

## COMMUNICATION

# Future directions in Systematics: A report from the 4th Systematic Biology Forum in China

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**Abstract** The 4th Systematic Biology Forum, China took place in December 2019, covering a vast array of topics across animals, bacteria, fungi, plants, and viruses in the fields of systematics and evolutionary biology. Here, we discuss the emergent themes of this meeting and how these and other interdisciplinary research programs can be synthesized to better understand evolution in a systematic framework.

**Key words** Taxonomy, phylogenomics, phylogenetics, evolution.

Systematists have long explored the dynamics of the tree of life, such as when life emerged, how life has evolved, and where life has adapted to, but the field is changing rapidly, perhaps quicker than ever before. As phylogenetic trees solidify, including volumes of taxa and data once thought impossible, we are beginning to use trees more interdisciplinarily, effectively blurring the lines between macro-evolution and micro-evolution. This could not have been more evident than at the 4th Systematic Biology Forum, China, hosted by the Institute of Zoology, Chinese Academy of Sciences in Beijing. Across four plenary talks and 34 invited presentations, covering animals, bacteria, fungi, plants, and even viruses, the >500 attendees from 101 research institutions saw the immense promise of integrating morphological, molecular, ecological, and other lines of evidence to better reconstruct and understand the history of life on Earth. It is clearer than ever before that China is at the forefront of the field, given significant recent funding increases for basic research and continued efforts at internationalization (Zhou & Leydesdorff, 2006; Zare & Winnacker, 2011; Qiu, 2014; Didham & Zhu, 2016; Yang, 2016; Tollefson, 2018).

The last few decades have seen great advances in molecular biology, and systematists have been some of the quickest to adopt these technologies. In fact, over half of talks used genomic methods (including reduced representation). Where once single-gene phylogenies enabled breakthroughs, it is now commonplace to use hundreds of loci via phylogenomic targeted bait methods and improved protocols for gleaning DNA from historical specimens. There has been a natural increase in data quantity as such, but we must not neglect to consider its fit for purpose, as multiple talks focused on the potential for systematic errors increasing support for incorrect relationships (Brown & Thomson, 2016), such as compositional bias, long-branch attraction, heterotachy, gene tree heterogeneity, poor model selection, paralogy, etc. Gene concordance factor metrics (gCF) (Ané *et al.*, 2007; Minh *et al.*, 2018) and internode certainty quantification (Salichos & Rokas, 2013; Zhou *et al.*, 2019) can complement classic branch support measures by quantifying gene tree incongruence. Ultra-conserved elements (UCEs) have been widely used, for instance, but we do not actually know what most of these loci do because they are selected for genomic architecture rather than function (Bossert & Danforth, 2018; Zhang *et al.*, 2019b). Although most UCE reconstructions appear reliable, we cannot easily check these results, as they represent just one marker type. Low-coverage genome sequencing may help solve these issues, as multiple marker sets (UCEs, BUSCOs, SNPs, *etc.*) may be designed and

used from generalized sequencing runs (Zhang *et al.*, 2019a), making marker design a likely hotspot for future research in phylogenomics.

As sequencing becomes less expensive and data become more plentiful, knowledge synthesis is quickly becoming an imperative. Such efforts are vital because studies differ in their datasets and species selections, often reconstructing differing relationships. By bringing all of these results together in one place, it becomes possible to compare and contrast their differences, evaluate why they might differ, and ultimately find some consensus among studies (Maddison *et al.*, 2007; Kumar *et al.*, 2017). Numerous platforms exist that seek to build such a system, but it seems likely that a singular resource will eventually be decided to consolidate these efforts at a unified tree of life.

The use of morphological characters for tree reconstruction was largely eclipsed by these molecular methods in the talks at the Forum. Indeed, morphology has been largely neglected outside of cladistics in recent years, but there is great promise in its future use. The most obvious line is that of fossils; as trees become increasingly species-dense, additional calibration points will be needed to accurately date them. Further, Bayesian tip-dating analyses can now feasibly employ both molecular and morphological data to better incorporate these calibrations into trees (Ronquist *et al.*, 2012; Luo *et al.*, 2019). Even when not using it to reconstruct trees, morphology is invaluable for making sense of how form and function have changed over time; fossils offer invaluable clues as to whether relationship and ancestral state reconstructions are correct, inclusive even of large-scale geological models such as the formation of the Qinghai-Tibetan Plateau (Su *et al.*, 2019). Linked together with contemporary specimens and their functional traits, enabled by powerful new technologies like microCT and 3D imaging combined with evidence such as physiological or behavioral data, we can reconstruct how groups, species, and populations evolved. This type of integrative approach is exemplified in recent high-profile papers on ruminant evolution (Chen *et al.*, 2019; Lin *et al.*, 2019; Wang *et al.*, 2019) that incorporate systematics, genomics, physiology, and more, that, when applied broadly across additional taxa, will enable a holistic view of life on Earth.

Globalization of science will play an increasingly vital role in systematics. Many species are regionally restricted, so, naturally, we must all work together to reconstruct a unified tree of life. Even for well-studied groups, where species-dense phylogenies already exist, cross-border collaboration is necessary to discover the unexplored natural history of these species, such as diet, nesting preferences, thermal tolerance, and more (Staab *et al.*, 2015), all of which can be key drivers of evolution. This is especially true for insects and other poorly-known invertebrates, where the vast majority of species remain undescribed or even undiscovered (Stork, 2018). Such studies will require direct knowledge of these species, linking back to classical life history and taxonomic work, which can help revitalize these undervalued fields (Lee, 2000; Agnarsson & Kuntner, 2007).

China is poised to become a regional hub for this type of integrative research, given its continued and substantial funding for foundational, basic research (Qiu, 2014; Yang, 2016) as part of its commitment to the principles of a more sustainable, ecological civilization (Xu *et al.*, 2019). Given that most Asian countries are classified as developing, there is great potential for China to partner with its neighbors and developed countries to build systematic capacity for the betterment of regional scientific progress, including through larger-scale frameworks such as the Belt and Road Initiative. These kinds of capacity building efforts will be key to improve and standardize practices in the region, but only through additional partnerships with developed countries will a truly global scientific community become a reality.

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