Microbial systematics

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"We will be more likely to realize a full understanding of microbial diversification if we accept that the word 'species', for all its utility, may have no precise referent"

W Ford Doolittle, 2006[1]

This special issue of *Microbiology Australia* covers *microbial systematics*. In guest-editing this issue my intention has been to bring world experts together to discuss the past, present and future of microbial systematics with a view on the technical and theoretical advancements in the field. While the global debate continues on how to define "microbial species" in the light of recent advances, expert authors contribute insights into how sound taxonomical analyses can benefit this process of redefinition.

Reflection of theoretical renaissance on microbial systematics

Systematics has experienced a theoretical renaissance in terms of evolutionary and environmental adaptation, and systematists have begun to make extensive use of molecular biology and computer programs (bioinformatics) to study organisms[1-3]. *Genomics*, which explores the biology of organisms through their genetic blueprints, has profoundly affected the field leading to a revision of our definitions of microbial entities, their capabilities, as well as our methods and approaches to their study. Its influence on various sub-disciplines of microbiology and its interaction with related disciplines has also been unrivalled[4].

Redefining diversity

Advancements through the use of molecular and genomic tools have also greatly expanded our understanding of *microbial ecology*. Cultivation-independent methodologies analyse the small-subunit ribosomal RNA (rRNA) genes of mixed microbial populations from environmental samples, revealing the diversity of the uncultured prokaryotic world and providing the basis for studies of microbial biogeography[1-3]. Prediction of the ecological role of members of these communities requires access to the genome, rather than a single gene, and high-throughput genome sequencing methodologies leading to *metagenomics* provide that access[5].

With the use of specific primers, amplification and sequence of 16S genes from un-fractionated environmental samples is now possible[1,6]. However, it has been reported that the number and diversity of species with few 16S sequences assignable at the 97% level to cultivated species from the same sampling site astonishes microbiologists[1]. Furthermore, many species with 97% 16S identity cut-off are reported themselves to be represented by multiple different but similar individual sequences in any sample. Diversity in gene sequences has also matched gene content diversity, for example, *Escherichia coli* (O157:H7) with 1,387 genes not present in another *E. coli* strain (K12)[1].

Species concept

Questions in microbial systematics range from the species level to the phylum[1,3,7]. The availability of genome data from multiple strains of a species promises to provide a quantitative measure of genome relatedness and hence species status. At the other end of the taxonomic spectrum, analysis of members of poorly represented phyla should reveal the true diversity of microbial genomes and allow us to better resolve phylogenetic relationships between the phyla. The interface between microbial systematics, evolution and genomics also provides an opportunity to re-evaluate the genome as a static entity, particularly its susceptibility to acquisition and loss of genes by lateral gene transfer (LGT) within and across the species boundary[1,3,6,7].

The yet-unclear effect of gene flow, in particular lateral gene transfer, makes the line of descent difficult, if not impossible, to describe. However, even in the face of genomic fluidity, it seems that the typical geno- and phenotypic characteristics of a taxon are still maintained, and are sufficient for reliable classification and identification of Bacteria and Archaea[1,3,6,7]. There are many well-defined genotypic clusters that are congruent with known species delineated by polyphasic approaches. Comparative sequence analysis of certain core genes, including rRNA genes, may be useful for the characterisation of higher taxa, whereas various character genes may be suitable as phylogenetic markers for the delineation of lower taxa, resulting in the escape of some organisms from reliable classification[7].

More genomically-based criteria are likely to be adopted soon but there can be no precise mapping to any unitary model of diversification and adaptation and, therefore, it seems unlikely that the scientific world will soon, if ever, have a uniform species concept to allow definition-independent answers such as how many prokaryotic species there are, at some particular site, or in the whole world[1,7].

Experts revisiting systematics for *Microbiology Australia* in the light of current advancements

In the present special issue, Erko Stackebrandt defines molecular taxonomic parameters in the light of the ongoing conceptual renaissance; Barny Whitman guides us through *Bergey's Manual of Systematic and Evolutionary Microbiology* in "What's up with Bergey's?". Martha Trujillo provides insights into the importance of taxonomic subcommittees and the need for minimal standards for the description of prokaryotes. Jim Staley focuses on how to capture and tame "World's wild microbes" while John Fuerst discusses microbial diversity beyond *E. coli*.

