Expanding the ‘Digital Protologue’ Database (DPD) to ‘Current Microbiology’: An Offer to Scientists and Science

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The recent introduction of a standardized format for bacterial and archaeal species (Roselló-Mora et al. [3]) for ‘original material associated with a newly published name, comprising its description or diagnosis and any of a number of other elements such as illustrations, synonymy etc.’ (protologue, <https://en.wiktionary.org/wiki/protologue>), constitutes a milestone in the rapid mobilization of taxonomic machine-readable data into existing electronic databases. These exist in ample versions in strain catalogues of public microbial resource centres, dedicated microbial databases, e.g. BacDive (<http://bacdiv.dsmz.de/>) or Mycobank (<http://www.mycobank.org/>) and nomenclatural databases such as LPSN (<http://www.bacterio.net/>), LPT (<https://www.arb-silva.de/projects/living-tree/>), WDCM (<http://www.wdcm.org/>) or EzTaxon (<http://www.ezbiocloud.net/>).

New significant developments, considered to be a paradigm shift, require adaption of traditional thinking and procedures to the new situation. For more than a hundred and thirty years bacterial taxonomists followed individual strategies, which in the 1970ies were combined and subsumed under ‘polyphasic’ [1]. This approach saw the inclusion of new approaches and techniques into the traditional spectrum of properties to characterized novel microbial species. Examples were the determination of the base composition of DNA, DNA–DNA hybridization, gene sequencing, automated phenotypic tests, riboprinting, MALDI-TOF and lately, though still fragmentary only, entire or draft genome sequences. As a consequence, the range of describing properties of a novel species

significantly increased the knowledge base of the cultured micro-biodiversity. Taxonomists may feel uneasy with the increasingly time-consuming and laborious data generation but also collection curators and scientists find it difficult to manually search for specific properties and comparative data.

As indicated by Roselló-Mora et al. [3] other journals are encouraged to follow the examples of *Antonie van Leeuwenhoek*, *Systematic and Applied Microbiology* and, recently, *Archives of Microbiology* [4]. Current Microbiology, another journal that effectively publishes a significant number of novel prokaryotic species, now follows their example. Another main advantage lies in the opportunity for authors and any other scientists to use the data format for retrospectively adding data of previously published taxa.

A curated and managed high quality database will overcome key problems that hamper data exchange and interoperability between mBRCs and third party databases. The use of incorrect or invalid names results in heterogeneous, incomplete and fragmented datasets for the users. The use of Taxon Number, similar to the policy regarding the deposition of information of novel fungal taxa in MycoBank [2] will facilitate machine-readable linkages to data sources to be made reducing human error and speeding up connectivity in the ever expanding mass of data.

The present initiative is fully in line with the ideas of the ESFRI project Microbial Resource Research Infrastructure (MIRRI) to link data to resources available in public microbial resource centres. Based on a long tradition, not-for-profit mBRCs were established to allow facilitated and legal access to resources worldwide, to add value to known and yet unknown microbial biodiversity and to exploit unknown sources and knowledge to discover and disclose for the bioeconomy and bioscience generally. MIRRI is

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being established to provide access to the combined resource and knowledge base currently disparate and not easily connected and to respond to user needs through coordinated policy and strategy. At the heart of these efforts are the ambitions, (i) to facilitate access to resources and knowledge to offer solutions to the development goals and specifically the bioeconomy, and (ii) to facilitate user communications by providing a gate to a knowledge-based platform.

It is the ultimate aim of the MIRRI project to take the interoperability and accessibility of resources and data to a higher level, recognizing that better-managed resources will lead to further discovery in all areas of the Life Sciences.

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