EDITORIAL

Forsaking the tome—a worms’ eye view of taxonomy

Living creatures adopt strategies for survival that involve “recognition” of objects in the surrounding environment, and a suitable response to their presence. An earthworm recognises buried vegetable matter as edible and eats it; retracts into its burrow when pecked by a bird, and so on. The shape of the leaf and the position and force of the bird’s peck can take many different forms, but nevertheless they evoke an appropriate class response despite this polymorphism. Essentially, the earthworm has “classified” its observed universe into groups of phenomena, can “generalise” from a particular, possibly unique, set of sensory inputs to assign (“identify”) the stimulant to a category, and can then mount an appropriate response. Children categorise their much wider universe, and, by adolescence, have subconsciously classified the objects which they have encountered into tens of thousands of subtly different, sometimes overlapping classes and subclasses. They can identify new objects from minimal sensory data in a fraction of a second, and can communicate this knowledge to others through language. Microbial taxonomists, after a century of effort, have been somewhat less successful.

The purpose of classification is to divide bacteria into named, homogeneous and distinct genera and species, and to describe their characteristics in such a way that new isolates can be simply, rapidly and economically identified as members of one of these groups. Preliminary identification from a few tests allows an isolate to be shunted into one of a few schemes for further biochemical and susceptibility tests, tailored to give an identification and information on appropriate therapy. The species name that is finally assigned to the isolate implies information that is not (and often cannot be) obtained in laboratory tests, and is the basis for clinical advice and further action.

For medical bacteriologists, the implied information covers pathogenic capacity, probable sources of infection, prognosis, cross-infection potential, and contributes to optimisation of treatment. The accuracy of this deduced information depends on the accuracy of identification, species homogeneity and accuracy in attributing these characters to the species; its scope depends upon accumulated case reports of infections caused by the organism.

Classifications provide the technical language of species and genus names that communicate this implied information in a shorthand form. Like the earthworm, the laboratory team analyses and identifies the stimulus, then mounts an appropriate response. Unlike the earthworm, the response is founded upon a classification and knowledge gathered by many individuals over many years.

Most of the problems in bacterial taxonomy are due to an unnatural division between those who produce classifications and those who use them. On the one side, taxonomy is often an academic exercise, on the other, it is the basis for organisation of a simple, rapid and sensible flow of isolates through laboratory tests, and a mainstay in determining clinical advice. The divergence of purpose and philosophy between taxonomists and users has increased since the 1960s and is being further aggravated by current changes. If both sides ignore the importance of their contributions and responsibilities in the taxonomic process, it is possible that the worm might face a choice between divorcing itself from central control, or hiding from leaves and attempting to eat birds.

Diagnostic laboratories now encounter “occasional” pathogens of increasing variety and with increasing frequency, due to changes in disease patterns and medical care. The list of species recognised as pathogens only in the last 20 years run from *Arcanobacterium (Corynebacterium) haemolyticum* to *Xanthomonas (Pseudomonas) maltophilia*; failure to include the entire alphabet may merely reflect the scarcity of genus names beginning with *X*. Many of these new pathogens have been moved to new genera during their rise to medical interest, compounding the confusion of unfamiliar names. Taxonomic changes are occurring faster than they can be incorporated in new editions of textbooks; *Corynebacterium jeikeium*, for example, does not appear in the current edition of Bergey’s Manual.

One approach to the confusion is to retract into the wormhole of familiar, older classifications, by reporting, for example, all coagulase-negative staphylococci as “*Staphylococcus epidermidis*” or even “*Staphylococcus albus*”. However, this is not an option for many of the new pathogens. A better strategy is to attempt to understand the origins of the problems, and to participate in their solution. Diagnostic microbiologists must realise that revision is a necessary natural process in classification, because improvements are made by a cyclic succession of hypothesis, criticism, exploration and revision, as in all science. If the changes occur in a sensible manner, the revisions can lead to improvements in the accuracy and scope of the implied information predicted from identification.

