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Automated Ribotyping of Bacteria: “Bar-coding” or Genetic Fingerprinting for Bacterial Identification and Characterization

Jong Ok Kim and Je Hyeon Lee
Takara Korea Biomedical Inc.

Recently the Microbiology has been developed rapidly. It is known that the conventional method is insufficient for complete classification of separated bacteria and to investigate the movements of the source of infection. Although analyzing identity used recently for bacteria has been improved substantially in comparison to the conventional method, the former has the problems, such that it takes long for analysis, that it shows different results up to the status of a bacillus, that it is impossible to identify each between same species, that the accuracy is mostly dependent on user's special experience, and so on. In the industrial area that have to be cautious especially to bacteria infections or other field in which bacteria inspection is essential, like medical institutions of hospitals, etc., reduction of analyzing time, accuracy of analysis, and credibility improvement are essential conditions. The followings are showing the current analysis standards of microorganism. i) Nutritions used for growing ii) Ingredient types and contained quantity of Fatty acid in the membrane iii) DNA or RNA standards, etc. Among above conditions, as a solution to overcome problems, such as data credibility, subjective analysis, data sharing unreliable and difficult, time consuming, network application, etc. which are happening during analysis by conventional method, we will introduce the system of identifying bacterium by operating genetic fingerprint(Ribotyping) automatically. The genetic fingerprint(Ribotyping) method used as an innovative one identifying under DNA standard applies with the multi-formation of bacterium ribosome RNA genes in sub-species.