

The Right Time for Synthesis in Evolutionary Biology

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BioScience

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The Right Time for Synthesis in Evolutionary Biology

It is 2005, and I find myself leading the new National Evolutionary Synthesis Center (NESCent) in Durham, North Carolina. NESCent is funded by a \$15 million grant from the National Science Foundation (NSF) to help bring about a broad synthesis of the biological sciences. This major award follows on the heels of other ambitious NSF initiatives to jump-start evolutionary studies, such as the Tree of Life initiative, which aims to assemble an evolutionary tree for all 1.7 million described species.

Before I explain why 2005 is a propitious time to launch NESCent, let me reflect on why 1989 would have been a lousy year to attempt a grand biological synthesis around the unifying principle of evolution. In 1989 I was a graduate student at Yale, where most of the molecular biology graduate students I knew treated evolutionary biology with extreme skepticism. Evolutionary biology seemed ethereal and ultimately untestable. Ironically, 1989 was the year that the Yale molecular biology groups led by Frank Ruddle and William McGinnis made the most important macroevolutionary discovery of the decade—that the body plans of mice and flies are mapped by the same family of genes. This discovery, with lovely details like the shared colinear mapping of homeotic genes in mice and flies, truly brought home the fact that nothing in molecular biology makes sense except in the light of evolution.

Lest I sound patronizing to molecular biologists who dismissed the promise of evolutionary biology, I was soon to join many of my colleagues in criticizing the Human Genome Project. What was the point of mapping the human genome, I wondered, with no other genomes for comparison? We were confident that all that money—in our hands, at any rate—could be put to far better use. Of course, we now know that the very sequencing of the human genome brought with it the technology that allows us each to contemplate the sequencing of our “favorite” genome. And of course we know that the very methods we were using to infer phylogenetic relationships of species were perfectly suited for comparing other genomes.

The fact that we can now quietly chuckle at our past naïveté is exactly why 2005 is the perfect time to attempt evolutionary synthesis. An amazing confluence of scientific threads facilitates this process. Medical researchers have been using evolutionary methods and software for over a decade. The dazzling successes of paleontological and DNA-sequence databases have inspired any number of efforts to create databases for all kinds of behavioral and morphological data.

In our first two years alone, NESCent will sponsor 15 postdoctoral fellows and 10 sabbatical faculty, and organize 20 working groups involving nearly 500 scientists and educators from all disciplines. I consider the path to successful synthesis to be one where everyone involved is inspired to a grander, collaborative vision, one that brings them to a new playing field with so much room that their old territories are forgotten. Achieving such a vision is easiest when it simply involves working with an amazing person you've just met at NESCent—and that's exactly what we hope to encourage.

CLIFF CUNNINGHAM
Director, National Evolutionary Synthesis Center

Editor's note: AIBS is providing education and outreach services for NESCent through a subcontract. See page 183.