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On the fitness of microbial taxonomy

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Microbial taxonomy seems to be an expanding discipline especially in Asian countries. By contrast, the number of taxonomists in Western countries are in decline, and the reasons for this could either be economic or due to interest. Losing taxonomy expertise could have consequences for Western countries.

Taxonomists play an important role in describing the extent of biological diversity and framing it in a classification schema that is of general scientific purpose. However, only a very small proportion of the scientific community possesses expertise in this field. There is a general feeling that such expertise is slowly disappearing, a fact that may act negatively on the understanding of hitherto undiscovered biological diversity. Results of a bibliographic survey of the current state of the taxonomist community researching prokaryotes seem to warn Western countries, who were the leaders in this field in the 20th century, about losing taxonomy expertise.

In several recent letters in *Trends in Ecology & Evolution* [1–3], taxonomists of eukaryotes discussed whether taxonomists are in decline or not, and whether the extent of diversity to be described would be achievable by the current set of available taxonomists. Contrary to the decline in microbial taxonomists previously hypothesized [4], there are increasing numbers of systematists studying taxonomy of *Bacteria* and *Archaea*, although there is much more work to be done on the microbial side. It is estimated that 80% of eukaryotic diversity is undiscovered [5]. However, the situation for prokaryotes is much more dramatic, where the approximately 9000 species hitherto described represent far less than 0.1% of the existing diversity, and it would take at least 16 000 years to achieve the complete catalog given the current set of active experts [6].

The low coverage of microbial diversity is partly because classification of prokaryotes is a much younger discipline than eukaryotic classification. Serious classifications started at the end of the 19th century when methodological developments in microbiology allowed the study of microscopic organisms. Low classification coverage is also partly due to the difficulties that microbiologists come across when trying to classify a new taxon. The main problems arise from the need to isolate new taxa as living pure cultures in the laboratory, and the lack of morphological complex structures that force the study of metabolic and chemical traits in addition to genetic properties. Although the compulsory need for pure cultures for taxonomic

purposes hampers the speed of the classification process, it guarantees the perpetuation of the living material in culture collections making the type specimens available to the scientific community [6], which does not occur in other disciplines.

In this regard, the classification of microorganisms largely depends on technological developments that allow more accurate descriptions of the microorganism's properties. In fact, methodological innovations importantly influenced the method and speed of taxa descriptions [7]. A good example of this is shown in Figure 1a, where a clear shift in the speed of descriptions of new taxa occurred in the early 1990s. In that decade, the use of the 16S rRNA gene sequence as a molecular clock facilitated the description of new species promoting an arithmetic growth of publications with new species descriptions. In fact, the presence of such sequences (now over 3.5 million; <http://www.arb-silva.de>) in public repositories has increased exponentially (Figure 1a), but most of the sequences (over 99%) are from environmental DNA of hitherto uncultured organisms, for which no formal classification is yet possible. It seems that in the past 6 years we have reached a plateau of descriptions per year (Figure 1a and 1d). This observation can be better explained by constraints in publishing space in specialized journals together with the load capacity of editors and reviewers, rather than a decrease of interest or expertise, as will be discussed below. In this regard, it is remarkable that the increase in new classifications since 2000 is accompanied by an increase in the number of issues in each volume of the *International Journal of Systematic and Evolutionary Microbiology* (IJSEM; the largest source of new classifications, publishing more than 70%), which increased from four to six issues in 2000 and to 12 issues in 2006.

It is important to note that the shift in the early 1990s was also accompanied by a change in the habits (Figure 1b) and also nationalities of the experts (Figure 1c). Traditional descriptions were based on isolating several representative strains of the same taxon and studying them simultaneously in order to explain the intraspecific extent of diversity. Use of molecular phylogenetic methods to reveal the genealogy of organisms was accompanied by an explosion of descriptions based on a single specimen for each taxon, abandoning the effort to try to isolate more representatives of the same taxonomic unit (Figure 1b). These kinds of descriptions promote lower quality information on the genetic and phenotypic diversity of prokaryotes, and thus the whole classification system suffers from this lack of information. However, single strain species descriptions (SSSDs) have significantly sped up

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Keywords: microbial taxonomy; species description; culture collection.

