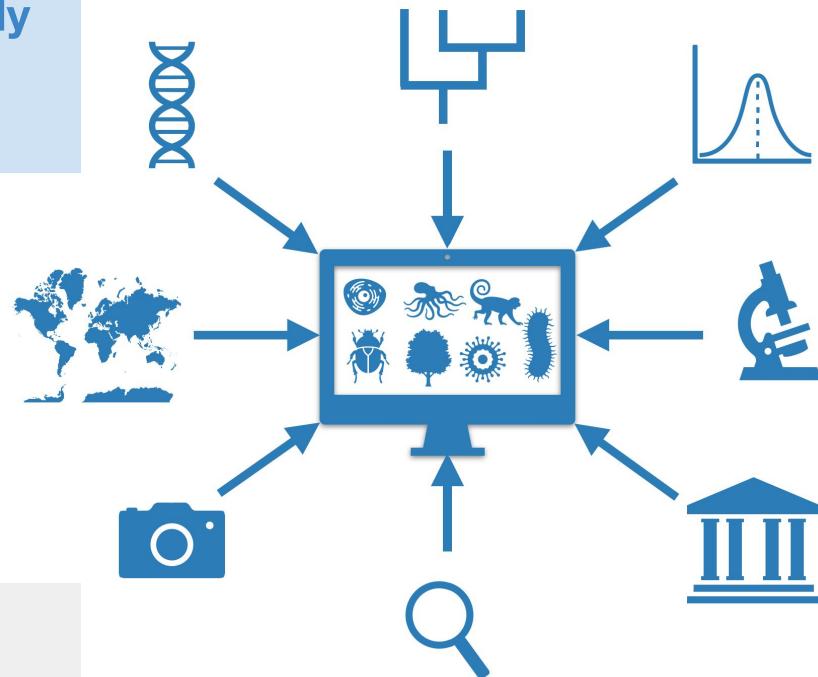


Revitalizing monographs

Marymegan (Meg) Daly
The Ohio State U
daly.66@osu.edu

Felipe Zapata
UCLA
fzapata@ucla.edu



Knowinnovation
Costa Michailidis
Malachi Greaves



Supported



Monographs: treatments that centralize biodiversity information for groups of organisms. This information includes accurate and precise description of morphological variation, phylogeny, species delimitation, genetic diversity, literature, nomenclature, geographic distribution, images, etc

The critical baseline data on biodiversity included in taxonomic monographs is used by biologists *and* non-experts alike.

Observations about taxonomic monographs

- **The practice of monography has changed little in over 200 (or more) years:** monographs are still the “same” kind of documents (even the digital ones).
- **Components of monographs are mainstream research in systematic biology using modern data, tools, and approaches:** species delimitation, phylogenomics, biogeography, speciation, etc.
- **Few students and professionals engage in monographic research (despite the fundamental role of monographs in biodiversity research):** training, “impact”.

Observations about science/technology 2010-20

- **Changes in publication models/types of products:** novel interfaces to databases, semantic web, science reproducibility, integration/crowdsourcing.
- **Advances in tools and approaches that relate to monographs:** specimen digitization (iDigBio), 3D imaging, databases, genomics, phenomics, machine learning, artificial intelligence, cyberinfrastructure, ontologies, natural language processing, etc.
- **Funding:** e.g., PEET, ARTS: but we should aim for transformative monographic research (not more of the same).



Taxonomy must engage with new technologies and evolve to face future challenges

To the Editor — Despite taxonomy being fundamental to biology for discovering, describing and identifying the units of analysis across disciplines, it is generally agreed that the perceived importance of taxonomy is diminishing¹. In the face of this paradoxical decline, we argue that fulfilment of a long-promised ‘taxonomic renaissance’² must be strategic because few permanent taxonomic positions exist, little funding is available, and challenges are manifold.

