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# A decade of open biodiversity data in the Azores: closing knowledge gaps and building a foundation for long-term monitoring

**Guilherme Oyarzabal, Ricardo Costa, Rosalina Gabriel, Pedro Afonso, Claudine Ah-Peng, Nuno Vaz Álvaro, Isabel Amorim, Rui Andrade, José Azevedo, Enric Ballesteros, Luís Barcelos, João Barreiros, Mário Boieiro, Isabel Borges, Andrea Botelho, Mariana Brito, Eva Cacabelos, Hugo Calado, Pedro Cardoso, Rui Carvalho, Márcia Coelho, Rúben Coelho, Rita Cordeiro, Ana Costa, Carina Costa, Luís Crespo, Eva Cuesta, Alexandra Dal Lago, Almudena Duenas-Rojas, Rui Elias, William Farnham, Maria Teresa Ferreira, Robert Fletcher, Amélia Fonseca, Jorge Frias, Laura González García, Artur Gil, Vítor Gonçalves, Sofia Goulart, Ruben Heleno, Débora Henriques, Lucas Lamelas-Lopez, Abrão Leite, Sébastien Lhoumeau, David Lopes, Gábor Lövei, Rúben Luz, Jagoba Malumbres-Olarte, José Marcelino, Catarina Melo, David Milla-Figueras, Paulo Monjardino, Sandra Monteiro, Ignacio Moreu, Leila Morgado, José Mota, Raul Neto, Elisabete Nogueira, Rui Nunes, Manuela Parente, Laurine Parmentier, Rita Patarra, Enésima Pereira, Fernando Pereira, Maria Pereira, Andrea Petrone, César Pimentel, Silvia Poponessi, Gabor Pozsgai, Afonso Prestes, Pedro Raposeiro, Roberto Resendes, François Rigal, Ana Rodrigues, António Rodrigues, Alejandra Ros-Prieto, Ana Santos, Michael Schülke, Cecília Sérgio, Luís Silva, Lurdes Silva, Gabriela Silveira, Nelson Simoes, Manuela Sim-Sim, António Soares, Mariana Sousa, Martin Souto, Peter Stüben, Stephanie Suciu, João Tavares, Mário Teixeira, Noelline Tsafack, Duarte Toubarro, Virgílio Vieira, Martha Vounatsi,**

**Sophie Wallon,** **Paulo Borges**

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# A decade of open biodiversity data in the Azores: closing knowledge gaps and building a foundation for long-term monitoring

Guilherme Oyarzabal[‡,§], Ricardo Costa[‡,|,§], Rosalina Gabriel[‡], Pedro Afonso[¶,#], Claudine Ah-Peng[¤], Nuno Vaz Álvaro[«,»], Isabel R. Amorim[^,˅], Rui C. A. Andrade[‡], José M. N. Azevedo[¶], Enric Ballesteros[¦], Luís M. D. Barcelos[‡], João P. Barreiros[‡,⁷], Mário Boieiro[ˆ,˅], Isabel Borges[¢], Andrea Z. Botelho[ℓ], Mariana R. Brito[�unk], Eva Cacabelos[℗,Ⱥ], Hugo R. M. Calado[¢], Pedro Cardoso[ƨ,ı], Rui Carvalho[F,ı], Márcia C. M. Coelho[‡], Rúben Coelho[₮], Rita Cordeiro[ℓ], Ana C. Costa[ℓ], Carina Costa[₦], Luís C. Crespo[‡], Eva Cuesta[Ⱪ], Alexandra Dal Lago[₲], Almudena Duenas-Rojas[ʔ,Ⱪ], Rui B. Elias[‡], William Farnham[₩], Maria Teresa Ferreira[₸,ǂǂ], Robert L. Fletcher[₩], Amélia Fonseca[§§], Jorge Frias[ǁ], Laura González García[¶,¶¶], Artur Gil[###,¢], Vítor Gonçalves[ℓ], Sofia Goulart[�unk], Ruben Heleno[¤¤], Débora S. G. Henriques[««], Lucas Lamelas-Lopez[‡], Abrão Leite[»»], Sébastien Lhoumeau[‡], David H. Lopes[‡], Gábor Lövei[ˆˆ,‡], Rúben Luz[ℓ], Jagoba Malumbres-Olarte[‡,ı], José Marcelino[‡], Catarina Melo[‡,˅˅], David Milla-Figueras[¶], Paulo Monjardino[ǁ], Sandra Monteiro[ℓ], Ignacio Moreu[¢], Leila N. Morgado[‡], José A. Mota[ʔʔ], Raul M. A. Neto[ʂʂ], Elisabete C. Nogueira[�unk], Rui Nunes[‡], Manuela I. Parente[ℓ], Laurine M. Parmentier[‡], Rita F. Patarra[¢¢,¢], Enésima Pereira[‡], Fernando Pereira[‡], Maria J. Pereira[ǁ], Andrea Petrone[‡,₲], César M. M. Pimentel[�unk], Silvia Poponessi[ℓℓ,ꝺꝺ], Gabor Pozsgai[‡], Afonso C. L. Prestes[ℓ,℗℗,ⱥⱥ], Pedro M. Raposeiro[ℓ], Roberto Resendes[ƨƨ], François Rigal[FF,‡], Ana C. P. Rodrigues[₹₹], António F. Rodrigues[»], Alejandra Ros-Prieto[‡], Ana M. C. Santos[₦₦,ʔ,‡], Michael Schülke[ⱪⱪ], Cecília Sérgio[ƨ], Luís Silva[ℓ,ⱥⱥ,℗℗], Lurdes B. Silva[₲,ⱥⱥ,℗℗], Gabriela M. Silveira[ʔʔ], Nelson Simoes[ǁ], Manuela Sim-Sim[ƨ], António Onofre Soares[¢,₩₩], Mariana A. Sousa[₸₸], Martin S. Souto[ℓ], Peter E. Stüben[ǂǂ], Stephanie R. A. Suciu[¶], João Tavares[ǁ], Mário B. Teixeira[ǁ], Noelline Tsafack[‡,§§§], Duarte Toubarro[ǁ], Virgílio Vieira[¢], Martha Vounatsi[‡], Sophie Wallon[‡], Paulo A. V. Borges[‡,˅,ǀǀǀ]

‡ University of the Azores, CE3C - Centre for Ecology, Evolution and Environmental Changes, Azorean Biodiversity Group, CHANGE - Global Change and Sustainability Institute, School of Agricultural and Environmental Sciences, Rua Capitão João d'Ávila, Pico da Urze, 9700-042, Angra do Heroísmo, Azores, Portugal

§ These two authors contributed equally to this article, Angra do Heroísmo, Azores, Portugal

| LIBRe – Laboratory for Integrative Biodiversity Research, Finnish Museum of Natural History, University of Helsinki, P.O.Box 17 (Pohjoinen Rautatiekatu 13), 00014, Helsinki, Finland

¶ University of the Azores, OKEANOS - Institute of Marine Sciences, Doutor Frederico Machado, 4, 9901-862, Horta, Azores, Portugal

# IMAR - Institute of Marine Research, University of the Azores, Horta, Azores, Portugal

¤ Université de La Réunion, UMR PVBMT - Unité Mixte de Recherche sur les Peuplements Végétaux et Bioagresseurs en Milieu Tropical, Pôle de Protection des Plantes, 97410 Saint-Pierre, La Réunion, France

« University of the Azores, CCMMG - Center for Climate, Meteorology, and Global Change, Rua Capitão João d'Ávila, Pico da Urze, 9700-042, Angra do Heroísmo, Azores, Portugal

» University of the Azores, IITAA - Institute for Agricultural and Environmental Research and Technologies, Rua Capitão João d'Ávila, Pico da Urze, 9700-042, Angra do Heroísmo, Azores, Portugal

^ University of the Azores, CE3C - Centre for Ecology, Evolution and Environmental Changes, Azorean Biodiversity Group, CHANGE - Global Change and Sustainability Institute, Rua Capitão João d'Ávila, Pico da Urze, 9700-042, Angra do Heroísmo, Azores, Portugal

˅ IUCN - International Union for the Conservation of Nature, SSC - Species Survival Commission, Atlantic Islands Invertebrate Specialist Group, Angra do Heroísmo, Azores, Portugal

¦ CSIC - Centre d'Estudis Avançats de Blanes, Carrer Accés Cala Sant Francesc, 14, 17300, Blanes, Girona, Spain

ʔ IUCN - International Union for the Conservation of Nature, Groupers and Wrasses Specialist Group, Hong Kong, Hong Kong

