

## A Wish List for Systematic Biology

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*Abstract.*—“When you’re movin’ in the positive, your destination is the brightest star.”

Stevie Wonder, “Master Blaster (Jammin’),” 1980

This is the last of several commentaries solicited by the Editor on the occasion of the 50th anniversary of our society. Whereas previous installments have reflected on key episodes in the past, this one concerns the future. The distant future is hard to predict, except in the most uninteresting terms. So, instead, I’ve put together a wish list—some of the things I would most like to see happen to *Systematic Biology*, to the Society of Systematic Biologists, and to our discipline in general. I’m optimistic enough to think that all of these will eventually come to pass, or that, at least, the ideas will get a fair hearing. But, I’m realistic enough to concede that some probably won’t happen in my lifetime.

First, though, a brief commentary on the recent past and immediate future. Systematic biology has blossomed over the last few decades. Most obviously, we have witnessed a phylogenetic revolution. Having very nearly died out at the hands of the modern synthesis, who could possibly have imagined the centrality of phylogeny in evolutionary biology at the turn of the century? In fact, the pervasive impact of tree-thinking is the one indisputable major change in the entire landscape of evolutionary biology since the synthesis. At the same time, the frightening loss of biodiversity has reemphasized the need for basic knowledge about the structure of diversity and highlighted how far we are from achieving an adequate description of it.

Overall, our basic mission now seems much clearer than it did when I began graduate school in the mid-1970’s. Our task is to chart the diversity of life, in its entirety, from the tiniest tips of the Tree to every one of its branches. If we can keep our eyes focused on this big prize, the future looks exceedingly bright. Incidentally, I specifically mean to make no distinction between phylogenetic systematics and so-called “alpha taxonomy.” In my view we’re all working on the same

grand project, and such subdivision is counterproductive, especially if we end up bickering among ourselves about how to divide up the meager resources. Our work is so exciting and fundamental that the whole pie simply has to get bigger.

Now for some concrete wishes. With respect to *Systematic Biology*, we need to take a hard look at whether we continue to publish the systematics papers we think are really the most exciting and significant. Even if we are not troubled by this at the moment, it might become a serious issue as venues for systematics articles continue to expand. What can we do to continue to attract the most interesting work? The key, I think, is publishing papers that are controversial because they push the envelope in one way or another. In this connection, I’m concerned about the “Points of View” and “Book Review” sections. In the 1970’s and 1980’s these generated a lot of excitement and were must reading for everyone in the field. My impression is that they have lost their edge. “Points of View” are now mostly mini-research papers that don’t spark much debate, and book reviews are few and far between. I don’t think we have any less to argue about or that there are fewer relevant books. But this sort of dialogue is not likely to re-emerge unless we actively support it and keep it squarely focused on ideas (as opposed to personal attacks).

With respect to SSB we have made some brilliant moves over the last few decades. Changing *Systematic Zoology* to *Systematic Biology* (Hillis, 2001) was an excellent idea, and we are now enjoying the fruits of that effort in the form of papers by botanists, mycologists, and others, as well as their participation in the business of the society. Holding annual meetings with the Society for the Study of Evolution (SSE) has also been critical to our recent success. My two wishes for SSB relate to playing an even bigger role. First, I think we need to make special efforts to

represent the international systematics community. There have been some attempts to build alliances overseas (see "Report of Society Business" for 1989 and 1999; *Syst. Biol.* 48: 228, 838), but despite our intentions, we are still mainly a North American outfit. Holding meetings and workshops abroad on some regular basis would go a long way toward solving this problem. We should also be sure that SSB is represented wherever there are important discussions that concern our membership. We are still, for example, having limited impact on global change initiatives.

Second, I think we need to lead by example when it comes to databasing our findings. The systematics community has a set of obvious commitments related to phylogenetic analyses, yet we have so far failed to ensure that these data are accessible. Attempts are made, of course, to archive datasets, but a flat archive is a far cry from a real database, which would allow meaningful searches and syntheses. In fact, in comparing *Systematic Biology* over the last four years with *Mycologia*, *Systematic Botany*, and the *American Journal of Botany*, I found *Mycologia* to be at the top and *Systematic Biology* to be at the bottom of the list in terms of the ability to electronically retrieve phylogenetic data published in their pages. I think a key to turning this around is to actively support grass-roots efforts along these lines, such as the Tree of Life project (<http://ag.arizona.edu/tree/phylogeny.html>) and TreeBASE (<http://www.herbaria.harvard.edu/treebase/>), and to adopt them as official SSB outlets. At the same time, it makes perfect sense for us to get behind efforts to database taxonomic names, specimen data, and so on, which are now mainly shouldered by our museums. At the very least we might fill a significant void by providing, through our Web pages, a clearinghouse for such resources.

It is worth noting that the word "advancement" appears prominently in the names of some well known scientific societies, such as the "American Association for the Advancement of Science." I don't think we need to change our name-but we should be more proactive in advancing our discipline as a whole and in reaching out to the rest of science and society. This sentiment segues naturally into my wishes for our discipline in general.

First, I think that the vitality of our enterprise depends critically on making connections to other disciplines. Whereas phylogenetic systematics has fused almost imperceptibly with, for example, the study of molecular evolution and development, we have made much less headway in connecting with our paleontological colleagues, or to many aspects of ecology (e.g., community and ecosystem ecology). This has little to do, I think, with the potential for productive interchange and more to do with sociology. So, we need to try harder.