We need to start with digitization and online accessioning of type specimens, prioritizing those taken from their countries of origin³, as well as capacity building to enable taxonomists in developing countries to perform the best work possible and to collaborate globally. Via high-resolution imaging technology, virtual taxonomy laboratory (VTL) approaches can accelerate taxonomic collaboration and productivity online. As these setups may be expensive, federal governments should prioritize establishing at least one such centre nationally to collaboratively write diagnoses, descriptions and manuscripts. Through mutually beneficial partnerships involving training and specimen exchanges, integrative approaches that incorporate many lines of evidence could become feasible worldwide.

Integrating this evidence efficiently will require a singular, centralized data storage system (rather than separately in GenBank, Barcode of Life Data (BOLD) System, Global Biodiversity Information Facility (GBIF) and so on), including a unified species list as well as taxonomic history, relevant literature, original and updated morphological descriptions, high-quality images, life history data, molecular and morphometric resources for coalescent or other analyses (for example, barcodes), and even ecological linkages and economic valuations. Ideally, this will be accomplished through an internationally funded institute or alliance for biodiversity and integrative taxonomy, but this will necessitate policy support. Such an institute would encourage increased hiring and advocate better recognition for primary data generation and their use, as well as encouraging metrics that value magnitude of contribution to papers rather than authorship order.

Once species data become accessible worldwide, the potential for collaboration between data providers and other researchers will be boundless. Unlimited multi-faceted data could be assembled and assessed in a truly integrative taxonomic framework. This will support incorporation of artificial intelligence methods to guide species delimitation analyses, as people are actively attempting for identification^{4–6}. These algorithms could be trained with examples of well-resolved groups and then optimized weighting schemes could be used for other groups.

Deep-learning can also identify both new instances of the same species and new species via comparison with known species^{7,8}. For each known species, a morphological, ecological, distributional and genomic variation ‘space’ would be defined, and specimens exceeding the limits of these spaces would be flagged for examination by experts, expediting sorting immensely while also preventing erroneous records. These integrative species definitions could be continuously updated and improved by experts, and once suitable they could even be applied to citizen-science data to gather an immense number of new records while also encouraging public participation in and appreciation of science. Conservation will also benefit, as accumulated distributional information, once verified, will enable the development of continually updated, accurate biodiversity hotspot maps, with approaches helping to compensate for under-sampling and under-description in species-rich areas such as the tropics, where taxonomic work is most needed.

These suggestions may seem a dramatic departure from current approaches, dismissing the human element of taxonomy, but this could not be more false. Taxonomists must modernize along with the field, while maintaining traditional practices and the invaluable knowledge they provide, which means embracing new technologies for species discovery, delimitation and identification, just as we have with molecular methods and new imaging technologies. Technological advances allow for unprecedented taxonomic approaches, but existing methods must be better integrated into a broader vision encompassing species

discovery, rendering accessible rich data about known species, and scaling up analytical pipelines to meet urgent societal needs pertaining to biodiversity conservation and ecosystem conservation and management. □

Michael C. Orr Rafael R. Ferrari¹,
Alice C. Hughes Jun Chen²,
John S. Ascher¹, Yue-Hong Yan³,
Paul H. Williams Xin Zhou⁴, Ming Bai⁵,
Andrey Rudov⁶, Feng Zhang⁶, Ke-Ping Ma⁶
and Chao-Dong Zhu

¹Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China. ²Landscape Ecology Group, Centre for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menghai, China. ³Department of Biological Sciences, National University of Singapore, Singapore City, Singapore. ⁴Key Laboratory of National Forestry and Grassland Administration for Orchid Conservation and Utilization, The National Orchid Conservation Centre of China and The Orchid Conservation and Research Centre of Shenzhen, Shenzhen, China. ⁵Natural History Museum, London, UK. ⁶Department of Entomology, China Agricultural University, Beijing, China. ⁷Department of Entomology, College of Plant Protection, Nanjing Agricultural University, Nanjing, China. ⁸Institute of Botany, Chinese Academy of Sciences, Beijing, China.

