Marine and Fishery Sciences 39 (1): xxx-xxx (2026)
https://doi.org/10.47193/mafis.3912026010111

POINTS OF VIEW

Closing the genomic gap: the need for coordinated fish genomics in Argentina

Alejandro S. Mechaly[1, 2, 3, *] and Yamila P. Cardoso[3, 4]

[1]Instituto de Investigaciones en Biodiversidad y Biotecnología (INBIOTEC-CONICET), Mar del Plata, Argentina. [2]Fundación para Investigaciones Biológicas Aplicadas (FIBA), Mar del Plata, Argentina. [3]Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Buenos Aires, Argentina. [4]Laboratorio de Sistemática y Biología Evolutiva, Facultad de Ciencias Naturales y Museo (FCNyM), Universidad Nacional de La Plata (UNLP), Paseo del Bosque S/N, B1900FWA - La Plata, Argentina.
ORCID *Alejandro S. Mechaly* https://orcid.org/0000-0002-4396-0955

ABSTRACT. Fish genomics has become an essential tool to explore the genetic basis of biological processes, such as biodiversity, evolution, and adaptation, as well as for direct applications in conservation, aquaculture, and fisheries management. Argentina, home to more than 1,100 fish species and diverse aquatic ecosystems, holds enormous potential for genomic research. Although historically underrepresented in global databases, recent progress (including genome sequencing of commercially and ecologically important species) signals growing momentum in the field. This note provides an overview of the current state of fish genomics in Argentina, highlights notable contributions, and underscores the need for high-quality genome assemblies, national coordination, and broader taxonomic coverage to ensure that the country's biodiversity is adequately represented and preserved.

Key words: Conservation genetics, aquaculture genomics, genetic diversity, fisheries, genome.

Cerrando la brecha genómica: la necesidad de una genómica de peces coordinada en Argentina

RESUMEN. La genómica de peces se ha consolidado como una herramienta clave para comprender los procesos biológicos fundamentales, como la biodiversidad, la evolución, la adaptación, pero también en aplicaciones directas en conservación, acuicultura y manejo pesquero. Argentina, con más de 1.100 especies de peces y una gran diversidad de ecosistemas acuáticos, presenta un enorme potencial para el desarrollo de estudios genómicos. Aunque históricamente subrepresentado en las bases de datos globales, el país ha comenzado a generar avances significativos (incluyendo la secuenciación de especies de importancia comercial y ecológica). Esta nota resume el estado actual de la genómica de peces en Argentina, destaca aportes relevantes y enfatiza la necesidad de promover ensamblajes genómicos de calidad, esfuerzos nacionales coordinados y una mayor cobertura taxonómica para preservar adecuadamente la biodiversidad acuática del país.

Palabras clave: Genética de la conservación, genómica en acuicultura, diversidad genética, pesquerías, genoma.

*Correspondence:
amechaly@inbiotec-conicet.gob.ar

Received: 12 August 2025
Accepted: 9 December 2025

ISSN 2683-7595 (print)
ISSN 2683-7951 (online)

https://ojs.inidep.edu.ar

Journal of the Instituto Nacional de Investigación y Desarrollo Pesquero (INIDEP)

Fish genomics has become a fundamental tool for exploring the genetic basis of physiological functions and biodiversity in aquatic species, offering critical insights for both basic and applied research. Over the past two decades, global initiatives such as the Vertebrate Genomes Project (Rhie et al. 2021), Fish-T1K (Fan et al. 2020), and large-scale teleost sequencing consortia have revolutionized the field, producing hundreds of high-quality reference genomes that serve as baselines for comparative and conservation studies. Together with recent global reviews summarizing the current landscape of fish genomics (e.g. Hughes et al. 2018; Lu and Luo 2020), these initiatives have established a robust framework for understanding fish biodiversity, adaptation, and applied genomic innovation across taxa.

In Argentina, a country distinguished by its rich aquatic biodiversity and wide array of freshwater and marine ecosystems, genomic approaches have the potential to significantly advance the understanding and preservation of native fish species. The country's diverse habitats, from the extensive freshwater basins of the Paraná and Uruguay rivers to the vast Atlantic coastline, support a broad range of fish species, many of which are endemic or of high ecological and economic relevance (Hirt-Chabbert et al. 2024). Unfortunately, many fish groups remain poorly studied, and it is estimated that various new species remain to be discovered. New molecular tools have boosted integrative taxonomic studies, attempting to address this gap in basic knowledge of the country's ichthyology (Cardoso et al. 2016, 2019).

