What does the Name Change Entail? Differentiation of Strains for Bacterial Names

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Abstract

The frequent change of bacterial names and the consequences have been discussed in brief, with recent examples of *Bacillus spp*, and *Lactococcus spp*.

Keywords: Bacterial classification, *B. paralicheniformis*, *B. licheniformis*, *L. plantarum* and *L. pentosus*

Opinion

The bacterial classification change of names "*Bacillus licheniformis* into *B. paralicheniformis*, Lactobacillus plantaruam, *L. pentosus* and *L. paraplantarum*" and implications. The change of a strain name creates many hurdles in representing, patenting, and in academic events. Even more important, patents filed under the previous name may disappear as the new name appears. The incorporation of a new name locally is easy, but this is a major concern globally. In 2019, we filed a patent on the Bioprocess developed for the purification of (*B. licheniformis*), bacteriocin as a result, the patent granted. During the submission of the whole genome sequence (WGS) in the NCBI portal, we were informed that this is *B. paralicheniformis*, but based on 16S rRNA sequence it was *B. licheniformis*. Identical incident observed involving L. plantarum, after submitting the genome sequence, it was informed as *L. pentosus*. Current microbial classifications based on 16S rRNA gene sequences, and also a few housekeeping genes [1-4] have several limitations. They begin with low phylogenetic resolution at various taxonomic ranks [5], followed by missing diversity because of primer mismatches [6], finally formation of corrupt tree topologies by drawing together various disparate groups [7].

Subsequently, we discovered the incidents that led to a change in the names of a few bacterial strains. It was a certain type of nucleotide changes to non-standard housekeeping genes such as rec A. Surprisingly, if the 99.9 % similarities found in the 16S rRNA right away it may be sequence blasted at nucleotide level and given a specific name. If not, above 99.0 % sequence similarity may be considered as another but, without considering the 16S rRNA.

The dependence more on other than 16S rRNA sequence may be followed/considered/ ignored. These kinds of sudden changes in the name, causes lot of complications. The change in the name sometimes disqualifies the strain for human applications, as it has not listed in the local food safety guidelines. The name changes also created irreparable damage in commercializing the products. At the end, we should understand and accept that nothing changes the nature of the objects under classification the level of variations needs accounted for in any proposal. The classification scheme could be measured based on the number of people subscribe to it. Therefore, we may conclude that classification schemes of changing the names are rarely "right" or "wrong" but considered as simple and formal procedures to relax the complexity. This subsequently, provides a common acceptable nomenclature.

Funding information

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