

FIRST MOLECULAR RECORDS AND GENETIC LINKS AMONG *CRASPEDACUSTA SOWERBII* (CNIDARIA, HYDROZOA) POPULATIONS IN ARGENTINA AND BRAZILDeserti, M. I. <sup>(1, 2)</sup>, Guerín, D. M. A. <sup>(3)</sup>, Acuña, F. H. <sup>(1, 2)</sup> & Stampar, S. N. <sup>(4)</sup><sup>1</sup> Instituto de Investigaciones Marinas y Costeras (IIMyC -CONICET); Facultad de Cs. Exactas y Naturales, Universidad Nacional de Mar Del Plata, Mar Del Plata, Argentina. Email: desertiirene@gmail.com<sup>2</sup> Estación Científica Coiba (Coiba-AIP), Clayton, República de Panamá.<sup>3</sup> Escuela de Filosofía, Facultad de Filosofía y Humanidades, Universidad Nacional de Córdoba, Argentina.<sup>4</sup> Laboratory of Evolution and Aquatic Diversity (LEDALab), Bauru, São Paulo, Brazil.*C. sowerbii* fo San Luis province (Argentina SL (1-4))

Hotel Lake Canada BECA(H-100)  
Stowell Lake Canada - BECA(H-95)  
McKenzie Lake Canada 2 - BECA(H-93)  
Maltby Lake Canada - BECA(H-71)  
Killarney Lake Canada 2 - BECA(H-30)  
Klein Lake Canada - BECA(H-69)  
Killarney Lake Canada 1 - BECA(H-104)  
Nagano Japan 1 - CSNZ012  
Nagano Japan 2 - CSNZ013  
Nagano Japan 3 - CSNZ014  
Italy - MH230079.1  
Brazil 4 - Ariranha do Ivaí Parana M7  
Chile 29 - MF177122.1  
Chile 15 - MF177116.1  
Chile 31 - MF177133.1  
Chile 33 - MF177131.1  
Chile 20 - MF177111.1  
Chile 1 - MF177110.1  
Chile 10 - MF177101.1  
Chile 19 - MF177112.1  
Chile 24 - MF177127.1  
Chile 27 - MF177124.1  
Chile 5 - MF177106.1  
Chile 25 - MF177126.1  
Chile 17 - MF177114.1  
Chile 22 - MF177129.1  
Chile 18 - MF177113.1  
Chile 2 - MF177109.1  
Chile 23 - MF177128.1  
Chile 14 - MF177117.1  
Chile 28 - MF177123.1  
Chile 6 - MF177105.1  
Chile 26 - MF177125.1  
Chile 9 - MF177102.1  
Chile 13 - MF177118.1  
Chile 32 - MF177132.1  
Chile 30 - MF177121.1  
Chile 16 - MF177115.1  
Chile 8 - MF177103.1  
Chile 7 - MF177104.1  
Chile 12 - MF177119.1  
Chile 11 - MF177120.1  
Chile 4 - MF177107.1  
Chile 3 - MF177108.1  
Chile 21 - MF177130.1  
Brazil - Ariranha do Ivaí Parana M11  
Brazil 3 - Ariranha do Ivaí Parana M8  
Argentina SL (3)  
Brazil 2 - Ariranha do Ivaí Parana M10  
Argentina SL (4)  
Argentina SL (1)  
Argentina SL (2)  
Crim Dell Lake Canada - BECA(H-59)  
McKenzie Lake Canada 1 - BECA(H-94)  
Glen Lake Canada 1 - BECA(H-84)  
Florence Lake Canada - BECA(H-78)  
Dawangling Hainan China 1 ???  
Dawangling Hainan China 2 - HNSM-BT  
Brazil 8 - Videira, Santa Catarina SC2  
Brazil 7 - Videira, Santa Catarina SC3  
Brazil 6 - Videira, Santa Catarina SC4  
Brazil 5 - Videira, Santa Catarina SC5  
Brazil 9 - Videira, Santa Catarina SC1  
Singapore - CSS001  
China 1 - KF510026.1  
Germany 2 - FJ423613.1  
Germany 4 - FJ423618.1  
Germany 8 - FJ423620.1  
Germany 6 - FJ423615.1  
Morocco 2 - MK600508.1  
Morocco 1 - MK600509.1  
Germany 5 - FJ423617.1  
Germany 1 - FJ423616.1  
Germany 7 - FJ423614.1  
Germany 3 - FJ423619.1  
Olindias 2 phosphorica  
Olindias 3 muelleri  
Olindias sambaquiensis

