence time of 3.49 days (Lana et al., 2001). The salinity varies from 14.6 to 30.0 and temperatures range between 16.9 and 29.3°C. This area experiences a significant freshwater input, especially during the summer (rainy season, December to May), when freshwater discharge is five times higher than in winter (dry season, June to November) (Mantovanelli et al., 2004). The region holds considerable ecological and economic importance for the entire southern region (Bumbeer and Rocha, 2016), where numerous nautical structures, including marinas and ports, are situated. Notably, the Port Complex of Paraná represents the largest grain port in Latin America and the second largest public port in Brazil (Menem et al. 2019; Portos do Paraná 2023).

To confirm the species identification, on February 15, 2023, fourteen individuals possibly belonging to the species *P. viridis*, were sampled at a depth of 2 meters on the artificial structures of Ponta do Poço Marina Club (25°32'55"S and 48°23'19"W) (Figure 1). In the sampling area, some of the collected individuals were forming agglomerates (clusters), while others were individually dispersed. For species evaluation, the entire specimens, including shells and tissues, were carefully detached from the artificial substrata using a metal spatula, placed in plastic containers, and transported on ice to the laboratory, where they were stored in the freezer.

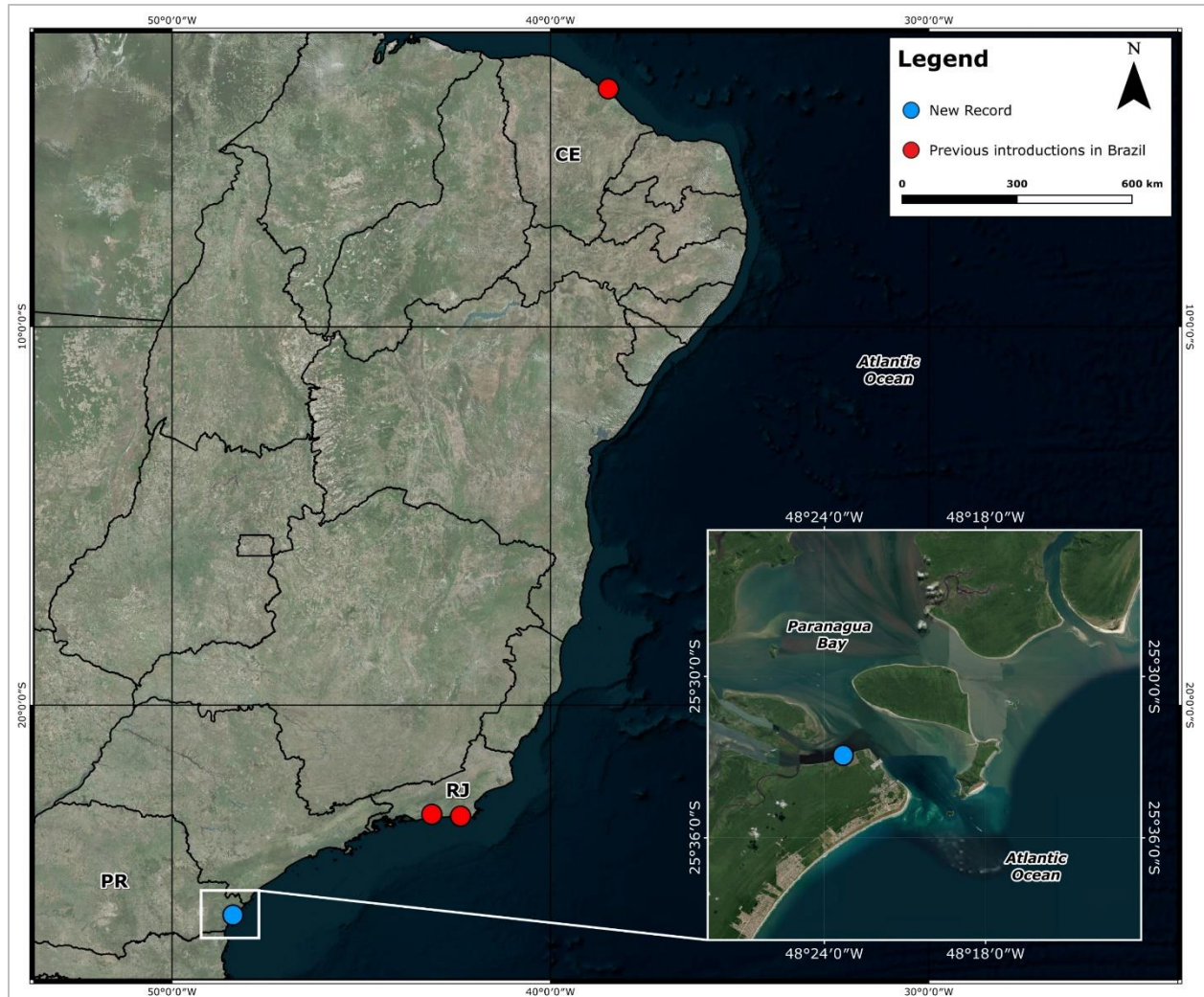


Figure 1. The range expansion of the Asian green mussel *Perna viridis* in Brazil. Red dots indicate areas where the mussel has already been recorded, and a blue dot marks the location of the new record in the Paranaguá Bay Estuarine Complex, southern Brazil. CE, Ceará. RJ, Rio de Janeiro. PR, Paraná.

The extraction of genomic DNA from the mussel samples was carried out using the commercial DNeasy Blood & Tissue kit (Qiagen, Germany). Subsequently, the DNA was quantified via spectrophotometry on the NanoQuant Infinite M200 Pro equipment (Tecan, Switzerland). The DNA was then used as a template for PCR amplification of the gene encoding for cytochrome oxidase subunit I (COI). For this, the primer forward dgLCO-1490 (5'-TAAACTTCAGGGTGACCAAARAYCA-3') and reverse dgHCO-2198 (5'-GGTCAACAAATCATAAAGAYATYGG-3') were used, according to Meyer (2003). The 25  $\mu$ l



