Paths and obstacles to an evidence-based, reproducible, and dynamic Plant Taxonomy

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Paths and obstacles to an evidence-based, reproducible, and dynamic Plant Taxonomy

Título em português:

Caminhos e obstáculos para uma taxonomia de plantas baseada em evidências, reprodutível e dinâmica

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Running Head: Evidence-Based Plant Taxonomy

Abstract

Plant taxonomy, though historically foundational in the biological sciences, has been slow to incorporate modern standards of scientific rigor. Traditional reliance on morphology and purely descriptive practices, with limited use of statistical and phylogenetic analysis, has resulted in low reproducibility and limited scientific robustness. This essay advocates for a shift toward an evidence-based and reproducible plant taxonomy, aligning plant systematics practices with contemporary principles of open science. For such an endeavor, it is highly recommended to adopt integrative and analytical approaches to taxa delimitation. In such an approach, taxa are not factual data, but rather conclusions drawn from analysis. Practical recommendations are offered to guide journals, researchers, and institutions toward a more robust and scientifically credible taxonomic practice.

Resumo

A taxonomia vegetal, embora historicamente fundamental nas ciências biológicas, tem sido lenta na incorporação de padrões modernos de rigor científico. A dependência tradicional em macromorfologia e em práticas puramente descritivas, com uso limitado de análises estatísticas e filogenéticas, vem resultando em baixa reprodutibilidade e robustez científica limitada. Este ensaio defende uma mudança em direção a uma taxonomia vegetal baseada em evidências e reprodutível, alinhando as práticas de sistemática vegetal com os princípios contemporâneos da ciência aberta. Para tal, é altamente recomendável a adoção de abordagens integrativas e analíticas para a delimitação de táxons. Nessa abordagem, os táxons não são dados factuais, mas sim conclusões extraídas de análises. Recomendações práticas são oferecidas para orientar periódicos, pesquisadores e instituições em direção a uma prática taxonômica mais robusta e cientificamente confiável.

Palavras-chave: Ciência aberta; delimitação de espécies; sistemática

Keywords: Open Science; species delimitations; systematics

The methods we use to name and classify plant life shape how we understand, conserve, and communicate about biodiversity. Yet, many foundational taxonomic practices have remained unchanged for decades or even centuries, despite major advances in biology, data science, and analytical tools. If plant taxonomy is to function as a scientific discipline, it must evolve with the very evidence it helps organize. Despite the long-standing achievements of taxonomic classification in organizing plant diversity, much of the current taxonomic literature does not meet fundamental scientific standards such as methodological transparency, reproducibility, or integration of evidence. These issues weaken the reliability of taxonomic conclusions and hinder the field's ability to evolve alongside modern biology. This essay presents a rationale for adopting evidence-based and reproducible practices in plant taxonomy, advocating for a conceptual and methodological alignment with broader scientific principles.

Scientific disciplines differ in their questions and tools, but share core principles: formulation of hypotheses, reliance on empirical evidence, logical reasoning, and transparent communication of results (Box, 1976; Ioannidis, 2005). Reproducibility is central to these principles, ensuring that independent researchers can validate findings using the same data and methods. Replicability, the ability to achieve consistent results across studies addressing the same question with new data, further strengthens the reliability of conclusions (Whitlock, 2011; Nosek *et al.*, 2015; UNESCO, 2021). Scientific knowledge grows through iterative testing, revision, and generalization. Models and hypotheses must accommodate uncertainty and variability, and scientific claims should remain open to scrutiny and refinement. These norms should be foundational to any field aiming to produce reliable knowledge (Garnett & Christidis, 2017).