[✉]e-mail: michael.christopher.orr@gmail.com; zhuad@ioz.ac.cn

Published online: 10 November 2020
<https://doi.org/10.1038/s41559-020-01360-5>

References

- Wiley, E. O. *Phil. Trans. R. Soc. B* **359**, 739 (2004).
- Pearson, D. L., Hamilton, A. & Erwin, T. L. *BioScience* **61**, 58–63 (2011).
- Lamont, J. B. ‘Taxonomy, lacking in prestige, may be nearing a demise’, *The New York Times* (10 December 1991). <http://go.nature.com/3bmj9y>
- Ferrari, R. R. *Zootaxa* **4564**, 1–17 (2017).
- Orr, M. C., Ascher, J. S., Bai, M., Chester, D. & Zhu, C.-D. *Arctia* **27**, 203–212 (2020).
- Gomes, S. T. et al. *PLoS Biol.* **18**, e3000784 (2020).
- Williams, P. H. et al. *Eur. J. Taxon.* **719**, 1–120 (2020).
- Asche, J. S. et al. *Methods Ecol. Evol.* **11**, 922–931 (2020).
- Huang, Y. et al. *PLoS Biol.* **18**, e3000782 (2020). <https://doi.org/10.1371/journal.pbio.3000782> (2020).
- Wheeler, Q. D. *The New Taxonomy* (CRC Press, 2008).

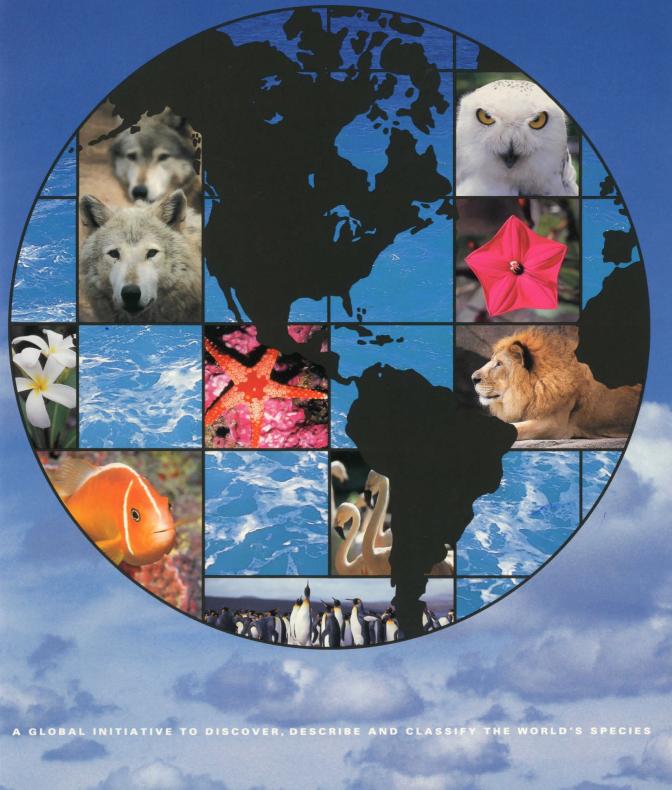
Acknowledgements

M.C.O., R.R.F. and C.-D.Z. were mainly supported by grants from the National Science Foundation,

1990s

SYSTEMATICS AGENDA 2000

CHARTING THE BIOSPHERE



2010s

Special Essay

Syst. Biol. 61(4):549–552, 2012.
 © The Authors 2012. Published by Oxford University Press on behalf of Society of Systematic Biologists.
 This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (<http://creativecommons.org/licenses/by-nc/3.0/>) which permits non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.
 DOI:10.1093/sysbio/sys044
 Advance Access publication on March 4, 2012

