

**THE MODERN TAXONOMY OF THE GENUS *MYCOBACTERIUM*:  
THE ROLE OF GENOTYPE AND PHENOTYPE**

Enrico Tortoli

Regional Reference Center for Mycobacteria, Florence, Italy

Although the need to class living creatures is natural to humans, the taxonomy started to be a real science only in the 18<sup>th</sup> century when Carl van Linné proposed the binomial Latin system which is still used today. The genus *Mycobacterium* was first proposed in 1896 when *M. tuberculosis* and *M. leprae* were described. Very fruitful, for the taxonomy of mycobacteria, were the years, at the end of 20<sup>th</sup> century, in which it was under the control of the International Working Group of Mycobacterial Taxonomy founded by L. Wayne. In this period important studies based on numerical taxonomy were carried on and highly reproducible techniques were developed. The approach based on phenotypic features, was however brought into question in the last decade of the 20<sup>th</sup> century as a consequence of the extraordinary progress of genetic disciplines. The keystone was represented by the detection, within the genome, of variable nucleotide traits interspersed within highly conserved regions. Although the analysis of such genetic regions confirmed, to a great extent, the previous taxonomic knowledge based on phenotypic characters, at the same time, many previously unrecognized species were described on the basis of the detection of strains with new, unreported sequences. The euphoria produced by the increasing availability of automatic instrumentations gave rise, in few years, to the conviction that the phenotypic age had reached its end. It is now evident that the genus *Mycobacterium* is much more complex than it was acknowledged a few years ago but probably the time is ripe for new rules, based on consensus of scientific community, aiming to bring again under control the description of new species, too often based on minimal genotypic diversities and disregarding any phenotypic investigation.