AphidTraits: an open dataset of temperature-dependent trait responses in aphids (Hemiptera: Aphididae)

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Abstract

Aphids are among the most destructive and economically impactful group of agricultural pests. Their successful management hinges on integrative and sustainable control practices. Given the global scope of aphid impacts, mathematical models are invaluable for developing informed control strategies, particularly in the context of changing climate. Such models typically require detailed empirical data to adequately quantify relationships between environmental factors and aphid life history traits. However, appropriate data are often spread throughout the literature or are in disparate formats that hinder model building efforts. To address this issue, we have developed AphidTraits, a fully open, machine-readable dataset that adheres to VecTraits standards. AphidTraits focuses on the temperature dependence of multiple types of traits (e.g., life-history, behavioral, morphological) in aphid species and consolidates experimental data from diverse published literature. The current data product contains 36,417 trait records from 257 publications, representing 93 aphid taxon names across 48 genera and studies published between 1939 and 2025. AphidTraits captures further trait variation across species, populations, and environmental conditions, providing a valuable resource for novel secondary analyses across studies.

Keywords: Aphididae, aphid, thermal biology, temperature-dependent traits, life-history traits, trait database, ecological modelling, climate change, agricultural pests

Background and Summary

Aphids (Hemiptera: Aphididae) are among the most destructive groups of agricultural pests, inflicting direct damage to many economically important crops through feeding activities (Kamphuis et al., 2013; Van Emden & Harrington, 2007). They are also some of the most significant vectors of pathogens in plants and are implicated in the transmission of more than 200 plant viruses (Harris & Maramorosch, 2014; Ng & Perry, 2004). The pressure of aphid infestations leads to both direct loss of crops and reduced agricultural yields, making aphids a threat to commercial agricultural operations, and more broadly, global food security (Guerrieri & Digilio, 2008; Luo et al., 2022).

The success of aphids as pests is due to a number of factors, including rapid reproductive rates, complex life cycles, and global distribution throughout temperate growing regions (Du et al., 2020; Singh & Singh, 2021; Van Emden & Harrington, 2007). Temperature is a key environmental driver of both aphid population dynamics and their capacity to transmit pathogens (Brabec et al., 2014; Sylvester, 1964; Vickerman & Wratten, 1979). Given their poikilothermic physiology, temperature influences nearly every facet of aphid biology, including survival, fecundity, developmental rates, feeding behavior, dispersal, and viral transmission cycles (Sylvester, 1964; Vickerman & Wratten, 1979; Zhou et al., 1995). Consequently, variability in temperature can have profound effects on aphid populations, disease transmission, and phenological patterns.

The significant agricultural impact of aphids calls for effective pest and disease management (Guerrieri & Digilio, 2008; Luo et al., 2022). Mathematical models are useful tools in the development of sustainable control practices, such as forecasting disease activity or predicting the efficacy of biological controls on populations (Van Emden & Harrington, 2007). Given the influence of temperature on aphid biology, predictive models of aphid infestations or disease outbreaks typically rely on trait data collected or measured across a range of temperatures (Ryan et al., 2026). In the past this has presented a challenge, as existing trait data on aphids are not centralised, instead scattered across diverse studies that differ in methodology and reporting standards. Here we present `AphidTraits`, an effort to compile and standardise existing temperature-dependent aphid trait data. The resulting data product will support modeling efforts to better understand aphid population dynamics and agricultural disease risk, particularly in the face of changing climate.

Methods

Literature Search

We conducted an extensive search of the published scientific literature on aphids to identify studies with data for inclusion in `AphidTraits`. Following PRISMA (Preferred Reporting Items for Systematic Reviews) guidelines for conducting and reporting systematic literature reviews (Page et al., 2021), we implemented a global literature search across multiple electronic databases, including PubMed, Web of Science, and Scopus. Searches were conducted in September 2025, with no restrictions placed on date of publication or language. Searches were implemented in each database using Boolean operators with the following terms:

- (“Aphid” AND “Temperature” AND “Trait”)
- (“Aphid” AND “Temperature” AND “Life History”)
- (“Aphid” OR “Aphididae” AND “Temperature” AND “Survival” AND “Development”)
- ([Species name] AND “Temperature” AND “Survival” AND “Development”)