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ˢ University of Lisbon, CE3C - Centre for Ecology, Evolution and Environmental Changes, CHANGE - Global Change and Sustainability Institute, Faculty of Sciences, Campo Grande, 1749-016, Lisbon, Portugal
¢ University of the Azores, CE3C - Centre for Ecology, Evolution and Environmental Changes, Azorean Biodiversity Group, CHANGE - Global Change and Sustainability Institute, School of Agricultural and Environmental Sciences, Rua da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
ℓ University of the Azores, CIBIO - Research Center in Biodiversity and Genetic Resources, InBIO - Associate Laboratory, Faculty of Sciences and Technology, Department of Biology, Rua da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
৯ LIFE CWR - LIFE project “Ecological Restoration and Conservation of Praia da Vitória Coastal Wet Green Infrastructures”, Praia da Vitória, Azores, Portugal
₱ Centro Oceanográfico de Vigo, Instituto Español de Oceanografía (IEO-CSIC), Vigo, Spain
₳ Hydrosphere. Laboratorio Ambiental para el Estudio de Ecosistemas Acuáticos, Vigo, Spain
₴ University of Lisbon, CE3C - Centre for Ecology, Evolution and Environmental Changes, CHANGE - Global Change and Sustainability Institute, Faculty of Sciences, Campo Grande 016, 1749-016, Lisbon, Portugal
₣ LEAF-Linking Landscape, Environment, Agriculture and Food Departamento de Ciências e Bioengenharia de Biossistemas, Instituto Superior de Agronomia - Universidade de Lisboa, Liaboa, Portugal
₹ Secretaria Regional do Ambiente e Alterações Climáticas, Rua do Galo nº 118, 9700-040, Angra do Heroísmo, Azores, Portugal
₦ Parque Terra Nostra, Largo Marquês da Praia e Monforte, 9675-037, Furnas, Azores, Portugal
₭ Universidad Autónoma de Madrid, TEG-UAM - Terrestrial Ecology Group, Departamento de Ecología, C. Darwin, 2, Fuencarral-El Pardo, 28049, Madrid, Spain
₲ University of Bologna, Via Zamboni, 33, 40126, Bologna, Italy
⁇ Universidad Autónoma de Madrid, Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Calle Darwin 2, 28049, Madrid, Spain
₩ University of Portsmouth, Institute of Marine Sciences, Department of Biological Sciences, Ferry Road, Eastney, Portsmouth, United Kingdom
₸ Regional Secretariat of Environment and Climate Change, Project LIFE BEETLES (LIFE 18 NAT/PT/000864), Rua do Galo n118, 9700-040, Angra do Heroísmo, Azores, Portugal
‡‡ Secretaria Regional da Agricultura e Alimentação, Project LIFE POLINIZACORES (LIFE24-NAT-PT-LIFE POLINIZACORES-101215702), Vinha Brava, 9700-08140, Angra do Heroísmo, Azores, Portugal
§§ University of the Azores, Faculty of Sciences and Technology, Rua da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
|| University of the Azores, CBA – Centre of Biotecnology of the Azores, Faculty of Sciences and Technology, Rua Madre de Deus, 9500-321, Ponta Delgada, Azores, Portugal
¶¶ Futurismo Azores Adventures, Portas do Mar 24-26, 9500-771, Ponta Delgada, Azores, Portugal
## University of the Azores, IVAR - Research Institute in Volcanology and Risk Assessment, Rua da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
¤¤ University of Coimbra, Centre for Functional Ecology, Associate Laboratory TERRA, Department of Life Sciences, Calçada Martim de Freitas, 3000-456, Coimbra, Portugal
«« Banco Genético Vegetal Autóctone, Empresa Municipal Cascais Ambiente, Estrada de Manique, n.º 1830. Alcoitão 2645-138, Lisbon, Portugal
»» Rua Fernando Pessoa, nº99 R/C DTO 2765-483, Estoril, Portugal
^^ Aarhus University, Department of Agroecology, Flakkebjerg Research Centre, Forsoegsvej 1, DK-4200, Slagelse, Denmark
ˇˇ University of Coimbra, CFE - Centre for Functional Ecology, Department of Life Sciences, Calçada Martim de Freitas, 3001-401, Coimbra, Portugal
¦¦ University of the Azores, CBA – Centre of Biotecnology of the Azores, School of Agricultural and Environmental Sciences, Rua Capitão João d'Ávila, Pico da Urze, 9700-042, Angra do Heroísmo, Azores, Portugal
⁇ Direção de Serviços de Agricultura, Direção Regional de Agricultura, Secretaria Regional de Agricultura e do Desenvolvimento Rural, Quinta de São Gonçalo, 9500-343, Ponta Delgada, Azores, Portugal
ˢˢ N/A, Ponta Delgada, Azores, Portugal
¢¢ Expolab - Ciência Viva Science Centre, Avenida da Ciência - Beta, n.º 8, Ponta Delgada, Azores, Portugal
ℓℓ Universidade de Cagliari, Via Università, 40, 09124, Cagliari, Italy
৯৯ Institute for Alpine Environment, Eurac Research, Viale Druso 1, 39100, Bolzano, Italy
₱₱ UNESCO Chair – Land within Sea: Biodiversity & Sustainability in Atlantic Islands. University of the Azores, Rua da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
₳₳ University of Porto, BIOPOLIS/CIBIO - Biodiversity and Genetic Resources Research Center, Campus de Vairão, Rua do Crasto, nº 765, 4485-684, Vairão, Portugal
₴₴ University of the Azores, School of Science and Technology, Department of Biology, Rua da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
₣₣ Institut Des Sciences Analytiques et de Physico Chimie pour L'environnement et les Materiaux UMR5254, Comité National de la Recherche Scientifique – University de Pau et des Pays de l'Adour, Pau, France
₹₹ Secretaria Regional do Ambiente e Acão Climática, Direção Regional do Ambiente e Ação Climática, Rua Cônsul Dabney, Colónia Alemã, Apartado 140, 9900-014, Horta, Azores, Portugal

ⁿⁿ Universidad Autónoma de Madrid, TEG-UAM - Terrestrial Ecology Group, Departamento de Ecología, C. Darwin, 2, 28049, Madrid, Spain
ₖₖ Museum für Naturkunde - Leibniz Institute for Research on Evolution and Biodiversity, Blankenfelder Straße 99, D-13127, Berlin, Germany
₠₠ University of Montpellier, CBGP - Centre de Biologie pour la Gestion des Populations, INRAE - French National Institute for Agricultural Research and Environment, CIRAD - French Agricultural Research Centre for International Development, Institut Agro, 755 avenue du Campus Agropolis, Montpellier, France
⁇ Fundação Gaspar Frutuoso, University of the Azores, R. da Mãe de Deus, 9500-321, Ponta Delgada, Azores, Portugal
₩₩ IUCN - International Union for Conservation of Nature, SSC - Ladybird Specialist Group, Ponta Delgada, Azores, Portugal
₸₸ University of the Azores, Mestrado em Gestão e Conservação da Natureza, Rua Capitão João d´Ávila, Pico da Urze, 9700-042, Angra do Heroísmo, Azores, Portugal
‡‡‡ CURCULIO Institute e.V., Hauweg 62, D-41066, Mönchengladbach, Germany
§§§ Avignon Université, Aix Marseille Université, CNRS IRD IMBE, 84911, Avignon, France
||| IUCN - International Union for the Conservation of Nature, SSC - Species Survival Commission, Monitoring Specialist Group, Angra do Heroísmo, Azores, Portugal

Corresponding author: Paulo A. V. Borges (paulo.av.borges@uac.pt)

## Abstract

Ten years of dedicated biodiversity research and coordinated open-data publication have built an extensive, reusable knowledge base for the Azores. We synthesize this collective achievement through the AZORES BIOTA and BioMonI-Plot collections, evaluating its contribution to addressing the Wallacean and Prestonian shortfalls and identifying priorities for future research and monitoring. Focusing on the nine islands of this North Atlantic archipelago, we review publications issued between 2016 and May 2026, encompassing terrestrial and marine organisms across six kingdoms. We combine curated publication and dataset metadata with Darwin Core occurrenceID-linked species and subspecies records to assess spatial, taxonomic, temporal and methodological coverage, species accumulation by colonization status, and island species–area relationships. Across 91 publications, the collections document 931 animal, 1,185 plant and 742 fungal species and subspecies, alongside taxa from three additional kingdoms, and identify 598 additions to the Azorean Biodiversity Portal reference list. This sustained effort has substantially expanded accessible knowledge of species distributions, contributing to reducing the Wallacean shortfall. Arthropod abundance datasets and repeated standardized surveys also alleviate the Prestonian shortfall by enabling assessments of population and community change. Together, these resources establish valuable baselines for biodiversity assessment, invasion surveillance and conservation planning. The synthesis also reveals uneven coverage among islands, taxa and habitats, with spatial differences in research effort complicating interpretation of species–area relationships. The Azorean experience demonstrates the substantial scientific value of sustained regional expertise, collaboration and standardized open-data publication for understanding island biodiversity. By consolidating achievements and making remaining gaps explicit, this synthesis provides a foundation for targeted investment in underrepresented biota, spatially balanced surveys and sustained abundance

monitoring, strengthening the evidence base for future biodiversity research and conservation.

## Keywords

Biodiversity database, Darwin Core, FAIR data, GBIF, island biodiversity, occurrence data, open data, Prestonian Shortfall, species accumulation, Wallacean Shortfall.

## Introduction

Oceanic islands make a disproportionate contribution to global biodiversity, harboring unique biotas characterized by high levels of endemism and distinct species assemblages shaped by geographic isolation, environmental heterogeneity and evolutionary history (Whittaker and Fernández-Palacios 2007, Whittaker et al. 2017, Pyšek et al. 2020, Fernández-Palacios et al. 2021). Their exceptional evolutionary heritage endows islands with high intrinsic conservation value, while their ecosystems support important ecological functions and contribute to human well-being and cultural identity. Moreover, their restricted area, isolation and often small-ranged biotas make them particularly vulnerable to habitat degradation, climate change and biological invasions (Whittaker and Fernández-Palacios 2007, Whittaker et al. 2017, Pyšek et al. 2020, Fernández-Palacios et al. 2021). The Azores Archipelago represents a particularly relevant example, combining high conservation value and distinct island biotas with extensive historical landscape transformation (Gabriel et al. 2014, Gabriel et al. 2024a, Gabriel et al. 2024b, Pozsgai et al. 2024, Borges 2025).

To safeguard this biodiversity and develop effective conservation strategies, access to reliable information is essential, yet such information is often fragmented across projects, publications and institutional databases. This knowledge fragmentation is a pervasive challenge across the Azores, limiting our capacity to document species distributions, abundances and the respective changes across time (Cardoso et al. 2011a, Hortal et al. 2015, Meyer et al. 2016, Troudet et al. 2017). Consequently, integrating scattered biodiversity information across the archipelago is essential for identifying and progressively reducing three complementary knowledge gaps: the Wallacean shortfall, arising from incomplete knowledge of species' geographic distributions; the Prestonian shortfall, reflecting limited information on species abundances and their spatial and temporal dynamics; and the Darwinian shortfall, arising from incomplete knowledge of species' phylogenetic relationships and evolutionary history (Lomolino and Heaney 2004 , Cardoso et al. 2011b, Hortal et al. 2015). In this context, the AZORES BIOTA and BioMonI-Plot (Biodiversity Monitoring of Island Ecosystems) collections in the Biodiversity Data Journal have been providing individual datasets as a distributed data infrastructure for archipelago-scale synthesis and monitoring. Their rapid accumulation creates both an opportunity and an urgent need to synthesize this information into an integrated evidence base for conservation and policy. Such synthesis is particularly important for establishing robust long-term ecological baselines against which future biodiversity change,

biological invasions, habitat restoration, and conservation outcomes can be detected and evaluated (Dornelas et al. 2013, Borges et al. 2019, Borges 2025). This emerging tradition of standardized biodiversity inventory through open data papers has helped reduce knowledge shortfalls by publishing structured occurrence, event, and checklist resources with explicit metadata, sampling protocols, and taxonomic decisions.

Here, we synthesize a decade of coordinated biodiversity data publication through the AZ ORES BIOTA and BioMonI-Plot collections to evaluate how sustained regional research and open-data mobilization have advanced knowledge of the Azorean biota and contributed to addressing the Wallacean and Prestonian shortfalls (Lomolino and Heaney 2004, Cardoso et al. 2011b, Hortal et al. 2015). Specifically, we assess the temporal development of this evidence base and its coverage across taxonomic groups, islands, habitats and sampling approaches; examine patterns of species and subspecies documentation and new distribution records; and identify where abundance data and repeated standardized surveys provide baselines for assessing biodiversity change. By considering these achievements alongside remaining gaps and biases, we identify priorities for future surveys, monitoring and data mobilization. We then discuss how this consolidated knowledge can inform conservation action and biodiversity policy through three complementary applications: (i) surveillance and early warning of biological invasions; (ii) assessment of population and community change and evaluation of restoration and other conservation interventions; and (iii) development of biodiversity indicators and evidence-based prioritization of conservation actions across the archipelago. In doing so, we examine how sustained investment in regional expertise and standardized data publication can strengthen the foundations for biodiversity assessment and conservation on oceanic islands (Dornelas et al. 2013, Borges et al. 2018b, Borges 2025).