Transparency in data, methods, and interpretation is crucial for reproducibility. Open access to specimen data, character definitions, measurement protocols, analytical code, and statistical models allows others to verify and build upon taxonomic studies (Whitlock, 2011). Despite the availability of repositories and publishing platforms, many journals, including Acta Botanica Brasilica (ABB), still lack mandatory policies requiring the sharing of underlying data and code. However, ABB, supported by SciELO and guided by its Open Science alignment policies, provides authors with a SciELO Data repository (https://data.scielo.org/dataverse/brabb) as a platform for sharing their research data. Indeed, scientific societies and institutions must promote infrastructure for long-term preservation and sharing of taxonomic evidence. Notable initiatives include Dryad (https://datadryad.org/), SciELO data (https:// data.scielo.org), MorphoBank (https://www.morphobank.org/), and GBIF (https://www.gbif.org/), which provide open-access repositories for data and metadata. For botany specifically, platforms such as Jabot (https://jabot.jbrj.gov.br/) and Flora e Funga do Brasil (https://floradobrasil.jbrj.gov.br/) represent efforts toward structured botanical data sharing in Brazil. A coordinated network of curated, interoperable repositories would greatly enhance reproducibility and accessibility in plant taxonomy. Without such standards, plant taxonomy risks remaining an opaque practice rather than a scientific enterprise.

Plant taxonomy was consolidated in the 18th century with the work of Linnaeus, who, influenced by Platonic thought and the Christian worldview predominant in Europe, sought to classify living beings based on a few fixed characteristics considered essential and immutable (Stuessy, 2009). Linnaeus saw species as types created by God, immutable since creation, reflecting the belief in the stability and perfection of divine nature (Larson, 1971; Stevens, 1994). This typological approach, based on ideal categories, founded the organization of botanical knowledge at the time, but it proved to be limited in the face of intraspecific variability, the discovery of new lineages and fossils, and, of course, the proposal of evolutionary theory (Judd *et al.*, 2016; Rouhan & Gaudeul, 2021). Nevertheless, the taxonomic practice has remained greatly unchanged ever since. Today, integrative taxonomy and evolutionary theory bring together morphological, molecular, ecological, and phylogenetic methods to build evidence from specimen data. This is essential to move beyond the fixist taxonomic paradigm, providing classifications that more accurately represent the dynamic patterns of diversity and the processes resulting in evolutionary relationships and phenotypic diversification of organisms (Dayrat, 2005; Padial *et al.*, 2010).

Current traditional taxonomic practice largely fails to be reproducible because it does not isolate and present individual character data (see Box 1). Descriptive characters are often categorical, compressing variation into broad ranges (e.g., *petal shape obovate to ovate*; *scale color brownish to reddish-brown*). When numerical traits are chosen, they are usually limited to simple measurement ranges derived from the minimum and maximum values observed in a few specimens (e.g., *height 1-3 m*), without statistically characterizing the actual distribution of morphological traits (Cardini, 2020). In addition, it is a widespread practice to disconnect individual measures from vouchers, only presented as a list of analyzed specimens. Such practices omit rigorous quantification of size and shape variation and cannot provide true means, medians, and variance, nor distinguish them from measurement noise (Adams *et al.*, 2004). Besides, morphological diagnosis alone does not necessarily result in knowledge from phenotypic diversity; it is usually designed with a view to species differentiation, rather than the processes that may have led to phenotypic divergence.

Unlike sampling in some zoological studies, botanists typically do not collect a series of specimens, i.e., a sampling of population variation in a given location. As a result, it is often not possible to assess the usual phenotypic variation of a specific locality or population. However, it is well-known that phenotypes can be plastic, expressed in different forms from the same genotype under varying environmental conditions (West-Eberhard, 1989; Paaby & Testa, 2017). Phenotypic plasticity, along with natural phenotypic variation within and among populations, indicates that organisms are not the result of a predetermined genotype-to-phenotype pathway, but rather systems shaped by genotype–environment integration, as the genotype encodes a range of potential phenotypes (Sultan & Stearns, 2005). Adding to this complexity, internal phenotypes (at the cellular, tissue, and physiological levels) and external phenotypes (such as macromorphology and phenology) also vary throughout an organism’s life and in response to environmental interactions (Houle *et al.*, 2010). Conversely, phenotypes are modular, with different functional modules grouping traits that may evolve independently of others (Porto, 2018). Additionally, phenotypic variation can be constrained by developmental and evolutionary contingencies (Jablonski, 2017). This collection bias often leads to a sampling bias toward extremes, individuals that deviate from the median population phenotype. Beyond the possibility of aberrant individuals, those occurring at the edges of their ecological niche may exhibit atypical or outlier morphologies, since stressful environments can uncover, generate, and amplify phenotypic and genetic variation among individuals in a population (Badyaev, 2005).

