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Systematics Agenda 2020: The Mission Evolves

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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 role of systematics within biology (e.g., Blackmore and Cutler 1996; Cracraft 2002; Halanych and Goertzen 2009), in education (e.g., Krishtalka 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” was held during 2009–2010 to evaluate progress in the field and identify new directions and opportunities. Workshop participants reviewed SA2K as a way to rapidly achieve common 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 suggest 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 partly achieved. Workshop participants acknowledge the continued relevance—indeed centrality—of all three

TABLE 1. Systematics Agenda 2020. Missions 1 and 2 are largely congruent with the corresponding elements of Systematics Agenda 2000 (SA2K). Mission 3 is new; see text for discussion. Mission 4 maps to Mission 3 of SA2K but emphasizes dissemination rather than the organization of information

Systematics Agenda 2020

Mission 1: To discover and document past and present life on earth

Mission 2: To analyze and synthesize the information derived from this global discovery effort into a history of life and predictive classification system

Mission 3: To understand the evolutionary mechanisms that explain the origin, maintenance, and loss of biodiversity

Mission 4: To communicate and apply this knowledge to science and society

of these missions to researchers across the life sciences. The group also argues that the success of these missions likely relies on updated credit models that reward more than just peer-reviewed publications as knowledge currency (Ebach et al. 2011; McDade et al. 2011).

Although SA2K embraces the discovery of evolutionary *pattern* (i.e., phylogeny, SA2K Mission 2), it is remarkably silent with respect to the evolutionary *processes* that generate the diversity of life on Earth. The overwhelming consensus among workshop participants was that, in the intervening years, systematists have embraced study of evolutionary processes as integral to their science. Many of the questions that drive the research programs of systematists focus on processes including speciation and the evolution of characters ranging from DNA sequences to morphology and behavior; reciprocally, a great deal of evolutionary biology depends on the context provided by phylogenetic systematics. The power and potential of robust phylogenies largely built from molecular data have led a growing number of researchers across the life sciences to take on questions about evolutionary patterns and processes and at the same time have led evolutionary biologists to embrace tree-thinking. For example, a more nuanced understanding of rates of molecular evolution and better methods for estimating the timing of divergence (e.g., Sanderson 2003; Drummond and Rambaut 2007; Ho and Phillips 2009) have improved the construction and contextualization of phylogenies within earth history. Such advances are at the same time fueling research on genome evolution (e.g., Jiao et al. 2011) and the biological consequences of environmental change (e.g., Smith and Donoghue 2010). The more we learn, the more complex (and exciting) the dual problems of the phylogenetic *pattern* and evolutionary *processes* that together reveal the history of life become. Thus, we argue for an explicit and central role for evolution in a revised agenda for systematics and propose this as the new Mission 3 in SA2020 (Table 1).

Mission 2 of SA2K calls implicitly for deducing phylogenies but emphasizes predictive classification as the goal of analysis and synthesis of biodiversity data. In the intervening years, formal classification has to some extent taken a back seat to elucidation of phylogenetic relationships and to presentation of phylogenetic trees as the product of analysis and synthesis. Part of this

may be due to the debate regarding the Phylocode (Benton 2007; Lee and Skinner 2007; Mishler 2009; Cantino and de Queiroz 2010) or to the reluctance of systematists to propose formal classifications with attendant nomenclatural novelties when work is still very much in progress. However, we argue that it also reflects a focus on phylogenies and tree-thinking as the organizational underpinning of systematic knowledge. Phylogenies function extremely well as metaphors for what we know about evolution and have substantial heuristic power to suggest additional questions in comparative biology. Being more succinct and visually engaging, trees are more attractive than classifications and have found their way into life science textbooks from the introductory to specialized levels. Notably, the workshop groups did not reach consensus on the topic of whether or not classification remains a central mission of systematics. Given that phylogenetically based investigation of biological process seems to have eclipsed the importance of classification as a motivating theme in systematics, the role of classification in the future of our science merits further consideration within the systematics community.

