

From the Editors

The Zuckerkandl Prize

We are pleased to award the second annual Zuckerkandl Prize to Dr. Gustavo Caetano-Anollés for the best article published in the *Journal of Molecular Evolution* in the calendar year 2002. Dr. Caetano-Anollés' paper,

“Evolved RNA Secondary Structure and the Rooting of the Universal Tree of Life” (*J Mol Evol* 54:333–345, 2002)

was selected by the Editors from six excellent papers that were nominated for the award by our Associate Editors. The prize was established by Springer-Verlag to honor Dr. Emile Zuckerkandl, the founder and Editor Emeritus of our journal.

Dr. Zuckerkandl helped found the field of molecular evolution. (An excellent brief chronicle of his life and scientific contributions can be found at <http://hrst.mit.edu/hrs/evolution/public/profiles/zuckerkandl.html>.) As a postdoctoral fellow with Linus Pauling in the late 1950s and early 1960s, he carried out the very first evolutionary comparisons of proteins—hemoglobin sequences from primates and other taxa—and noted that sequence divergence tracked phylogeny. This insight led him to formulation of the “molecular clock.”

The modern science of molecular phylogenetics arose from this seminal finding, and with the aid of faster computers, has made ever-accelerating progress. However, the data used in modern phylogenetic analyses have largely remained the same as those pioneered by Dr. Zuckerkandl—conserved and evolved changes in the primary sequences of molecules.

Controversy surrounding the conceptual underpinnings of the molecular clock has relevance to this year's prize-winning paper. Constancy in the rate of protein evolution was considered by Dr. Motoo

Kimura as primary evidence in support of his seminal theory of neutral molecular evolution. Since the rate of neutral substitution is expected to be equal to the mutation rate to neutral alleles, then so long as the majority of changes are selectively neutral and the mutation rate is roughly constant per year, then so too should be the rate of protein evolution.

The assumption of neutral mutation driving protein evolution runs into problems, however, when one considers its applicability to phylogenetic inference. A basic tenet of molecular phylogenetics is that molecules should be chosen to have a rate of evolution that is appropriate for the time-depth of the taxonomic comparisons being made. In particular, resolving ancient relationships requires very slow-evolving molecules. But a slow-evolving molecule, if it is to be useful for this purpose, cannot be evolving completely neutrally: Were this to be the case, the sites incurring changes, though few in number, would each be mutationally saturated.

The purpose of this explication is not to recount the history of thinking about this interesting problem, but rather to point out that natural selection (positive and/or negative) must be operating on evolved changes in phylogenetically informative molecules. But selection acts principally on the secondary and higher-order structural changes these mutations produce, and not the primary sequence changes themselves. And so it stands to reason that evolutionary analysis of structural changes in “conserved” molecules will be especially informative, both from the perspective of phylogenetic inference as well as from the perspective of evolutionary mechanisms.

Dr. Caetano-Anollés' prizewinning paper lays out a methodological approach for unification of phylogenetics with structural biology, to the benefit of both. In selecting this work for the Zuckerkandl

Prize, the Editors couldn't help but notice the obvious intellectual heritage of this scientific achievement.

* * * * *

We are pleased to announce that the *Journal of Molecular Evolution* will soon be implementing a web-based electronic submission, administration and

review system. This new system, "Manuscript Central," will speed up every step in the process from manuscript submission to acceptance. We encourage authors who plan on submitting manuscripts to us in the coming months to first contact us by email about this option. The formal launch of Manuscript Central is expected to be Summer 2003.