PCR reaction consisted of: 1x SuperFi™ II Buffer (ThermoFisher Scientific), 0.2mM dNTP, 0.5mM of each primer, 1U Invitrogen™ Platinum™ SuperFi™ II DNA Polymerase (ThermoFisher Scientific), 50ng genomic DNA, and the final volume was adjusted with ultrapure water. The PCR reaction was conducted on the thermocycler (Veriti®, Applied Biosystems®), with the program: 94°C for 2min, 35 cycles of 94°C for 15sec, 58°C for 30sec, and 72°C for 30sec, with a final extension of 72°C for 2.5min. To confirm the amplification, the PCR products were evaluated through agarose gel electrophoresis (1%) and compared with the molecular marker DNA ( $\lambda$  Hind III, Invitrogen). The fragments were sequenced by the GoGenetics company, in both directions using the BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, USA), with the mentioned primers and the product evaluated on the ABI 3500x Genetic Analyzer (Applied Biosystems, USA) as described by the manufacturer.

The sequencing results were processed using the bioinformatics package CLC Genomics Workbench v. 6.5.2 (QIAGEN, Denmark). Initially, the sequences obtained in both directions were subjected to a step of eliminating low-quality segments (<Q30) using the Trim tool. Then, the shared regions between the two sequences were recognized and overlapped in order to obtain a single continuous segment of the COI gene, using the DNA Assemble tool. Finally, the obtained segment was then analyzed on the Barcode of Life Data System - BOLD Systems v.4 (RATNASINGHAM; HEBERT, 2007) portal in order to carry out the first molecular identification step. The sequence was compared to those available in the Species Level Barcode Records database. In this database, every COI barcode record with a species-level identification and a minimum sequence length of 500bp is included.

The second molecular identification of the mussel was done through a comparative analysis of its COI sequence and that of other specimens within the same genus, including the same species. This was done by searching for published COI sequences in the NCBI nucleotide bank that also had the location in which they were sampled from (Table 1). Then, their sequences were aligned using the ClustalW algorithm embedded in MEGA11 software. The Maximum Likelihood phylogenetic tree was then built in the same software, with sequences from *P. perna*, *P. viridis* and *P. canaliculus*, using the Hasegawa-Kishino-Yano model (HASEGAWA; KISHINO; YANO, 1985), and using *Aulacomya atra* as an outgroup. The test was made with the bootstrap method, using 1000 replications.

