Next Generation Sequencing in Clinical Microbiology, Applications and Challenges

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Abstract:

Next Generation Sequencing (NGS) combined with bioinformatics has open a new era in public health, and infectious diseases (1). NGS combined with bioinformatics has been used successfully worldwide in infectious diseases research for most prevalent pathogens affecting the public health (2). NGS allows sequencing of the whole genome of multiple pathogens in one sequencing run (1). In the last two decades, NGS has been an attractive option for clinical laboratories around the world as both investment and running cost have decreased dramatically (3). NGS has different applications in the clinical setting such as: outbreak management, molecular case finding, characterization, surveillance and rapid identification of pathogens, taxonomy, meta genomics approaches on clinical samples (1). In addition, during the in the beginning of the COVID-19 pandemic, NGS has played a critical role in the early fight against this novel coronavirus for his first identification and sequencing analysis which is used as reference to develop any vaccine (4,5). However, implementing of high quality NGS and bioinformatics in public health diagnostic can be challenging (2). These challenges may include: the presence of well-trained staff, the selection of the convenient NGS method, the right use and interpretation of the bioinformatics tools. Here we will discuss the application of NGS in the analytical and post analytical phase in the clinical diagnostic cycle with emphasize on bacteriology, as well as summarize some bioinformatics tools and procedures used for sequences and genome analysis. There is no doubt that such an opportunity will sooner than later profoundly change the routine laboratory practice together with the means of conducting microbiological diagnosis.

Biography:

Get my PhD in November 2017, at the University Hospital institute of infectious diseases, Aix-Marseille University, Marseille, France. Expertise in antibiotic susceptibility testing methods, antibiotic combination and synergistic study. Build a strong background in molecular epidemiology, antimicrobial resistance. I have been building my expertise in Next generation sequencing for bacteriology three years later. I get experienced for different NGS platforms (Illumina, Oxford Nanopore, MGI), with strong troubleshooting mind. Bioinformatics analyses of NGS data using different linux based tools. I supervise master student, train technicians. My dream is to become an expert in my domain, learn more and to build an exceptional researcher.

Recent Publications:

1. Prevalence of Molecular Mechanisms of Carbapenem Resistance in Pseudomonas aeruginosa clinical isolates from Saudi Arabia

2. Molecular Characterization of Carbapenemase Producing Acinetobacter Baumannii and Pseudomonas aeruginosa from Tertiary Care Hospitals in Mecca - Saudi Arabia

3. Draft genome and description of Chryseobacterium phocaeense sp. nov.: a new bacterial species isolated from the sputum of a cystic fibrosis patient