

What Does the Name Change Entail: Differentiation of Strains for Bacterial Names

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DESCRIPTION

Bacterial strain composing, or recognizing microscopic organisms at the strain level, is especially significant for analysis, treatment, and epidemiological reconnaissance of bacterial diseases. This is particularly the situation for microbes showing undeniable degrees of anti-infection opposition or harmfulness, and those engaged with nosocomial or pandemic diseases. Strain composing additionally has applications in considering bacterial populace elements. Throughout the most recent twenty years, atomic techniques have logically supplanted phenotypic tests to type bacterial strains. In this article, we audit the current bacterial genotyping strategies and characterize them into three fundamental classifications: (1) DNA banding design based techniques, which arrange microbes as per the size of pieces created by enhancement as well as enzymatic absorption of genomic DNA, (2) DNA sequencing-based techniques, which study the polymorphism of DNA groupings, and (3) DNA hybridization-based techniques utilizing nucleotidic tests.

The bacterial classification change of names “*Bacillus licheniformis* into *B. paralicheniformis*, *Lactobacillus plantarum*, *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 new name may be incorporated locally with ease 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. When submitting 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*. 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 a non-standard house-keeping genes such as *rec A*. Surprisingly, if the 99.9 % similarities found in the 16S rRNA right away it may be 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 change 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.

Bacterial strain-composing techniques have been quickly advancing over late years. The field has been advancing toward PC helped plan/examination and expanding mechanization, goal, throughput, and reproducibility. In the genomic period, bacterial genotyping benefits progressively from bioinformatics, for example, PC based determination of composing markers; plan of composing system; stockpiling, trade, and examination of genotyping information (DNA banding designs, DNA arrangements, microarray profiles); advancement of further developed investigation instruments; and phylogenetic examination. Genotyping data sets containing banding designs, DNA arrangements, or DNA microarray profiles are advantageous for interlaboratory examination, review considers, and long haul epidemiological reconnaissance of bacterial contaminations.

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