Table 1. All sequences used to build the phylogenetic tree, organized by species name, location from where it was collected, its GenBank Accession, its nucleotide length, and references. *P. viridis*, *Perna viridis*; *P. perna*, *Perna Perna*; *P. canaliculus*, *Perna canaliculus*.

Species	Location	Genbank Accession	Nucleotide length	Reference
<i>P. viridis</i>	Parana-Brazil	PP702447.1	608	-
<i>P. viridis</i>	Kochin-India	JN179068.1	650	(GILG et al., 2013)
<i>P. viridis</i>	Kochin-India	JN179072.1	650	(GILG et al., 2013)
<i>P. viridis</i>	Hong Kong	GQ497818.1	650	(GILG et al., 2013)
<i>P. viridis</i>	Hong Kong	JN179047.1	650	(GILG et al., 2013)
<i>P. viridis</i>	Singapore	HQ197379.1	650	(GILG et al., 2013)
<i>P. viridis</i>	Singapore	JN179049.1	650	(GILG et al., 2013)
<i>P. viridis</i>	Chennai - India	DQ917612.1	617	(WOOD et al., 2007)
<i>P. viridis</i>	Southern India	DQ917586.1	617	(WOOD et al., 2007)
<i>P. viridis</i>	Philippines	DQ917599.1	617	(WOOD et al., 2007)
<i>P. viridis</i>	Thailand	DQ917590.1	617	(WOOD et al., 2007)
<i>P. viridis</i>	Vietnam	DQ917584.1	617	(WOOD et al., 2007)
<i>P. perna</i>	Luanda-Angola	KC692001.1	614	(CUNHA et al., 2014)
<i>P. perna</i>	Punta D'Ouro-Mozambique	KC692009.1	614	(CUNHA et al., 2014)
<i>P. perna</i>	Swakopmund-Namibia	KC692005.1	614	(CUNHA et al., 2014)
<i>P. perna</i>	Muscat-Oman	KC692013.1	614	(CUNHA et al., 2014)
<i>P. perna</i>	Gans Bay-South Africa	KC691990.1	614	(CUNHA et al., 2014)
<i>P. perna</i>	Bizerte-Tunisia	KC691986.1	614	(CUNHA et al., 2014)
<i>P. perna</i>	Africa	DQ917618.1	617	(WOOD et al., 2007)
<i>P. perna</i>	Venezuela	DQ917588.1	617	(WOOD et al., 2007)
<i>P. perna</i>	Santa Catarina-Brazil	DQ917594.1	617	(WOOD et al., 2007)
<i>P. perna</i>	Sao Paulo-Brazil	DQ917592.1	617	(WOOD et al., 2007)
<i>P. canaliculus</i>	Houhora-New Zealand	DQ917607.1	617	(WOOD et al., 2007)
<i>P. canaliculus</i>	Castlepoint-New Zealand	DQ917613.1	617	(WOOD et al., 2007)
<i>P. canaliculus</i>	Gore Bay-New Zealand	DQ917608.1	617	(WOOD et al., 2007)
<i>P. canaliculus</i>	Fiordland-New Zealand	DQ917609.1	617	(WOOD et al., 2007)
<i>P. canaliculus</i>	Nelson-New Zealand	HG005373.1	706	(POCHON et al., 2013)
<i>Aulacomya atra</i>	Wellington-New Zealand	DQ917614.1	620	(WOOD et al., 2007)

## Results

Through the comparison of the mitochondrial gene COI from the mussel collected in Paranaguá Bay Estuarine Complex (*Perna viridis*, GenBank: PP702447.1), with sequences from all three species within the *Perna* genus, obtained from NCBI's nucleotide bank, it has been confirmed that the collected specimen corresponds to the exotic mussel *Perna viridis* (Linnaeus, 1758) (Figure 2 e Figure 3 ).

