

A collaborative, integrated and electronic future for taxonomy

Norman F. Johnson

Department of Evolution, Ecology and Organismal Biology, The Ohio State University, 1315 Kinnear Road, Columbus, OH 43212, USA. Email: johnson.2@osu.edu

Abstract. The Platygastridea Planetary Biodiversity Inventory is a large-scale, multinational effort to significantly advance the taxonomy and systematics of one group of parasitoid wasps. Based on this effort, there are some clear steps that should be taken to increase the efficiency and throughput of the taxonomic process. Increased collaboration among taxonomic specialists can significantly shorten the timeline and add increased rigor to the development of hypotheses of characters and taxa. Species delimitations should make use of multiple data sources, thus providing more nearly independent tests of these hypotheses. Taxonomy should fully embrace electronic media and informatics tools. Particularly, this step requires the development and widespread implementation of community data standards. The barriers to progress in these areas are not technological, but are primarily social. The community needs to see clear evidence of the value added through these changes in procedures and insist upon their use as standard practice.

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In the year 1220, under the direction of the Archbishop Walter de Gray, the construction of the York Minster Cathedral was begun. Today, its three towers rise 60 m into the air, providing an expansive view of the ancient city of York. Whenever I visit such old church buildings in Europe, I feel a strong emotional impact. I think that this arises both from a feeling of nearly tangible community with generations of predecessors, as well as a simultaneous sense of the smallness of individual humans and the greatness of what can be built together. The construction of cathedrals in the Middle Ages was, literally, a monumental task completed by generations of individual workers, common labourers and talented craftsmen alike. This work required decades or even centuries to complete, or at least to be declared to have been finished. In the process, the architects' original plans were often modified, sometimes so substantially as to result in a peculiar mixture of styles in the final product.

Since the publication of the 10th edition of *Systema Naturae* (Linnaeus 1758), we zoological taxonomists have been working on our own edifice. The pace of the work has ebbed and flowed over the decades. The guiding principles have dramatically changed over the years, beginning as an attempt to elucidate divine inspiration and then absorbing the Darwinian revolution, the integration of genetics and evolution in the 'New Synthesis', and now becoming more and more influenced by the current era of molecular biology. Through this time it has been a collective enterprise, one generation following the next, working to discover and document the diversity of the living world and to put order to this great richness of species.

Gould and Lewontin (1979) used cathedral architecture as a powerful image in their seminal paper in evolutionary biology. The metaphor of a cathedral also came to my mind as I thought about my expectations and aspirations for the future of taxonomy.

Like any science, taxonomy builds upon the accomplishments of the past, and we have both a rich tradition and our full share of anachronisms. And, as with any profession steeped in tradition, we have the conflict between a reflexive conservatism and a rebellious, self-assured new generation. My own training as a graduate student was embedded in the intellectual context of the first two generations of scientists who followed the development of the 'New Synthesis.' Initially, I was taught using the textbooks of Ernst Mayr and his collaborators (e.g. Mayr 1963, 1969), before the days of personal computing and DNA sequencing. Much has changed in systematics, evolutionary biology and even taxonomy since that time, but the task of constructing that cathedral, brick by figurative brick, is an ongoing challenge. More recently, the context of this viewpoint is primarily the efforts we have made over the past decade to find ways to accelerate the growth in understanding of our own group of interest – the parasitoid wasps of the superfamily Platygastridea – through the development and application of new informatics tools. This work was supported in part by the US National Science Foundation Planetary Biodiversity Inventory Program. As in many invertebrate taxa, we are confronted by a surprisingly large number of species and too few people available to do the work. There are some 5000 species that are currently considered valid and, on the basis of our current work, I estimate that this is somewhere between only one-tenth to one-third of the actual number. Today there are, at most, 3–4 professional scientists whose research efforts are concentrated on platygastroid systematics and taxonomy. Therefore, to make substantial progress we need to make the most effective use possible of the time and energy of these specialists.