Search results were initially screened to remove duplicate records. Title and abstract screening of the remaining records was managed using Rayyan (Ouzzani et al., 2016), followed by full-text review for data extraction. In addition, we manually screened the reference section of selected articles to review any potential studies that were not returned in literature searches. Our inclusion criteria focused on studies that generated empirical data to explore temperature-dependent traits in aphids. For example, laboratory or field experiments to establish relationships between life history traits, physiology, or disease transmission and temperature. As such, studies selected for inclusion had to meet four criteria:

1. the study must feature an experiment conducted under controlled laboratory or field settings (i.e., no surveillance-based entomological studies);
2. the study must report a measurable life history trait for an aphid species (e.g., survival, developmental time, growth rates, behavioral outcomes);
3. the study must record life history traits in relation to temperature; and
4. data must be collected in sufficient detail to support standardisation into a machine-readable format.

The database searches yielded 4,944 records after removal of duplicates. Title and abstract screening excluded 4,592 records, leaving 352 reports sought for retrieval from the database searches. Author-led manual searching and citation snowballing identified a further 34 reports, giving 386 reports sought for retrieval in total. Of these, 41 reports could not be accessed or located, and 345 were assessed for eligibility by full-text review. A further 88 reports were excluded because they contained no eligible or extractable aphid trait data ($n = 38$); were modelling, review, mapping, abundance, or unsuitable field studies ($n = 22$); focused on non-aphid organisms, including predators, parasitoids, or pathogens ($n = 14$); contained no eligible temperature comparison ($n = 11$); or contained data already represented in `AphidTraits` ($n = 3$). The final data product contained records from 257 publications (Fig. 1).

Data extraction

Studies that met our inclusion criteria were reviewed in full for data extraction. When possible, we made requests for raw datasets directly from the corresponding authors indicated on the publication. When original datasets were not available, data were digitised from publications. Data presented in tables were inputted into a digital table format. For the initial human-only component of `AphidTraits`, data presented in figures were digitised using WebPlotDigitizer v4.8 (Rohatgi, 2024) and compiled into table format. This human-only component contains 11,265 records from 129 publications.

The dataset was subsequently expanded using a rule-based, human-supervised GPT workflow. GPT was provided with the full paper and instructed to extract temperature-dependent primary biological traits from text, tables, and figures, while preserving biological and experimental context. The human supervisor reviewed the outputs, supplied paper-specific corrections and general rule clarifications, and required the statistical error unit to be recorded exactly as named by the source. Visible error bars were not assigned to SD, SE, SEM, CI, or another statistical category unless that statistic was explicitly identified in the paper. Where an error magnitude or other value could not be supported by its recorded provenance, the value was left blank rather than inferred. Figure-derived observations were retained when they provided data not otherwise available in text or tables, including recoverable zero-survival or zero-development observations at temperature extremes.

For papers not written in English, the source passages required to determine study eligibility and extract methods, collection provenance, trait definitions, units, tables, and figure captions were

