

PERSPECTIVE

ShareTrait: Towards interoperable and reusable individual trait-based data in ectotherms

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Handling Editor: David Costantini**Abstract**

1. More and more data on species traits are being collected and made openly available. Despite these efforts, effective syntheses of trait data to comprehend how species respond to and affect their environment are hampered by inadequate standards for publishing the data and the associated metadata, which limits the interoperability and reuse of data across studies.
2. We have developed *ShareTrait* (<https://sharetrait.org/>), a novel initiative that consolidates individual-level trait data and associated metadata in an interoperable and reusable format, enabling standardised and integrated use. As a proof-of-concept, we initially focus on three core traits of ectotherms: metabolic rate, development time and fecundity. These traits, measurable in almost all animals, are fundamental to an organism's overall fitness.
3. *ShareTrait* enables researchers to share their (meta)data with the research community. To date, researchers from diverse fields have contributed 28,692 individual-level data records to *ShareTrait*. These records originated from 45 datasets and are just the tip of the iceberg of existing data, highlighting the potential of *ShareTrait* to be a valuable community resource for meta-analyses and comparative approaches.

For affiliations refer to page 3133.

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4. Future directions of ShareTrait will focus on accumulating more records, expanding to cover more traits, including those measurable at the population level, and partnering with journals in relevant fields (ecology, physiology, evolution) to make sharing standardised trait data part of the standard publication process.
5. We envision ShareTrait, along with its digital infrastructure and comprehensive metadata, to be a catalyst for collating trait data across species. ShareTrait can streamline research efforts, minimise duplication and empower researchers to explore patterns and broader ecological, evolutionary and physiological questions among taxa (e.g. via meta-analyses and comparative approaches). This way, ShareTrait will unlock new frontiers in trait-based approaches, enhancing our understanding of species–environment relationships.

KEYWORDS

FAIR principles, metabolism, metadata, metazoans, ontogeny, phenotypes, reproduction, species traits

1 | INTRODUCTION

A fundamental objective in ecology and evolutionary biology is to uncover universal principles that govern the interactions between species and their environments. These principles can then be applied to safeguard biodiversity, maintain ecosystem integrity, and understand how distinct populations within a species adapt to shifting environmental conditions. Trait-based ecology has played a key role in advancing this objective (McGill et al., 2006). During recent decades, several influential studies have shaped the development of this field (e.g. de Bello et al., 2021; Díaz & Cabido, 2001; Kraft et al., 2008; Violle et al., 2007). By focusing on species' traits, rather than taxonomic identity, ecological studies can be compared across locations with differing species compositions (Chown et al., 2004; Marshall et al., 2012; Verberk et al., 2013). For instance, despite local variation in species composition, grouping species by trophic guild reveals regularities in the distribution of trophic guilds that respond consistently to global gradients in temperature and energy availability (González-Trujillo et al., 2025). Thus, the trait-based approach reduces context-dependency and enhances our ability to predict ecological responses across environmental gradients and across diverse ecosystems (Degen et al., 2018; Luza et al., 2023; McGill et al., 2006).

1.1 | The opportunity: More and more trait data are being collected

The success of trait-based ecology is evident in the growing number of publications on this topic, fuelled by the increasing collection of trait data for a wide range of species (Kattge et al., 2020; Klausmeier et al., 2020; Zakharaova et al., 2019). With the advent of open science, there is a strong emphasis on making trait data

openly available for reuse in meta-analyses and comparative studies (Keller et al., 2023; Schwanz et al., 2022), leading to substantial progress in implementing the FAIR principles (Findability, Accessibility, Interoperability and Reusability) for trait data (Culina et al., 2021; Gallagher et al., 2020). Most journals now encourage the practice of publishing data in online appendices or repositories, including trait data.

A multitude of comprehensive trait databases have emerged across various disciplines, such as TRY (Kattge et al., 2020), AusTraits (Falster et al., 2021) and BIEN (Enquist et al., 2016) for plant traits, FishBase (Froese & Pauly, 2024), WoRMS (Ahyong et al., 2024), Addmy-Pet (Marques et al., 2018) and AVONET (Tobias et al., 2022) for animal traits, and the Open Trait Network (<https://opentraits.org/datasets>), which currently lists 259 datasets. While these databases have greatly improved the findability and accessibility of trait data, significant challenges persist in ensuring interoperability between datasets from different studies, which limits their full potential for reusability in ecological research.

1.2 | The obstacles: Barriers to interoperability and reusability

Currently, three primary challenges hinder the implementation of the FAIR principles, particularly regarding interoperability and reusability, in animal trait data. First, the vast diversity of animal body plans and life histories poses a significant obstacle to trait standardisation (Moretti et al., 2017). This stands in evident contrast to molecular biology, where the abundance of ubiquitous nucleotide and protein sequences has facilitated the successful adoption of FAIR principles (Federhen, 2012). While molecular biology benefits from a relatively uniform foundation, animal ecology deals with a broader range of traits, most of them

specific to various taxonomic groups. This diversity manifests in pronounced differences in body plans, elemental composition, mobility and numerous other characteristics, each subject to unique evolutionary trade-offs. Consequently, the field of animal ecology must contend with a far more complex landscape when attempting to standardise and integrate trait data. Ectotherms, which represent over 99% of animal diversity, exemplify this challenge. Traits such as flight capacity or egg size are only relevant to specific taxonomic groups capable of flying or egg-laying, respectively. Moreover, applying standardised trait measurement protocols across taxonomic groups is often impractical, as methods for measuring a given trait must be tailored to suit the species biology (Moretti et al., 2017). To overcome this difficulty, separate trait databases have been created for specific taxonomic groups such as World Spider Trait database (Pekár et al., 2021) and Collembase (Timmermans et al., 2007) or selected traits such as GlobTherm (Bennett et al., 2018) and MetaR (Leiva et al., 2024).