Systematics Agenda 2020: The Mission Evolves

MARYMEGAN DALY^{1,*}, PATRICK S. HERENDEEN², ROBERT P. GURALNICK^{3,4}, MARK W. WESTNEAT⁵, AND LUCINDA McDADE⁶

¹Department of Evolution, Ecology and Organismal Biology, The Ohio State University, 1315 Kinnear Road, Columbus, OH 43212, USA; ²Chicago Botanic Garden, 1000 Lake Cook Road, Glencoe, IL 60022 USA; ³University of Colorado Museum of Natural History, Bruce Curtis Building, UCB 265, University of Colorado, Boulder, CO 80309 USA; ⁴Department of Ecology and Evolutionary Biology, University of Colorado, Ramaley N122, Campus Box 334, Boulder, CO 80309-0334, USA; ⁵Department of Zoology, Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, IL 60605-2496, USA; and ⁶Rancho Santa Ana Botanic Garden, 1500 N College Avenue, Claremont, CA 91711, USA;

*Correspondence to be sent to: Department of Evolution, Ecology and Organismal Biology, The Ohio State University, 1315 Kinnear Road, Columbus, OH 43212, USA; E-mail: daly.6@osu.edu.

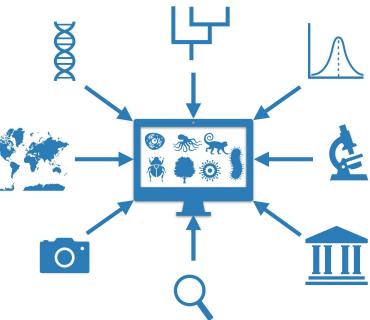
In the early 1990s, a comprehensive set of missions and goals for the discipline was articulated by a global community of systematists; these were presented as Systematics Agenda 2000 (1994). Abbreviated here as SA2K, this agenda spurred awareness of the field and initiated discussions about the future of systematics within biology (e.g., Blackmore and Cutler 1996; Cracraft 2002; Halanych and Goertzen 2009), in education (e.g., Krishnapolu and Humphrey 2000; Thanukos 2010), and public policy (e.g., Prance 1995). After nearly 20 years of achievement and growth in systematic biology, a series of four US National Science Foundation-sponsored workshops on "Future Directions in Biodiversity and Systematics Research" were held during 2009–2010 to evaluate progress in the field and identify new directions and opportunities. Workshop participants reviewed SA2K and may be rapidly to have come to ground and to jump-start our discussions. We did not plan to undertake a formal revision of SA2K, but our discussions led to consensus on a number of relevant points. We share these here with the intention of generating further reflection and discussion toward advancing our field and its missions.

The clear consensus from the 85 participants was that, progress notwithstanding, the three interlinked missions of SA2K: (1) to discover, describe, and inventory global species diversity; (2) to analyze and synthesize the information derived from this global discovery effort into a predictive classification system that reflects the history of life; and (3) to organize the information derived from this global program in an efficiently retrievable form that best meets the needs of science and society, remain central to discipline. It is a testament to the comprehensive vision of SA2K that much of that document, now nearly 20 years old, remains relevant. In light of these workshop discussions, we align the mission statements of SA2K with emerging priorities and opportunities and articulate four missions that embrace the changes in technology, infrastructure,

and science since the publication of this influential document and recast them as Systematics Agenda 2020 (Table 1). This revised agenda maintains emphasis on the discovery and synthesis of biodiversity, incorporates evolution as a driving process and organizing theme, and emphasizes communication within the biological sciences community and to the general public.