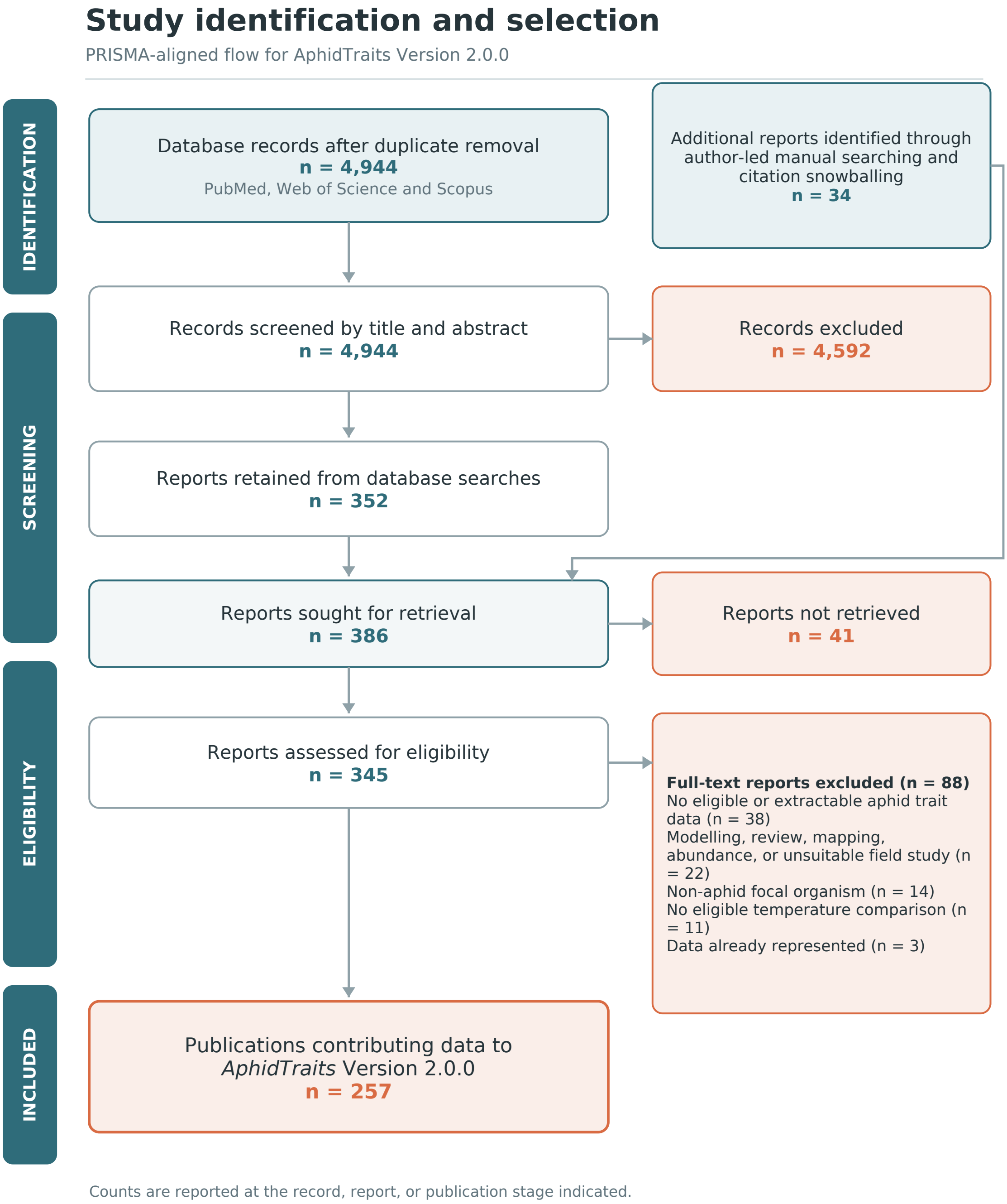

Figure 1: PRISMA-aligned flow diagram for study identification, screening, retrieval, eligibility assessment, and inclusion in `AphidTraits` Version 2.0.0. The 4,944 database records are the deduplicated set; 34 additional reports were identified through author-led manual searching and citation snowballing.

translated into English using GPT within the supervised extraction session. Scientific names, numerical values, units, and statistical notation were preserved. Translations were interpreted in page and figure context, and ambiguities that could not be resolved from the source were recorded rather than silently inferred.

All extracted data used to build `AphidTraits` were formatted into the standard data template established by the VectorByte initiative (`https://www.vectorbyte.org`). VectorByte provides a global platform for open-access data on disease vector traits (VecTraits; Johnson et al., 2023) and vector population dynamics (VecDyn; Rund et al., 2023) as well as standardised formats for each of these. As we focused on trait data in this study, we used the VecTraits format. Information extracted from included publications and standardised into the VecTraits format include insect vector species, life-history stage, location, GPS coordinates, experimental settings (e.g., temperature treatments), rearing conditions (e.g., temperature, humidity, photoperiod), measurable traits (numerical observations with units of measurement), sample-size information, and citation details. To ensure downstream usability of data, minimum reporting standards were used when data were digitised, following the VecTraits standard. These included recording the number of generations since field collection where reported, distinguishing planned or reconstructed sample sizes from exact analysis sample sizes, and retaining separate machine-readable codes for evidence source, reconstruction status, uncertainty, and analysis eligibility.

When a paper reported a named field collection locality but did not provide coordinates, decimal latitude and longitude were assigned using a defensible centroid for the finest named locality. The reported place name was preserved, and the coordinate was identified as derived rather than paper-reported. The field source locality was used in preference to the laboratory measurement location. Coordinate precision was standardised as SITE, LOCALITY, ADM2, ADM1, REGION_NON_ADMIN, ADM0, MULTIPLE_LOCALITIES, or MISSING. Commas and semicolons were removed from the final citation field to reduce delimiter-related problems in downstream machine processing, while DOI and other identifiers were retained in separate fields.