The second challenge to interoperability and reusability stems from the disparate data formats employed, which complicate the process of combining and synthesising data. These formats range from Excel spreadsheets to machine-readable databases, encompassing measurements at various organisational levels (individual, population and species). Magnifying this challenge is the lack of uniform taxonomic identification, which exacerbates interoperability concerns, particularly when attempting to merge trait datasets that have undergone different taxonomic harmonisation processes. These factors not only introduce ambiguities in data interpretation but also hinder integration with other data types, such as phylogenetic information, geographical data and relevant environmental variables. This data sparsity and complexity contrast with plant biology, a field where the implementation of rigorous standards has largely resolved similar issues (Cornelissen et al., 2003).

A third challenge involving interoperability and reusability among animal trait datasets is the incomplete provision of metadata. Here, metadata are defined as *data for the data* (Jenkins et al., 2023) and include (but are not limited to) detailed information about environmental conditions (e.g. temperature, humidity, oxygen, photoperiod), organism-specific information (e.g. age/size, life stage, sex/mode of reproduction, place of origin, life history), experimental conditions (e.g. sampling design, incubation volume) and measurement techniques (e.g. different protocols and instruments). These metadata provide the relevant context in which the trait measurements were made and often greatly influence the outcome of these trait measurements. Previous studies compiling trait data have often been tailored to specific research questions and therefore do not report the full set of metadata (Dahlke et al., 2020; Herberstein et al., 2022; Makarieva et al., 2008). Incomplete sets of metadata limit our ability to assess the quality and appropriateness of data for reuse and prevent the integration of databases, hindering the broader application of trait data across studies and disciplines (Sielemann et al., 2020).

1.3 | Towards a solution: ShareTrait

To tackle the main challenges to interoperability and reusability of animal trait data, a systematic and coordinated approach is needed that develops and implements standardised protocols for trait measurements, comprehensive metadata standards and interoperable data formats. In response to this pressing need, we introduce ShareTrait, an innovative initiative aimed at enhancing the interoperability and reusability of trait data. Currently, ShareTrait focuses on three fundamental traits: metabolic rate, development time and fecundity, and important metadata, such as body mass and temperature. These traits, measurable in almost all animals, are considered the most fundamental life history traits because they directly govern the energy budget of organisms and how it is allocated to development and reproduction. In other words, these traits have direct links to fitness (Brown et al., 2004; Ricklefs & Wikelski, 2002; White et al., 2022; Zera & Harshman, 2001). ShareTrait is also designed with scalability in mind, allowing for the inclusion of additional traits in future versions.

A distinctive feature of ShareTrait is its capacity to store individual-level trait data, which is defined as a trait value that is measured on a single individual. The importance of including individual-level trait data has been recognised in some databases (e.g. plant traits in AusTraits), but most existing trait databases for animals typically operate at species or population levels (e.g. GlobTherm; Bennett et al., 2018). This granular focus enables researchers to explore trade-offs between traits and trait plasticity, and enhances the accuracy and predictive power of ecological models by incorporating intraspecific trait variation rather than assuming functional equivalence across all individuals (Kearney et al., 2021). Moreover, the availability of individual-level data allows for maximum analytical flexibility: researchers interested in population or species patterns can readily aggregate ShareTrait data to the desired level.

Another key feature of ShareTrait is its relational database structure (Figure 1). The internal architecture comprises multiple interconnected tables, linked through primary keys, ensuring non-redundant data storage. This structure improves accuracy, reduces storage demands and allows for versatile data incorporation without requiring a complete reorganisation of existing records. This design facilitates the addition of new traits and integration with existing datasets. Data retrieval is highly flexible; users can query any table or combination of tables using Structured Query Language (SQL), enabling them to customise datasets according to specific research requirements. This adaptability, combined with the R package RMySQL (Ooms et al., 2024), ensures efficient and user-friendly access to ShareTrait's datasets for R users, allowing them to connect to MySQL databases for ease of exploration and analysis.

In developing ShareTrait, we have prioritised the comprehensive inclusion of metadata, ensuring that both the trait data and associated contextual information are shared effectively. This approach is fundamental for the reuse of trait data in addressing