## Material and methods

### Study location

This study focuses on the Azores, a remote volcanic archipelago in the North Atlantic Ocean comprising nine main islands distributed among the Western, Central and Eastern island groups (Fig. 1). The Western group includes Corvo and Flores, the Central group Faial, Pico, São Jorge, Graciosa and Terceira, and the Eastern group includes São Miguel and Santa Maria. The archipelago has a temperate oceanic climate and comprises a mosaic of terrestrial, freshwater and marine habitats, including native forest remnants, agricultural landscapes, exotic forests, cave ecosystems, urban habitats and freshwater and coastal ecosystems that are represented unevenly across biodiversity datasets (Borges et al. 2019).

All species and subspecies (hereafter taxa) records were referenced against the Azorean Biodiversity Portal (ABP), which maintains the reference list of all Azorean biota and serves as the baseline against which all data in this study were compared. Azorean taxa

were classified into four colonization-status categories: (i) endemic, comprising taxa restricted to the Azores; (ii) native non-endemic, comprising taxa occurring elsewhere but considered to have colonized the archipelago naturally; (iii) introduced, comprising taxa presumed to have arrived through human-mediated dispersal; and (iv) indeterminate, comprising taxa for which the available evidence is insufficient to establish native or introduced status (Carlton 1996, Borges et al. 2006, Borges and Wunderlich 2008, Borges et al. 2022a). This categorization is central for interpreting conservation value, species protection, monitoring priorities, anthropogenic impact and invasion risk (Borges et al. 2019, Castro et al. 2024, Oyarzabal et al. 2024). The synthesis therefore treats the archipelago as both a biogeographic unit and as a set of island-level sampling units, because apparent diversity differences among islands can be shaped by both intrinsic biogeographic processes and unequal sampling intensity.

## Data sources, inclusion criteria and compilation

We compiled data from two thematic collections in the Biodiversity Data Journal (BDJ), published between 2016 and May 7th 2026, both of which mandate public data deposition in GBIF, the Pensoft BDJ platform, or other recognized repositories. The AZORES BIOTA collection collates publications on the taxonomic diversity of Azorean terrestrial and marine biota. The collection includes Research Articles, Taxonomic Papers, Data Papers, Alien Species Profiles, and Species Conservation Profiles. The BioMonI-Plot (Biodiversity Monitoring of Island Ecosystems) collection collates cross-taxon and cross-ecosystem biodiversity and ecosystem functioning data at the plot scale, globally. It encompasses biodiversity surveys focused on trait sampling, eDNA integration, and remote-sensing data, published as Research Articles, Taxonomic Papers, or Data Papers. Both collections include a majority of publications that include datasets organized according to the Darwin Core format. This is a standardized vocabulary and data format used to share biodiversity information, maintained by the Biodiversity Information Standards (TDWG) organization. It defines a common set of terms (fields) for describing taxa occurrences, events, and associated metadata, ensuring that data from different sources can be easily integrated and compared (Wieczorek et al. 2012).

Most studies selected passed both of the following criteria: i) concerned the Azores; ii) were published within the AZORES BIOTA or BioMonI-Plot collections from Biodiversity Data Journal. We additionally included GBIF datasets known to be in preparation for publication in either collection. Except for three datasets (Wallon et al. 2026b [10.15468/unbsgv], Petrone et al. 2026a [10.15468/hgyfh3], Carvalho et al. 2026) all GBIF datasets incorporated in this study have since then been published in either AZORES BIOTA or BioMonI-Plot collections. For most analyses, we retained only datasets containing records with an occurrenceID, the Darwin Core term used to uniquely identify individual biodiversity occurrence records and enable their consistent referencing and tracking across data infrastructures such as GBIF (Wieczorek et al. 2012). Eligible datasets contained occurrence, checklist or species-incidence information accompanied by sufficient metadata to assign records to a publication year, taxonomic group and island.

Publications lacking this level of record-level information were retained only for descriptive summaries of the overall AZORES BIOTA and BioMonI-Plot collections and were excluded from analyses requiring species-level occurrence data. Each dataset was treated as a single bibliographic unit, whereas datasets spanning multiple islands were partitioned into separate island-level analytical units to ensure that their contribution to spatial coverage was attributed to each island represented (Costa et al. 2026; Suppl. material 1).

The studies providing occurrenceID-linked records covered multiple taxonomic groups, namely: Arthropoda (Borges et al. 2018a, Malumbres-Olarte et al. 2019, Borges et al. 2021, Carvalho et al. 2021, Costa and Borges 2021, Marcelino et al. 2021, Soares et al. 2021, Borges et al. 2022a, Borges et al. 2022b, Borges et al. 2022c, Lhoumeau et al. 2022b, Lhoumeau et al. 2022a, Vieira et al. 2022, Lamelas-López et al. 2023b, Lamelas-López et al. 2023a, Teixeira et al. 2023, Wallon et al. 2023, Boieiro et al. 2024, Lhoumeau et al. 2024, Sousa et al. 2024, Teixeira et al. 2024, Boieiro et al. 2025, Borges et al. 2025b, Borges et al. 2025c, Borges et al. 2025a, Calado et al. 2025b, Crespo et al. 2025a, Crespo et al. 2025b, Duenas-Rojas et al. 2025, Lhoumeau et al. 2025, Borges et al. 2026, Leite et al. 2026, Wallon et al. 2026a, Wallon et al. 2026b, Vounatsi et al. 2026a, Vounatsi et al. 2026b), Bryophyta (Gabriel et al. 2019, Gabriel et al. 2024b, Gabriel et al. 2024a, Sousa et al. 2024, Gabriel et al. 2025, Carvalho et al. 2026, Morgado et al. 2026, Silveira and Gabriel 2026), Chordata (Goulart et al. 2019, Lamelas-López et al. 2020, Barcelos and Barreiros 2022, Barcelos et al. 2023, Lamelas-López and Borges 2023, García et al. 2023, Sousa et al. 2024, Boieiro et al. 2025, Borges et al. 2025c), Fungi ( Melo et al. 2020, Rodrigues et al. 2024, Borges et al. 2025c, Monjardino et al. 2026, Silveira and Gabriel 2026), Macroalgae (Neto et al. 2020b, Neto et al. 2020d, Neto et al. 2020a, Neto et al. 2020c, Neto et al. 2021b, Neto et al. 2021a, Neto et al. 2021c, Milla-Figueras et al. 2024), Tracheophyta (Elias et al. 2019, Costa et al. 2023, Silva et al. 2023, Sousa et al. 2024, Borges et al. 2025b, Borges et al. 2025c, Calado et al. 2025a, Andrade et al. 2026, Carvalho et al. 2026, Lago et al. 2026, Parmentier et al. 2026, Petrone et al. 2026a, Petrone et al. 2026b, Petrone et al. 2026c) and some other groups ( Luz et al. 2020, Souto et al. 2021, Luz et al. 2022, Suciu et al. 2025). All the studies considered provided biodiversity data obtained at the islands and marine areas belonging to the Azores.

Overall taxa occurrence analyses across realms, years and islands were based on a file with the summarized information compiled from each publication (e.g. authors, date of publication, doi, protocols used in the methodology, number of sites, number of months sampled, overall number of taxa sampled, and number of new records for the islands individually and for Azores as a whole) allowing records to be linked to published papers. Taxonomic information provided by the papers (e.g. taxa scientific name, genus, family, etc) was cross-checked with information obtained from the Azores Bioportal platform to update the taxonomy of older publications, to obtain the proportion of taxa studied based on the known pool and to identify new additions to the biodiversity known for the archipelago. For arthropods, taxonomic validation also followed the most recent published checklist (Borges et al. 2022d). The obtained scientific names were treated as

unique name strings for corpus-level accumulation and summaries (e.g. identifying the main phyla). To develop standard vocabularies, improve cross-publication comparability, and to make synthesis tables reusable for future monitoring work, metadata categories were harmonized into broad analytical classes for realm, habitat, sampling protocol, and dataset type (e.g. analytical vs data paper) (Wieczorek et al. 2012, Wilkinson et al. 2016). When information was incomplete or ambiguous, the original terminology was manually curated rather than forced into uncertain classifications.

## Data structuring and analyses

To study sampling and publication effort, we first summarized the number of dataset entries by year, dataset type, realm (terrestrial or aquatic) and higher taxonomic group to evaluate temporal growth and structural composition of the corpus. We then summarized spatial coverage per island. To evaluate the taxonomic coverage and representativeness of the occurrence data mobilized through AZORES BIOTA and BioMonI-Plot, the analyses presented below were restricted to known taxa and those with occurrenceID-linked information, across islands, colonization-status categories, and major eukaryotic phyla (see results for missing groups). All the following analyses were performed using R software (R Core Team 2026).

To assess the temporal patterns, we constructed taxa accumulation curves restricted to macroalgae, bryophytes, tracheophytes and terrestrial arthropods (due to insufficient data for other groups, see Results) across four colonization-statuses (Endemic, Native, Introduced, and Indeterminate). Occurrence records with valid identifiers were filtered to retain only the first record of each taxon, defined as the earliest publication year in which the taxa appeared in the dataset. Only records from 2018 onward were considered, as this marks the point from which records began following the Darwin Core occurrenceID pattern. For each colonization status within each taxonomic group, we calculated the cumulative number of unique taxa recorded over time by summing new additions per year. Total taxon richness for each colonization status was calculated as the number of distinct taxa. These totals were displayed as horizontal reference lines on the accumulation curves to indicate the total known taxa pool for each colonization status and taxonomic group. We tested differences in annual taxa documentation rates among colonization statuses using a generalized linear mixed-effects model (GLMM) with a negative binomial distribution, with the help of the *lme4* package (Bates et al. 2015). The response variable was the number of new taxa per year, and colonization status was used as a predictor variable, while year of publication was a random effect, to account for temporal autocorrelation and variation among years in taxa documentation rates. We selected the Negative Binomial distribution to accommodate overdispersion in the count data. Overdispersion and R-squared were checked with the 'performance' package ( Lüdecke et al. 2021).

To evaluate how richness scales with island area across taxonomic groups and colonization categories, we fitted Species–Area Relationship (SAR) models with the *sars* package (Matthews et al. 2014, Matthews et al. 2019). For this, we also included only

taxa with valid occurrenceID. For each combination of phylum group (limited to bryophytes, tracheophytes, fungi, terrestrial arthropods and terrestrial chordates) and colonization status (Endemic, Native, Introduced, and Indeterminate), we calculated richness as the number of unique taxa recorded per island, and paired with the corresponding island area (km²). We fitted the SAR models using the Power model (S = c × A^z), where S represents richness, c is the intercept, A is island area, z is the slope describing the rate at which richness increases with area (Triantis et al. 2011). We parameterized models using non-linear regression, with a partial grid search procedure to optimize starting parameter values, checking model convergence. For each model, we extracted the intercept (c), slope (z), Akaike Information Criterion (AIC), corrected AIC (AICc), Bayesian Information Criterion (BIC), $R^2$, and the adjusted $R^2$ to assess model fit and support model comparison. The z-value quantifies the strength of the species–area relationship, with higher values indicating a steeper increase in taxon richness with increasing island area.