Despite our completely obvious connections to evolutionary biology, for some reason "pattern cladistics" still exists (if you doubt this, see, for example, Brower, 2000). I wish this would finally disappear. However necessary it once may have seemed to proclaim our "independence"—distancing systematics from evolution in this way has long since outlived its usefulness. Now it's just embarrassing. We should be marching arm-in-arm with our friends studying population genetics, adaptation, speciation, etc. Despite repeated proclamations to the contrary by some colleagues, our gene trees, not to mention our biogeographic data, are crucial to these efforts, and vice versa.

Our long-term success in connecting to the rest of the world depends ultimately on getting our own house in order. Most importantly, we need to continue to shed remnants of arbitrariness in the way we do our business. Thanks largely to Willi Hennig's brilliant arguments (1966), a giant step in this direction has already been taken—the resolve to give names only to clades. However, it looks like the next logical step—eliminating the traditional taxonomic ranks—will be much harder. As bad luck would have it, at a very early stage one of our most important endeavors—naming—got tied to something arbitrary—ranking. Though it will be painful to disentangle these, after so many years, I believe it will be increasingly harmful to our discipline to maintain current nomenclatural practices. Given the fundamental nature of the problem, I think the best way out (for us and for the user community) is not to try to patch up the old system, but instead for the systematics community to adopt something like the PhyloCode (<http://www.ohiou.edu/phylocode/>). Among other things this would force us to abandon the false security of standard ranks, and

to develop much better ways of communicating about biodiversity. For example, instead of reporting (as though it means something) that there are 20 families in area A as compared with 10 in area B, we'll have to focus instead on the properties that actually interest us—perhaps the number of species, the degree of disparity, or the depth of time represented by taxa in those locations.

One of the nasty side effects of arbitrary decisions is that they necessitate an appeal to authority. In the past, these authorities have been individual taxonomists (e.g., for years Arthur Cronquist was a prime authority on ranks in plants), but I fear we will soon see other (well-intentioned) efforts along the lines of the "Angiosperm Phylogeny Group" ordinal classification of angiosperms (APG, 1998). Although at first blush this may look like progress, arbitrary acts carried out by a large number of people are every bit as arbitrary, and ranking by tribunal may only make it more difficult to question the wisdom of the system.

Finally, on the phylogeny front I hope we will soon experience a subtle but important shift in research style. A standard formula these days makes a virtue of analyzing as many sequences as possible and then drawing attention to whatever significant results happen to emerge. We analyze hundreds—even thousands—of *rbcL* sequences, for example, and highlight whichever nodes within angiosperms seem to be well supported, whether or not these were of particular interest to us at the outset. Although significant results have surely been obtained in this way, we're left with a sizable residue that also just happens to contain many of the most vexing phylogenetic problems (cf. Bininda-Emonds et al., 2000). In angiosperms we're still more or less clueless about, say, the closest relatives of the monocotyledons. A more targeted, hypothesis-testing, approach has paid off recently in some important cases (e.g., the root of angiosperm), and this shift might be happening naturally as the initial round of excitement over large molecular studies subsides.

A corollary of this view is the need for much more attention to synthesizing well-founded, independently obtained, phylo-

genetic results. This will be increasingly important for comparative studies, where larger trees are needed to make more powerful statements about, for example, rates of diversification and character change (Ree and Donoghue, 1999). Fortunately, recent attention to the problem of assembling a backbone Tree of Life (<http://research.amnh.org/biodiversity/features/feat.html>) is highlighting the need for "phyloinformatics" and for the synthetic tools that this would enable.

Reflecting on these wishes, most of them are about broadening our effort and forging new connections. When new approaches yield great successes (and we've certainly had our share in recent years), disciplines may instead move in the opposite direction—turning inward and settling into familiar routines (parsimony analysis of lots of sequences, mapping some characters for good measure). Such formulas will continue to be productive, but my hope is that we won't become complacent. Progress over the past few decades has been absolutely enormous, but the biggest hurdles are ahead of us, and we'll need all of the positive energy we can muster to reach our destination.

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#### REFERENCES

- ANGIOSPERM PHYLOGENY GROUP (APG). 1998. An ordinal classification for the families of flowering plants. *Ann. Missouri Bot. Gard.* 85:531–553.
- BININDA-EMONDS, O. R. P., S. G. BRADY, J. KIM, AND M. J. SANDERSON. 2000. Scaling of accuracy in extremely large phylogenetic trees. Pages 547–558 in *Pacific Symposium on Biocomputing 2001* (R. Altman, A. Dunker, L. Hunter, K. Lauderdale, and T. Klein, eds.). World Scientific Publishing, Singapore.
- BROWER, A. V. Z. 2000. Evolution is not a necessary assumption of cladistics. *Cladistics* 16:143–154.
- HENNIG, W. 1966. *Phylogenetic Systematics*. Univ. Illinois Press, Urbana, IL.
- REE, R. H., AND M. J. DONOGHUE. 1999. Inferring rates of change in flower symmetry in asterid angiosperms. *Syst. Biol.* 48:633–641.