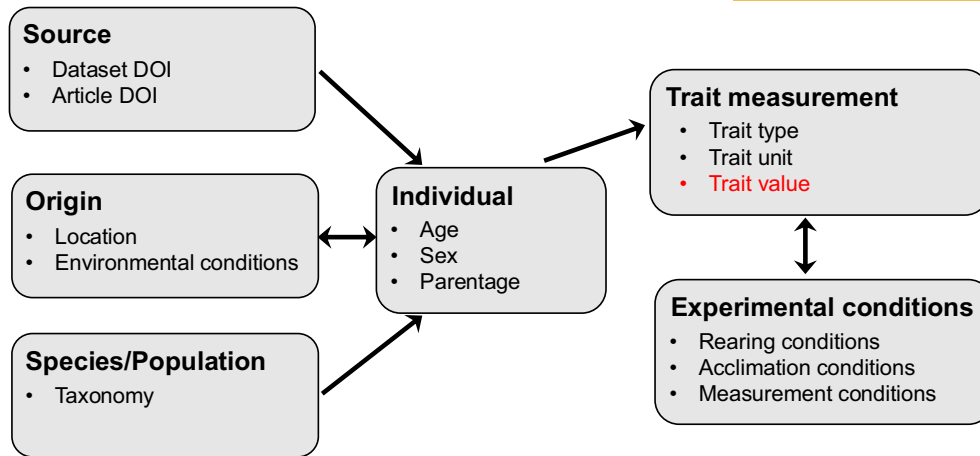


FIGURE 1 Schematic illustration of the structure of the ShareTrait relational database, which links traits measurements to their associated metadata. Here, metadata (indicated in black) refers to any information other than the trait value (e.g. metabolic rate, development or fecundity, indicated in red) measured at the individual level, providing essential contextual information regarding the data source, origin, species or population, individual specimen, trait measurement and experimental conditions. Individual specimens are linked to specific trait measurements and experimental conditions. Each specimen is traceable to its origin, complete with environmental data and is classified by population and species. For a detailed overview of the database structure, see [Figure S1](#).

diverse research questions, as it provides the necessary context to control for potentially confounding factors and isolate variables of interest. The metadata standards are designed to cover the requirements that are common across most trait-based studies. They adhere, where possible, to protocols and guidelines established by the research community (e.g. Killen et al., 2021; Leiva et al., 2024; Moretti et al., 2017; Wu et al., 2024), and include additional information deemed essential in expert panel interviews. For each trait (metabolic rates, development time, fecundity), we held three online expert panel interviews. Each panel included at least six researchers—ranging from early career to professors—with expertise in at least one of the traits under discussion. We conducted semi-structured interviews to gather feedback on the proposed metadata standards. Prior to these sessions, we provided experts with a current metadata list for review. While the experts did not reach complete agreement on every point, there was broad consensus regarding both the essential metadata to be reported and the proposed structure of the database. In a few cases, we followed up with additional discussions or emails to clarify or complete metadata.

The integration of these features within the ShareTrait database unlocks exciting opportunities for the exploration, curation, and analysis of trait (inter)relationships. [Figure 2](#) showcases several of these possibilities. For example, the database, encompassing both data and metadata, facilitates the examination of intraspecific variation among species and the identification of trade-offs between fundamental biological processes ([Figure 2a](#)). Also, the comprehensive dataset unveils new avenues for the identification of macrophysiological relationships such as patterns in energy usage and expenditure across the animal kingdom, and detection of potential outliers representing taxon-specific adaptations ([Figure 2b](#)). Leveraging the associated metadata, researchers can account for diverse sources of variation, including influences

from the environment, locality or study design, thereby enhancing the statistical rigour and precision of parameter estimation ([Figure 2c](#)) and enabling more refined interpretations of ecological and evolutionary phenomena.

By providing a comprehensive platform for trait data and associated metadata, ShareTrait prevents duplication of research efforts. Moreover, by promoting the sharing of all research data, regardless of findings, ShareTrait addresses the issue of publication bias favouring significant results (the file drawer problem, Rosenthal, 1979). Even data that fail to support a particular hypothesis holds value to the scientific community, enabling more rigorous hypothesis testing or exploration of alternative theories. Thus, ShareTrait serves as a catalyst for a more inclusive, representative, transparent and collaborative scientific process. In the following sections, we (i) describe the design of ShareTrait, including its workflow and key data considerations; (ii) present the trait data currently available in ShareTrait; and (iii) discuss the caveats and currently unresolved issues of ShareTrait. We conclude by outlining future steps for the development and expansion of ShareTrait.

2 | SHARETRAIT DESIGN AND WORKFLOW

ShareTrait is an open, community-driven initiative for animal trait data, empowering researchers to contribute their data or utilise available datasets on traits of interest. To enhance the interoperability and reusability of animal trait data, ShareTrait adopts the following approach ([Figure 3](#)):

- a. Only datasets that are archived elsewhere with a DOI (digital object identifier) can be submitted, ensuring that ShareTrait is not the primary archive. An online, interactive platform streamlines