To evaluate spatial and temporal patterns of research effort across the Azorean archipelago, we quantified the number of published papers reporting taxa records for each of the nine islands, with each unique DOI entry treated as a distinct publication record. Azorean islands were grouped into the three recognized geographical groups of the archipelago, as presented in the previous 2.1 Study location section. Moreover, to assess temporal trends in taxa documentation, we calculated the cumulative number of new taxa records per island over time. New records were defined as unique entries per island and year, identified using the new records field in the dataset. We also calculated an archipelago-wide cumulative curve by summing annual records across all islands.

## Data resources

All individual data is publicly available in GBIF. The harmonized dataset used for this synthesis is available in Zenodo (Costa et al. 2026) and see also Suppl. material 1.

## Results

The current compilation includes 91 publications spanning 2016 to May of 2026 (Suppl. material 1). The associated datasets comprise taxa occurrence records from six kingdoms of life, with Plantae and Animalia contributing the greatest richness. Plantae was the most diverse kingdom in terms of unique entries, with 1,185 taxa represented by occurrenceIDs (~29% from the nearly 4,000 Plantae registered in the ABP), while Animalia were represented by 931 taxa with occurrenceIDs (~16% from the nearly 6,000 Animalia registered in the ABP) (Fig. 2). For Fungi, from the known 2,000 taxa, sampled richness reached 742 taxa with occurrenceID (~37%) (Fig. 2). Chromista, Protozoa and Bacteria, from which only 342 taxa are registered for the Azores, 282 have occurrenceIDs (Fig. 2). In total, 598 taxa were new additions (595 with occurrenceIDs), corresponding to taxa that had not been registered into the ABP. Moreover, 830 taxa (322 with

occurrenceIDs) were mentioned in published work as newly recorded in the Azores at the time of publication.

The total richness varied substantially among Macroalgae, Fungi, Arthropoda, Chordata, Bryophytes, and Tracheophytes as well as according to their colonization status (Fig. 3). Among tracheophytes, introduced and native taxa dominated, while endemic tracheophytes comprised a smaller proportion (Fig. 3). Bryophytes, Fungi and Macroalgae showed lower overall richness, with native taxa predominating in comparison with the other colonization statuses (Fig. 3). Chordates, included for comparative purposes, represented the smallest pool among the focal groups (Fig. 3). In general, a substantial majority of taxa in each category had at least one georeferenced occurrence record, although some groups, like endemic Chordata, did not.

## Analyses through time

Analyses through time using taxa accumulation curves could only be performed for four taxonomic groups, macroalgae, bryophytes, tracheophytes and terrestrial arthropods, owing to insufficient data for the remaining groups.

### Macroalgae

Annual documentation rates differed significantly among macroalgae phyla. Chlorophyta (green algae), the reference category, had a significant baseline log-rate of 1.918 (SE = 0.818, p = 0.019), corresponding to an estimated mean of approximately 59 new taxa over 3 years, a mean of 19.7 ± 24.2 taxa/year (Fig. 4). Rhodophyta (red algae) also showed a significantly higher documentation rate (β = 1.479, SE = 0.141, p < 0.001), corresponding to approximately 4.4-fold higher documentation rate than Chlorophyta, with 259 new taxa over 3 years, a mean of 86.3 ± 95.8 taxa/year. Ochrophyta (brown algae) did not differ significantly from Chlorophyta (β = 0.185, SE = 0.172, p = 0.282), with approximately 71 new taxa over 3 years, a mean of 23.7 ± 26.0 taxa/year (Fig. 4), indicating comparable documentation rates between these two groups. Model diagnostics indicated no overdispersion (dispersion ratio = 0.980, p = 0.928). The model explained near-complete variation in documentation rates (conditional $R^2$ = 0.998), although fixed effects alone accounted for a modest proportion (marginal $R^2$ = 0.115), indicating that interannual variability played a substantial role.

Using endemic taxa as the reference category (intercept: β = −1.858, SE = 1.216, p = 0.127), all three other colonization-status categories showed higher documentation rates: indeterminate (β = 3.632, SE = 0.752, p < 0.001), introduced (β = 2.878, SE = 0.755, p < 0.001), and native (β = 5.446, SE = 0.740, p < 0.001) (Fig. 5). These large rate ratios should be interpreted cautiously given the extremely low endemic baseline (a single record). At the same time, natives dominated macroalgal documentation, accounting for 313 new taxa over three years at a mean rate of 104 ± 117 taxa/year. Indeterminates followed with 51 new taxa over three years (17 ± 21.2 taxa/year) and introduced with 24 new taxa over three years (8 ± 7.6 taxa/year) (Fig. 5). Model

diagnostics indicated no overdispersion (dispersion ratio = 0.992, p = 0.992), with the model explaining near-complete variation in documentation rates (conditional $R^2$ = 0.998) and colonization status explaining a considerable share of the variance (marginal $R^2$ = 0.424). Finally, the accumulation curves also showed that none of the colonization statuses had reached a clear asymptote by 2026. Hence, additional taxa remain to be documented across all categories.

## Bryophytes

Annual documentation rates varied significantly among bryophyte groups. Anthocerotophyta (hornworts), used as the reference category, had a non-significant baseline log-rate of 0.535 (SE = 0.778, p = 0.491), equivalent to approximately 3 new taxa documented over 2 years, averaging 1.5 ± 0.707 taxa per year (Fig. 6). In contrast, Bryophyta (mosses) exhibited a significantly higher documentation rate (β = 2.921, SE = 0.717, p < 0.001), with 153 new taxa recorded over 4 years and an annual mean of 38.2 ± 26.9 taxa. Marchantiophyta (liverworts) also showed a significantly higher rate than the reference group (β = 2.329, SE = 0.744, p = 0.001), with approximately 114 new taxa documented over 4 years, corresponding to a mean of 28.5 ± 39.7 taxa per year (Fig. 6). Model diagnostics revealed no evidence of overdispersion (dispersion ratio = 0.850, p = 0.784). The model accounted for a substantial proportion of variation in documentation rates (conditional $R^2$ = 0.896; marginal $R^2$ = 0.627), suggesting that interannual variability contributed considerably to the observed patterns.

Bryophytes exhibited the least pronounced accumulation trajectories among the three origin groups examined (Fig. 7). Endemic bryophytes, the reference category, had a non-significant baseline log-rate of 0.388 (SE = 0.457, p = 0.395), corresponding to an estimated mean of approximately 8 new taxa over 3 years, a mean of 2.67 ± 2.89 taxa/year. In contrast, native bryophytes significantly dominated the records, accounting for 260 new taxa over 4 years at a mean rate of 65 ± 60.7 taxa/year, with a significantly higher accumulation rate (β = 3.481, SE = 0.311, p < 0.001). Introduced bryophytes showed a lower documentation rate, although the difference was not statistically significant (β = −1.151, SE = 0.657, p = 0.079), while we do not have occurrenceID for Indeterminates to perform this analysis (Fig. 7). The extremely limited sample sizes for non-native bryophyte categories, however, warrant cautious interpretation of these comparisons. Coefficients of variation were high for both natives (95.2%) and endemics (108.2%), again indicating episodic rather than continuous taxa documentation.

Model diagnostics indicated no overdispersion (dispersion ratio = 1.035, p = 0.864) and explained near-complete variation in discovery rates, with both conditional ($R^2$ = 0.992) and marginal $R^2$ values ($R^2$ = 0.866). This indicates that colonization status was a strong predictor of bryophyte discovery patterns and that interannual variability played a comparatively minor role. However, the high marginal $R^2$ primarily reflects the overwhelming dominance of natives relative to the negligible contributions of other colonization categories, rather than a balanced comparison across all groups. Finally, none of the bryophyte accumulation curves approached an asymptote by 2026, although

the limited and sporadic records for non-native taxa suggest that additional sampling effort is needed to reliably assess accumulation trajectories for the groups (Fig. 7).

### Tracheophytes

Annual documentation rates differed significantly among tracheophyte groups. Magnoliophyta (flowering plants), used as our reference category, used as the reference category, had a significant baseline log-rate of 4.351 (SE = 0.463, $p < 0.001$), corresponding to approximately 535 newly documented taxa over five years and a mean of 107 ± 62.1 taxa per year (Fig. 8). Pteridophyta showed a significantly lower documentation rate than Magnoliophyta ($\beta = -2.475$, SE = 0.156, $p < 0.001$), with 45 newly documented taxa over five years and a mean of 9 ± 9.08 taxa. The remaining tracheophyte groups also showed a significantly lower documentation rate ($\beta = -3.277$, SE = 0.255, $p < 0.001$), comprising approximately 16 newly documented taxa over three years and a mean of 5.33 ± 2.31 taxa per year (Fig. 8). Model diagnostics indicated no overdispersion (dispersion ratio = 1.038, $p = 0.76$), and the model explained a substantial proportion of variation in documentation rates (conditional $R^2 = 0.993$; marginal $R^2 = 0.660$), which suggest interannual variability contributed considerably to the pattern found.

The accumulation curve pattern was even more pronounced in tracheophytes. Endemic tracheophytes, the reference category, had a significant baseline log-rate of 2.235 (SE = 0.511, $p < 0.001$), corresponding to an estimated mean of approximately 73 taxa over 5 years, with a mean of 14.6 ± 16.0 taxa/year. Introduced tracheophytes though, contributed to 407 new taxa over 5 years at a mean rate of 81.4 ± 48.4 taxa/year ($\beta = 1.993$, SE = 0.399, $p < 0.001$), significantly exceeding the endemic baseline. Indeterminate tracheophytes showed the significantly lowest rates, with 27 taxa over 4 years and 6.75 ± 6.4 taxa/year ($\beta = -0.884$, SE = 0.450, $p = 0.050$). Finally, although native tracheophytes had a rate of 93 taxa over 4 years, with a mean of 23.2 ± 16.7 taxa/year, this difference was not statistically significant ($\beta = 0.370$, SE = 0.409, $p = 0.366$) (Fig. 9).

The coefficients of variation ranged from 72–109% for tracheophytes, which indicate considerable interannual variability in discovery rates. Moreover, model diagnostics indicated no overdispersion (dispersion ratio = 0.346, $p = 0.432$), and the models explained substantial variation in discovery rates, with conditional $R^2 = 0.881$, while colonization status explained a considerably larger share for tracheophytes (marginal $R^2 = 0.512$). This indicates that taxonomic identity was a stronger predictor of discovery patterns in tracheophytes (Fig. 9).