Peter Kampfer and Stefanie Glaeser review prokaryotic taxonomy in the sequencing era with an emphasis on the MLSA in classification. John Bowman reviews proteomic applications in microbial taxonomy while Joachim Wink reveals how taxonomy and natural product research can work together. Artem Men, Kirby Siemering and Susan Forrest visit new toolboxes for microbial systematics taking us to metagenomics and beyond. Johannes Groenewald, Marizeth Groenewald and Pedro Crous tell us novel advancements in fungal and yeast systematics. The expertise then moves on to viruses and looks at the classification and systematics of bacteriophages and viruses with Stephen Abedon, Hans Ackermann and Adrian Gibbs.

An article on the World Federation for Culture Collections (WFCC) is also included in this issue co-authored by Philippe Desmeth and myself, stressing once more the importance of depositing newly described species, and culture collections in microbial systematics. Information on the mission and activities of the WFCC and the World Data Centre of Microorganisms (WDCM; http://new.wfcc.info) dating back to Professor Skerman's days at the University of Queensland in the 1960s is also included. I am hoping that collections and individuals will become members of the Federation from Australia, which also offers the Skerman Award every three years to a microbiologist for a significant contribution to the field of systematics.

I would also like to draw attention to the newly established *Bergey's International Society for Microbial Systematics* (BISMiS) and encourage microbiologists to become a member of the Society (http://www.bergeys.org/index.html).

Finally, I would like to thank all the contributing experts and hope that this issue will further strengthen the importance of microbial systematics in Australia and perhaps encourage young members to define a career path in the field.

References

1. Doolittle, W.F. (2006) Species. *Microbiol. Today* 33, 148–151.
2. Moore, E.R.B. *et al*. (2010) Microbial systematics and taxonomy: relevance of a microbial commons. *Res. Microbiol.* 161, 430–438.
3. Achtman, M. and Wagner, M. (2008) Microbial diversity and the genetic nature of microbial species. *Nature Rev. Microbiol.* 6, 431–440.
4. Ward, N. and Fraser, C.M. (2005) How genomics has affected the concept of microbiology. *Curr. Op. Microbiol.* 8, 564–571.
5. Ward, N. (2006) New directions and interactions in metagenomics research. *FEMS Microbiol. Ecol.* 55, 331–338.
6. von Mering, C. *et al.* (2007) Quantitative phylogenetic assessment of microbial communities in diverse environments. *Science* 315, 1126–1130.
7. Schleifer, K.H. (2009) Classification of Bacteria and Archaea: past, present and future. *Syst. Appl. Microbiol.* 32, 533–542.

Biography

Dr Kurtböke is currently the Vice-President of the World Federation of Culture Collections (WFCC). She has been working in the field of biodiscovery and has been an active member of the international actinomycete research community since 1982. She is engaged with studies related to actinomycete diversity and taxonomy, particularly uses of actinophages to define suborder boundaries of the order *Actinomycetales.* She currently conducts research and teaches in the field of applied microbiology and biotechnology and is senior lecturer at the University of the Sunshine Coast, Queensland.

Molecular taxonomic parameters

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The parameters in place for the circumscription of taxonomic ranks increase with the description of lower ranks; only one or a few, mostly genomic properties, for phyla, classes and orders, while those for families, genera and, above all, for species, are described with increasing complexity, including molecular, chemotaxonomic, morphological and biochemical properties. Even the attempt to list a few examples for species-rich genera or for a phylogenetically diverse range of taxa would go beyond the scope of this communication. Rather, the presently applied molecular approaches for delineation should be revisited here. For a broad overview on the use of the wide spectrum of phenotypic methods recommended today the reader is referred to a recent publication by Tindall *et al.*[1].

Since the early 1980s 16S rRNA gene sequence identities have been included in the description of mainly higher taxonomic ranks. The phylogenetic superiority of this molecule over other genes to place an organism next to its nearest neighbour has been well covered in the literature[2]. The primary structure of this gene, however, is too conservative to differentiate among strains of species as well as among closely related species (for