Mission 4, as we have recast the Mission 3 of SA2K, involves communication of the data and results of systematic biology to multiple audiences in part to support the application of systematic biology to key societal issues. These objectives, together with all the missions of systematic biology, rely on and benefit from capabilities of the internet that were nascent or nonexistent in the early 1990s. Advances have been much more extensive and rapid than could have been anticipated 20 years ago. As importantly, the internet has achieved far greater *penetration* than almost any of us would have believed possible in terms of depth and breadth of both web-based content and users. The result is that knowledge is being discovered and constructed, interrelated, and disseminated in ways that could not have been envisioned at the time of formulation of SA2K. Improving data curation practices and remarkable technological improvements in data publishing platforms have revolutionized our ability to discover and access biodiversity data and knowledge products. All SA2K missions have greatly benefited from free global access to reference material about species through a number of large-scale projects (e.g., Genbank, TOLWeb, TreeBASE,

EOL, BHL, GBIF, and Wikipedia). At the same time, new web tools have been and are being developed that help to ordinate these data in ways that are beginning to allow assembly and linking together of trees and the characters used to construct them (e.g., Barcode of Life Data Systems, Morphobank, and Morphbank,). Further, standards are being developed for reporting phylogenies and phylogenetic inference methods in a way that will promote the accessibility and their reuse (MIAPA Wiki; Leebens-Mack et al. 2006). Advances in technology and media have raised the bar in terms of expectations, and many significant challenges remain to develop full interoperability within and between systematics-oriented knowledge bases.

Specifically with regard to Mission 4, revolutionary informatics approaches have opened the door to more creative ways to integrate data and communicate results to students, colleagues, and the public. As the information age has transformed biodiversity science and phylogenetic systematics, so too has the rise of web media and social networking transformed our ability to reach wider audiences. Systematic biologists have a great opportunity, indeed a responsibility, to engage a diverse set of audiences in biodiversity science and systematics. Web tools and visualization approaches can make the power and logic of evolutionary tree-thinking intuitive and accessible to a wide public audience in ways that are fun and exciting, yet nonthreatening to preexisting belief systems. There are numerous new ways to teach these concepts from modern broadcast approaches (e.g., Web sites, lectures, and videos) to more interactive web media (e.g., web games, virtual worlds, social networks, and augmented reality in exhibits) that the systematics community should embrace as our science takes firm root in the digital realm. The emphasis of communication over organization reflects the centrality of communication to everything that we do. In fact, one of our main tasks as systematists must be to communicate the wonder and excitement of systematics, and its centrality within the biological sciences, to our colleagues in other scientific disciplines and to the general public.

We are in a modern “age of discovery”: we have access to novel data and rigorous analytical methods that enable us to address both the patterns and the processes that have built the tree of life. These discoveries change the way we think about the evolution of plants and animals, fungi, and microbes, change research programs, and excite people well beyond the community of systematists. For example, the New York Times has covered the story that the formerly obscure New Caledonian plant *Amborella trichopoda* is the closest living relative to all other flowering plants (Mathews and Donoghue 1999; Parkinson et al. 1999; Qiu et al. 1999; Soltis et al. 1999) at least six times since that discovery was announced. This year, the date of the split between placental and marsupial mammals, as estimated from molecular evidence, was corroborated by new fossil evidence (Luo et al. 2011) in a story that was covered by nearly 200 media outlets in more than 40 countries

in just the first month or so postpublication. A recent article in Wired magazine (http://www.wired.com/magazine/2011/09/mf_microbiome/) explains the human microbiome, which was discovered and catalogued through application of phylogenetic systematic approaches. Clearly, we are far from alone in finding systematics research to be compelling. Our task as a community is to communicate the excitement of modern systematic biology and its direct relevance to all other disciplines within biology and to the public at large. If we can do this, we will certainly continue to advance our discipline while recruiting a new generation of creative and motivated students to join in the endeavor.