Extensive progress has been made in species discovery and documentation (SA2K Mission 1), with accelerating rates of taxonomic description for some taxa (Joppa et al. 2011), especially those that have benefited from focused and funded research projects (e.g., National Science Foundation's Planetary Biodiversity Inventory projects). However, despite these achievements, much remains to be done in terms of biodiversity discovery and documentation (e.g., Mora et al. 2011). Workshop participants suggested elsewhere that we need to fundamentally change how we work in order to speed that process and lobby for changes to many aspects of the permitting system as it applies to scientific collecting. Progress toward SA2K Mission 2, "analysis and synthesis" of knowledge about biodiversity in the form of understanding the patterns of phylogenetic relatedness among organisms, has arguably been even more dramatic than advances in our discovery and documentation of them. There has been a remarkable upswing in the number of phylogenetic trees published annually over the last 10 years and increasing resolution of relationships at both deep and shallow branches and across all domains of life, with the possible exception of prokaryotes. Still, much remains to be learned at all levels of the phylogenetic hierarchy. Likewise, numerous internet-based information repositories (e.g., EOL, GBIF) have been launched but remain very much works in progress, which makes it clear that Mission 3 of SA2K, to "organize biodiversity knowledge and make it readily retrievable", remains only partially achieved. Workshop participants acknowledge the continued relevance—indeed centrality—of all three

2020s



Revitalizing monographs

- **Workshop 1 (AMNH-2018):** Bottlenecks and opportunities in monographic research.
- **Workshop 2 (UCLA 2019):** New technologies to energize and unify monographic research.
- **Workshop 3 (Online 2021):** Generate creative strategies and new research collaborations aimed at revitalizing—reinventing—monographs to fulfill the needs of modern biology.

From our workshops

- What are the **core goals** of monographs?
 - Precise **descriptions** and a clear analysis of character variation (phenotype, genotype, geography, phenology, phylogeny, etc).
 - **Species delimitation:** rationale, raw data/analyses
 - **Classification:** phylogeny
 - **Identification**
 - Enable **further analysis:** link with other taxa, other users who may not be taxonomists

From our workshops

- What are the **core components** of monographs?
 - **Specimens:** in the microbial world DNA/culture/eDNA.
 - **Specimen-based data/metadata:** raw morphological measurements, scores for qualitative traits, geographic distribution, genomics, ecology.
 - **Taxon-based data:** literature, previous hypotheses, historical nomenclature.

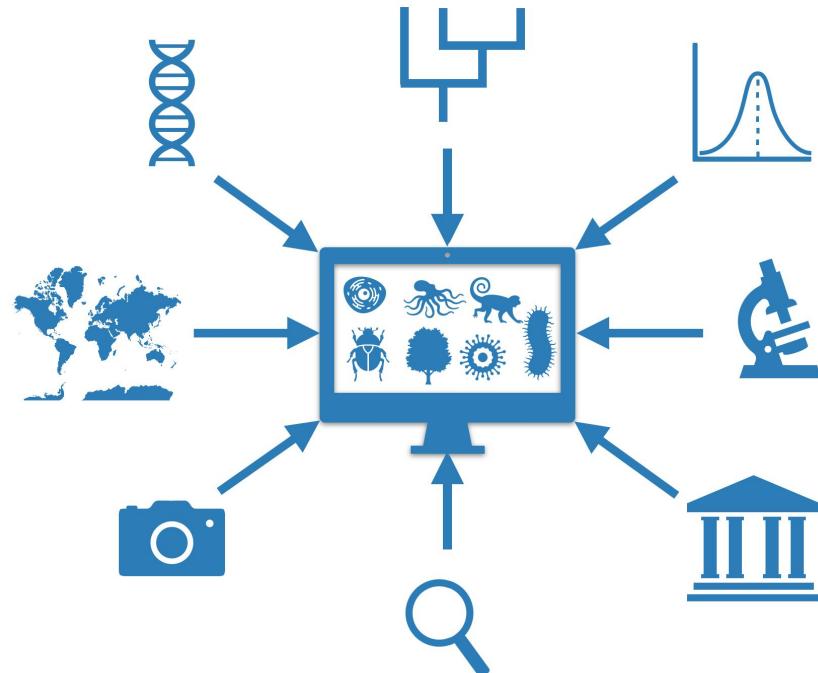
From our workshops

- What are **limiting steps** of monographs?
 - **Specimen gathering**
 - **Morphological measurements**: gathering data and no centralized repository to build from.
 - **Tree building**: automatic generation with genome scale/eDNA.
 - Incorporate and propagate **measurements of uncertainty** throughout workflow.
 - Assess **data quality** and use of citizen data.
 - **Integration** with other resources
 - **Nomenclature**: lack of centralized, curated repositories.
 - **Publications** are largely impenetrable to most users, and publications are static, no versioning, largely not queryable (measurements, genes)

Revitalizing monographs

Workshop 3

What?
How?