Finally, the accumulation curves also showed that none of the colonization statuses had reached a clear asymptote by 2026. Hence, additional taxa still remain to be documented across all categories. The steepest accumulation trajectories were consistently observed for introduced taxa though, which continued to show substantial annual additions up to the final year analyzed. Endemics, despite having the lowest total richness, exhibited relatively consistent accumulation patterns, with new taxa added in most years (Fig. 9).

## Terrestrial arthropods

Annual documentation rates differed markedly among terrestrial arthropod groups. Arachnida, used as our reference category, had a significant positive baseline log-rate of 2.240 (SE = 0.389, $p < 0.001$), equivalent to approximately 117 new taxa documented over 8 years, averaging 14.6 ± 18.8 taxa/year (Fig. 10). We have found for Insects also a significant positive documentation rate ($\beta = 2.088$, SE = 0.382, $p < 0.001$), but with many more new taxa, counting 607 new taxa recorded over 7 years, an annual mean of 86.7 ± 62.3 taxa. Lastly, other arthropod classes (which include, for instance, other Hexapoda and Myriapoda) showed a lower but non-significant documentation rate ($\beta = -0.758$, SE = 0.454, $p = 0.095$), with 40 new taxa documented over 5 years, corresponding to a mean of 8 ± 11 taxa/year (Fig. 10). Model diagnostics showed no overdispersion (dispersion ratio = 0.400, $p = 0.576$), with the model explaining substantial variation in documentation rates (conditional $R^2 = 0.859$; marginal $R^2 = 0.592$), indicating a considerable contribution of interannual variability.

The accumulation curves revealed substantial variation in both the total number and rate of taxa reported occurrence among colonization statuses of terrestrial arthropods (Fig. 11 ). Endemic arthropods, the reference category, had a baseline log-rate of 2.411 (SE = 0.376, $p < 0.001$), corresponding to an estimated mean of approximately 100 new taxa over 7 years, a mean of 14.3 ± 13.5 taxa/year. Introduced arthropods showed a significantly higher documentation rate ($\beta = 0.982$, SE = 0.326, $p = 0.023$) with 325 new taxa over 8 years, a mean of 40.6 ± 38.3 taxa/year. In contrast, native arthropods did not differ significantly from endemics ($\beta = 0.536$, SE = 0.324, $p = 0.098$), with 224 new taxa over 8 years, a mean of 28 ± 25.4 taxa/year, nor did Indeterminate in origin arthropods ($\beta = -0.062$, SE = 0.364, $p = 0.863$), with 115 new taxa over 6 years, a mean of 19.2 ± 20.5 taxa/year, although Indeterminates showed a slightly lower point estimate than the endemic baseline (Fig. 11).

The high standard deviations relative to the means (coefficients of variation exceeding 90% for all colonization statuses) indicated a high interannual variability in discovery rates, suggesting episodic rather than continuous taxa accumulation. Model diagnostics indicated no overdispersion (dispersion ratio = 1, $p = 0.792$), with the model explaining substantial variation in discovery rates (conditional $R^2 = 0.748$), although fixed effects alone accounted for a modest proportion (marginal $R^2 = 0.1168$), indicating that interannual variability played a considerable role.

Finally, the accumulation curves showed that none of the colonization statuses had reached a clear asymptote by 2026 (Fig. 11), suggesting that additional taxa remain to be documented across all groups. The steepest accumulation trajectory was observed for introduced taxa, which continued to show substantial annual additions through the final year. Endemics, despite having the lowest total richness, exhibited a relatively consistent accumulation pattern, with new taxa added in most years

## Species-Area Relationship

Species–Area Relationship (SAR) models revealed substantial variation in the strength and fit across taxonomic groups and colonization categories (Fig. 12). The Power model (S = c × A^z) explained between 21% and 83% of the variation in taxa richness across the Azorean islands, depending on the group considered (Table 1). The highest $R^2$ values were observed for native bryophytes ($R^2$ = 0.83, adjusted $R^2$ = 0.67) and endemic bryophytes ($R^2$ = 0.69, adjusted $R^2$ = 0.38), indicating that island area strongly predicted richness for bryophytes. Indeterminate Tracheophytes also showed a good fit ($R^2$ = 0.69, adjusted $R^2$ = 0.54). In contrast, the poorest fits were found for native tracheophytes ($R^2$ = 0.21, adjusted $R^2$ = - 0.10), suggesting that factors other than area play a more prominent role in determining richness for this group. Among terrestrial arthropods, model fit was moderate and relatively consistent across colonization categories, with $R^2$ values ranging from 0.42 (Indeterminate) to 0.47 (Native), though adjusted $R^2$ values were considerably lower (0.22–0.26).

The slope parameter z, which quantifies the rate at which richness increases with island area, varied markedly among groups. The steepest slopes were observed for Indeterminate Tracheophytes (z = 0.66), followed by endemic bryophytes (z = 0.52), introduced tracheophytes (z = 0.52), and native bryophytes (z = 0.45). Terrestrial arthropods displayed moderate and relatively consistent z-values, ranging from 0.34 (Introduced) to 0.41 (Native). These differences indicate that taxa richness in tracheophytes (particularly Indeterminates) increases more rapidly with island area (Fig. 12).

## Research effort through the Azores

Research effort varied considerably across the Azorean islands, both in the number of publications reporting taxa records and in the cumulative documentation of new records (Figs 13, 14). Terceira and Pico (Central group) accounted for the highest number of publications, followed by São Miguel (Eastern group), while Corvo and Flores (Western group), together with Graciosa and São Jorge (Central group), showed substantially fewer publications, indicating comparatively limited research attention (Fig. 13). This pattern was mirrored in the cumulative number of terrestrial new records, which increased across all islands between 2018 and 2026 but at markedly different rates (Fig. 14). Terceira exhibited the steepest accumulation trajectory, consistent with its higher research effort, while Pico and São Miguel showed intermediate rates. The remaining islands displayed comparatively shallow trajectories, with limited annual additions of new records. The archipelago-wide cumulative curve (Azores total) reached approximately 115 records by 2026, with no indication of an asymptote.

## Discussion

Our results clearly show the continuous growth in documenting taxa in the Azores, driven by the AZORES BIOTA and BioMonI-Plot collections. However, this progress must be interpreted through the lens of three well-established biodiversity knowledge shortfalls.

First, the Wallacean shortfall, the incomplete knowledge of species geographic distributions, is starkly evident in our data. Occurrence records are heavily concentrated on the three largest islands (São Miguel, Terceira, and Pico), while smaller islands, particularly in the Western group (Corvo and Flores), remain severely under-sampled, reflecting the concentration of research infrastructure and historical collecting effort on the larger, more accessible islands. This is particularly problematic in the case of Flores which has the largest native forest fragments of the archipelago compared to its area (around 11%) (Gaspar et al. 2008). This spatial bias implies that the true distribution of most Azorean taxa across the archipelago remains unknown, limiting the dataset's utility for conservation planning, protected area designation, and invasion monitoring on less-studied islands (Hortal et al. 2015, Reilly et al. 2023).

Second, the Prestonian shortfall, namely the lack of abundance data and temporal population trends, is reflected in the episodic nature of occurrence reporting across all taxonomic groups. The high coefficients of variation (>90% for arthropods, 72–109% for tracheophytes) indicate that records accumulate in pulses rather than through systematic monitoring. Although many source datasets include abundance (all the arthropod datasets) or sampling-event information, the present synthesis mainly analyses species incidence and occurrenceID-linked documentation; therefore, it remains limited for evaluating population size, viability or abundance trends. Abundance data is important to distinguish between stable populations and those persisting at critically low numbers, a distinction essential for extinction risk assessment (Cardoso et al. 2011a, Hortal et al. 2015).

Third, the Darwinian shortfall, the limited knowledge of species' phylogenetic relationships and evolutionary history, constrains the interpretative power of the dataset ( Diniz-Filho et al. 2013, Hortal et al. 2015). Occurrence records document where taxa are found but provide little information on the evolutionary history represented by those records. This gap is particularly relevant in the Azores, where the evolutionary origins and relationships of many endemic lineages remain incompletely resolved. More comprehensive phylogenetic frameworks would allow conservation assessments to incorporate evolutionary distinctiveness and identify taxa representing disproportionate amounts of unique evolutionary history (Diniz-Filho et al. 2013, Hortal et al. 2015). Bridging the Darwinian shortfall therefore requires greater integration of molecular phylogenetic information with the existing occurrence-data infrastructure.

Progress is also being made towards reducing the related Hutchinsonian shortfall, which concerns incomplete knowledge of species' ecological attributes and niches (Cardoso et

al. 2011a, Hortal et al. 2015). A recent example is the publication of a comprehensive functional-trait database for Azorean arthropods (Oyarzabal et al. 2026), which consolidates trait information of the type already used to investigate ecological responses and conservation vulnerability in Azorean arthropods (e.g. Oyarzabal et al. 2024, Oyarzabal et al. 2025).

Therefore, while our primary objective of demonstrating continued temporal growth in taxa documentation was met, the data simultaneously reveal the depth of remaining knowledge gaps in the Azores archipelago. Addressing these shortfalls will likely require a strategic shift towards spatially balanced survey designs, systematic abundance monitoring, and sustained temporal sampling, without which the Azorean biota will remain incompletely known, and conservation decisions will continue to be made under considerable uncertainty.

## Imbalance in spatial and taxonomic coverage

Our results reveal marked imbalances in both taxonomic and spatial coverage. Although the collections capture a meaningful fraction of the known Azorean biota, important data-mobilization gaps persist, particularly for less-studied or range-restricted taxa and for marine biodiversity. The SAR analyses further indicate that island area alone cannot explain observed taxon richness. Unequal survey effort is likely to contribute substantially to these patterns: São Miguel, Terceira and Pico have received disproportionately greater research attention, whereas several smaller islands, particularly Corvo and Flores, remain comparatively under-sampled. Consequently, the higher observed richness of larger islands may partly reflect greater survey completeness in addition to genuine biogeographic effects. This interpretation is consistent with other findings, where intensive, long-term sampling substantially increased the number of documented taxa, demonstrating that observed richness can be strongly dependent on survey effort even in relatively well-studied protected areas (Saunders and Ward 2018, Ichter et al. 2022, Pitogo et al. 2026). Consequently, the SAR models presented here should be interpreted as reflecting both genuine biogeographical patterns and the legacy of spatially biased research effort across the archipelago, as they represent an entanglement of genuine biogeographical processes and spatially non-random research effort (Drakare et al. 2005 , Guedes et al. 2023).