An additional ‘trap’ rising from the typological and morphological diagnosis view derives from herbarium specimens that can be artificially assembled. Some researchers mount specimens with parts from more than one individual in a population, for instance, combining a flowering branch from one plant and a fruiting branch from another, producing a hidden (not explicit, inaccessible) hybrid specimen that does not represent a natural individual in nature. Such 'Frankenstein' specimens also reflect subjective judgments made in the field, usually derived solely from the collector's opinion based on visual diagnosis. Alarmingly, some of these composite specimens could be designed as type material. For clear scientific and methodological reasons, such practice should be banned from the endeavour of systematizing biodiversity.

BOX 1 - Example of specimen data record. Leaf morphometrics partial data from *Chamaecostus acaulis* (S. Moore) T. André & C.D. Specht in André *et al.* (2015)

Herbarium	Specimen code	Longitude	Latitude	Leaf blade length (cm)	Leaf blade width (cm)	Leaf area (cm^2)	Leaf apex degree	Leaf base degree
A	59644	-51.88	-17.32	14.0	5.0	110.0	73	45
IAN	129572	-46.93	-15.80	17.7	8.9	247.4	90	60
INPA	41821	-60.64	-9.19	23.5	8.3	306.4	50	75
INPA	88765	-63.05	-9.95	24.3	8.7	332.1	45	52
MG	160936	-52.33	-3.48	22.3	8.9	311.7	60	51
MG	166827	-52.02	-3.18	30.3	8.2	390.3	33	35
MO	2895800	-63.62	-10.59	20.5	6.4	206.1	50	42
MO	4842491	-65.63	-11.01	25.3	9.8	389.5	79	39
NY	8338	-65.46	-9.66	15.5	7.0	170.4	97	42
NY	194385	-52.50	-4.80	24.8	8.4	327.2	63	49
R	208178	-50.52	-20.26	14.5	7.0	159.4	91	82
RB	395800	-55.93	-9.60	11.5	7.2	130.1	87	72

RB	500170	-55.93	-9.80	20.5	8.2	264.0	79	50
UB	55182	-52.25	-15.88	21.5	7.5	253.3	51	30
UB	55190	-46.81	-15.88	17.5	6.5	178.7	90	40

*Herbaria acronyms follow Index Herbariorum (https://sweetgum.nybg.org/science/ih/).

**Specimens are indexed by herbarium code since collector name and number are often produced as duplicates, which makes them poor indexes for actual measured specimen sheets.

On the other hand, integrative approaches can allow the interpretation of patterns from the acknowledgment of processes, bringing methods into a much more inclusive realm. For instance, Buitrago-Aristizábal *et al.* (2020) showed that leaf blade symmetry and eccentricity categorized for species in the genus *Ischnosiphon* (Marantaceae) proposed in traditional monographic descriptions and identification keys (*e.g.* Andersson, 1977), were highly variable within species and formed a continuous of overlapping variation between species, hindering its objective use for understanding species (typological) concepts or diagnosis (Figure 1). Moreover, the continued use of merely qualitative concepts and terminology without replicable definitions or landmarks hampers reproducibility and limits broader interpretability across studies (Feitosa e*t al.*, 2023). These important limitations highlight the need for open data coupled with transparent, statistically robust frameworks that incorporate adequate individual specimen data, sampling schemes, sample sizes, quantitative morphometric analyses, accuracy measurements, and universal descriptive standards to ensure consistent and reliable species descriptions and diagnoses.