Concurrently, taxonomists have turned to molecular biology, in the belief that comparison of genomic data yields “truer” classifications reflecting the evolutionary relatedness of species. This search for the
“holy grail” of a natural classification, whatever its academic merits, is a siren song that deafens taxonomists to the practical purposes of classification. Most taxonomic revisions based on these techniques are undoubtedly valid. However, surprisingly few have improved the homogeneity of species and the pathogenic predictivity of identification, and some have generated genospecies, with little description of pathogenesis, that no diagnostic laboratory can identify reliably. The trend towards an absolute requirement for genotypic characterisation of any proposed new species places bacterial classification firmly in the hands of a tiny minority of microbiologists who often have little contact with routine bacteriology.

This technological change has removed the opportunity for diagnostic microbiologists to participate in classification studies. Their participation, and, presumably, its tempering effect, has decreased markedly in recent years. Although an ardent supporter of numerical taxonomic principles, I must admit that this began with the introduction of numerical taxonomy. Few non-academic microbiologists had the time, computing facilities and mathematical knowledge to take up this advance. Although Sneath and Cowan concurrently emphasised that the only purpose of taxonomy was to produce a working classification for use in practical identification, the influence of this contention has waned with time.

Furthermore, the genetic methods are complex, multi-stage processes with such a low throughput that few strains can be examined. A single mis-labelling accident, one genetically atypical strain, or an unnoticed slip in technique could distort the classification of a species for many years. Diagnostic microbiologists might justifiably place little faith in the homogeneity of a species proposed on the basis of less than five supposedly representative strains, some of which are not of clinical origin.

Clearly, these developments have widened the gap between diagnostician and taxonomist, and it appears that little is being done to prevent the two groups from diverging further. As a diagnostic microbiologist with an interest in taxonomy I recognise an urgent need for both groups to come to a consensus on their objectives and responsibilities.

The clinical microbiologist should be the source of isolates and information on the pathogenicity of new groups. If an infecting isolate is identified to a species with little or no record of pathogenicity, then other bacteriologists would benefit from a clearly documented report of the strain's characteristics, circumstances surrounding the infection, the symptoms, treatment and outcome. This type of publication has become rarer in recent years, but accumulated anecdotal case reports remain the mainstay for optimisation of diagnosis and treatment. They also highlight species that are heterogenous in phenotypic and pathogenic characteristics and require subdivision, e.g., Streptococcus milleri. If an isolate is unidentifiable, then it should be reported, and submitted to an interested person, who can accumulate strains, and eventually revise the classification.

Routine laboratories should be encouraged to have an interest in a genus, and be supplied with the means to accumulate isolates and clinical details from other laboratories. The role for the interested person with a keen eye for anomalies has increased in importance with the increasing range of pathogens, as have the opportunities for useful, publishable, contributions to knowledge. Academic taxonomists should not be averse to supplying expertise for co-operative investigations. Most importantly, microbiologists in diagnostic laboratories should forsake their customary apathetic retreat into old classifications, and complain loud and long about changes that they consider unnecessary, confusing or impractical.

Academic taxonomists should recognise that their product is the working technical language of microbiology. If the practical purposes of the language are ignored, the users are likely to forsake the tone of academically correct species names, and evolve their own language. A species that cannot be identified or reliably discriminated from others by tests available to a routine laboratory has no practical purpose. Incidental information to define its ecological and pathogenic properties will be not accumulated. The users also require terms to describe distinguishable groups with clearly defined pathogenic properties, whatever their academic merit.

The requirements of the routine laboratory should be considered in all taxonomic changes. The addition of new species names should be considered not simply for academic validity, but also for their impact on practicing microbiologists. Proposals for new species should include a suggested scheme for routine identification, an assessment of error rates in identification, and some reasonable basis for prediction of ecological and pathogenic properties. These requirements would place a lower limit on the number of isolates described, discouraging excessive splitting of genera, and provide a practical basis for the work in the routine laboratory.

Piecemeal re-arrangements at genus level cause much confusion and divergence of terminology. They might be better introduced in batches, presaged by reviews of the changes and their reasons in journals commonly read by those whom the changes will affect.

The earthworm bears the consequences of an inappropriate response immediately. By contrast, feedback between the users and producers of bacterial classifications is minimal and slow. We need to re-establish a basis for mutual understanding, so that the worm's aspirations to ultimate understanding remain compatible with its ability to feed and avoid predation.

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