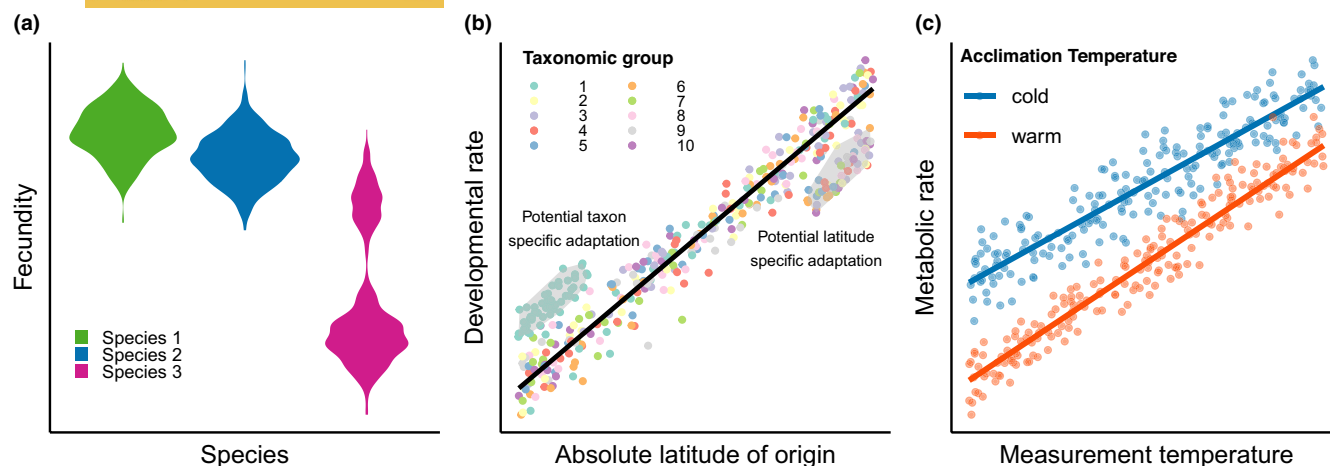


FIGURE 2 Conceptual illustration, using simulated data, showing how trait data and associated metadata can be utilised to address diverse research questions. (a) Comparing fecundity trait data among species: For a given species, natural selection can act on heritable variation across individuals. Species 3 exhibits a bimodal distribution, potentially indicating different cohorts following distinct developmental pathways or indicating disruptive selection. (b) Development rate (normalised to a single temperature across studies) increases towards higher latitudes and shorter seasons, exemplifying the use of location metadata associated with trait data. Deviations from the general trend may indicate specific adaptations in certain taxa, warranting further analysis. (c) Metabolic rate responses to the thermal environment highlight the contrasting effects of measurement conditions and acclimation conditions. Typically, metabolism increases with acute warming. However, when measured at a common temperature and standardised by body mass, animals acclimated to colder conditions often exhibit higher metabolic rates compared to their counterparts acclimated to warmer temperatures.

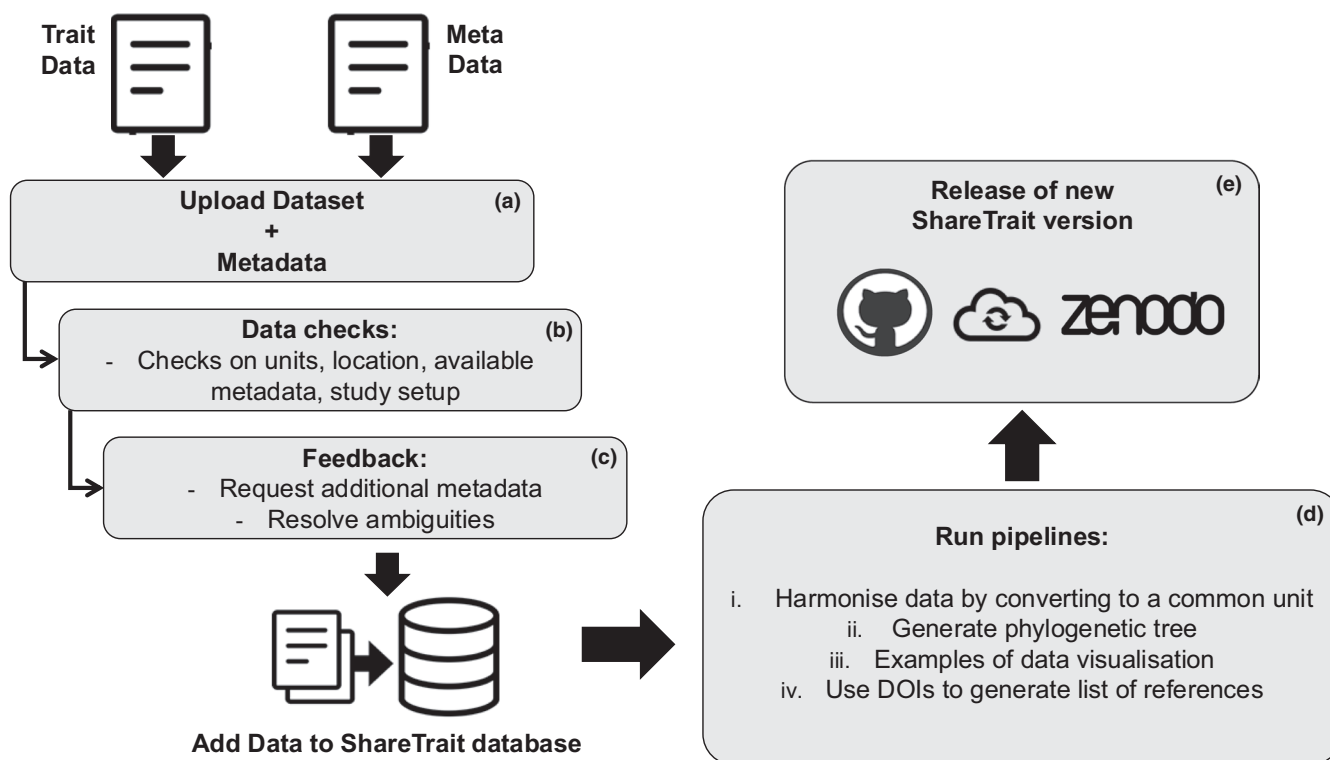


FIGURE 3 General workflow of ShareTrait. The process encompasses the following: (a) data submission with metadata; (b) rigorous quality controls; (c) feedback and problem resolution with contributors; (d) data standardisation via pipelines and (e) version control and continuous updates integrated with platforms like GitHub and Zenodo. This approach ensures data interoperability and consistency within ShareTrait.