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REFERENCES

- Benton M.J. 2007. The Phylocode: beating a dead horse? *Acta Palaeontol. Pol.* 52:651–655.
- Blackmore S., Cutler D. 1996. *Systematics Agenda 2000: the challenge for Europe*. London: Linnean Society.
- Cantino P.D., de Queiroz K. 2010. Phylocode. International code of phylogenetic nomenclature. International Society for Phylogenetic Nomenclature. Available from: <http://www.ohio.edu/phylocode/>.
- Cracraft J. 2002. The seven great questions of systematic biology: an essential foundation for conservation and the sustainable use of biodiversity. *Ann. MO Bot. Gard.* 89:127–144.
- Drummond A.J., Rambaut A. 2007. BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol. Biol.* 7:214. doi:10.1186/1471-2148-7-214.
- Ebach M.C., Valdecasas A.G., Wheeler, Q.D. 2011. Impediments to taxonomy and users of taxonomy: accessibility and impact evaluation. *Cladistics.* 27:550–557.
- Halanych K.M., Goertzen L.R. 2009. Grand challenges in organismal biology: the need to develop both theory and resources. *Integr. Comp. Biol.* 49:475–479.
- Ho S.Y.W., Phillips M.J. 2009. Accounting for calibration uncertainty in phylogenetic estimation of evolutionary divergence times. *Syst. Biol.* 58:367–380.
- Jiao Y., Wickett N.J., Ayyampalayam S., Chanderbali A.S., Landherr L., Ralph P.E., Tomsho L.P., Hu Y., Liang H., Soltis P.S., Soltis D.E., Clifton S.W., Schlarbaum S.E., Schuster S.C., Ma H., Leebens-Mack J., dePamphilis C.W. 2011. Ancestral polyploidy in seed plants and angiosperms. *Nature.* 473:97–100.
- Joppa L.N., Roberts D.L., Myers N., Pimm S.L. 2011. Biodiversity hotspots house most undiscovered plant species. *Proc. Natl. Acad. Sci. U.S.A.* 108:13171–13176.

- Krishtalka L., Humphrey P.S. 2000. Can natural history museums capture the future? *BioSciences*. 50:611–617.
- Lee M.S.Y., Skinner, A. 2007. Stability, ranks, and the PhyloCode. *Acta Palaeontol. Pol.* 52:643–650.
- Leebens-Mack J., Vision T., Brenner E., Bowers J.E., Cannon S., Clement M.J., Cunningham C.W., DePamphilis C., DeSalle R., Doyle J.J., Eisen J.A., Gu X., Harshman J., Jansen R.K., Kellogg E.A., Koonin E.V., Mishler B.D., Philippe H., Pires J.C., Qiu Y.-L., Rhee S.Y., Sjölander K., Soltis D.E., Soltis P.S., Stevenson D.W., Wall K., Warnow T., Zmasek C. 2006. Taking the first steps towards a standard for reporting on phylogenies: minimum information about a phylogenetic analysis (MIAPA). *OMICS*. 10:231–237.
- Luo Z.-X., Yuan C.-X., Meng Q.-J., Ji Q. 2011. A Jurassic eutherian mammal and divergence of marsupials and placentals. *Nature*. 476:442–445.
- Mathews S., Donoghue M.J. 1999. The root of angiosperm phylogeny inferred from duplicate phytochrome genes. *Science*. 286:947–950.
- Mishler B.D. 2009. Three centuries of paradigm changes in biological classification: is the end in sight? *Taxon*. 58:61–67.
- Mora C., Tittensor D.P., Adl S., Simpson A.G.B., Worm B. 2011. How many species are there on Earth and in the ocean? *PLoS Biol.* 9(8):e1001127.
- Parkinson C.L., Adams K.L., Palmer J.D. 1999. Multigene analyses identify the three earliest lineages of extant flowering plants. *Curr. Biol.* 9:1485–1488.
- Prance G.T. 1995. Systematics, conservation and sustainable development. *Biodiv. Conserv.* 4:490–500.
- Qiu Y.-L., Lee J., Bernasconi-Quadroni F., Soltis D. E., Soltis P.S., Zanis M., Zimmer E.A., Chen Z., Savolainen V., Chase M.W. 1999. The earliest angiosperms: evidence from mitochondrial, plastid and nuclear genomes. *Nature*. 402:404–407.
- Sanderson M.J. 2003. r8s: inferring absolute rates of molecular evolution and divergence times in the absence of a molecular clock. *Bioinformatics*. 19:301–302.
- Smith S.A., Donoghue, M.J. 2010. Combining historical biogeography with niche modeling in the Caprifoliaceae clade of Lonicera (Caprifoliaceae, Dipsacales). *Syst. Biol.* 59:322–341.
- Soltis P.S., Soltis D.E., Chase M.W. 1999. Angiosperm phylogeny inferred from multiple genes as a tool for comparative biology. *Nature*. 402:402–403.
- Systematics Agenda 2000. 1994. Systematics agenda 2000: charting the biosphere. Technical Report. New York: Systematics Agenda. p. 1–34.
- Thanukos A. 2010. Views from understanding evolution: evolutionary trees from the tabloids and beyond. *Evol. Edu. Outreach*. 3:563–572.