Taxonomically, arthropods dominate the dataset, followed by tracheophytes, while other groups remain comparatively underrepresented or almost entirely missing such as the case of Mollusca (Fig. 15). This imbalance likely reflects not only genuine differences in taxa richness but also the historical availability of taxonomists. Arthropods are both the most speciose major group in the Azores and the best represented in the present corpus, reflecting sustained specialist attention over recent decades, including comprehensive checklists and dedicated sampling programmes (Borges et al. 2010, Costa and Borges 2021, Borges et al. 2022b, Borges et al. 2022c, Lhoumeau and Borges 2023, Pozsgai et al. 2024). Similarly, tracheophytes have received considerable attention due to the existence of well-established endemic, native and introduced floras, and their

prominence in habitat characterization studies (Gabriel et al. 2014, Elias et al. 2016, Sousa et al. 2024). However, this relatively strong taxonomic knowledge does not necessarily imply that endemic diversity is fully resolved, as molecular evidence has revealed previously overlooked genetic lineages within several endemic plant taxa, suggesting that current taxonomic circumscriptions may underestimate the true extent of endemic diversity (Schaefer et al. 2011, Roxo et al. 2026).

Bryophytes offer an instructive counterpoint (Fig. 15). Despite their relatively small total taxon pool, they have attracted considerable specialist attention in the Azores, including targeted survey efforts and repeated taxonomic revisions (Gabriel and Bates 2005, Gabriel et al. 2014, Gabriel et al. 2024a, Gabriel et al. 2024b, Henriques et al. 2017). This sustained effort, combined with the naturally low endemic richness of Azorean bryophytes, has resulted in the early documentation of nearly all known endemic bryophyte taxa, with the sole exception of *Trematodon perssoniorum* P.Allorge & Thér. ex V.Allorge (1951). However, comprehensive coverage of the endemic flora does not translate into comprehensive coverage of the group as a whole, because endemics represent only a fraction of Azorean bryophyte diversity (Gabriel and Bates 2005, Gabriel et al. 2024a, Gabriel et al. 2024b). The remaining taxa, predominantly native non-endemics, are far more numerous yet remain under-documented in published, occurrenceID-linked datasets. The causes are twofold: identification requires microscopic examination and specialized training, which slows specimen processing; and much of the existing material is held in herbaria or referenced in grey literature that has not been digitized or published in standardized formats. The consequence is that overall bryophyte representation in the dataset remains disproportionately low relative to the taxonomic effort the group has received. Closing this gap requires not only sustained taxonomic work but targeted investment in molecular tools and dedicated data papers to accelerate the flow of existing collections into accessible databases, particularly for the speciose native (Macaronesian) flora (Vanderpoorten et al. 2007). This is especially relevant given that several islands still lack any published study, meaning that bryophyte records from those islands may exist but remain unavailable for synthesis.

In contrast, chordates and fungi remain markedly underrepresented, though for fundamentally different reasons (Fig. 15). Chordates suffer from a lack of georeferenced occurrence data, reflecting both the inherent demands of systematic vertebrate surveys and the archipelago's isolation, which complicates inter-island logistics and concentrates research on the most accessible islands. These constraints are compounded by the limited number of taxonomic specialists, a tendency for opportunistic sightings to be published without precise coordinates, and the fact that many observations remain unpublished or inaccessible in technical reports and institutional databases (Meyer et al. 2015, García-Roselló et al. 2025). For instance, for mobile or pelagic species, point localities are inherently ambiguous: records from tourism operators are concentrated along island coasts and vessel routes, potentially reflecting patterns of observation effort rather than species distributions alone coasts, where those vessels operate, reflecting operational pattern rather than ecology. Precision thresholds also differ between realms: a 10-metre GPS error is negligible on land, but at sea it can represent a meaningful

displacement relative to a vessel-based observation, where coordinates may be recorded at any point along the vessel's track (Moudrý and Devillers 2020). Marine chordate records therefore require explicit georeferencing protocols, and spatial analyses should account for substantially greater positional uncertainty than for terrestrial taxa (Fig. 15). This scarcity should not, however, be read as an absence of observations: iNaturalist alone hosts over 18,000 chordate records for the Azores (at: https://www.inaturalist.org. Accessed September 17th 2026), showing that citizen science may be highly effective for this taxon. The gap is thus one of mobilization into standardized, occurrenceID-linked datasets rather than of observational effort, and integrating such complementary sources could substantially improve coverage. Fungi face a different but equally constraining set of challenges. Although more than 570 species being documented recently (Souto et al. 2024, Monjardino et al. 2026), fungi remain underrepresentation stems from the ephemeral and cryptic nature of fungal fruiting bodies, which makes systematic survey work highly seasonal and weather-dependent, and from the increasing reliance on molecular methods for accurate species-level identification, as morphological characters alone are often insufficient (Cannon 1999, Yahr et al. 2016, Truong et al. 2017). These barriers are now partly mitigated by molecular methods. DNA-based approaches, including amplicon and shotgun sequencing, can substantially improve taxonomic resolution, particularly where morphological characters alone are insufficient (Monjardino et al. 2026). However, molecular workflows require specialized infrastructure, bioinformatic expertise, and well-curated reference databases, and they still depend on taxonomic specialists for validation and interpretation (Waterhouse et al. 2022). Coupled with the ongoing global shortage of fungal taxonomists, this means that even well-collected and well-stored specimens may remain unidentified for extended periods.

Collectively, these patterns reveal that taxonomic representation in the Azorean dataset reflects the historical geography of research effort rather than ecological importance. The two most striking cases, chordates and mollusks, defy global expectations: chordates are the most intensively studied animal group worldwide (Hochkirch et al. 2020, Caldwell et al. 2024), and land snails are recognized for exceptionally high endemism and rapid speciation (Holland and Cowie 2009, Drost et al. 2018, Proios et al. 2021, Osborne et al. 2024); both would be expected to feature prominently in any biodiversity inventory, yet both remain poorly documented locally. Conversely, spiders and beetles, far from "high-profile" taxa, are comparatively well represented, reflecting the legacy of dedicated local expertise rather than global research priorities. This configuration indicates that data gaps in the Azores are shaped less by inherent taxonomic difficulty than by the contingent presence or absence of sustained specialist communities.

Ironically, the pattern we found is not unique to the Azores archipelago. Globally, prioritization constrained by limited funding tends to reinforce existing biases by channeling resources toward taxa with established research communities, accessible identification pathways, or active conservation programmes, while data-poor groups are deprioritized precisely because their knowledge gaps appear prohibitively expensive to close (Hochkirch et al. 2020, Caldwell et al. 2024). The Azorean case nonetheless

demonstrates that this dynamic is contingent rather than deterministic: where local expertise has been cultivated, even taxonomically challenging groups have been documented effectively. Without deliberate intervention, however, the shortfalls described above will persist, perpetuating uneven evidence availability and potentially reinforcing biases in conservation attention. Closing them will require reorienting research investment toward a more balanced portfolio that combines spatially balanced surveys, sustained taxonomic training, international collaboration, and molecular tools, including environmental DNA (eDNA) (Taberlet et al. 2012), to accelerate documentation of undersampled taxa and islands.

## Supporting invasion early warning and restoration targeting

Our results establish an important baseline for monitoring biological invasions, although its interpretation must account for the uneven spatial coverage of the underlying data. Introduced taxa exhibited the steepest accumulation trajectories in both terrestrial arthropods (317 taxa; 39.6 ± 39.7 taxa/year) and tracheophytes (407 taxa; 81.4 ± 48.4 taxa/year), indicating ongoing additions to the introduced biota. However, the episodic nature of occurrence reporting reveals an uneven sampling effort across the different islands, as discussed above, which limits the capacity for early detection of new introductions critical for effective invasion management (Venette et al. 2021, Howard et al. 2022). This limitation is compounded by the dataset's strong spatial bias toward larger islands (São Miguel, Terceira, and Pico), meaning that new arrivals on less-studied islands, particularly those in the Western group (Corvo and Flores), may remain undetected for longer periods, allowing populations to establish and spread before management actions are initiated. Hence, any attempt to restore native communities on smaller islands must contend with an unknown baseline of invasive taxa pressure, making it difficult to set realistic recovery targets or to determine whether management interventions are succeeding. As suggested by other authors, without systematic monitoring across all islands, restoration efforts risk being undermined by undetected invasions that erode hard-won conservation gains (Watari et al. 2013, Cordell et al. 2016, Nogué et al. 2017).

Effective invasion management requires an integrated strategy operating across three complementary lines: prevention through regulation of introduction pathways, systematic monitoring and prospection of high-risk areas, and eradication or containment of established taxa (Hortal et al. 2015, Boieiro et al. 2023, Gabriel et al. 2024, Gabriel et al. 2024a, Gabriel et al. 2024b, Oyarzabal et al. 2024). A systematic review of 260 documents identified early detection, rapid response, and robust biosecurity protocols as primary strategies for invasion management globally, yet implementation across the Azorean archipelago remains inconsistent (Castro et al. 2024). Therefore, strengthening stakeholder involvement in biosecurity and early-detection programmes is essential, as human-mediated transport, particularly shipping, may be the major pathway for species introductions to oceanic islands (Lenzner et al. 2020, Costa and Borges 2021). Improving the archipelago's capacity for early detection and rapid response will require more spatially balanced monitoring and surveillance programmes that target both high-traffic

ports and currently undersampled islands. Although stakeholder participation in the Azores shows strong interest and positive attitudes, actual engagement remains limited across sectors (Calado 2019, Bettencourt et al. 2023). Our study, together with the broader AZORES BIOTA and BioMonI-Plot collections establishes a strong baseline for an expanded monitoring framework. However, realizing its potential depends on sustained investment in systematic, archipelago-wide surveillance and on converting stakeholder willingness into long-term active participation.

## Conclusions

The AZORES BIOTA and BioMonI-Plot collections demonstrate the value of structured, open and standardized biodiversity-data publication for building a long-term knowledge base in a remote oceanic archipelago. However, our synthesis also shows that data mobilization remains uneven across islands, taxa, habitats and time. The Darwinian shortfall persists, as phylogenetic information and evolutionary context remain largely absent from the dataset, limiting its capacity to inform phylogenetically informed conservation planning. The Wallacean shortfall is evident in the strong spatial bias toward larger islands, confounding species–area relationships and undermining restoration baselines for smaller islands whose documented richness may be artificially depressed by lower sampling effort. Finally, the Prestonian shortfall is considerably alleviated within AZORES BIOTA because all arthropod datasets include abundance data rather than simple presence records. Moreover, long-term initiatives such as the implementation of the BALA (Pozsgai et al. 2024, Pozsgai et al. 2026) and SLAM ( Lhoumeau et al. 2022a, Lhoumeau et al. 2022b, Borges 2025) protocols provide repeated standardized surveys that enable the assessment of population trends for many species. However, long-term demographic information is still unavailable for several taxonomic groups (such as fungi, chordates, land snails, marine invertebrates, and most arthropod orders other than a few well-studied beetle and spider groups) and habitats (such as cave systems, deep-sea environments, freshwater ecosystems, and coastal environments). Taxonomically, these shortfalls are compounded by persistent biases: arthropods and tracheophytes dominate the dataset, while chordates and fungi remain critically underrepresented, and Mollusca is almost absent. Bryophytes, despite near-complete endemic coverage, lack comprehensive digitized records for their native species, illustrating that research intensity alone does not guarantee data mobilization.