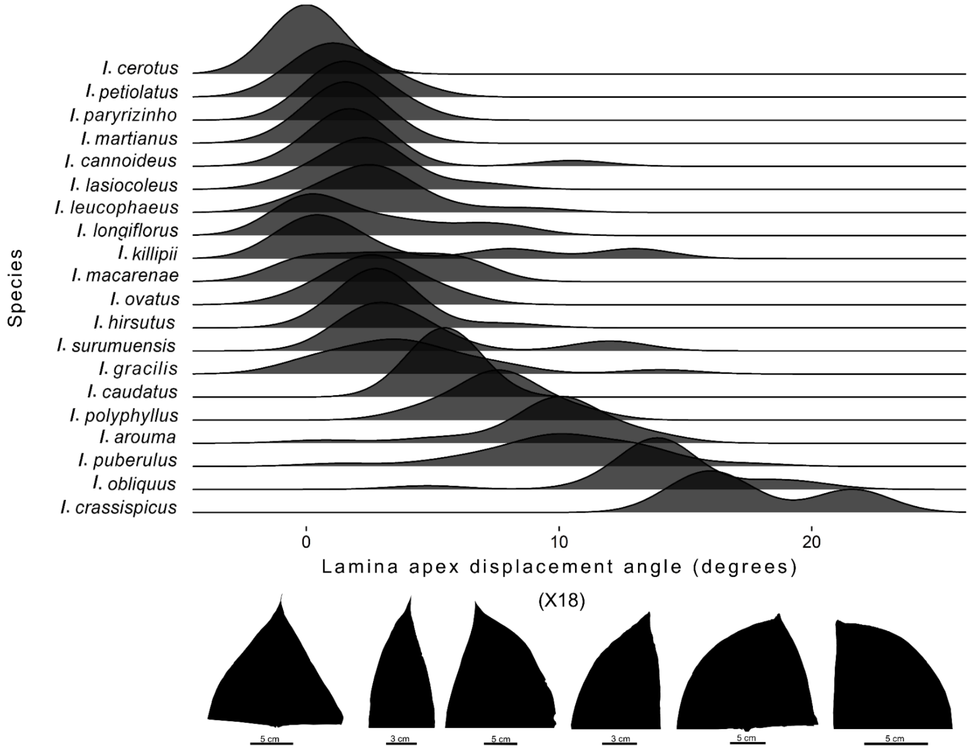

Figure 1. Density plot of lamina symmetry along 21 *Ischnosiphon* species. From left to right: silhouettes representing leaf apices from *I. cerotus* (Schunke-Vigo 3216), *I. cannoideus* (Prance 14254), *I. ovatus* (Kuhlmann s.n.), *I. puberulus* (Andersson 1776), *I. obliquus* (Plowman 2584), and *I. crassispicus* (Plowman 2584). Original M.A. Buitrago-Aristizábal *et al.* (2020), Accommodating trait overlap and individual variability in species diagnosis of *Ischnosiphon* (Marantaceae), Botanical Journal of the Linnean Society, Volume 194, Issue 4, December 2020, Pages 469–479,

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Species are currently understood as evolving lineages composed of interbreeding populations over time (de Queiroz, 1998). It is therefore a trans-temporal entity. These lineages are also often permeable (Wu, 2001; Mallet *et al.*, 2016), where species boundaries are not always rigid and may vary through time or across populations, producing non-bifurcating species phylogenies (Mallet *et al.*, 2016; Bock *et al.*, 2023). Species - and any other taxa for that matter, since every genus, family, etc., was once an ancestral lineage - are not fixed entities but dynamic and context-dependent. There is rising evidence of multiple routes to diversification through whole-genome duplication (e.g., Soltis *et al.*, 2009; Jiao *et al.*, 2011; Carta *et al.*, 2020), and most speciation events in plants took place in sympatry (Hernandez-Hernandez *et al.*, 2021). Although discontinuities among organisms and populations can be observed in nature, speciation is a continuous process that may even be reversed through gene flow (Vaux *et al.*, 2016). Even after lineage separation, reticulation processes—such as hybridization and introgression—make it difficult to delineate hermetic species definitions that accurately reflect evolutionary history (Galtier, 2018).

Traditional taxonomy assumes that morphological differences reflect distinct entities. However, a direct relationship between phenotypic divergence and lineage separation is not always observed in nature (Vaux *et al.*, 2016). Closely related but distinct lineages can remain phenotypically similar over geological timescales through stasis (Cerca *et al.*, 2019), drift, or phylogenetic niche conservatism (Wiens *et al.*, 2010; Crisp & Cook, 2012). However, as lineages diverge, evolutionary processes beyond drift—such as stabilizing selection, pleiotropy, gene flow, linkage of co-adapted traits, or biotic factors like competition and herbivory (Cooper *et al.*, 2010; Crisp & Cook, 2012)—may explain why descendant lineages retain phenotypic similarities. Conversely, convergent evolution can make distantly related lineages morphologically similar despite distinct evolutionary trajectories (Speed & Arbuckle, 2017). Defining and identifying species using qualitative morphological traits becomes particularly challenging when taxa belong to species complexes. These complexes consist of incompletely separated or divergent lineages where reproductive barriers remain weak (Pinheiro *et al.*, 2018). Conversely, the same taxonomic problem arises with cryptic species, reproductively isolated lineages exhibiting little to no morphological distinction (Bickford *et al.*, 2007; Haufler, 2008; Struck *et al.*, 2018). In plants, hybridization, introgression, and broad phenotypic plasticity further complicate species delimitation and pose significant challenges for taxonomic and conservation efforts (Vaux *et al*., 2016).