data submissions. Data owners can contribute (meta)data through a user interface via www.sharetrait.org. Interoperability is strengthened through meta-data standards that describe trait measurements using uniform terminologies and by importing

(meta)data into a relational database structure. The user interface facilitates and standardises the entry of metadata through user-friendly dropdown menus and the provisioning of tailor-made templates for data submission. Metadata comprises information

- on the experimental conditions (e.g. temperature, oxygen level and humidity that the individuals experienced either prior to or during the trait measurements), biological aspects (e.g. body mass, the sex or life history stage of the individual and information on its parents), information related to the collection event (e.g. geographical coordinates of the collection site, date of collection, environmental conditions during collection) and experimental technique. In total, the database currently accommodates 113 different metadata variables (for an overview, see [Figure S1](#)).
- b. Rigorous data quality checks are performed on each submitted dataset. Standard quality control procedures are applied, including automated checks for missing data and anomalous values within variables, for example, values outside the range previously reported for the specific trait.
 - c. Feedback is requested from data contributors to obtain additional metadata that was missing or to resolve ambiguities. If an issue is identified during this feedback process, the data owner is contacted to verify the data or to resolve any errors. Once all feedback is incorporated and issues are addressed, the data are added to the ShareTrait database.
 - d. We have developed and implemented four pipelines in R (R Development Core Team, [2023](#)) to standardise the data, a critical step in ensuring consistency across different datasets:
 - (i) The first pipeline converts trait units into a unified format. The process involves harmonising trait expressions (e.g. unifying 'number of eggs' and 'number of offspring' to 'offspring number') and providing comprehensive metadata (e.g. specifying the developmental interval for 'developmental time', such as from hatching to first moult or from hatching to adulthood). This standardisation is facilitated through dropdown menus with predefined terminology in the user interface during data submission. Additionally, for metabolic rates, the script converts all oxygen consumption and carbon dioxide production units to milligrams of oxygen per hour per individual ($\text{mg O}_2 \text{ h}^{-1} \text{ ind}^{-1}$), a common unit used in comparative approaches and databases (Froese & Pauly, [2024](#); Leiva et al., [2024](#)).
 - (ii) A second pipeline involves the construction of a phylogenetic tree. Incorporating phylogenetic data in the form of a tree enhances the capacity to conduct comparative analyses (Felsenstein, [1985](#); Grafen, [1989](#)). The phylogenetic tree, derived from the Open Tree of Life (OTL; Rees & Cranston, [2017](#)), is pruned to retain only the species present in the most recent database version, utilising the 'rotl' package (Michonneau et al., [2016](#)). To mitigate the constant reorganisation of species identities, which can occur when species are removed or renamed due to published taxonomic revisions, the original species names (synonym) as reported in the datasets are retained in the current database and this feature will be maintained if a new version of ShareTrait is released with updated taxonomy. By keeping the original species names, we ensure that users can always trace the data back to its source, regardless of subsequent taxonomic changes.
 - (iii) The third pipeline enables users to visualise the data through maps that illustrate the geographic origins and geographic bias of selected data, as well as provide illustrative examples for exploring, analysing and visualising the available data. These examples demonstrate how the dataset can be employed to uncover biological patterns, such as the scaling relationship between metabolic rates and body mass (an important metadata variable), the temperature dependence of developmental time and environmental temperature or the association between fecundity and parent size (here considered as part of the metadata). For illustrative purposes, data points in these visualisations are segregated by species from different realms: freshwater, marine, intertidal and terrestrial. Researchers, however, retain the flexibility to apply alternative realm categorisations. By offering these tools and examples, we aim to enhance the accessibility and utility of ShareTrait, empowering researchers to explore and leverage the trait data from ShareTrait in their own studies.
 - (iv) The fourth pipeline facilitates attribution, which enables the generation of a list of references for the primary data sources utilised. This component is particularly important, as it recognises and highlights the work of data contributors, providing clear value and incentive for participation. To achieve this, we employed the function 'GetBibEntryWithDOI' from the 'RefManageR' package (McLean, [2017](#)), which retrieves bibliographic citations from DOIs associated with the primary sources. These citations are subsequently saved to a BibTeX file for efficient citation management. Alternatively, users can access the publicly available library on Zotero (<https://www.zotero.org/groups/4659193/sharetrait/collections/SZEVAKN2>), ensuring that the contributors' work are visible and easily citable by the research community.
 - e. The database is version-controlled and continuously updated on the project's website, with integration on platforms such as GitHub and Zenodo. Each release generates a suite of resources, including record maps and phylogenetic trees for the included taxa and a dictionary covering all the different columns in the database. A DOI is assigned to every version, enabling ShareTrait users to cite the specific database iteration they have utilised. To ensure reproducibility as new versions of ShareTrait are updated or corrected, we implement version control via GitHub and adhere to the Semantic Versioning Specification (SemVer, <https://semver.org/>). All the code required to replicate this workflow, including both the harmonisation and taxonomy processes, and the versioning of R packages used in the pipelines, is available at a GitHub repository (<https://github.com/ShareTraitProject/ShareTrait>).