Closing these interconnected shortfalls and constraints requires more than continued data accumulation. It demands deliberate investment in under-sampled taxa and islands, systematic abundance monitoring, sustained temporal sampling, taxonomic capacity, international collaboration, molecular tools and stakeholder engagement. Addressing these dimensions together would allow conservation planning in the Azores to move beyond documenting species occurrence towards understanding how biodiversity is distributed, how populations are changing and where conservation intervention is most needed. Continued data publication, combined with taxonomic expertise, harmonized metadata and sustained monitoring, can therefore enable AZORES BIOTA and BioMonI-

Plot to evolve from an open archive of biodiversity records into a comprehensive monitoring infrastructure supporting biodiversity-change detection, biosecurity, restoration and conservation planning across the archipelago.

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## Conflicts of interest

The authors have declared that no competing interests exist.
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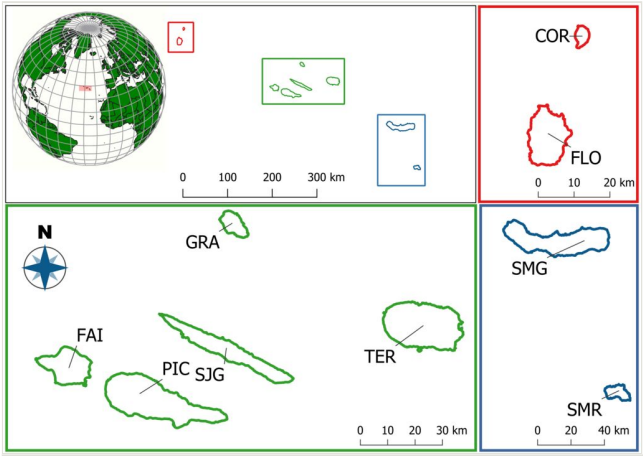



Figure 1.

The Azores archipelago. Top left shows the position of the three island groups: Western – red for Corvo (COR) and Flores (FLO); Central – green for Faial (FAI), Pico (PIC), São Jorge (SJG), Graciosa (GRA), and Terceira (TER); and Eastern – blue for São Miguel (SMG) and Santa Maria (SMR). Adapted from Oyarzabal et al. (2025).

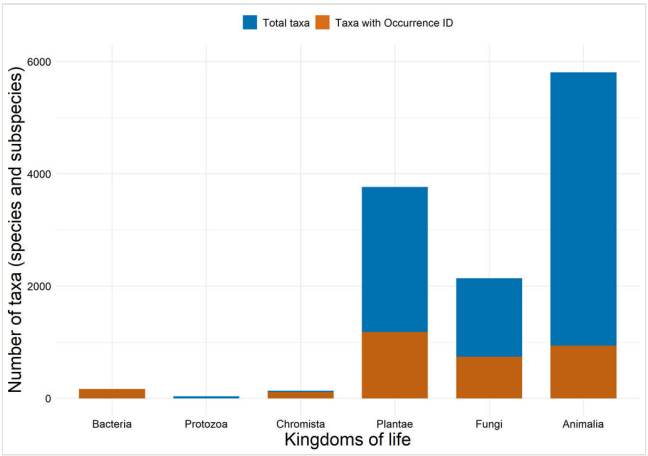



Figure 2.

Taxa (species and subspecies) richness across kingdoms of life in the Azorean biodiversity dataset. Dark blue bars represent the total number of unique taxa recorded per kingdom; orange bars indicate the subset of taxa with valid occurrenceID-linked and georeferenced records.

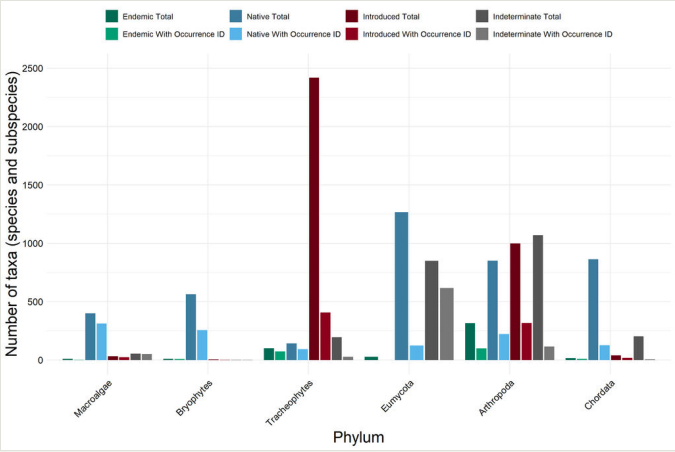



Figure 3.

Taxa (species and subspecies) richness by phylum and colonization status. Colonization statuses are shown as Endemic (green), Native (blue), Introduced (red), and Indeterminate (grey). For each color, darker shades represent total unique taxa per category known for the Azores; lighter shades indicate taxa with valid occurrenceID-linked and georeferenced records.

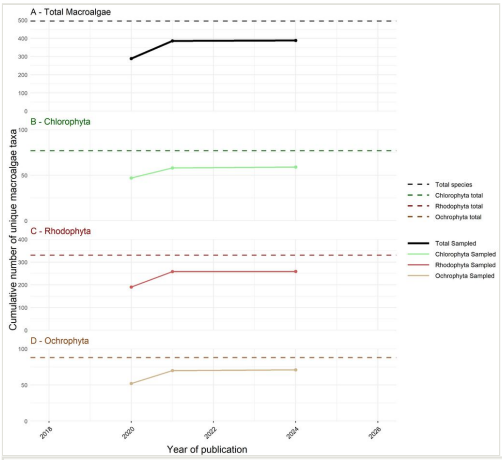



Figure 4.

Taxa (species and subspecies) accumulation curves for macroalgae across groups (2018–2026). A - cumulative curve for all macroalgae combined. B–D display cumulative curves for Chlorophyta, Rhodophyta and Ochrophyta taxa, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among taxonomic groups.

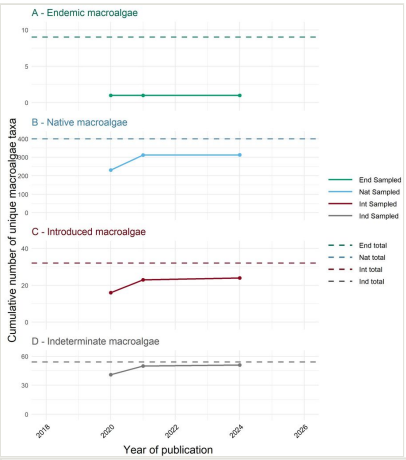



Figure 5.

Taxa (species and subspecies) accumulation curves for macroalgae across colonization statuses (2018–2026). A–D display cumulative curves for Endemic, Native, Introduced, and Indeterminate taxa, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richnesss among colonization statuses.

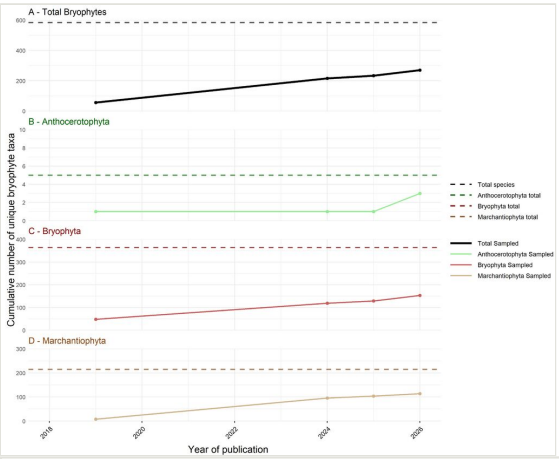



Figure 6.

Taxa (species and subspecies) accumulation curves for bryophytes across groups (2018–2026). A - cumulative curve for all bryophytes combined. B–D display cumulative curves for Anthocerotophyta, Bryophyta and Marchantiophyta taxa, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among taxonomic groups.

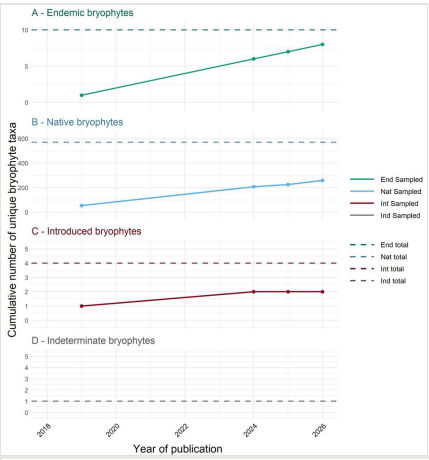



Figure 7.

Taxa (species and subspecies) accumulation curves for bryophytes across colonization statuses (2018–2026). A–D display cumulative curves for Endemic, Native, Introduced, and Indeterminate taxa, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among colonization statuses.

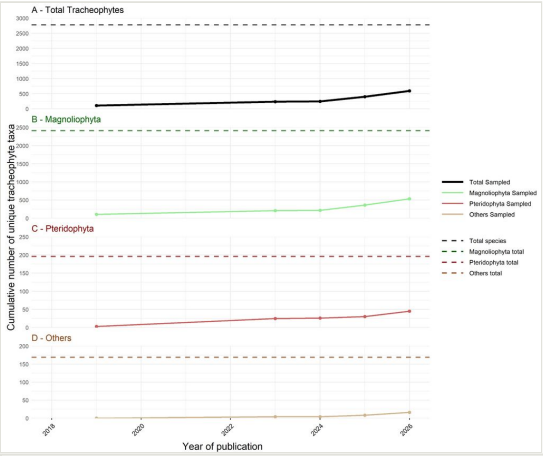



Figure 8.

Taxa (species and subspecies) accumulation curves for tracheophyte across groups (2018–2026). A - cumulative curve for all tracheophyte combined. B–D display cumulative curves for Magnoliophyta and Pteridophyta taxa and other minor groups, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among taxonomic groups.

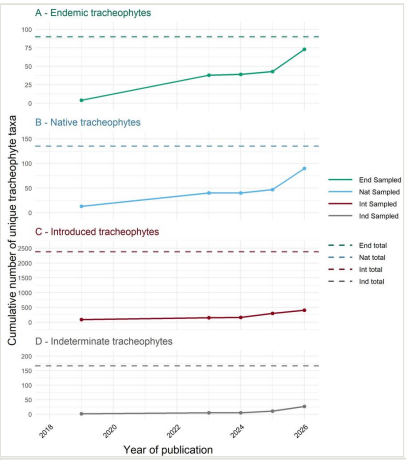



Figure 9.

