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Re-defining microbial diversity from its single-celled building blocks

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It would be an astonishing experience for an environmental microbiologist of 1985 to be teleported straight into 2015! Few things have remained the same in this dynamic research field, and our understanding of the abundance, diversity and activities of microorganisms on the planet Earth has been thoroughly revamped. Research technologies that were unimaginable in 1985 are producing data of unprecedented quantity and quality. But there may be a distressing moment as well: realizing that microbial community composition data collected with so much effort in 1985 is rarely looked at in 2015, even when trying to understand decadal and longer-term environmental changes. The reasons are deeper than science fads and difficulties accessing non-digitized records: most analyses of the composition of natural microbial assemblages of 1985 are considered incorrect and incompatible with the science of 2015.

Now let us imagine that we can be teleported into 2045. Most likely we would see technological and conceptual advances exceeding those that took place between 1985 and 2015. Unfortunately, we would likely see Earth's environment continuing to undergo significant change, largely as a result of anthropogenic perturbations. Hopefully, we would also see human societies that are increasingly cognizant of their interdependence with the rest of Earth's biota, in particular with the predominant, microbial component of it. By 2045, microbiology may become one of the key areas of expertise required to understand, predict and mitigate global environmental changes. Historical records will be of key importance. Will suitable data exist? Will scientists of 2045 look back at the results of microbial community composition in oceans, soils and other environments collected in 2015 to draw meaningful conclusions about ongoing alterations?

Chances are high that the answer to the question above will be 'no'. Although today's studies of microbial diversity are no longer prone to cultivation limitations of 1985, they are still predominantly framed around operational, technique-based definitions rather than a deep understanding of the underlying biology. As research techniques change, operational definitions change, too. Therefore, many microbial species, genera and even broader taxonomic units of 1985 have no relevance today (Garrity and Lyons, 2003), while many of today's operational taxonomic units and associated data may lose relevance in a few years or decades from now despite the enormous (at least by 2015 standards) datasets produced around them. We can say that this is part of science progress. However, I cannot stop thinking that there must be a smarter way to go about it. How come we confidently recognize many animals and plants described in millennia-old texts using long-gone languages, while some microbial taxonomic units turn unintelligible in a matter of decades?

There are good reasons to believe that the upcoming decade will place microbial diversity research on more solid footing. The recent emergence of single-cell genomics (SCG) will likely play a critical role (Lasken, 2012; Stepanauskas, 2012). Already, SCG offers routine recovery of genomic blueprints of microbial groups that used to be inaccessible because of the absence of their pure cultures (Marcy *et al.*, 2007; Rinke *et al.*, 2013; Swan *et al.*, 2013). This may lead to a long-overdue reconciliation of the robust biological nomenclature of cultivated taxa (Garrity and Lyons, 2003) with the chaotic world of naming conventions for the remaining 99+% of microorganisms. However, the potential of SCG goes beyond descriptive analyses of uncultivated lineages. By focusing on the most fundamental units of biological organization – individual cells – SCG breaks free from the necessity to bin microbial community molecular data into arbitrary taxonomic units. Furthermore, unlike other cultivation-independent methods, SCG is well-suited to analyze genomic rearrangements, horizontal gene transfer and the organization of hereditary information in multiple DNA molecules in a cell, all of which likely play key roles in the non-Darwinian evolution of microorganisms and their rapid adaptation to a changing environment (Ochman *et al.*, 2000; Shapiro, 2010). This is starting to offer a fresh, assumptions-free view of the microbial genomic diversity and underlying ecological and evolutionary processes at unprecedented detail (Kashtan *et al.*, 2014; Engel *et al.*, 2014). As SCG and complementary techniques grow in scale, biological patterns may emerge to inspire natural rather than operational definitions of microbial diversity. These definitions may differ substantially from the current biological

species concept, which was specifically designed for multicellular eukaryotes that constitute only a few, relatively young branches of the tree of life. We may find out that the evolutionarily much older and more diverse world of unicellular *Bacteria*, *Archaea* and *Eukarya* is organized and evolves in ways that defy our current, anthropocentric conventions. Such prospects justifiably make environmental microbiology a very dynamic and futuristic field that leads the way for improved understanding and stewardship of Earth's predominant, unicellular biota.

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