As a consequence of such a complex diversification context, describing taxa should require more than listing arbitrarily defined scientific names, specimens, and macromorphological categorical attributes; it demands analytical frameworks in the realm and scale of the biological evolutionary processes producing patterns and capable of testing lineage boundaries and gene flow, particularly by using phylogenetic, genomic, and demographic data (Dufresnes *et al.*, 2023). Therefore, taxonomic categories should be treated as hypotheses about evolutionary lineages, not static data or as assumed factual entities found in nature. In such a perspective as the one proposed here, taxonomic decisions should be based on multidisciplinary evidence and probabilistic reasoning, distinct from arbitrarily, often solely opinion-based, categories.

Like any scientific model, taxa, as hypotheses, must be testable, subject to revision, and grounded in reproducible evidence. Yet, plant taxonomy has been emphasizing description and classification, often without the analytical rigor expected in hypothesis-driven research. In a formal sense, plant taxonomy can be defined as the set of procedures for naming, describing, and classifying organisms, primarily based on observable traits and guided by nomenclatural rules (Simpson, 2006; Judd *et al.*, 2015). Systematics, by contrast, is the broader scientific discipline that seeks to understand evolutionary relationships among organisms, integrating data from all of the biological sciences, including, but not limited to, genetics, morphology, and ecology (Wiley & Lieberman, 2011). It includes plant taxonomy as a component, often a practical result of biological patterns, but extends further to evolutionary processes, population genetics, and phylogenetic inference (Zachos, 2018). While these terms are sometimes used interchangeably, their conceptual distinction is colossal. Considering this distinction, taxonomy can be viewed as a method, and its specialists, as any specialist in a method, a technician. Therefore, academia, science funding agencies, and journals should be investing in graduating, funding, and publishing systematic biology, a proper biological science, which can, as a consequence, produce solid taxonomy based on the integration of factual biological data (see Box 2 for practical recommendations).

Another major concern that arises from current outdated practice is the phenomenon known as taxonomic inflation (Isaac *et al.*, 2004; Garnett & Christidis, 2017), which occurs when evolving lineages are excessively split based on limited or non-integrative data, often without sufficient or any evolutionary justification. It can have huge impacts on conservation efforts or proper species management (Garnett & Christidis, 2017; Zachos, 2018). One common driver of taxonomic inflation is the reliance on a single line of evidence—such as macromorphological traits—without corroboration from genetic or reproductive data, which can provide evidence of lineage cohesion, isolation, and relatedness. While morphology remains a foundational tool in plant taxonomy, its subjective definition, interpretation, plasticity, and convergent evolution can mislead taxonomic inference. To ensure scientific robustness, new taxa should be proposed only when supported by consistent signals across multiple, independent datasets, and particularly, with evidence of relatedness, which most often comes from molecular data or phylogenetic interpretation of phenotype when considering fossil taxa without molecular data. Classifications and taxon descriptions derived solely from morphological traits or based on a single specimen should be avoided, as they usually lack robust empirical support. Many historical cases, such as early misclassifications, illustrate how limited and biased evidence can lead to unnatural taxonomic arrangements. For example, early classifications used pteridophytes (*e.g.* Kramer & Green, 1990), grouping ferns and lycophytes, two distinct lineages (Pryer *et al.*, 2001), or fern allies for lycophytes, horsetails, and whisk ferns (*e.g.* Tryon & Tryon, 1982), the latter two now known to be nested in the fern lineage (Pryer *et al.*, 2001). Moreover, the Angiosperm Phylogeny Group I (APG, 1998) did not accommodate a long-standing Dicotyledoneae taxon to properly reflect angiosperm diversification under a phylogenetic-based classification. An integrative, evidence-based, phylogenetic approach mitigates such risks and ensures greater scientific reliability at any taxonomic level.