## INTRODUCTION &amp; AIM

*Craspedacusta sowerbii* Lankester, 1880, is a freshwater hydromedusa native to the Yangtze River in China, recognized for its remarkable invasiveness and widespread global distribution. In South America, records of *C. sowerbii* remain scarce and scattered, and there is a marked lack of information on its genetics, ecology, and effects on local communities. This lack of data not only limits our understanding of its population dynamics but also our ability to identify its colonization events and its phylogenetic and biogeographic relationships with congeners from other regions of the world. This knowledge gap restricts assessments of its potential impact on continental freshwater ecosystems, including its effects on trophic structure and the composition of native fauna.

## METHOD

*C. sowerbii* was collected at Dique Berta Vidal de Battini (33°10'15.1" S, 66°09'17.5" W), San Luis Province, Argentina, Ariranha do Ivaí (24°24'38"S, 51°34'45"W), and Videira (27°04'23"S, 51°06'24"W), Paraná and Santa Catarina respectively, from Brazil. The whole genome was extracted using the EasyPure® Genomic DNA Kit (TransGen Biotech) protocol. Subsequently, we used mlCOLintF (Leray et al. 2013) and jgHCO2198 (Geller et al. 2013) primers to obtain the region of the cytochrome c oxidase subunit I (COI) fragments of ~370 bp. The purified DNA was processed using the Ludwig Biotechnologia kit, followed by Sanger sequencing through an outsourced service. Forward and reverse sequences were assembled and edited using Geneious Prime version 2023.0.4 (Kearse et al. 2012). The COI sequence datasets were aligned in MAFFT v7.53 using the L-INS-I algorithm and "--maxiterate 1000" option (Katoh et al. 2009). Maximum likelihood (ML) reconstruction was performed using IQ-Tree2 (Minh et al. 2020). Branch support was assessed through 1000 SH-like approximate likelihood ratio test (SH-aLRT) replicates (Guindon et al. 2010), 1000 ultrafast bootstrap (UFBoot2) replicates (Hoang et al. 2018), as well as parametric aLRT (Anisimova and Gascuel 2006), and approximate Bayes tests (Anisimova et al. 2011). The resulting trees were edited and visualized using TreeGraph v2 (Stöver & Müller 2010).

## RESULTS &amp; DISCUSSION

The phylogenetic analysis showed that the **Argentina** sequences form a well-supported clade together with **Brazilian** samples from Paraná, suggesting a biogeographic connection and genetic cohesion among these groups. These samples also integrate into a broader lineage that includes records from **Chile, Japan, Italy, and Canada**, reaffirming the cosmopolitan nature and invasive potential of *C. sowerbii*. The differences observed between the Santa Catarina and Paraná populations could be attributed to several factors: geographic barriers and distinct hydrographic basins that limited direct genetic exchange. The genetic proximity among Argentina, Paraná, and Chile may reflect both historical dispersal and human-mediated colonization. In contrast, the genetic divergence observed in the Santa Catarina population could be explained not only by its isolation due to natural barriers but also by following a dispersal route different from Paraná and Argentina, which has kept it more genetically separated.

## CONCLUSION

These preliminary results should be interpreted with caution, as they are based on a single marker and a limited number of samples. However, given the ecological impact of the species, monitoring its presence is crucial to understanding potential alterations in local communities. This context highlights the importance of expanding molecular and ecological studies, integrating hydrological and anthropogenic information, which will guide management strategies that respect regional conservation practices. This study represents an essential starting point for understanding the genetic structure, dispersal pathways, and potential ecological impact of *C. sowerbii* in South American freshwater ecosystems. It also highlights the importance of assessing its influence in this region, where information on invasive cnidarians and their ecological consequences remains scarce. Evaluating the impact of *C. sowerbii* is crucial for understanding how non-native species can alter community composition, trophic dynamics, and the integrity of biodiversity in the region.

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