It seems that taxonomy has been held in low regard long before the advent of molecular biology. Even in 1928 it was compared by

Walther Horn to the mind-numbing scholasticism of the Middle Ages (Horn 1928). This impression is reinforced since the primary sources of taxonomic characters are the same arcane details of anatomy that were used in the 18th and 19th Centuries, and the results of taxonomy are published as classifications and descriptions, both widely misunderstood to be subjective in nature and inherently unscientific. Yet there have been many examples of taxonomists eagerly adopting the latest developments in both theory and instrumentation. Witness the rapid adoption, at least by the younger practitioners, of the biological species concept in the 1940s and 1950s and of cladistics two decades later. Taxonomists have embraced the use of scanning electron microscopes, global positioning systems, and extended-focus imaging (Winston 1999). This belies the notion that taxonomy is a moribund enterprise, and offers the reasonable hope that the field can continue to grow and to take advantage of the new opportunities that present themselves. Startling advances in molecular biology and information technologies over the past 10–15 years have revolutionised many aspects of both science and everyday life. So it should come as no surprise that I anticipate that the same fields will exert a strong and positive influence on the future of taxonomic practice.

The data that taxonomists use in their work come from a range of quite disparate domains (Johnson 2007; Thessen and Patterson 2011). These include, but are not limited to, taxonomic names and classifications, geography, time, stratigraphy, biological and ecological associations, imagery, literature and features. This last category encompasses information on anatomy, physiology, phenology, behaviour, karyotypes, protein and nucleic acid sequences, and genome structure, just to hit a few of the high points. Taxonomists generate and test hypotheses of both characters and taxa on the basis of these data in a process akin to the reciprocal illumination of phylogenetic systematics (Hennig 1966; Johnson 2010).

Unfortunately, many of these data are hidden, found only as labels on specimens in locked cabinets, embedded in some sort of summary statement (such as a distribution map), or not presented at all. Yet there is much that can be done with these resources, not only for the conduct of taxonomy itself, but also to address questions beyond the scope of the original paper or to combine the data from different studies in meta-analyses. In this way, data that are gathered at great effort and expense can find use by a wider range of scientists, thus having broader impact and achieving more citations. To accomplish this, I believe that it should be standard and expected practice that all of the specimens used in a taxonomic study have globally unique identifiers and, as a minimum, the accompanying label data on provenance – place, time, and method of collection, life stage, sex (if applicable), identification, and depository – be recorded in publicly accessible, online databases. Ideally, of course, this would be true for the entire holdings of all natural history collections, thus transferring or at least sharing the tasks of data recording and dissemination from the individual scientist to an institution that can house and protect the information for the long term. This need not result in further bloating of the size of publications. Reference to the unique identifiers can be included in supplementary information as is the common practice in many journals in biology.

Is this feasible and, if so, is it desirable? I believe that the answers to both questions are an emphatic yes! On its website, the Global Biodiversity Information Facility (GBIF: www.gbif.org) boasts more than 300 million specimen records. (More precisely, these are primary species occurrence records, including specimens as well as other documented records such as images or sightings.) GBIF does not maintain these records, but caches copies of core data elements and acts more or less in the role of a broker, providing a convenient place to discover where they are housed and curated. Nevertheless, a set of information exchange standards has been developed and implemented, thus allowing a user to query and merge datasets from disparate resources. The unfortunate aspect is that these electronic depositories of specimen data currently come from only 341 ‘publishers’ and a minority of both records and publishers deal with the holdings of invertebrate collections.

If the data were accessible, it would be possible to better understand and model geographic distributions, niche breadth, phenology and biological and environmental associations. It would be feasible to document changes in geographic distributions through time and to predict better the possible impacts of biological invasions or climatic change. Taxonomists beginning a study would be able to determine where material relevant to their work is deposited and include it in their project. I have sometimes heard the lament that taxonomy fares poorly in comparison with other disciplines such as oceanography, astronomy and physics in which the community bands together to use and share data from large, expensive instrumentation. I think that, in fact, we already have the ‘big instrument’ in hand, a biodiversity viewer: the global holdings of our natural history collections. The problem is that this viewer is still unassembled, broken into its individual components and spread around the world. It is time to put the pieces together and hold it up as an exemplar of large-scale, international scientific cooperation.