Taxa (species and subspecies) accumulation curves for tracheophytes across colonization statuses (2018–2026). A–D display cumulative curves for Endemic, Native, Introduced, and Indeterminate taxa, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among colonization statuses.

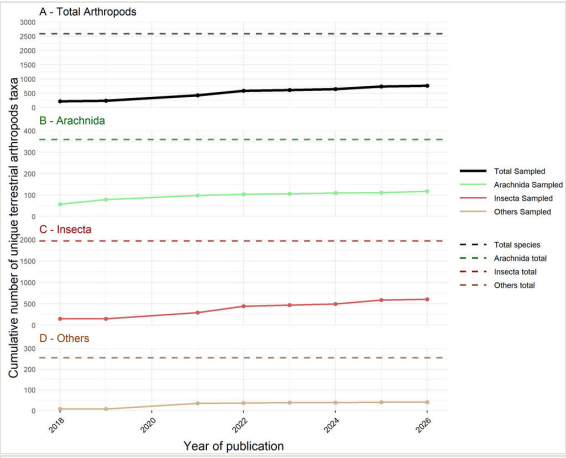



Figure 10.

Taxa (species and subspecies) accumulation curves for terrestrial arthropods across groups (2018–2026). A - cumulative curve for all terrestrial arthropods combined. B–D display cumulative curves for Arachnida and Insecta taxa and other minor groups, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among taxonomic groups.

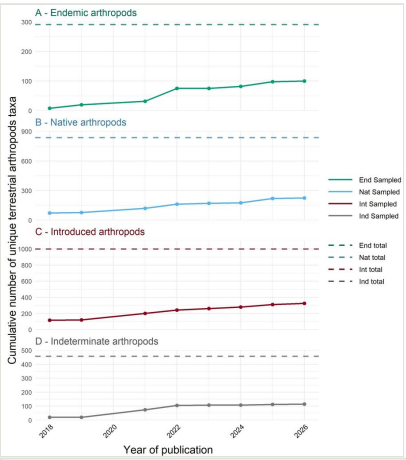



Figure 11.

Taxa (species and subspecies) accumulation curves for terrestrial arthropods across colonization statuses (2018–2026). A–D display cumulative curves for Endemic, Native, Introduced, and Indeterminate taxa, respectively. Solid lines represent the cumulative number of unique taxa documented over time, based on the earliest record of each taxon. Dashed horizontal lines indicate the total known taxon richness for each category. Note the different y-axis scales across panels, reflecting the substantial variation in taxon richness among colonization statuses.

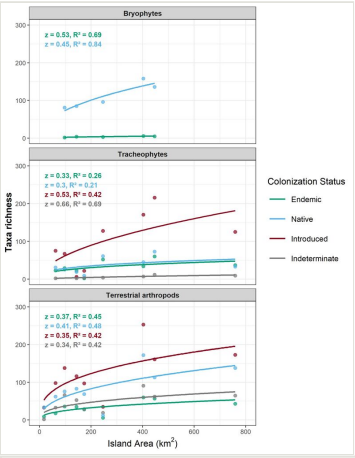



Figure 12.

Species–Area Relationship (SAR) with Power model (S = c × A^z) fitted for each phylum group and colonization status across the Azorean islands. z = slope of the SAR; colors indicate colonization status.

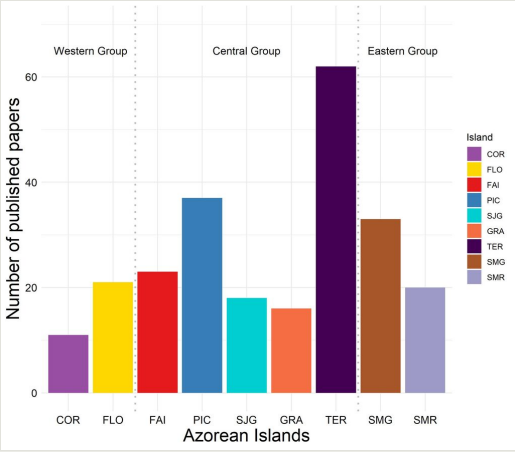



Figure 13.

Number of published papers reporting taxa records across the nine islands of the Azores archipelago. Islands are grouped by geographical region: Western group (COR: Corvo, FLO: Flores), Central group (FAI: Faial, PIC: Pico, SJG: São Jorge, GRA: Graciosa, TER: Terceira), and Eastern group (SMG: São Miguel, SMR: Santa Maria). Dashed vertical lines delineate the three island groups.

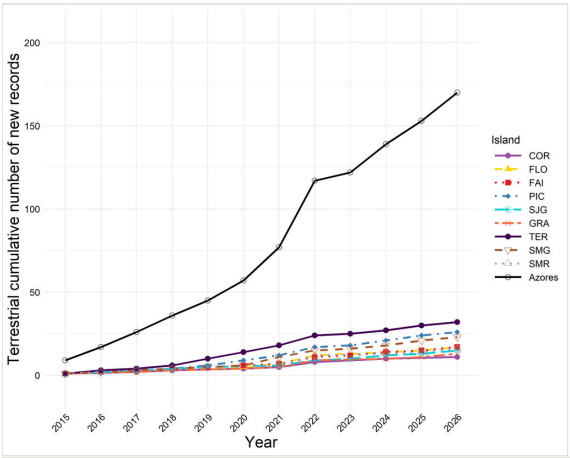



Figure 14.

Cumulative number of new terrestrial taxa records per island and for the Azores archipelago (black line) over the period 2016–2026. Curves represent the cumulative sum of unique new records reported annually for each island. The archipelago-wide total was calculated by summing annual records across all islands prior to accumulation.

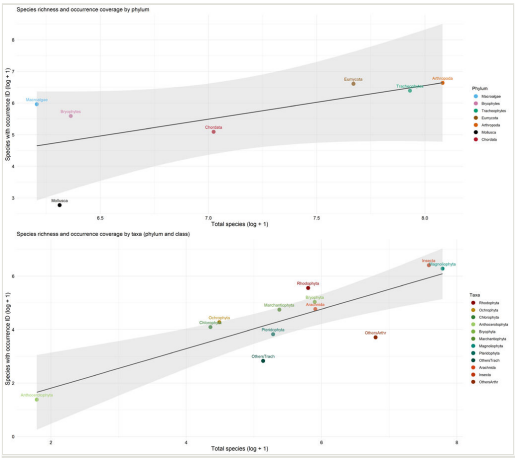



Figure 15.

Relationship between total known taxon richness and the number of taxa represented by occurrenceID-linked records across Azorean biodiversity groups. Points represent (A) phylum-level groups and (B) a finer breakdown separating other phyla and arthropod classes. Both axes are log-transformed (log + 1). The grey line shows a linear regression fitted across all groups, with 95% confidence intervals.

Table 1.

Species–Area Relationship (SAR) parameters for Azorean *taxa* across phylum groups and colonization statuses. Models were fitted using the Power model (S = c × A^z), where S is *taxa* richness and A is island area (km²). The c parameter represents the intercept, and z represents the slope of the species–area relationship. $R^2$ and adjusted $R^2$ indicate the proportion of variance in richness explained by island area.

| Phylum | Colonization Status | C value | Z value | R2 | Adjusted-R2 | Number of Islands |
|---|---|---|---|---|---|---|
| **Bryophyta** | Endemic | 0.21 | 0.52 | 0.69 | 0.38 | 5 |
| | Native | 9.10 | 0.45 | 0.83 | 0.67 | 5 |
| **Tracheophyta** | Endemic | 5.20 | 0.33 | 0.26 | -0.35 | 8 |
| | Native | 7.08 | 0.30 | 0.21 | -0.10 | 8 |
| | Introduced | 5.47 | 0.52 | 0.42 | 0.18 | 8 |
| | Indeterminate | 0.13 | 0.66 | 0.69 | 0.53 | 7 |
| **Terrestrial Arthropoda** | Endemic | 4.59 | 0.36 | 0.44 | 0.26 | 9 |
| | Native | 9.20 | 0.41 | 0.47 | 0.29 | 9 |
| | Introduced | 19.90 | 0.34 | 0.43 | 0.24 | 9 |
| | Indeterminate | 7.59 | 0.34 | 0.41 | 0.22 | 9 |

# Supplementary material

## Suppl. material 1: A decade of open biodiversity data in the Azores: closing knowledge gaps and building a foundation for long-term monitoring - Datasets

**Authors:** Ricardo Costa, Guilherme Oyarzabal, Rosalina Gabriel, Paulo A. V. Borges
**Data type:** Datasets
**Brief description:** Ten years of coordinated open-data publication in the Azores are consolidated in the AZORES BIOTA and BioMonI-Plot collections (Biodiversity Data Journal). Compiling 91 publications (2016–May 2026) across six kingdoms, they document 931 animal, 1,185 plant and 742 fungal species and subspecies, plus 598 additions to the Azorean Biodiversity Portal. These collections reduce the Wallacean shortfall and, through arthropod abundance data and repeated surveys, the Prestonian shortfall, establishing baselines for biodiversity assessment, invasion surveillance and conservation planning despite uneven coverage across islands, taxa and habitats.
READ_ME_Supplementary_Material_1_Tables_Informations.docx: This document contain all the information regarading the tables below, including their description and the description of each collum within them. It is higly recomended to take a look in this document first, before cheching the datasets.
Supplementary_Material_2_FullTable.csv: This table is a compilation of the scientific works and datasets present in the Biodiversity Data Journal collections of Azores Biota and Plot-based Surveys of Island Biodiversity – the BioMonI-Plot Network, as well as datasets that are currently published in the GBIF that have or will soon integrate publications in the Biodiversity Data Journal.
Supplementary_Material_3_Sampling.csv: This table is a compilation of the Standardized Protocols used in the scientific works and datasets present in the Biodiversity Data Journal collections of Azores Biota and Plot-based Surveys of Island Biodiversity – the BioMonI-Plot Network, as well as datasets that are currently published in the GBIF that have or will soon integrate publications in the Biodiversity Data Journal.
Supplementary_Material_4_New_Records_Azores.csv: This table is a compilation of the New records obtained for the studied islands in the scientific works and datasets present in the Biodiversity Data Journal collections of Azores Biota and Plot-based Surveys of Island Biodiversity – the BioMonI-Plot Network, as well as datasets that are currently published in the GBIF that have or will soon integrate publications in the Biodiversity Data Journal.
Supplementary_Material_5_New_Records_Islands.csv: This table is a compilation of the New records obtained for the archipelago in the scientific works and datasets present in the Biodiversity Data Journal collections of Azores Biota and Plot-based Surveys of Island Biodiversity – the BioMonI-Plot Network, as well as datasets that are currently published in the GBIF that have or will soon integrate publications in the Biodiversity Data Journal.

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