



Whole genome sequence analysis of pathogens

Abstract

Due to the constantly emerging diseases, the pathogenicity of the causative agents and their increasing antimicrobial resistance, and in the spirit of the “One Health” strategy, the efforts of all scientists have been redirected to the development of molecular and bioinformatics methods for the diagnosis and analysis of pathogens and in particular whole genome sequencing (WGS). Over the last decades, the world has been shaken by a genomic revolution that replaces conventional testing methods with whole genome mapping and characterization of pathogens in food and environment, human and animal isolates.

Facilitating scientist’s access to complete pathogen genome data and sharing data from each country in a single harmonized data platform offers an enormous opportunity to characterize pathogenic microorganisms: typing, outbreak characterization, food outbreaks, risk assessment, antimicrobial resistance, pathogenesis and WGS-based epidemiology. In addition to identifying and typing the pathogenic agent, whole genome sequencing provides an opportunity to predict on the basis of bioinformatics analysis and statistical data processing, pathogen distribution patterns, as well as refinement of monitoring plans, prediction of emerging outbreaks of infectious diseases, and not last but not least, the antimicrobial resistance of pathogenic bacteria and the strategy for the treatment of diseases.

Genomics as a constantly evolving science not only changes the diagnostic scheme / framework of the national reference laboratories involved in the research and monitoring of infectious diseases but also questions the completeness and accuracy of the risk assessment to date.

Outside the scientific aspects, a number of initiatives and publications related to WGS clearly mark the global trend of transforming from conventional methods of diagnosing pathogens to WGS, which provides better diagnostic readiness, is cheaper and faster as consumables and reagents, does not need a lot of staff, could handle about 3,000 isolates per week, and the information it provides is vast, comprehensive, and not just about isolation and typing of the infective agent.

Fundamental microbiology is shifted by informatics, genomics, bioinformatics and statistics.

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