The vast disparity between the size of the available workforce and that needed to accomplish the task of ‘completing’ the taxonomic enterprise has been referred to as the taxonomic impediment. When I entered graduate school, agnostic as to which taxon I wished to focus on, the advice that I received was to seek out a group with some general interest or importance for which specialists were few or entirely lacking. The rationale, of course, is to attempt to provide at least some coverage for these important groups of organisms and, thereby, to make at least slow advances in furthering our understanding across the broadest range of biological diversity. While I can still understand and appreciate the logic, I have since come to the conclusion that this is counterproductive. Graduate students commonly have to be self-trained because their major professor has no detailed expertise in the dissertation subject. Financial support for the students to conduct their research is limited to that which they can generate themselves. This strategy has fostered isolation among taxonomists, a lack of the beneficial effects of both competition and the synergy that can emerge from collaboration and, in the end, results in only sputtering advances in most groups of organisms.

I believe that taxonomy is already slowly evolving from this single-investigator paradigm to an integrated, collaborative enterprise. Cooperation will be facilitated by transparent

access to specimen data – both collection metadata and character data – and the availability of high-quality imagery of specimens. Internet-based tools to facilitate such collaboration are already in use: our own effort is a platform called vSysLab (Johnson 2010); the Scratchpads of the European Distributed Institute of Taxonomy are another such application (Smith *et al.* 2011). The development, testing, adoption or rejection of hypotheses of both characters and taxonomic concepts can be facilitated and made more rigorous by bringing more minds and perspectives to the work. It is my thesis that this stage of hypothesis development and testing is the critical bottleneck in the taxonomic enterprise, and the only effective way to attack it is to take full advantage of the intelligence and insights of as many people as possible. We may find that automated character extraction (such as that advocated by La Salle *et al.* 2009) will be effective in the future. I welcome such an advance, but remain rather skeptical that it can be operational in the near term.

It is fair to say that most taxonomists today incorporate phylogenetic analyses into their work program. In fact, it is very striking how such ‘tree-thinking’ now permeates almost all aspects of biology. This expansion of an approach that once was almost entirely limited to the systematics community has been greatly facilitated by the advances in technologies over the past two decades that have made it relatively easy to generate extensive character data for taxa, not from the arcane knowledge of anatomy, but from DNA sequences. Morphology has, of course, remained the primary coin of the realm for taxonomic work in many, perhaps most, groups. It is a rich, though not unlimited source of information, it has proven its worth (and weaknesses) over the past two and a half centuries, and is the only such source for some organisms, such as fossil or extremely rare taxa. Nevertheless, I believe the time is ripe for DNA sequence data to play a much more important role in fundamental taxonomy. I do not foresee this as a simplistic panacea for all the problems in species delimitation as in the characterisation, perhaps unfair, that is often associated with the concept of DNA bar-coding. Rather, I see the community moving closer to the idea of integrative taxonomy as espoused by Will *et al.* (2005), Schlick-Steiner *et al.* (2010) and Padial *et al.* (2010). In this scheme, DNA sequences, as well as many other sources of data, are used *along with* morphology as datasets that can independently test hypotheses of species. I suspect that morphology will be the prime source of data, simply because the characters can be more easily and comprehensively extracted. Incorporation of sequence data into the work flow will make it possible to assess species delimitations based on anatomy, to compare levels of character diversification and thereby to recognise, for example, that a single morphospecies is, in fact, a complex of species. There are many examples of molecular data leading to more highly refined species hypotheses and, on this basis, morphological features that were thought to be meaningless, individual variation are found to easily diagnose the species (e.g. Veijalainen *et al.* 2011). With the relative ease with which sequences can be generated from single legs or non-destructive extractions, I expect that integrative taxonomy will be the standard in the field in the near future. As with any change, this will also necessitate a reconsideration by curators of policies regarding such procedures and the deposition and ownership of both the resulting DNA extractions and the sequences.