3 | CURRENT DATA

ShareTrait was launched in November 2022, followed by two invitation events and a submission session aimed at engaging researchers

to contribute data, alongside a hands-on demonstration on the process of contributing data. The number of datasets contributed during this period is detailed in Figure 4. The current cumulative number of records across all datasets has already reached 28,692. This rapid accumulation of individual-level data demonstrates progress towards the realisation of the potential of ShareTrait as a resource for trait-based research.

The current version of ShareTrait predominantly comprises recent, peer-reviewed publications, with numerous studies reporting data on multiple traits (Alfaro-Tapia et al., 2022; Barneche et al., 2019; Burraco et al., 2019, 2020; Castañeda & Nespolo, 2013; Gebauer et al., 2007; Gomez Isaza et al., 2020a, 2020b; Hermaniuk et al., 2016, 2017, 2020; Hoffer et al., 2012; Jerbi-Elayed et al., 2021, 2022; Jorissen et al., 2023; Keinan et al., 2017; Le Goff et al., 2021; Le Lann et al., 2014; Leiva et al., 2015, 2016, 2018; Mesas & Castañeda, 2022; Molinet et al., 2023; Saeed et al., 2020; Semsarkazerouni et al., 2022; Shameer et al., 2018; Shokri et al., 2022; Tougeron et al., 2020, 2021; Tuni et al., 2016; van Dis et al., 2021; Verberk & Bilton, 2015; Vogels et al., 2021; Wu et al., 2015, 2018, 2022). The current version of ShareTrait includes 36 species, all of them represented in the Open Tree of Life. As a result, all species in ShareTrait v1.2.0 have associated phylogenetic information (Figure 5), which is particularly valuable for users who wish to incorporate this information into models that consider the shared evolutionary history of species.

4 | CREDIT AND ATTRIBUTION: QUESTIONS FOR THE RESEARCH COMMUNITY

Data sharing and reusing is a cornerstone of scientific progress, facilitating verification of methodologies, complementing replication of studies and the extension of existing knowledge. ShareTrait aims at serving as a valuable resource for the scientific community by providing open access to its foundational database under the CC BY 4.0 licence (<https://creativecommons.org/licenses/by/4.0/>). This licence allows users to freely access, share and adapt the database for any purpose, including commercial use, provided appropriate credit is given to the original contributors.

Despite the benefits of data sharing, researchers may be reluctant to share raw data due to concerns over losing control of its use or not receiving appropriate credit (Sequeira et al., 2024). It is crucial to acknowledge the considerable investment of time, effort and resources involved in acquiring primary data and curating datasets. Researchers contributing data deserve to be duly acknowledged for their contribution (Gallagher et al., 2020; Gomes et al., 2022). An effective way for acknowledging data contributors is to cite the original publications when utilising trait data (Lowenberg et al., 2019; Tenopir et al., 2011; Wood-Charlson et al., 2022). The practice of sharing data and consolidating it into databases offers numerous benefits beyond attribution, including the potential to foster

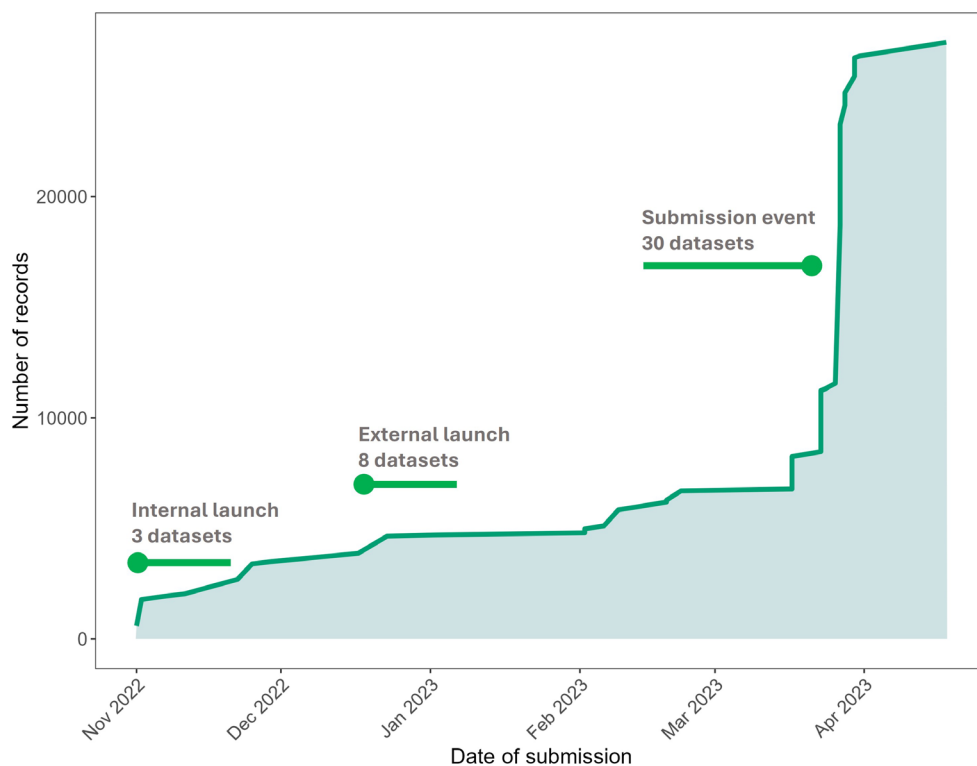


FIGURE 4 Cumulative records and datasets submitted to ShareTrait since November 2022. The internal and external launches, and the submission event are highlighted to show their impact on data accumulation for these particular events. In total, ShareTrait contains 45 datasets obtained from 34 published articles, which collectively correspond to 28,692 records. Note that some studies encompass multiple datasets, indicating the measurement of several traits per article.

