Bundling the forces in systematists

The past 15 years have witnessed a dramatic increase in our knowledge of the role of prokaryotes in early evolution (Doolittle, 2000; Woese, 2002; Martin & Embley, 2004) and a recognition of the vast diversity and ecological importance of prokaryotes (Hugenholtz *et al.*, 1998; Rappé & Giovannoni, 2003). Totally unexpected were the estimates of the astronomically large number of prokaryotic cells on this planet, their contribution to global cycles and food webs (Whitman *et al.*, 1998), the estimates about the number of potential prokaryotic species (Bull *et al.*, 2000; Dykhuizen, 1998), the depth and breadth of phylogenetically defined phyla (Dalevi *et al.*, 2001), and the genomic complexity of species (summarized by Pennisi, 2003). Furthermore, the role of horizontal and vertical gene transfer in shaping species was evaluated, which may lead to the development of the species concept(s) in bacteriology (Cohan, 2001; Spratt, 2004; Lan & Reeves, 2001).

This progress was stimulated by and runs parallel to the breathtaking developments in molecular methods. The ease with which these techniques can be applied to any biological specimen, either cultured or not yet cultured, has led to their widespread application. Microbiologists are now in a position to rapidly assess the phylogenetic novelty of isolates by comparing genomic properties, mostly the 16S rRNA gene sequence but increasingly sequences of genes encoding housekeeping proteins, with the database of similar sequences of archaeal and bacterial type strains. Studies have been published that correlate sequence diversity with taxonomic ranks (Fox *et al.*, 1992; Stackebrandt & Goebel, 1994; Keswani & Whitman, 2001). Indeed, the scientific literature contains many examples that point toward the presence of a putative novel taxon on the basis of significant differences between its 16S rRNA gene sequence and the phylogenetically nearest neighbour. A few members have been isolated and described subsequently, belonging to hitherto novel phylogenetic

lineages, with examples ranging from membership of new phyla (e.g. *Gemmatimonas aurantiaca*; Zhang *et al.*, 2003) to described genera (e.g. *Clostridium lacusfryxellense*; Spring *et al.*, 2003).

Despite the unparalleled diversity of prokaryotes, only about 6000 species have been described to date. This is due to the demanding process of naming species and to the lack of taxonomic expertise worldwide (Oren & Stackebrandt, 2002). Public collections of micro-organisms have the mandate to collect, maintain and distribute biological resources, primarily strains of scientific and applied interest as well as type strains of described species. Some of these centres perform excellent systematic studies on prokaryotic strains, and play a leading role in the development of quality control criteria for type strains and in the assessment of properties of novel isolates, which guides the description of novel species. Besides these centres, there are only a few other taxonomic centres worldwide able to perform the full range of tests needed in the polyphasic approach to prokaryotic systematics.

The majority of research groups, however, being able to isolate strains and to assess the phylogenetic diversity of their isolates, may have not have the expertise, the financial basis or the interest to continue the scientific work that would result in the description of a novel species or in the inclusion of the strain as a reference in other scientific projects. Such research groups may seek taxonomic help from one of the taxonomic centres mentioned above. However, if not, such a strain will most likely disappear from our scientific awareness and will often not be available, though its sequence is retrievable from public databases.

Many scientists would be willing to provide such strains to the community for subsequent scientific studies. In this instance, a new role of Biological Resource Centres (BRCs) can be defined, serving the

scientific community to expand the knowledge of prokaryotic diversity and to add to our understanding of the evolution of the broad spectrum of properties to be analysed in the context of systematics of prokaryotes. The strategy developed below should not be restricted to prokaryotes, including cyanobacteria, but should also include novel strains of yeasts, fungi and microalgae. In this scenario, the original investigator/isolator allows a BRC of choice to maintain in custody a strain that represents a phylogenetically distinct lineage, together with a record on a yet-to-be defined list of its properties [at least information as provided in the minimum dataset of CABRI (<http://www.cabri.org>), including the accession number of the sequence and an indication about the phylogenetic distance of its nearest neighbouring type strain].

The question remains, which BRC should play the role of a strain-broker collection? Certain functions should be guaranteed in order to regularly update the taxonomic status of the putative novel taxon. The centre should be committed to the following services.

- Maintaining the strain held in perpetuity and making available electronic lists of such strains.
- Facilitating communications between depositors and taxonomists who are interested in the strain, provided, if so requested by the depositor, by Material Transfer Agreement.
- Checking regularly the phylogenetic status of the strain by sequence analysis via, for example, BLAST (<http://www.ncbi.nlm.nih.gov/blast>).
- Updating the list of strains by addition of novel strains, removal of strains sent off and entering changes in the phylogenetic affiliation.

The advantage of transferring new responsibilities to BRCs lies in their expertise in collection management,

storage and long-term maintenance, dealing with a large number of accessions and distributions and their record-keeping. Being directly involved in the implementation on articles laid down in the Convention on Biological Diversity (<http://www.biodiv.org>), BRCs are used to tracking documents from the depositor to the customer and, by implementing Material Transfer Agreements, creating an atmosphere of trust between the two parties. In contrast to the established role of BRCs, providing the same resources to many customers, the role as a strain-broker for putative species is to guarantee that the strain is only sent to a single research group, unless otherwise decided by the original depositor. A strain forwarded must immediately be eliminated from the list of available strains but should be kept in the non-public collection.

The new task of BRCs adds to the responsible role of these collections in the world of increasing complexity of both biological material and information. Scientists are asked to contribute to this novel approach by approaching collections of their choice for the benefits of responsible use of funds and biological resources, and to expand the network of communication between systematists over laboratory and national borders.

BRCs that have already agreed to serve in this function are the BCCMTM, Gent, Belgium (<http://www.belspo.be/bccm/>) and the DSMZ, Braunschweig, Germany (<http://www.dsmz.de>). Other World Federation of Culture Collections (WFCC) member collections may follow.

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