Perhaps one of the most seriously anachronistic aspects of today’s taxonomy involves the process of publication. Under the current, fourth edition of the International Rules of Zoological Nomenclature, nomenclatural acts must be disseminated in a published work and one of the defining criteria for such a work is that ‘it must have been produced in an edition containing simultaneously obtainable copies by a method that assures numerous identical and durable copies’ (Article 8.1.3). This requirement for durability, together with the explicit exclusion of ‘text and illustrations distributed by means of electronic signals (e.g. by means of the World Wide Web)’ (Article 9.8) have generally been taken to mean that zoological taxonomic publications must be produced in a hard copy format, preferentially ink on paper. As a result, many of the powerful advantages of electronic documents are severely constrained. These include incorporation of hypertext links from one document to another, dynamically produced pages, the effective abolition of restrictions on the number of pages or illustrations, the incorporation of illustrative material other than static images (such as movies and sounds), and the incorporation of semantic markup into the documents. A few publishers have found effective workarounds to this limitation by producing these works in two forms: in a traditional printed form, produced in small numbers and distributed to a few major institutions; and fully electronic versions as PDFs, HTML web pages, and XML documents. The most cogent argument of those who advocate retention of the hard-copy requirement is that ink on paper is the best-tested method to assure the durability and availability of works in the long term. I personally believe that this important need for archiving can and will be effectively met by the same agents that have always been responsible for that role: libraries. Library and information science is deeply involved in this issue already. Archiving published works is perhaps the prime directive of libraries, and I think we can continue to trust in their capability to fulfil it.

There are further, more important issues in taxonomic publication beyond this issue of hard-copy versus electronic formats. I believe that we need to conclusively move away from the expectation that a taxonomic work is ‘definitive.’ This seems to contribute to the inertia of the publication process, the often vain hope that just a few more specimens will turn out to be the key to the resolution of the last remaining questions. A taxonomic paper often plants the very seeds of its own obsolescence. The publication usually stimulates other workers, resulting in new discoveries of species, distribution records, ecological associations, temporal extensions and the like. These new data tidbits may be relatively trivial individually, but in the aggregate they make significant contributions to our understanding of most species. Development of a platform – perhaps something along the lines of the web taxonomy proposed by Godfray (2002) and its initial implementation as the CATE project (Clark *et al.* 2009) – that can reflect the current state of the dynamic growth and maturation in taxonomy would be a tremendous step forward.

As we move towards electronic publication, it is critical that we develop and implement community standards for the important elements in these documents. These elements include primary occurrence data (time, place, method and agent of

collection or observation), taxonomic concepts, characters, analytical techniques, phylogenies, classifications, etc. Standards are critical to the integration of information across different platforms. Several of these are already under development or have been approved under the auspices of the international organisation Biodiversity Information Standards TDWG (formerly the Taxonomic Databases Working Group). These include the Darwin Core and ABCD for primary occurrence data; the Taxonomic Concept Schema; Structure of Descriptive Data; query protocols such as DiGIR and TAPIR; and support for the use of Life Sciences Identifiers.

In addition to providing a mechanism to integrate database applications over the Internet, these standards should also be used within publications. Life sciences identifiers need not be intrusive to the reader as they can be included as hidden tags for elements within the text. Their presence provides an explicit link between the literature and external information resources around the world. Beyond the individual data elements, most taxonomic literature shares common structural features, a *de facto* standard if you will. The core of this structure is the taxon treatment. Addition of semantic markup, for example using schemata such as Taxpub (Penev *et al.* 2011), can define the boundaries of treatments and their major components, including nomenclatural information, lists of material examined, diagnoses, etymologies, descriptions and diagnoses. This markup, in turn, can provide the context that is important to effective, computer-driven data mining of the literature. Addition of such markup to the legacy literature is a daunting proposition: much of it is written in a style in which key elements, sometimes even the description of new taxa, are embedded in a narrative and therefore difficult to parse, even for human readers. Nevertheless, significant progress can be made (e.g. Cui 2010, 2012). Prospective literature is much more promising. In my own ideal, a taxonomic authoring application – built atop existing word processing applications – could be used to automatically facilitate the incorporation of much of this semantic markup, thus freeing authors, editors, and publishers to focus on producing and disseminating the science itself.