Data Records

The current `AphidTraits` data product contains 36,417 temperature-dependent trait records in 155 fields (Fig. 2). Following the format of other taxon-specific trait datasets (Da Re et al., 2025; Huxley et al., 2025), the data represent 257 publications, 48 aphid genera, and 93 unique genus–species combinations as recorded in the source data. The contributing studies were published between 1939 and 2025. These include prominent agricultural pests such as the green peach aphid (*Myzus persicae*), cotton aphid (*Aphis gossypii*), mustard or turnip aphid (*Lipaphis erysimi*), potato aphid (*Macrosiphum euphorbiae*), and others.

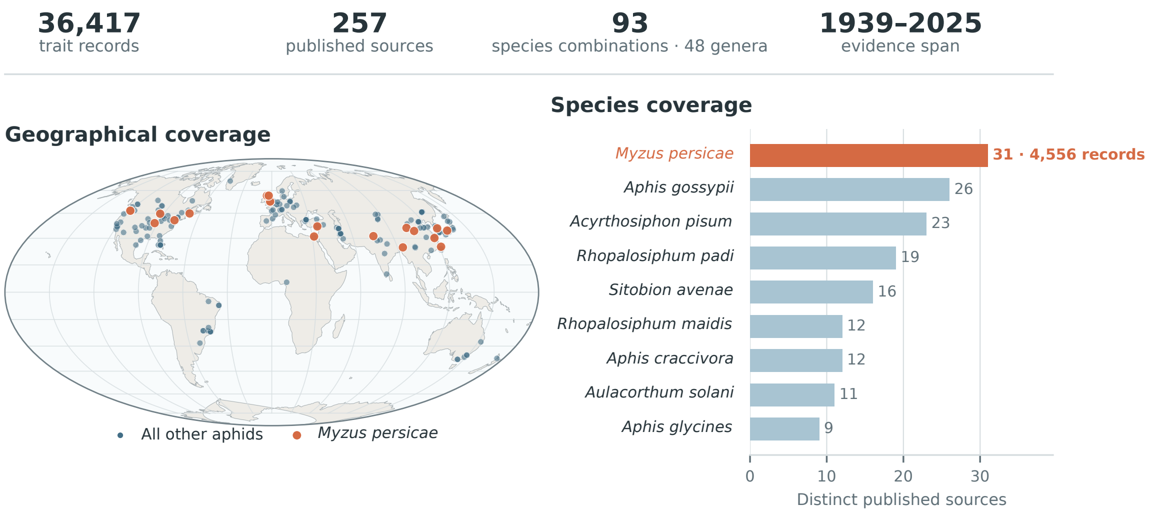

Figure 2: Overview of `AphidTraits` Version 2.0.0, showing dataset scale, publication span, geographical coverage, and the aphid taxa represented by the greatest number of contributing publications. Map points represent records with a single latitude–longitude pair; taxon counts show distinct contributing publications.

Data from studies were standardised using naming and reporting conventions established by VecTraits (Johnson et al., 2023; Ryan et al., 2026). Temperature-dependent aphid traits from digitised studies are recorded in fields such as "originaltraitname" and "originaltraitdef", which describe trait response data using names and definitions from the original studies. Original values, units of measurement, and errors for these traits are stored in "originaltraitvalue", "originaltraitunit", "originalerrorpos", "originalerrorneg", and "originalerrorunit", respectively. The conditions of environmental and experimental settings are described using fields such as "habitat", "labfield", "ambienttemp", and "ambientlight", among others, which capture the surroundings and experimental setup under which the observations were collected. Geographical data are reported in fields including "locationtext", "locationtype", "standardisedcoordinateadminlevel", "latitude", and "longitude". Temperatures that specimens were exposed to during experiments are stored in the "interactor1temp" and “interactor1tempunit” fields, respectively. Fields including “interactor1stage” and “interactor1sex” are used to indicate the life stage and sex of the species observed. Fields indicated with “secondstressor” were used to record additional temperatures and variables when included in publications (e.g., humidity, host plant, pesticides). Publication and data lineage are provided in fields such as “figuretable”, “citation”, and “doi”. The “notes” field provides extended machine-readable provenance and contextual metadata.