In taxonomic practice, it is essential to recognize that the sampling unit is the individual specimen collected or observed, and not the taxon itself, since taxonomic inferences derive from empirical data obtained from specific specimens (Stuessy, 2009). This distinction is essential to ensure statistical validity and reproducibility, central principles of experimental design (Sokal & Rohlf, 1995). The mistake of treating the taxon as a primary unit can lead to undue and biased generalizations, hiding intra-lineage variability, and compromising comparative analyses and evolutionary inferences. Thus, modern taxonomy must adopt rigorous sampling procedures, with a clear definition of sample units, independent replicates, and documentation and quantification of intraspecific variability, in line with good scientific experimentation practices (Quinn & Keough, 2002).

Historically, the training of taxonomists has followed a model of artisanal learning, based on the transmission of tacit knowledge through prolonged coexistence with experts, resulting in diagnostic decisions often supported by arbitrary criteria and little methodological transparency (Wheeler, 2004; Ebach *et al.*, 2011). This approach, perhaps effective in consolidating practical knowledge, limits critical autonomy and the ability to integrate multiple lines of evidence (Padial *et al.*, 2010; Yeates *et al.*, 2011). Given the growing complexity of biological datasets and the need to reconstruct natural classifications that are consistent with evolution, it is essential to provide emancipatory training for systematists, capable of formulating explicit hypotheses, handling large volumes of morphological and molecular data, applying robust phylogenetic methods and interpreting biodiversity patterns on broad scales (Dayrat, 2005; DeSalle et al., 2005; Godfray & Knapp, 2004). Training in integrative taxonomy favors replicable and testable approaches, reducing the subjectivism inherent in arbitrary taxon diagnosis (Schlick-Steiner *et al.*, 2010; Packer *et al.*, 2009). Thus, to address the global taxonomic crisis without taxonomic inflation and ensure scientific evidence-based classifications, it is crucial to transition from apprentice and procedural taxonomists to critical systematists (see Figure 2), i.e., researchers capable of collecting and analyzing factual data in the context of evolutionary theory and contemporary biological sciences (Wheeler *et al.*, 2012; Padial *et al.*, 2010; DeSalle *et al.*, 2005).