It appears to me that since much of the value of publications in the future is to be found in their electronic avatars, the natural next step is that the literature of zoological taxonomy will follow other sciences and become entirely electronic. Given the ease with which anyone equipped with a computer can produce and distribute a publication, that would seem to harbour a potentially disastrous flood of works of, shall we say, dubious quality. This may be true, but it is neither new nor unique to electronic publications. One approach to dealing with the issue is to develop a registry of ‘accepted’ publication venues for the proposition of nomenclatural acts. Currently, taxonomic works are published in hundreds of different periodicals. In my own group, the Platygastroidea, papers have appeared in 427 different journals; for ants the number increases to 753. This is clearly too many to be on anyone’s regular reading list, and if the number of journals available electronically increases, then the magnitude of the problem simply becomes greater. A registration procedure need not involve a subjective judgment of ‘quality’ nor the extreme case of funnelling all papers through a single outlet, but only an objective set of standards that ensure that the

content is available, archived and accessible to machine-based data mining.

Publications in the future should be multi-authored works, ideally with the roles played by the individuals specified in a meaningful way. This will exacerbate the disconnect that already exists between the authors of a paper and the authors of new taxa described in that paper. Also, as collaborative work becomes the accepted norm in taxonomy, perhaps the combination of non-identical sets of multiple authors may (finally) lead the community to abandon the practice of treating taxon author names as part of the scientific name itself. This may have made sense in the context of an earlier time in which including the name of the taxon author functioned as a shorthand citation to scientific publications. As such, they have always been flawed in that they provide insufficient information to actually locate the publication. An alternative justification is that they are useful in differentiating among homonyms, unless, of course, the same author is responsible for both names. Both of these functions are more effectively achieved through the use of unique identifiers to the taxonomic concepts, identifiers that when resolved lead to a complete citation or, even better, to a copy of the publication itself. Wägele *et al.* (2011) have recently suggested that the publications in which taxa are originally described be formally included in the literature cited sections of publications that use scientific names. The sentiment underlying the proposal is laudable. We teach undergraduate students that it is necessary to cite sources of information. Why should it be different for the discovery and delimitation of new species? I would only amend the proposal of Wägele *et al.* to note that the taxonomic concept of the original describer is often not the concept in current use. Therefore, logic would dictate that citations should be demanded for both the paper of the original description as well as that circumscribing that actual taxonomic concept being used. If this seems to a difficult requirement, then that is a strong argument for promoting the development of complete, annotated taxonomic catalogues of the world’s biodiversity that are developed and maintained by domain experts.

Perhaps my expectations and hopes for the future practice of taxonomy are limited. For each of these topics raised, preliminary work has already been done, and the tools to put them into effect are available. What will it take to put these – and other pieces – together into a whole that exceeds the sum of its parts? The primary obstacle, clearly, is not technological, but social. Any significant transformation will await two shifts in attitude. Both users and producers of taxonomic products must find value in the tools. That is, they must find it possible to answer questions and to do so more effectively than before. Second, use of these tools must become an expectation of good taxonomy. These sociological changes are much more difficult to put into place and the time needed to do so will undoubtedly be much longer than anyone may want.

I must admit that I waver between two very different views of whether this kind of view of the prospects for taxonomy will ever come about. On the one hand, I am deeply pessimistic. The quality of existing taxonomic publications varies widely: we certainly still consider works to be acceptable even though they fail even to meet the standards of the early 19th Century. The Code is understandably quiet on this issue, and the specialised knowledge required to competently judge the merits of papers makes peer

review extremely difficult. On the other hand, I believe that the benefits that will naturally be gained from greater collaboration, integration, and the shift to fully electronic ‘publications’ are so great and so self-evident, that the movement towards this change in methodology will be irresistible. I hope that the latter prevails, but I am not so sanguine as to expect that it will inevitably overcome the obstacles.

Of course, there is another profound factor that will affect the future of taxonomy. That is the continued loss of habitat and, presumably, species. So, even as we develop the tools to more rapidly build our taxonomic cathedral, the bell towers may never reach the height they could have, and we may never be able to appreciate the true dimensions that might have been attained. So it would behoove us to do the best we can to reach our goals as quickly as is prudently possible. I believe that we can make significant progress, not by waiting for technological breakthroughs, but by intelligently using and adapting the tools in hand. It took 253 years to build the York Minster Cathedral five centuries ago. It has now been 254 years since the seminal year of 1758, yet I know of no taxonomist who believes that our collective task is anywhere near its completion.

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