

## New Microbes New Infections promotes modern prokaryotic taxonomy: a new section “TaxonoGenomics: new genomes of microorganisms in humans”

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“New Microbes and New Infections” being devoted to new facts in infections and clinical microbiology comprises a “New Genomes of Microorganisms and Viruses in Humans” section featuring its own format. This section will evolve towards a “TaxonoGenomics: new genomes of microorganisms in humans” section to better take into consideration recent developments in prokaryote genome sequencing and incorporate the recent proposal that genome sequence and proteome must be part of the description of microbes of medical interest. Indeed, there is an impressive rise in bacterial genome sequencing, with 35,000 genomes currently available from virtually all major bacterial phyla. These sequences are an unprecedented source of information to develop molecular assays for detection or genotyping, to detect antibiotic resistance and virulence markers, to develop new culture media or to identify candidate antigens for vaccines [1]. A second breakthrough was the use of MALDI-TOF-mass spectrometry (MALDI-TOF-MS) for the routine identification of clinical isolates of bacteria and fungi [2,3]. Finally, the renewal of culture, through the culturomics strategy based on a diversification of culture conditions, enabled identifying more than 120 new human-associated bacterial species in a limited time [4]. These three tools have in common the advantage of producing data that can easily be shared and compared, either in international databases or culture collections.

Surprisingly, although it has undergone many changes over time according to the introduction of new diagnostic methods, microbial systematics has not been adapted to incorporate genomic sequence and MALDI-TOF-MS, despite the fact that these methods are now widely used worldwide. Currently, although there is no universal agreement on the rules and

criteria used for microorganism identification, several taxonomic criteria, based on phenotypic and genotypic characteristics [5–7], are used to determine whether a new bacterium fulfils the requirements to be classified as a new taxon. These include: i) routinely obtainable phenotypic properties (morphology, staining and antigenic properties, growth preferences, enzyme production, sugar metabolism, susceptibility to antibiotics, pathogenesis and habitat) [8]; ii) chemotaxonomic parameters such as the characterization of polar lipids, whole cell fatty acid content, respiratory quinones and peptidoglycan structure [9–11]; and iii) the determination of DNA-DNA hybridization (DDH) [12]. However, the latter two taxonomic criteria lack inter- and intra-laboratory reproducibility, require the use of methods restricted to few laboratories, are of no practical value for the routine identification of bacterial isolates.

Recently, several genomic tools have been proposed as alternatives of DDH for the taxonomic classification of prokaryotes, including average genomic identity of orthologous gene sequence (AGIOS), average nucleotide identity (ANI), digital DDH, maximum unique matches index (MUMi), multi-locus sequence analysis, multilocus sequence typing, and tetranucleotide regression [13], the former three of which have permitted the valid publication of several new species names [14–24]. In addition, a new polyphasic taxonomic strategy named taxono-genomics including both MALDI-TOF-MS instead of chemotaxonomic analysis and genome sequence analysis, in addition to common phenotypic criteria, was proposed to describe eight new bacterial species [17–24].

Therefore, there is now clear evidence that genomic and MALDI-TOF-MS data may be integrated as alternatives to chemotaxonomy and DDH, respectively, for the taxonomic description of bacteria, provided that the new isolates are compared to the phylogenetically closest species with standing in nomenclature.

Accordingly, “New Microbes and New Infections” will now accommodate two formats in the new “TaxonoGenomics” section, including a short 500-words format and one item to report on new genome of already described organism and a 1,500-word format and three items to report on new genome as part as the description of a novel organisms. This new section will accommodate only microbes of medical interest and not environmental ones without known connection with populations and patients.

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