The enormous potential of genomics-based studies lies in the generation of large databases that allow addressing both basic aspects of species biology and more applied aspects for the community. In addition to clarifying evolutionary relationships, genomic datasets are increasingly used to assess adaptive variation, monitor endangered species, and design genetic improvement programs in aquaculture. Fish represent the most species-rich group of vertebrates, with more than 35,000 recognized species worldwide (Fricke et al. 2025), and they perform essential functions in aquatic ecosystems. A number of fish species are threatened and are sensitive indicators of environmental health. Millions of people consume fish as a fundamental source of animal protein, and fishing plays an important role in the cultures, traditions, arts, and recreation (such as sport fishing) of many societies around the world.

The first whole-genome sequencing of a fish species, the tiger pufferfish (*Fugu rubripes*), was published in 2002, marking a landmark achievement in vertebrate genomics (Volf 2002). Since then, genome sequencing efforts have expanded across ichthyological diversity, propelled by rapid technological advancements and large-scale international initiatives (Mechaly et al. 2024). Globally, more than 3,000 fish genomes have been sequenced and deposited in public repositories such as NCBI, Ensembl, and DDBJ. These genomic resources span a wide spectrum of quality (from low-coverage drafts to high-quality, chromosome-level assemblies) and the number continues to grow rapidly as new projects and species are incorporated. However, despite this progress, the distribution of genomic resources remains highly uneven, with a strong bias toward northern hemisphere taxa and model species. Nevertheless, these initiatives have established international standards for genomic quality and data sharing, providing a framework that could guide similar coordinated efforts in less advanced regions of the world.

Argentina, which hosts 1,135 fish species, including native, introduced, and exotic taxa, remains notably underrepresented in this global genomic landscape (Bauni et al. 2022). To the best of our knowledge, genome sequencing has been reported for only 17 species, accounting for less than 1.5% of the country's ichthyofauna (Table 1). Neighboring South American countries such as Brazil and Chile have made substantial progress in generating and depositing fish genomes in public repositories, highlighting the importance of establishing similar national strategies in Argentina. Moreover, many of these Argentine assemblies remain in draft or unassembled form, limiting their practical utility for conservation genetics, selective breeding, and studies on adaptation and evolutionary biology. This situation reflects both funding limitations and the absence of coordinated genomic infrastructure across national research institutions. This disparity highlights the need for coordinated national efforts to expand genomic coverage, improve data quality,

Table 1. Genomic information available for fish species from Argentina. List of species with sequenced genomes, their main applications, and current status of genomic analysis.

Species (scientific name)	Common name (Spanish/English)	Application area	Genome status	References
Odontesthes bonariensis	Pejerrey/silverside	Fisheries, aquaculture, conservation	Draft genome (assembled, annotation)	Campanella (2014)
Piaractus mesopotamicus	Pacú/pacu	Fisheries, aquaculture	High-quality genome (assembled and annotated)	Mascali et al. (2022, 2024)
Paralichthys orbignyanus	Lenguado negro/black flounder	Fisheries, aquaculture	Draft genome (assembled, annotation)	Villarreal et al. (2024)
Salminus brasiliensis	Dorado	Fisheries, conservation	High-quality genome (assembled and annotated)	Graciano et al. (2022)
Dissostichus eleginoides	Merluza negra/ Patagonian toothfish	Fisheries	Draft genome (assembled, annotation)	Ryder et al. (2024)
Merluccius hubbsi	Merluza/Argentine hake	Fisheries	Draft genome (assembled, annotation)	Roa-Varon and Pirro (2022)
Lepidosiren paradoxa	Pez pulmonado sudamericano/South American lungfish	Evolutionary studies	High-quality genome (assembled and annotated)	Schartl et al. (2024)
Cichlasoma dimerus	Chanchita/dimerus cichlid	Reproductive behavior, nutritional and ecotoxicological studies	Illumina sequencing data available (not assembled)	Mechaly unpublished
Prochilodus lineatus	Sábalo/streaked prochilod	Fisheries	Draft genome (assembled, annotation)	Yazbeck et al. (2025)
Galaxias maculatus	Puyén/galaxiid	Fisheries	Draft genome (assembled, annotation)	Hughes et al. (2018)
Seriola lalandi	Pez limón/yellowtail kingfish	Fisheries, aquaculture	Draft genome (assembled, annotation)	Li et al. (2022)
Cnesterodon decemmaculatus	Madrecita de agua/toothed guppy	Conservation, bioindicator species	Illumina sequencing data available (not assembled)	Mechaly unpublished
Cynoscion guatucupa	Pescadilla/stripped weakfish	Fisheries	Illumina sequencing data available (not assembled)	Mechaly unpublished
Mustelus schmitti	Gatuzo/narrownose smooth-hound shark	Fisheries, conservation	Illumina sequencing data available (not assembled)	Mechaly unpublished
Cottoperca trigloides	Patagonian rock cod	Fisheries	High-quality genome (assembled and annotated)	Bista et al. (2020)
Eleginops maclovinus	Robalo/Patagonian blenny	Fisheries	High-quality genome (assembled and annotated)	Cheng et al. (2023)
Pagrus pagrus	Besugo/red porgy	Fisheries, aquaculture	High-quality genome (assembled and annotated)	Darwin Tree of Life Project/PRJEB87564