Revitalizing monographs



**e-Monograph
of the Caricaceae**

This website is a taxonomic resource for the papaya family. It will help experts and enthusiasts identify species, find its relatives and improve their understanding of the interesting family of flowering plants.

Contents:

- [Morphology](#)
- [Taxonomic history](#)
- [Identification keys](#)
- [Phylogeny](#)
- [Diseases](#)
- [Biogeography](#)
- [Sexual systems](#)
- [Sex chromosomes](#)

User interface: see above for filter and analysis. Page results in dynamic data grids; create maps and reports; and view illustrations and specimen images

Caricaceae, a small family of flowering plants comprising about 35 species in six genera. *Carica papaya*, better known as the papaya or pawpaw, is probably the best-known species in the family. It is not only for its delicious and nutritive fruits, but also because it contains the enzyme papain, which is extensively used in medicines, as meat tenderizer, for softening textiles, silk, leather, and in beer production. Several other species also have edible fruits and produce papain. For example, *Viscocalyx* and *Carica* spp. and *Asphodeles* show promising characteristics for further economic exploitation and development of new crops.

This website provides detailed information on the entire papaya's family. Specifically, data are provided on taxonomy, morphology, reproduction (sexual systems and sex chromosomes), evolutionary relationships , distribution, and systematics (e.g., how they related South American genera and diversified there). In addition, we present a brief account of the biology and ecology of the genus *Carica*, including the so-called heliotropic papayas from the Andes (*Viscocalyx* species) and the cold-tolerant species of papaya from Mexico, Guatemala, and El Salvador. For illustrations and detailed information on each genus and species, please use the search form.

Using the tabs at the top of the page, you can search for identifying genera and species, and search for herbarium specimens or taxa. You will find georeferenced collections, distribution maps, species descriptions, and illustrations (photos and drawings). For specially designed tutorials and other useful links, click on [Resources](#). All sources of information provided here are listed under [References](#). Links have been especially created to inform users about online available. Questions, comments, and contributions are especially welcome. Please write to antunesdf@gmail.com



ZooKeys Home Articles About About Zookeys person.net Home Monograph Zookeys (68): 1–124 DOI: 10.3897/zookeys.683 (2017) [4 Aug 2017]

A monograph of the Australopacific Saprininae (Coleoptera, Histeridae)