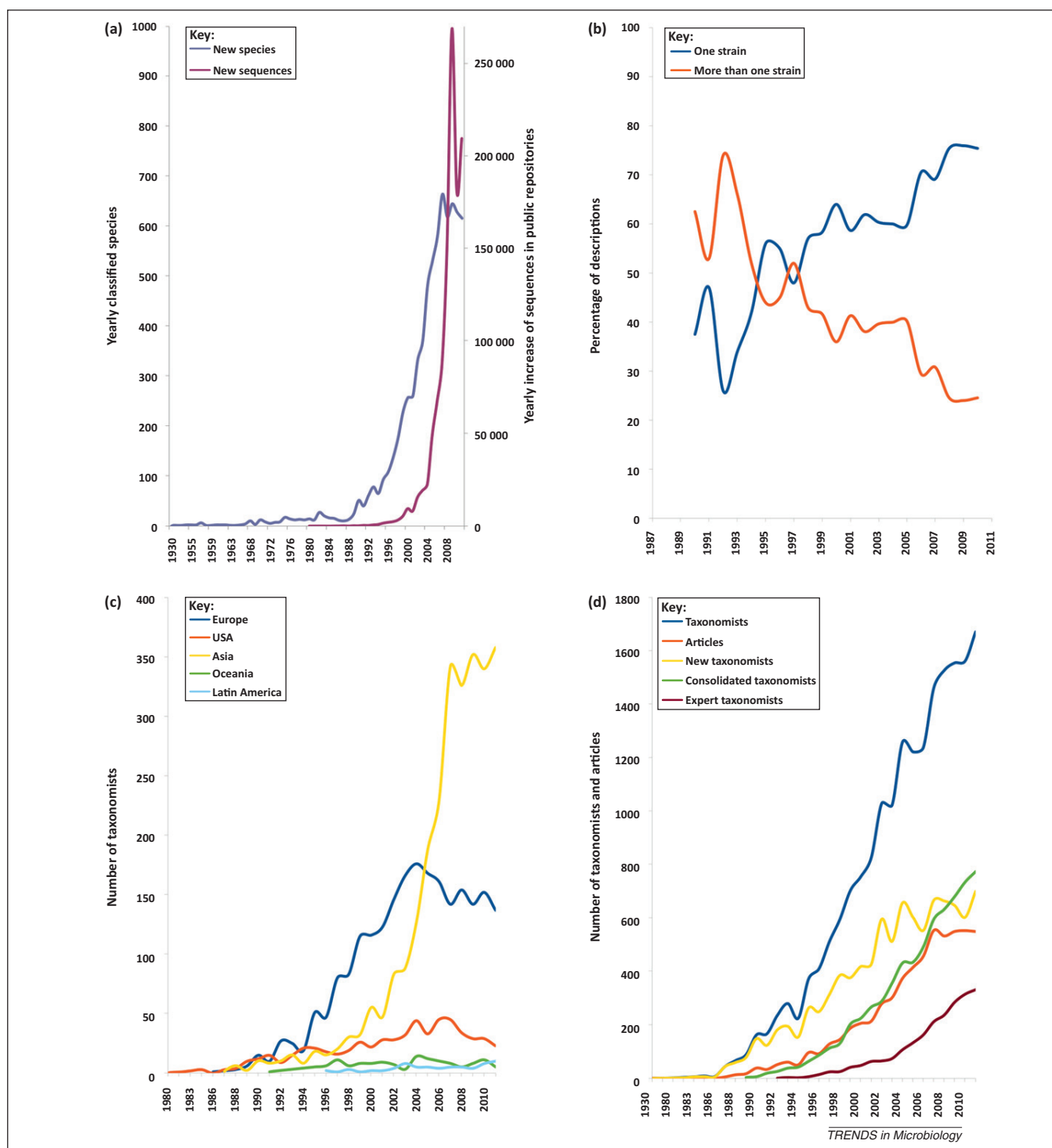


Figure 1. Trends over time in taxonomic practices in describing species of *Archaea* and *Bacteria*. **(a)** New species descriptions by year (left axis, blue line) and deposition of new 16S rRNA gene sequences in public repositories (right axis, purple line). **(b)** Yearly percentage of classifications with more than a single strain (orange line) or with just one isolate (blue line). **(c)** Number of taxonomists publishing new species from Europe (blue line), USA (orange line), Asia (yellow line), Oceania (green line), and Latin America (cyan line). In the graph, the countries that mainly contributed to the new descriptions are in descending order: China, South Korea, Japan, USA, Germany, France, UK, Russia, Spain, and India. **(d)** Number of taxonomists (blue line), newcomers (with only one description, yellow line), consolidated taxonomists (with at least three descriptions, green line), expert taxonomists (with at least ten descriptions, purple line), and articles on new classifications per year (orange line). All results are based on a bibliographic study of the Medline database, August 2012 (2012 baseline distribution plus updates; <http://www.nlm.nih.gov>), containing 21 566 046 references.

the activity of classifying prokaryotes, and currently approximately 80% of the descriptions are based on just one type specimen.

