

Living in the tree: a taxonomic perspective from within

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While early sketches of relationships (plants: Augustin Augier, 1801; palaeontology: Edward Hitchcock, 1840) included an creator for the origin of specimen, Jean-Baptiste Lamarck's evolutionary tree on animals from 1809 indicated a multiple descent of life form in parallel. The first one to publish an evolutionary tree was Charles Darwin (1837, 1859) who showed an abstract diagram of a theoretical 'Tree of Life' for species of an unnamed large genus with species evolving in time and space. Already 20 years later trees of life were commonly shown as those depicted by Ernst Haeckel between 1860 and 1880. It took, however, another 100 years to base evolutionary trees on a sound molecular basis, starting with the comparative analysis of protein sequences (e.g. Margret Dayhoff, 1978; Richard Ambler, 1981). This breakthrough, which for the first time linked the prokaryotes to the tree of life, originated from the pioneering paper of Emile Zuckerkandl and Linus Pauling (1965) on the chemical basis for molecular phylogeny. Protein sequencing was rapidly replaced by nucleic acid sequence analysis, first on viroids, 5S rRNA and 16S rRNA oligonucleotides (mastered by Carl Woese and colleagues), later, with the introduction of reverse transcriptase, on full length *rrn* genes and some genes coding for proteins. The PCR technology (1983), together with the previous discovery of restriction enzymes (around 1970) made gene sequencing a universally applied tool (from 1988 on). Among others, e.g., identification, ecology, and forensics, bacterial taxonomy is only some of the biological fields which were revolutionized. Its influence on re-shaping the Bergey's based classification above the species level was tremendous. For the first time in the history of microbiology scientists were able to evaluate the phylogenetic significance of taxonomic traits. However, hailed as the solution to all taxonomic problems once and forever, early hopes placing emphasis on gene sequence analyses failed for several reasons (no ranking implied): (i) historically , this approach was only second to the more widely accepted DNA-DNA reassociation technique for delineating species; (ii) the finding of lateral gene transfer shed doubt on the claim of ribosomal RNA genes and housekeeping genes to represent the evolution of the genome; (iii) the awareness that any hierarchic construct should take into consideration the maximum of phylogenetically relevant information; (iv) the phylogenetic tree evolved into a phylogenetic thicket, nevertheless with a cobweb structure; and (v) additionally, the evolutionary history of prokaryotic life forms, starting from a universal ancestor and leading to subsequently lower taxa stopped at the level of species where an artificial construct blocked the consequent translation of taxonomic data into practice. Having worked in taxonomy for 40 years, having seen the rise and fall of opinions, hypotheses and approaches, I conclude that with no doubt the discipline of systematics has progressed but a meaningful implementation of scientific findings into a fully developed hierarchic framework has to await the conceptual transition from taxon definitions to taxon concepts.

For references check the Internet