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From the Editor

The Zuckerkandl Prize

Editor's Note: In announcing this year's recipient of the Zuckerkandl Prize for the paper published in *JME* in 2003 judged best by our editorial staff, I have asked Dr. Hector Musto, a longstanding and dedicated Associate Editor to our journal, to write the announcement, which follows.

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Springer-Verlag established the Zuckerkandl Prize to honor Emile Zuckerkandl and his important conceptual contributions to molecular evolution. For 2003, the editors of the *Journal of Molecular Evolution* have selected Bryan Grieg Fry for his papers "Molecular Evolution and Phylogeny of Elapid Snake Venom Three-Finger Toxins" and "Isolation of a Neurotoxin (α-colubritoxin) from a Nonvenomous Colubrid: Evidence for Early Origin of Venom in Snakes." These papers are not about technical innovations or conceptual breakthroughs, the hallmarks of Dr. Zuckerkandl's many contributions, but rather they represent thorough applications of well-developed tools and methodologies in molecular evolution. They result, however, in startlingly new discoveries about the origin and evolution of the proteins we humans most love to fear. Indeed, E. O. Wilson, the great evolutionary biologist and a founder of sociobiology, even went so far as to argue for a genetic basis to our universal fear of snakes. Apparently he has not met Dr. Fry: in capturing over 2000 poisonous snakes for his studies (and dedicating one paper to a colleague killed by a snakebite), this is obviously one instance in which academic love (or a genetic mutation) has proven stronger than fear.

Bryan Grieg Fry

In the first paper (Fry et al. 2003a) the author studied the molecular evolution of the three-finger family of snake venom peptides. The genes encoding these molecules are encoded by a large and complex multigene family and show a diverse array of functional activities. Interestingly, the members of this multigene family, although rather short (only 60–74 residues), arc rich in disulfide bonds, with four such bonds being conserved in all known family members. As a consequence, all proteins in this femily have a similar pattern of folding that consists of three loops extending from a core containing the four conserved disulfide bridges. A comparison of the presumed species phylogeny with the gene tree, leads the authors to postulate a "birth-and-death" model to describe the evolution of this large multigene family. Originally formulated by Dr. M. Nei and colleagues to describe the evolutionary dynamics of genes in the major histocompatibility locus, it is a model allowing continual adaptive evolution of genes responding to a constantly evolving challenge.

In the second report (Fry et al. 2003b) the authors report the isolation and characterization of a polypeptide toxin (α-colubritoxin) isolated from *Coelognathus radiatus*, an Asian member of the nonvenomous family Colubrinae, commonly sold in pet stores. The pharmacological effect of the peptide

isolated from this house pet was shown to be a fully potent neurotoxin! Needless to say, this emphasizes the largely unexploitcd potential of colubrid venoms for biomedical research and drug design. From an phylogenetic perspective, the paper also shows that α-colxibritoxin is rooted within the gene tree of the elapid three-finger toxins described in the previous paper, which in turn suggests that this gene family originated within Colubroidea, and started to diversify before the origination of lineages leading to present-day venomous clades (snakes with front-fang toxin delivery systems).

These two papers (individually and taken together) are clear examples of the unexpected ways molecular evolution research, driven by purely academic interests, produces important implications for human health.

I have briefly summarized the scientific merits of these two deserving papers. However, I would also like to express a more personal opinion of the author. The field of molecular evolution has always been exciting to me because it deals with large intellectual issues – the origin of life and its unity, the evolution of the genetic code, the evolution of genomes, and mechanisms of evolution to name a few – where the main risk to the participant is defence of an incorrect idea or hypothesis (or perhaps acquiring a computer virus). All the work takes place in the security of our labs and offices. Now I see that there are some colleagues, such as Dr. Fry, who make very valuable contributions to the field but in doing so, they put not only their academic lives at risk, but their physical survival as well (just look at the accompanying picture or visit http://www.venomdoc.com). I must say that I admire these individuals, and I truly hope that this prize will further encourage them to continue with this kind of research, where certainly, I will never work!

Hector Musto

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