Regarding the number of microbial taxonomists, we cannot only observe an exponential increase in newcomers

(Figure 1d) but also in consolidated and expert taxonomists (those appearing in more than three and ten descriptions, respectively). These numbers are encouraging as it seems that microbial taxonomy may be more alive than ever. However, what is most striking is that the explosion in

taxonomists has occurred in Asian countries, nearly doubling those in Western countries (Figure 1c). In areas where taxonomy was a traditional practice, such as the USA and Europe, classification activities seem to be in decline. This probably has a financial explanation, as perhaps funding agencies do not promote enough research in the field of taxonomy, rather than a decline in the interest in classifying new organisms. Such discordant classification practices between Asian and Western countries may have important implications for the development of the compilation of microbial potential for different disciplines such as biotechnology and pharmaceuticals. Currently, one of the most important achievements in taxonomic research is that any new species type material must be deposited in two international strain collections of different countries for further maintenance of the living material. In this regard, researchers generally tend to deposit their strains in collections in their regions [8]. As the emerging Asian countries seem to be the most active in classification practices, and the Western ones seem to be in decline, in the future, Western collections may suffer a reduction in the deposition of type material. This will imply a decline of availability for the local industry.

Culture collections play an important role among taxonomists and users of the microbiological diversity. They authenticate the material in addition to being responsible for the perpetuation of such living biological resources. Collections do not only receive type material but also the deposit of important industrial, pharmaceutical, or biotechnologically relevant strains that need to be preserved. This deposit is done voluntarily by researchers, but very sporadically. Less than 1% of the published strains are deposited [9], hampering their availability for potential users. The compulsory deposit of type material for taxonomic purposes guarantees its availability, together with a description of the main metabolic and genetic properties. In the current era of genomics, the full genomic sequence may serve as a source for understanding the genetic potential of new species for basic research and industrial purposes. Unfortunately, genome databases are full of examples of sequences for which no culture deposit has been made, and also with dubious identities that may hamper further research [10]. It is the responsibility of taxonomists to provide accurate information about their new classifications. Given the relatively low costs of genome sequencing, encouraging taxonomists to provide full genome sequences as part of their descriptions should be one of the major goals of journal editors and also of the International Committee on Systematics of Prokaryotes (ICSP), as happened with the 16S rRNA gene sequence [11]. However, as often occurs, taxonomists do not receive sufficient economic support as classification activities do not seem to be a priority for funding agencies [12] and

perhaps for the scientific communities in Western countries. The benefits of their support may be invaluable in the future.

In short, it seems that microbial taxonomy is in good shape (at least in Asian countries), and that the extent of new descriptions is constrained by journal capacities, rather than taxonomists' activities. One of the most worrying problems is the increase of SSSDs that do not offer exhaustive descriptions of intra-taxon diversity. However, such classifications give us information about hidden microbial diversity as well as making invaluable living resources available when depositing their type material. Unfortunately, it seems that Western countries have suffered a major slowdown in comparison to the blooming activity in the East. Given the enormous extent of undiscovered prokaryotic diversity (over 99.9% of the total expected), it is important to encourage funding agencies to give support to newcomers to continue with their efforts in classifying *Bacteria* and *Archaea*, as the future benefits of revealing the biological potential of microbes cannot be underestimated.

Acknowledgments

The research of both authors is supported by the Spanish Plan Nacional CGL2009_12651-C02-02 and Consolider Ingenio CE-CSD2007-0005 projects both co-financed with FEDER support from the European Union and the European Project MIRRI (INFRA-2012-2.2.5, grant agreement 312251). The support of the German Academy of Sciences Leopoldina is also acknowledged.

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<http://dx.doi.org/10.1016/j.tim.2012.08.012> Trends in Microbiology, November 2012, Vol. 20, No. 11