

**Diethard Tautz, Max Planck Institute for Evolutionary Biology, Plön: “*De novo Evolution of Genes*”**

ABSTRACT: Discussions about the evolution of new genes started soon after the first (protein) sequences of genes became available. Already in 1970 Ohno developed major ideas on gene duplication models in a ground-breaking monograph. This was followed in 1977 by Francois Jacob's famous paper on "tinkering" where he considered specifically the question of whether new genes could emerge *de novo* out of non-coding DNA. He concluded with the often cited statement: "... creation of entirely new nucleotide sequences could not be of any importance in the production of new information." This has influenced the research agenda for a long time, and it turned in fact out to be very fruitful and to deliver abundant evidence for the model of gene emergence through duplication. On the other hand, this early conceptualization has also limited the experimental breadth and thinking towards focusing attention on conservation, rather than divergence of proteins. In another seminal paper, Cyrus Chothia concluded in 1992 that there might be not more than 1,000 basic folds that make up all known proteins. It was therefore a bit surprising that the very first systematic genome project, the sequencing of the yeast chromosome III in 1996 turned out to harbor a significant set of open reading frames that did not seem to be related to any previously known gene family. These were therefore termed "orphans". However, it was initially thought that this fraction of genes that could not be associated with any other gene would gradually disappear once more and more genomes were sequenced. But this was an expectation that was clearly not fulfilled. Every new genome turned out a similar high fraction of orphan genes, implying that the list of known orphans is currently expanding exponentially, while the list of known protein families comes indeed to saturation. Contrary to Jacob's expectation, it is now becoming clear that genes can indeed frequently arise *de novo* out of the genomic background and thus form new orphan genes. In my talk I will address the history of this conceptual

shift, as well as the implications for our understanding of the generation of evolutionary novelties.