Note: Species listed here are those for which genomic data are available, and which are known to occur in Argentina. However, other native or introduced species, especially those with broad distributions shared with other countries, may have been sequenced by international groups but have not yet been publicly released. Common names correspond to the vernacular names used in Argentina.

and ensure that Argentina's rich aquatic biodiversity is adequately represented in global genomic initiatives.

Over the last decade, fish species inhabiting Argentina have been studied using next-generation sequencing (NGS) technologies, particularly those of commercial and biological importance. Key aquaculture and fisheries species such as silverside (*Odontesthes bonariensis*) (Campanella 2014), pacu (*Piaractus mesopotamicus*) (Mascali et al. 2022, 2024), streaked prochilod (*Prochilodus lineatus*) (Yazbeck et al. 2025) and black flounder (*Paralichthys orbignyanus*) (Villarreal et al. 2024) have been the focus of whole-genome sequencing initiatives. These projects represent important milestones that demonstrate the feasibility of genomic research in South America despite economic and logistical limitations. Some of these advances were enabled by substantial investments from neighboring countries in national sequencing programs and training networks, such as Brazil's Embrapa Genomics initiative or Chile's Marine Genomics consortium. Incorporating Argentina into comparable collaborative frameworks would enhance regional representation and data sharing across South America, fostering a more integrated genomic landscape for Neotropical fish diversity.

Genomes of heavily exploited marine species, including the Patagonian toothfish (*Dissostichus eleginoides*) (Ryder et al. 2024) and hake (*Merluccius hubbsi*) (Roa-Varon and Pirro 2022), have also been sequenced (exclusively by international research groups) with no reported participation from Argentine institutions. While these genomic resources are critical for population structure analyses, stock assessment, and sustainable fisheries management, data, results, and conclusions drawn are all foreign. Developing local sequencing capacity capable of generating long-read and chromosome-level assemblies (e.g. PacBio HiFi or Oxford Nanopore) would represent a major step toward scientific independence and sustainability. In addition, strengthening bioinformatic infrastructure and training programs is essential. Access to high-performance computing and expertise in assembly, annotation, and population-genomic analyses will ensure that genomic data are efficiently used for conservation and aquaculture improvement. In these cases, the need to strengthen national capacities to actively contribute to international genomic initiatives that ensure the sustainable use of native species and national natural resources is highlighted.

Beyond commercially important taxa, genomic and transcriptomic data have been generated for species of ecological or evolutionary interest, such as the South American lungfish (*Lepidosiren paradoxa*) (Schart et al. 2022), toothed guppy (*Cnesterodon decemmaculatus*), and Dimerus cichlid (*Cichlasoma dimerus*), contributing to the understanding of phylogenetic relationships and adaptive evolution. Additional species, including narrownose smooth-hound shark (*Mustelus schmitti*), stripped weakfish (*Cynoscion guatucupa*), and galaxiid (*Galaxias maculatus*) have been included in preliminary genomic or transcriptomic surveys (see Table 1 for more details). Finally, cosmopolitan species with native populations in Argentina, such as the yellowtail kingfish (*Seriola lalandi*), possess chromosome-level genome assemblies and extensive genetic resources. These have been recently reviewed in detail by Mechaly et al. (2025). Collectively, these efforts underscore the growing momentum of fish genomics in Argentina and highlight the importance of expanding genomic initiatives to encompass a broader range of taxa, thereby enhancing the representation of the country's ichthyological diversity in global databases. Argentina's fish genomic representation is still well below the global average, indicating a critical gap between the country's diversity and what has been studied**.** Prioritizing species and coordinating national initiatives require greater investment in high-quality genome assemblies. A national repository or open-access database, linked to international platforms such as NCBI or Ensembl, would also facilitate data visibility and collaboration.