**New records. BRAZIL – Paraná • Paranaguá Estuarine Complex, Ponta do Poço Marina Club; 25°32'55"S, 48°23'19"W; 2 meters deep; 15.II.2023; E.I. Xavier leg.; artificial substrata; 14 spec.; metal spatula; UNIVALI collection (mol.PV1/PR).**

**Identification.** Green or bluish-green external color of shells; poorly developed mantle papillae; wavy S-shaped posterior pallial line; downward-pointing beak.



Figure 2. Left shell of *Perna viridis* sequenced for COI, collected in Paranaguá Estuarine Complex, Paraná, Brazil.

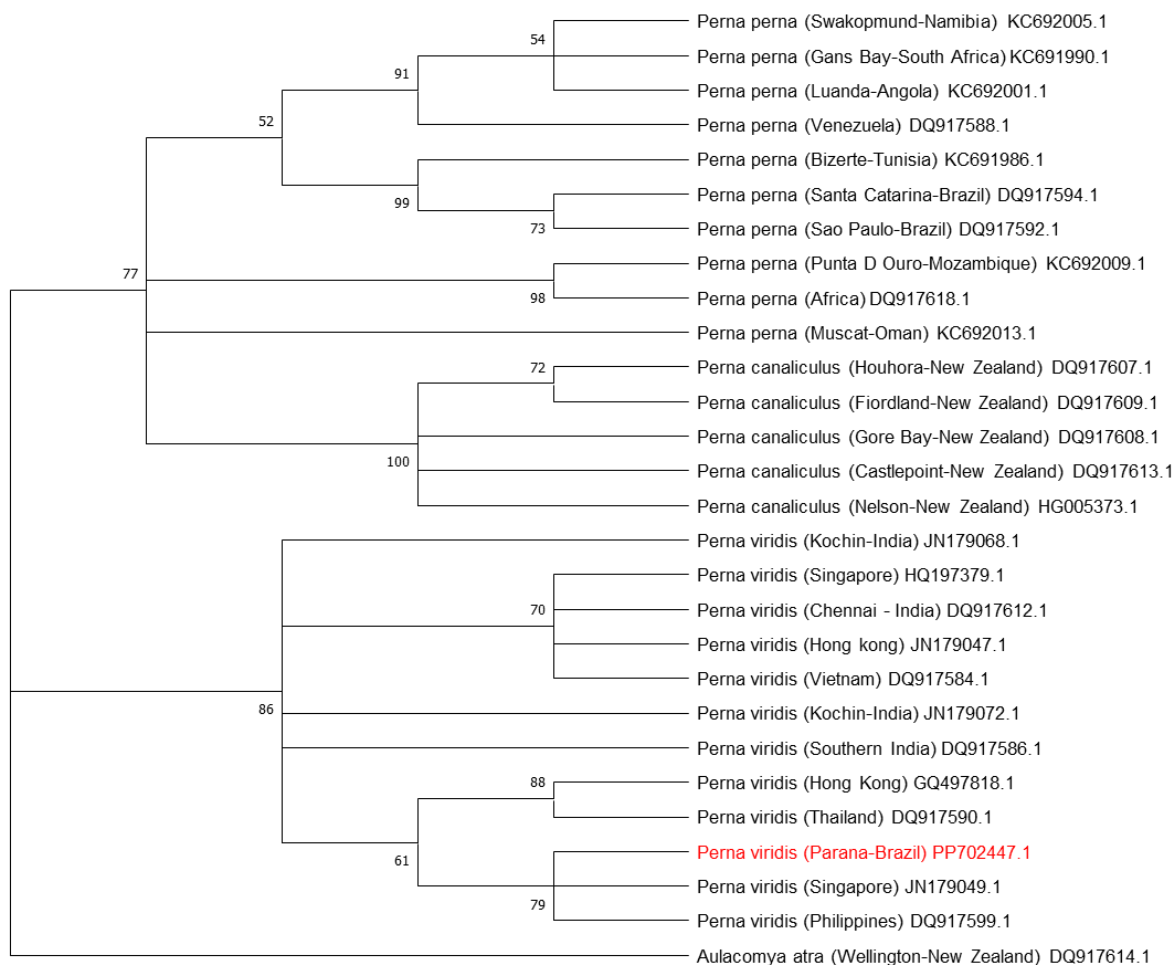


Figure 3. Maximum Likelihood phylogenetic tree (HKY+G+I) of various species within the genus *Perna*. Each node represents a different specimen's COI sequence, with its GenBank Accession and the location from where it was sampled from. Each branch has a label that represents its bootstrap percentage. Branches with less than 50% bootstrap value were condensed. This report's specimen is highlighted in red.

## Discussion

Based on the amplified COI gene, the present study is the first to confirm the occurrence of the exotic species *Perna viridis* in Brazil through molecular identification and represents the third Brazilian state where the presence of the mussel was recorded, expanding its range approximately 600 km south of the first recorded instance five years ago. The mussel has already been identified in the northeastern and southeastern regions of the Brazil (Messano et al. 2019; Soares et al. 2022;

Santos et al. 2023), and now its occurrence has been documented in the southern region, indicating that the country's coast presents optimal environmental conditions for the establishment and growth of the mussel. According to Siddall (1980), *P. viridis* has the capacity to disperse beyond its native range through step-wise larval dispersal or island hopping. However, due to the absence of rafting skills, members of the Mytilidae require vectors to move over long distances (Gracia and Rangel-Buitrago 2020). Due to these characteristics, ship ballast water and hull fouling have been identified as the main sources of the species' introduction (Bumbeer and Rocha 2016; Siriwardena 2022; Santos et al. 2023; Castro et al. 2023).