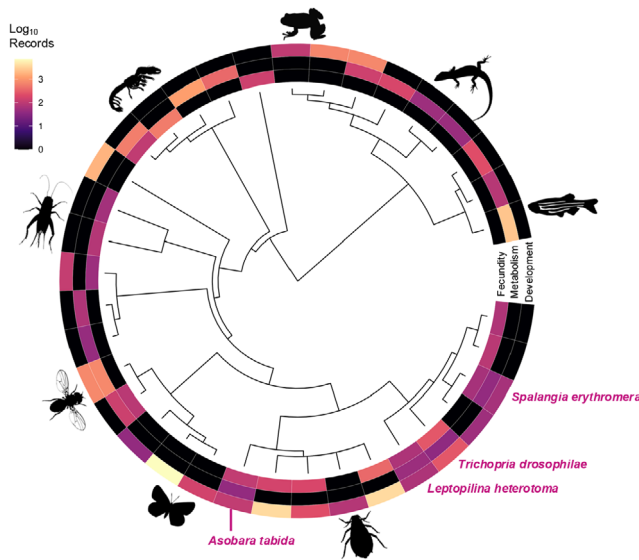


FIGURE 5 Distribution of record counts for animal traits and species and their phylogenetic relationships. The bars represent the number of records mapped for each of the 36 species present in the current version of ShareTrait. The main taxonomic groups are represented by silhouettes (available at www.phylopic.org under public domain). The four species containing measurements for fecundity, metabolic rates and development time are also indicated. Branch lengths were calculated using Grafen's method (Grafen, 1989). The figure was plotted using the R package 'ggtree' (Yu et al., 2017).

collaborations among researchers. For those wishing to cite the database in their work, we recommend referencing this paper and the latest version of ShareTrait published on Zenodo (version 1.2.0; Leiva et al., 2025).

ShareTrait aims to promote open access to trait data without imposing undue restrictions or obligations on researchers utilising the database. Researchers using ShareTrait data will be encouraged to invite data contributors as collaborators, but this is no requirement for data re-usage. This approach introduces several challenging questions that merit consideration within the scientific community (Groth et al., 2020; Piwowar & Vision, 2013). For example, in cases where a meta-analysis or comparative approach relies predominantly on data from a small number of researchers in the field, the question is *Should these contributors be invited to collaborate?* Such collaborations could enhance data interpretation, given the contributors' expertise in the study system. Nevertheless, there is a current lack of established ethical guidelines for data reuse, raising the questions of *Does the scientific community need to develop standards for collaboration?* and *What is the best approach to recognise and involve primary data contributors in subsequent research?* We feel these are open questions that warrant attention and underscore the intricate relationship between data sharing, attribution, and collaboration in scientific research. While collaborations may seem logical in certain contexts, they could also create barriers to research progress where, for example, researchers cannot be contacted, or where there may be contradiction between earlier and later interpretations of

archived data. We posit that these issues require further discussion and consideration by the broader scientific community as data sharing practices continue to evolve.

5 | CAVEATS OF THE CURRENT VERSION

To date, ShareTrait mostly contains articles published in recent years. This is partly because the data associated with recent publications are more likely to be publicly accessible, but also because the authors of these works often possess up-to-date insights into the experimental details related to the trait measurements of interest, ensuring comprehensive metadata coverage. Focusing exclusively on recent data can introduce considerable biases and constraints, hindering the understanding of temporal trends and ultimately compromising the reliability of ecological research (Tessarolo et al., 2017). Such biases are particularly problematic when examining links between trait plasticity (e.g. metabolic rate) and biodiversity trends, which are vital for understanding the consequences of climate change (Bozinovic et al., 2011; Bozinovic & Pörtner, 2015). A potential solution would be to manually extract data from figures, tables, or text in studies published in years before the emergence of data repositories, which is a common method for data compilation, for example, meta-analyses (García-Gómez et al., 2024; Leiva et al., 2019; Noble et al., 2018; Pottier et al., 2022). However, the process of data extraction from primary literature can be time-consuming and resource-intensive and often does not provide individual-level data. Therefore, ShareTrait users are encouraged also to upload data derived from older literature. By also contributing data to ShareTrait that is extracted from the literature, researchers can streamline efforts and avoid duplication.

Additionally, obtaining individual-level data is not always feasible for each trait or taxonomic group. For example, the size of the animal may prevent individual measurements, or its biology does not allow rearing in the laboratory. Currently, ShareTrait does not handle trait data at the population or replicate-group level, but future versions of ShareTrait will include the option to submit population averages, medians and proportions along with sample sizes and appropriate measures of variation. While individual-level data remain the preferred standard, this addition will help prevent the aforementioned potential bias and broaden the scope and utility of ShareTrait.

Finally, it is important to acknowledge the potential for incomplete submissions by contributors. The automated quality checks stage, which may require contacting data owners to resolve flagged issues, is particularly susceptible to interruptions in the submission process. In cases where data owners are unable to resolve potential errors, the dataset may still be included in ShareTrait, but with unresolved flags incorporated into the (meta)data. This approach allows future users to make informed decisions as to whether or not to include such data in their analyses, thus maintaining transparency and data integrity. In addition, future developments in artificial intelligence (AI) can help to resolve errors and extract additional metadata. For example, recent studies demonstrate that GPT-4 can achieve perfect accuracy

in extracting species location names from scientific articles (Castro et al., 2024); however, as acknowledged by Cornelius et al. (2025), the accuracy of such AI tools in extracting information about measured traits can be improved further. Thus, we foresee that in the future, integrated AI will help streamline the process and reduce the time required for users to input (meta)data into ShareTrait.