Beyond filling taxonomic gaps, genomic data provides an essential link between ecological, evolutionary, and applied research. They enable the study of local adaptation, population divergence, and speciation, while offering tools for sustainable fisheries management, aquaculture innovation, and biodiversity conservation. Integrating these perspectives will maximize the impact of genomic initiatives across Argentina's diverse aquatic ecosystems Recent genomic studies in Argentina have paved the way for more robust and comprehensive research, but resources and training need to be strengthened. Expanding local expertise in bioinformatics, molecular ecology, and evolutionary genomics will be critical to bridge the gap between field research and data interpretation. These efforts are not only vital for unraveling the genetic diversity and evolutionary history of native species but also for addressing pressing challenges in conservation, sustainable fisheries management, and aquaculture improvement. Moving forward, the expansion of genomic resources and collaborative projects will be essential to position Argentina as an active contributor to the global fish genomics landscape, ensuring that its rich aquatic biodiversity is adequately represented and preserved for future generations.

Author contributions

Alejandro S. Mechaly: conceptualization; writing-original draft; writing-review and editing. Yamila P. Cardoso: writing-review and editing.

REFERENCES

Bauni V, Bertonatti C, Giacchino A, Schivo F, Mabragaña E, Roesler I, Rosso JJ, Teta P, Williams JD, Abba AM, et al. 2022. Biodiversity of vertebrates in Argentina: patterns of richness, endemism and conservation status. ZooKeys. 1085: 101-127. DOI: https://doi.org/10.3897/zookeys.1085.76033

Bista I, McCarthy SA, Wood J, Ning Z, Detrich III HW, Desvignes T, Postlethwait J, Chow W, Howe K, Torrance J, et al. 2020. The genome sequence of the channel bull blenny, *Cottoperca gobio* (Günther, 1861). Wellcome Open Res. 5: 148. DOI: https://doi.org/10.12688/wellcomeopenres.16012.1

Campanella D. 2014. Evolutionary history and whole genome sequence of pejerrey (*Odontesthes bonariensis*): new insights into sex determination in fishes [PhD thesis]. Washington: The George Washington University. https://scholarspace.library.gwu.edu/etd/mp48sd085.

Cheng CHC, Rivera-Colón AG, Minhas BF, Wilson L, Rayamajhi N, Vargas-Chacoff L, Catchen JM. 2023. Chromosome-level genome assembly and circadian gene repertoire of the Patagonia blennie *Eleginops maclovinus*, the closest ancestral proxy of Antarctic Cryonotothenioids. Genes. 14:1196. DOI: https://doi.org/10.3390/genes14061196

Fan G, Song Y, Yang L, Huang X, Zhang S, Zhang M, Yang X, Chang Y, Zhang H, Li Y, et al. 2020. Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). Gigascience. 9 (8): 80. DOI: https://doi.org/10.1093/gigascience/giaa080

Fricke R, Eschmeyer WN, Van der Laan R, editors. 2025. Eschmeyer's catalog of fishes: genera, species, references. http://researcharchive.calacademy.org/research/ichthyology/catalog/fishcatmain.asp.

Cardoso YP, Brancolini F, Paracampo AH, Lizarralde MS, Covain R, Montoya-Burgos JI. 2016. *Hypostomus formosae*, a new catfish species from the Paraguay river basin with redescription of *H. boulengeri* (Siluriformes: Loricariidae). Ichthyol Explor Freshw. 27: 9-23.

Cardoso YP, Brancolini F, Protogino L, Paracampo A, Bogan S, Posadas P, Montoya-Burgos JI. 2019. An integrated approach clarifies the cryptic diversity in *Hypostomus* Lacépède 1803 from the Lower La Plata Basin. An Acad

Bras Cienc. 91 (2): e20180131. DOI: https://doi.org/10.1590/0001-3765201920180131

GRACIANO RCD, OLIVEIRA RS, SANTOS IM, YAZBECK GM. 2022. Genomic resources for *Salminus brasiliensis*. Front Genet. 13: 855718. DOI: https://doi.org/10.3389/fgene.2022.855718

HIRT-CHABBERT JA, MECHALY AS, TAPIA C. 2024. Seafood in Argentina: marine fish species, seasonal occurrence and prices. Rev Fish Biol Fish. 34 (2): 753-774. DOI: https://doi.org/10.1007/s11160-024-09836-4

HUGHES LC, ORTÍ G, HUANG Y, SUN Y, BALDWIN CC, THOMPSON AW, ARCILA D, BETANCUR-R R, LI C, BECKER L, et al. 2018. Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data. Proc Natl Acad Sci USA. 115 (24): 6249-6254. DOI: https://doi.org/10.1073/pnas.1719358115