Data overview

The dataset contains 1,154 distinct original trait names, preserving the terminology used by the source publications. Experimental temperature is populated for 31,974 records (87.8%), spanning −28.9 to 47.0°C. Sample-size information is available in the “replicates” field for 33,903 records (93.1%) and occurs in 243 of the 257 contributing publications. A numeric positive error or uncertainty magnitude is available for 10,996 records (30.2%) across 211 publications. Most records were generated under laboratory or laboratory-colony conditions (34,634 records; 95.1%), while 1,783 records (4.9%) originated from field, outdoor, mesocosm, or field-census settings. These dataset-level summaries are reported in Table 1.

Table 1: Summary of the current `AphidTraits` data product. Percentages use all 36,417 records as the denominator unless otherwise stated.

Dataset component	**Number**	**Percentage**
Trait records	36,417	100.0%
Source publications	257	–
Aphid genera	48	–
Unique genus–species combinations	93	–
Records with experimental temperature	31,974	87.8%
Records with sample-size information	33,903	93.1%
Records with numeric error or uncertainty	10,996	30.2%
Records with a single latitude–longitude pair	19,040	52.3%
Laboratory or laboratory-colony records	34,634	95.1%
Field or outdoor records	1,783	4.9%

The number of records and contributing publications was unevenly distributed across aphid taxa (Table 2). *Myzus persicae* was represented by the greatest number of publications (31) and 4,556 records. Other well-represented taxa included *Aphis gossypii* (26 publications), *Acyrthosiphon pisum* (23), *Rhopalosiphum padi* (19), and *Sitobion avenae* (16). These counts describe coverage within `AphidTraits` rather than the relative amount of research across the complete aphid literature, as not all studies identified during screening were included in the current data release.

Table 2: The ten aphid taxa represented by the greatest number of contributing publications. A publication may contribute multiple records and may include more than one taxon.

Taxon	**Publications**	**Records**
Myzus persicae	31	4,556
Aphis gossypii	26	2,012
Acyrthosiphon pisum	23	2,817
Rhopalosiphum padi	19	3,879
Sitobion avenae	16	2,160
Rhopalosiphum maidis	12	4,148
Aphis craccivora	12	1,614
Aulacorthum solani	11	1,191
Aphis glycines	9	1,403
Brevicoryne brassicae	8	559

A single decimal latitude–longitude pair is available for 19,040 records (52.3%) from 173 publications. Among all records, the standardised coordinate classification identifies 7,064 records at SITE precision, 7,008 at LOCALITY precision, 1,880 at ADM2, 1,690 at ADM1, 1,254 as REGION_NON_ADMIN, and 144 at ADM0. A further 1,448 records describe multiple collection localities that cannot be represented by one coordinate pair, and 15,929 records are classified as MISSING. These categories allow users to account explicitly for geolocation uncertainty rather than treating all coordinates as equally precise.

Data availability

`AphidTraits` Version 2.0.0 is available online via Zenodo (Huxley et al., 2026), and is also deposited and available through the VecTraits database (Johnson et al., 2023).

Code availability

All scripts used to apply the final source-adjudicated corrections, generate the cell-level change log, run structural checks, and reproduce the GPT–WebPlotDigitizer technical validation are archived with the data release (Huxley et al., 2026). The release also contains the pre-correction and corrected dataset versions required to audit the changes.

Technical Validation

All extracted records were subjected to structural checks, while targeted records and validation disagreements were subjected to source-level checks against the original publications. The final correction audit comprised 17 structural checks and 12 targeted verification checks, all of which passed. These checks included dataset dimensions, numeric coordinate pairing, coordinate-admin vocabulary, collection-date precision, citation punctuation, record identifiers, exact duplicate rows, and the absence of unintended changes to retained cells. Every changed, added, or deleted nonblank cell was preserved in a cell-level change log with the affected row, column, previous value, corrected value, governing rule, and evidence. The final release contains 36,417 rows and 155 columns, with zero unexpected changes outside the adjudicated corrections.

To provide an independent validation of figure digitisation, we compared `AphidTraits` with the separate human-only dataset in which all figure-derived values had been extracted using WebPlot-Digitizer. The human dataset was treated as an independent comparator rather than an error-free gold standard, and disagreements were adjudicated against the source PDF. Among 113 publications shared by the two datasets, 12 contained figure-derived rows in both workflows. Nine publications contained observations from the same figure, panel, biological series, and temperature treatment and could therefore contribute to numerical accuracy; the other three contained different within-paper figure coverage and were retained only in the coverage census.