6 | FUTURE DEVELOPMENTS AND OUTLOOK

ShareTrait aims to develop a comprehensive resource that empowers researchers to address diverse questions in animal ecology, physiology, and evolution, while promoting data standardisation and integration. We have described and implemented a series of steps that consolidate individual-level trait data and associated metadata in an interoperable and reusable format. As a complementary approach, we seek to implement future measures, as described below, focusing specifically on increasing the amount of (meta)data and expanding to further types of trait data.

6.1 | Promoting ShareTrait to the scientific community

Much of the data contributed to ShareTrait followed from specific invitations or workshops. Therefore, in the future, we will continue to promote ShareTrait to the scientific community at scientific events and symposia (e.g. Open Trait Network (OTN) meetings and annual meetings of relevant societies such as the Society for Experimental Biology (SEB), the Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology (SORTEE), the Ecological Society of America (ESA) and British Ecological Society (BES)). We will facilitate data contribution by organising workshops at these events.

6.2 | Partnering with academic journals

We envision a future where researchers share their trait (meta)data via ShareTrait as part of the publication process. Currently, more and more journals are asking researchers to deposit their data and code, and have partnered with data repositories such as Dryad (<https://datadryad.org/>) or Figshare (<https://figshare.com/>). However, the state of code and data sharing policies and their enforcement varies across journals in the fields of ecology, evolutionary biology and physiology (Parr & Cummings, 2005; Roche et al., 2015). We have contacted editors from a diverse range of scientific journals in these fields and informed them of our efforts. We are exploring potential collaborations to streamline the process for researchers to submit their data, paying specific attention to the format and inclusion of metadata, ensuring that both raw data and metadata are shared effectively. Initiatives such as the Global Biodiversity Information Facility (GBIF, <https://www.gbif.org/>) have demonstrated the value

of linking datasets to published research, significantly advancing ecological and biodiversity studies.

ShareTrait also aims to welcome submissions of embargoed data in the future. This feature will allow researchers to submit their data early in their workflow, which offers significant advantages. At this stage, the nuances of the work and associated metadata are still fresh in researchers' minds, making the sharing of (meta)data more efficient. This approach also supports partnering with journals to integrate data sharing into the publication process (see below). Embargoed data can be added to the database but will only be included in published versions after the specified embargo period expires.

6.3 | Expanding the range of traits

Currently, ShareTrait has only solicited data on three traits (fecundity, metabolism and development time), but our goal is to expand this scope by including additional traits, such as behavioural or morphological traits. Moreover, we also aim to include traits that are defined at the higher levels of biological organisation (e.g. of replicate groups, populations or species). For example, traits such as critical thermal limits or proportion survival are typically summarised across multiple individuals. To accelerate the expansion of ShareTrait, we will join forces with existing initiatives to collect large-scale trait data, such as our current collaboration with the European Thermal Fertility Network (<https://thermal-fertility-network-eseb.org/>; Bretman et al., 2024; Dougherty et al., 2024) to include thermal fertility measures. Similar approaches could include developmental viability or allometric scaling of metabolic rate.

7 | CONCLUSION

We envision ShareTrait as a valuable resource for researchers to answer their study questions, while promoting standardisation and data integration across the fields of animal ecology, evolution and physiology, and while preventing duplication of efforts. By promoting trait data interoperability and reusability, ShareTrait will allow researchers to unlock the full potential of trait-based approaches to advance our understanding of species–environment relationships, and attain a more interconnected scientific community that can effectively address complex ecological, physiological and evolutionary questions and contribute to informed conservation strategies.

AUTHOR CONTRIBUTIONS

Conceptualisation: Félix P. Leiva, Jacintha Eilers, Matty P. Berg and Wilco C.E.P. Verberk. *Data curation:* Félix P. Leiva. *Formal analysis:* Félix P. Leiva. *Funding acquisition:* Félix P. Leiva, Jacintha Eilers, Matty P. Berg, Steven L. Chown, Wilco C.E.P. Verberk. *Investigation:* Félix P. Leiva, Jacintha Eilers, Matty P. Berg, Wilco C.E.P. Verberk. *Data collection:* Félix P. Leiva, Jacintha Eilers, Diego R. Barneche, Luis E. Castañeda, Juan Diego Gaitán-Espitia, Paulina Gebauer, Daniel F. Gomez Isaza, Ian C. W. Hardy, Adam Hermaniuk, Sarah Jorissen,

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CONFLICT OF INTEREST STATEMENT

Natalie Pilakouta, Cristina Tuní and Diego R. Barneche are associate editors of *Functional Ecology*, but took no part in the peer review and decision-making process for this paper.

DATA AVAILABILITY STATEMENT

Data files and code supporting figures of this study are publicly available on GitHub (<https://github.com/ShareTraitProject/ShareTrait>) and are archived in Zenodo: <https://doi.org/10.5281/zenodo.14826294> (Leiva et al., 2025).

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Figure S1. Detailed structure of the relational database implemented in ShareTrait.

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