LI S, LIU K, CUI A, HAO X, WANG B, WANG H-Y, JIANG Y, WANG Q, FENG B, XU Y, et al. 2022. Chromosome-level genome assembly of yellowtail kingfish (*Seriola lalandi*). Front Genet. 12: 825742. DOI: https://doi.org/10.3389/fgene.2021.825742

LU G, LUO M. 2020. Genomes of major fishes in world fisheries and aquaculture: status, application and perspective. Aquac Fish. 5 (4): 163-173. DOI: https://doi.org/10.1016/j.aaf.2020.05.004

MASCALI FC, MASTROCHIRICO-FILHO VA, POSNER VM, RUBIOLO JA, HASHIMOTO DT, VILLANOVA GV. 2024. High-quality genome assembly and annotation of the pacu *Piaractus mesopotamicus*: an aquatic genetic resource of South American aquaculture. Aquacult Int. 32: 8981-9003. DOI: https://doi.org/10.1007/s10499-024-01601-5

MASCALI FC, POSNER VM, ROMERO MARANO EA, DEL PAZO F, HERMIDA M, SÁNCHEZ S, MAZZONI TS, MARTINEZ P, RUBIOLO JA, VILLANOVA GV. 2022. Development and validation of sex-specific markers in *Piaractus mesopotamicus*. Aquaculture. 558. DOI: https://doi.org/10.1016/j.aquaculture.2022.738374

MECHALY AS, AWRUCH C, CABRITA E, COSTAS B, FERNANDES JMO, GALLEGO V, HIRT- CHABBERT J, KONSTANTINIDIS I, OLIVERA C, RAMOS-JÚDEZ S, et al. 2024. Cutting-edge methods in teleost and chondrichthyan reproductive biology. Rev Fish Sci Aquac. 33 (1): 77-112. DOI: https://doi.org/10.1080/23308249.2024.2377999

MECHALY AS, ELIZUR A, ESCOBAR-AGUIRRE S, HIRT-CHABBERT J, INOHUYE RIVERA RB, KNIBB W, NOCILLADO J, PÉREZ-URBIOLA JC, PREMACHANDRA HKA, SOMOZA GM, et al. 2025. Yellowtail kingfish (*Seriola lalandi*) aquaculture: current situation, challenges, and future perspectives. Rev Aqua. 17: e70034. DOI: https://doi.org/10.1111/raq.70034

RHIE A, MCCARTHY SA, FEDRIGO O, DAMAS J, FORMENTI G, KOREN S, ULIANO-SILVA M, CHOW W, FUNGTAMMASAN A, KIM J, et al. 2021. Towards complete and error-free genome assemblies of all vertebrate species. Nature. 592: 737-746. DOI: https://doi.org/10.1038/s41586-021-03451-0

ROA-VARON A, PIRRO S. 2022. The complete genome sequences of 18 species of Gadiformes (Actinopterygii, Chordata). Biodivers Genomes. DOI: https://doi.org/10.56179/001c.56079

RYDER D, STONE D, MINARDI D, RILEY A, AVANT J, CROSS L, SOEFFKER M, DAVIDSON D, NEWMAN A, THOMSON P, et al. 2024. De novo assembly and annotation of the Patagonian toothfish (*Dissostichus eleginoides*) genome. BMC Genomics 25: 233. DOI: https://doi.org/10.1186/s12864-024-10141-4

SCHARTL M, WOLTERING JM, IRISARRI I, DU K, KNEITZ S, PIPPEL M, BROWN T, FRANCHINI P, LI J, LI M, et al. 2024. The genomes of all lungfish inform on genome expansion and tetrapod evolution. Nature. 634: 96-103. DOI: https://doi.org/10.1038/s41586-024-07830-1

YAZBECK GM, SANTANA NASCIMENTO GA, CAMPOS CARVALHO L, DIAS GRACIANO RC, DE PAULA SANTOS R, OLIVEIRA RS. 2025. A fractal pattern of hierarchical genetic population structure in mixed stocks across fish segregated by dams revealed by genomic resources for curimba *Prochilodus lineatus*. bioRxiv 2025.03.14.643328. DOI: https://doi.org/10.1101/2025.03.14.643328

Villarreal F, Burguener GF, Sosa E, Stocchi N, Somoza GM, Turjanski A, Blanco A, Viñas J, Mechaly AS. 2024. Genome sequencing and analysis of black flounder (*Paralichthys orbignyanus*) reveals new insights into Pleuronectiformes genomic size and structure. BMC Genomics. 27: 297. DOI: https://doi.org/10.1186/s12864-024-10081-z

Volff JN. 2002. The compact pufferfish genome. Genome Biol. 3: 59. DOI: https://doi.org/10.1186/gb-2002-3-11-reports0059