The same-observation dataset contained 178 paired central values. Of these, 145 pairs from eight publications represented direct figure digitisation by both workflows, while 33 pairs used a source-reported GPT central value and were classified as hybrid comparisons. Differences were normalised to the plotted y-axis span. Across the 145 direct pairs, the observation-weighted mean absolute error (MAE) was 1.277% of the plotted axis span (paper-cluster 95% confidence interval: 0.383–2.374%), and the paper-equal MAE was 1.031% (0.346–1.908%). In total, 127 of 145 direct pairs were within 2% of the plotted axis span. A source-adjudicated sensitivity analysis removed six direct pairs for which the PDF supported an error in the human comparator. Across the remaining 139 direct pairs, the observation-weighted MAE was 0.737% (0.383–1.187%), and 125 of 139 pairs were within 2% of the axis span.

The source explicitly named the error statistic for 75 paired error records. The recorded statistic matched the source in 75 of 75 GPT records and 67 of 75 human records. The eight remaining human mismatches arose from a single figure whose caption specified SD while the human comparator recorded SE. Ten error magnitudes were excluded from direct magnitude accuracy because their provenance did not support independent digitisation. Across the 65 eligible direct error-magnitude pairs from five publications, the observation-weighted MAE was 0.472% of the axis span (paper-cluster 95% confidence interval: 0.324–0.653%); all 65 were within 2% of the axis span.

Source adjudication identified errors in both workflows, including a wrong human axis calibration, omitted or miscoded treatment metadata, an exact duplicate GPT extraction block, a missing GPT point, unnamed GPT error bars, and incorrect error-statistic labels. The GPT defects were corrected before the validation statistics above were recalculated. Complete matched observations, coverage-only records, source-supported adjudications, and the applied correction history are archived with the dataset so that every denominator can be reproduced.

Usage Notes

Digitisation of publications and figures is a laborious process, and the introduction of errors is possible whenever data are extracted retrospectively. We minimised such errors by reviewing trait values throughout digitisation, using graphical methods such as frequency histograms, box plots, or scatter plots in R. Outliers identified through these visualisation techniques were cross-referenced against source publications to correct discrepancies. When available, raw datasets provided through supplemental materials or data repositories were used. The independent figure validation indicates that most direct digitisations agree closely relative to the plotted axis span, while also demonstrating that neither the supervised GPT workflow nor the human comparator should be treated as universally correct without reference to the source.

Users are advised not to use the dataset for fine-scale spatial modelling when coordinates were derived from broad administrative areas. The "standardisedcoordinateadminlevel" field should be used to distinguish precise sites and localities from ADM1, ADM0, non-administrative regional centroids, multiple localities, and missing coordinates. Georeferenced information for laboratory cultures should be treated with particular caution, as the measurement location may differ from the original field source.

The dataset preserves original trait definitions, measurement protocols, and experimental contexts. Similarly named traits may therefore differ in biological meaning across publications. Users should inspect "originaltraitdef", temperature context, life stage, sex, host plant, second stressors, sample-size basis, and the provenance codes retained in "notes" before combining records. Reported proportions and counts should be distinguished from reconstructed binomial counts, and strict analysis-eligibility fields should be used when analyses require only directly reported values.

Scientific Opportunities

Open datasets like `AphidTraits` are important for supporting the development of surveillance forecasting models and data-informed control strategies for agricultural pests like aphids. By collating and standardising aphid trait data from diverse sources, we are providing a comprehensive resource for researchers and policymakers to address current limitations in data availability with regards to species diversity, temporal coverage, and spatial extent. We have released `AphidTraits` to facilitate timely modeling efforts for aphid systems, while also recognising the need for future updates to the current data product as new data become available. The supervised AI-assisted workflow used to expand `AphidTraits` demonstrates the potential to increase the efficiency of data extraction while retaining explicit human oversight, source adjudication, and auditable provenance. This workflow also provides a foundation for future open-source software that can apply the same extraction and validation rules more consistently across new studies.

Measuring life history traits against temperature was the primary factor for inclusion in `AphidTraits`, and though we recognise that other variables may be of interest to researchers, the current dataset is limited to those studies that explicitly featured temperature as a variable. In future efforts to expand data availability for aphids, studies that examine life history traits against other environmental gradients could be prioritised.

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