The activities associated with port operations represent one of the most significant impacts on coastal environments worldwide, leading to alteration of aquatic ecosystems and the increasing presence of non-indigenous species (Madon et al. 2023). Regardless of the Paranaguá Estuarine Complex being considered a preserved coastal environment (UNESCO 2014), the region is exposed to numerous anthropogenic impacts, including port activities that may facilitate the invasion of species. This trend was as noted in previous investigations in the area, which have indicated that the port acts as an entry point for non-indigenous species. Neves et al. (2007) identified in a marina near Paranaguá Port the presence of four introduced species and another 30 cryptogenic species. In the study conducted by Bumbeer and Rocha (2016), which compared the Paranaguá Estuarine Complex and the adjacent open coast, the results evidenced that percentage of non-indigenous species was more pronounced in the estuary. Additionally, Rocha and Kremer (2005) confirm that the area is susceptible to non-indigenous species invasion.

Therefore, considering the potential for bioinvasion in the Paranaguá Estuarine Complex, primarily due to port activity, associated with the dispersal characteristics of *P. viridis*, and the distances between records of the species' occurrence in Brazil, the most likely means of mussel introduction in the study area is accidental — via ballast water or ship hull fouling — rather than natural dispersal.

Despite extensive discussions surrounding invasive species, this issue is globally acknowledged as the second largest threat impacting biodiversity, and its negative consequences are generally irreversible (Loehle and Eschenbach 2012; Latini and Resende 2016; Stanski et al. 2022). Therefore, following the proposal of Pyšek et al. (2020), it is suggested to implement an

integrated national invasive alien species surveillance program on the Brazilian coast, as well as to continue monitoring along the southwest Atlantic coastline to verify the range expansion of *P. viridis*. Future steps should include advancing the discussion about the recruitment and growth of *P. viridis* populations, as well as interactions and impacts on native species in places where their occurrence has been confirmed. This is important because the influence of alien species varies notably across species, regions, and ecosystems (Blackburn et al. 2014).

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### **Authors' Contributions**

Conceptualization: MCB. Validation: FLD. Investigation: MCB, NJRC, YOL, TDS Resources: FLD. Writing - Original draft: MCB, NJRC, YOL, TDS. Writing - Review and Editing: MCB, NJRC, YOL. Supervision: MCB. Project administration: MCB. Funding Acquisition: FLD.

### **Conflicts of interest**

The authors confirm that there are no conflicts of interest.

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