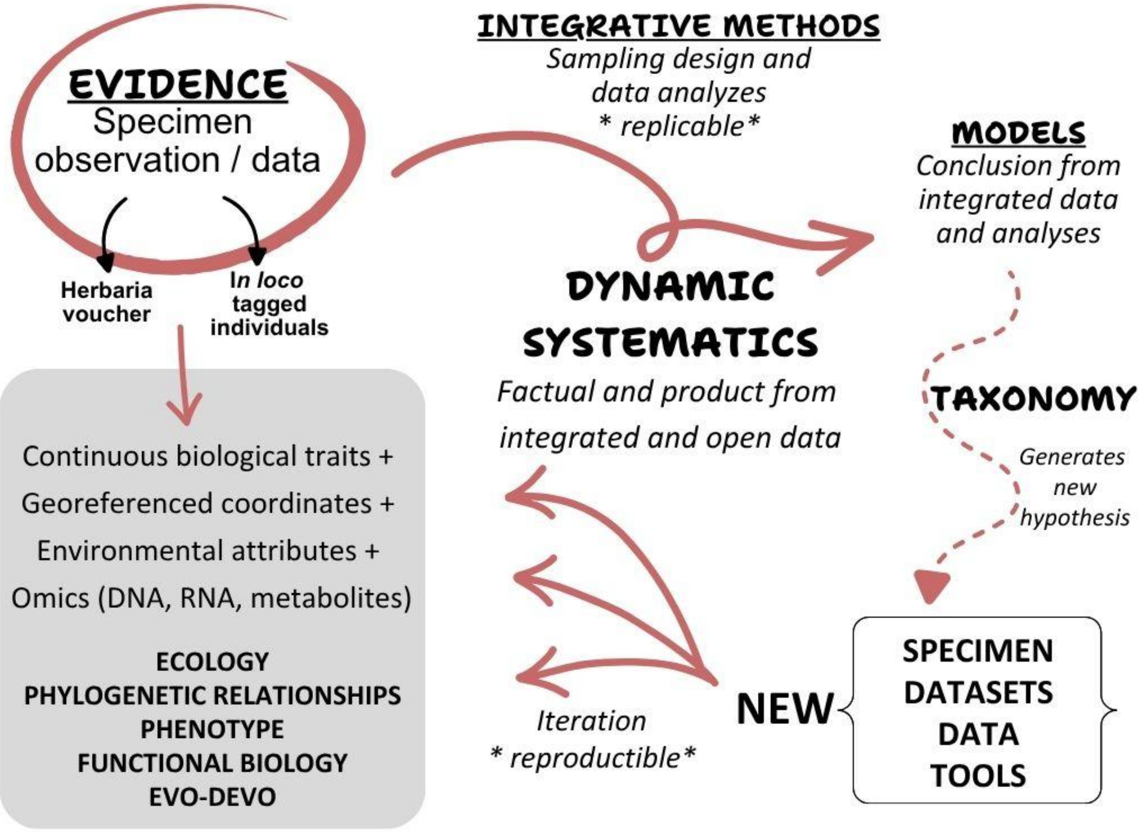

Figure 2. Conceptual workflow for evidence-based and dynamic Systematics. The workflow begins by investigating specimens (herbaria vouchers or *in loco* tagged individuals) as evidence, and then deals with replicable integrative multidisciplinary methods to analyze the specimens and produce taxonomic models/hypotheses. Then, new

specimens, datasets, data, and tools are used as evidence in a reproducible and iterative manner.

BOX 2. Some Practical Recommendations

Evidence integration: Taxonomic proposals should integrate multiple lines of evidence, including, but not exclusively based on, phenotype, reproductive biology, phylogenetics, genomics, and ecology.

Data transparency: Data and voucher information from analyzed specimens should be presented in a character x specimen matrix, not just as values ranges or specimens list, where it is impossible to recover original data per specimen. All datasets, code, and metadata used in taxonomic studies should be made publicly available. Phenotypic data should be presented with clear character definitions and methods for measurements and/or identification. .

Analytical rigor: Measurement uncertainty, character variability, and hypothesis testing should be clearly presented and justified.

Editorial reform: Following the Open Science recommendations, Journals should require the submission of underlying data and analytical protocols as part of the publication process. Initiatives like SciELO Data (https://data.scielo.org/) provide platforms to support these practices. Adopting tools such as transparency checklists or open science badges, already broadly used in fields like ecology, can help normalize these standards in plant taxonomy.

Institutional support: Scientific societies and funding agencies must support infrastructure for open data and reproducibility. Long-term initiatives, such as GBIF and Flora e Funga do Brasil, offer successful models of data stewardship in biodiversity science, demonstrating the feasibility and impact of sustained investment in digital resources.

Human resources and education: Universities and research institutions forming personnel should focus on an emancipatory curriculum, aligned with strong scientific project-based education strategies and critical reading and writing. An evidence-based and replicable systematics emphasizes science and not the scientist; therefore, it has the potential to change power relationships in a currently highly conflictual and hierarchical scientific community. Additionally, emancipatory teaching practices further stimulate user autonomy and context-dependent learning.

Plant taxonomy must evolve into a dynamic, evidence-based endeavor aligned with up-to-date standards of reproducibility and transparency. By treating taxa as hypotheses rather than facts and by grounding classification in testable, integrative models, plant taxonomy can fulfill its role as a rigorous scientific result of biological systematics. A truly scientific plant taxonomy is necessarily unstable in the best sense: it evolves with the accumulation of evidence, advances in analytical tools, and progress in theoretical frameworks. Changes in classification should be expected and welcomed as part of a dynamic scientific process. This transformation is not a rejection of tradition but an affirmation of plant taxonomy's scientific potential in the era of open, reproducible research.

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Authors' Contributions

TA: Conceptualization, Investigation, Writing – original draft, Writing – review & editing; TEA: Investigation, Writing – original draft, Writing – review & editing.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability Statement

No new data were created or analyzed in this study. Data sharing does not apply to this article.

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