Tomáš Lackner, Richard A. B. Leschen

Abstract –

The Australopacific Saprininae, containing twelve genera and forty species, are reviewed, illustrated and keyed to generic level. The genus *Hister* is transferred from the subfamily Histerinae, n. New World, to the subfamily Saprininae. *Saprinus* (Saprinus) *luteolus*, 1820 is designated as the type species of *Saprinus* (Saprinus) *luteolus*. *Saprinus* (Saprinus) *luteolus* sp. n. and four new species: *Saprinus* (*Saprinus*) *ravus* sp. n. (Australia), *Saprinus* (*Saprinus*) *chathamicus* sp. n. (Chatham Islands, New Zealand), *Saprinus* (*Saprinus*) *prosternalis* sp. n. (Chatham Islands, New Zealand) and *Saprinus* (*Saprinus*) *australis* sp. n. (Australia) are described. The distributional range of the genus is extended by a mixture of northern invasions that likely arrived to the region in early Cenozoic by “island hopping” from north (Hippocratea, Hippocrateina, several subgenera) and transoceanic autochthonous taxa either with uncertain phylogenetic affinities (Indonesian gen. sp., *Saprinoides* Lewis, 1891, *Aspidius* Gahan, 1923, *Leptosoma* Gahan, 1923, *Leptosomoides* Gahan, 1923, *Leptosomoides* Kongorong Maroul, 1862) or presumed recent (several species of *Saprinus* Erichson, 1834). Several *Saprininae* taxa (Chalcophoreinae, Schenck, 1890), (*Gnathodus* rotundulus (Fabricius, 1775), *Gnathodus* *gibbosus* (Fabricius, 1775), *Gnathodus* *longulus* (Fabricius, 1805), *Hypocaccus* (*Hypocaccus*) *intermedius* (Schenck, 1893), *Saphydrus* (*Saphydrus*) *claviger* (Blögl, 1867) and *Saprinus* (*Saprinus*) *erichsonii* Erichson, 1834) were introduced to the region with human activity. We report the first records of mycophagous (*Hippocratea memnonioides* gen. sp. n., *Hippocratea* sp. n., *Leptosoma* sp. n., *Leptosomoides* sp. n.) and saprophagous (all species of *Saprinus* (*Saprinus*)) taxa from the Australopacific Region. Ecotypes and paralectotypes of the following taxa are described here: *Saprinus australis* Lewis, 1900, *Saprinus galloensis* Schenck, 1894, *Saprinus* (*Saprinus*) *erichsonii* Maroul, 1862.

Contents Article Info Citation Metrics Comment Related PDFs Page Taxa Citations Metrics Download Cmd Int Code

Figure 1.  [Download](#)

Figure 2–9.  [Download](#)

Figure 10–13.  [Download](#)

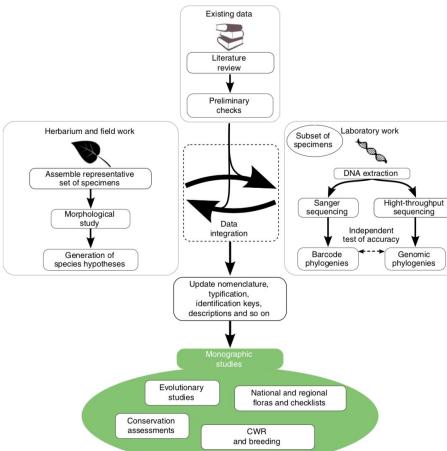
Figure 14–16.  [Download](#)

ARTICLES

nature
plants

A taxonomic monograph of *Ipomoea* integrated across phylogenetic scales

Pablo Muñoz-Rodríguez¹⁹, Tom Carruthers¹⁹, John R. I. Wood¹², Bethany R. M. Williams¹, Kevin Weitemeyer²⁰, Brent Kronmiller², Zoë Goodwin⁵, Alex Sumadjiya¹, Noelle L. Anglin⁶, Denis Filer¹, David Harris²⁵, Mark D. Rausher²⁷, Steven Kelly²¹, Aaron Liston⁸ and Robert W. Scotland^{21*}



?
**The same?
Something
else?**

Revitalizing monographs

What is the purpose of writing monographs?

Who are we writing monographs for?

Who uses monographs or might use them based on content?

Revitalizing monographs

Wouldn't it be great if...by...

Revitalizing monographs

Wouldn't it be great if we could speed up species discovery and validation **by** training artificial intelligence models inside monographs to “alert” the taxonomist of likely new species when more specimens are added to a database?

Wouldn't it be great if there was a machine that would take samples of say, water and generate minimum viable “monographs” automatically **by** separating content within the sample by size, sequence all organisms, image them, measure them and write output to a database for further validation/writing by a taxonomist?

Revitalizing monographs

Wouldn't it be great if we could crowdsource monographs **by** establishing worldwide collaborations and give proper credit?

Wouldn't it be great if we could reinvent monographs today, maybe by dropping the word monograph (historical baggage) and generate new types of documents?