

Microbiology & Applied Microbiology

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How genomic databases aid clinical mycobacteriology

Alina Minias

Polish Academy of Sciences, Poland

The introduction of high-throughput sequencing allowed for the sequencing of thousands of bacterial strains around the globe. We can currently look into the diversity of genomic composition of bacteria with great detail and on a large scale. We can analyze all mutations present in the entire bacterial genome, and we can do that with many strains. Data availability allows for bacterial population-based studies. We can use large genomic databases to identify DNA sequences that mark specific lineages, important from the clinical point of view. Further, we can analyze the variability of DNA sequences to estimate the level and the direction of evolutionary selection. Such information is valuable to indicate proteins essential for bacterial survival that can

be targeted for antibiotics or indicate mutations possibly involved in the generation of drug resistance. Finally, genomic databases provide a holistic view of the bacterial population's composition, drawing meaningful conclusions regarding epidemiology and pathogen transmission. All in all, genomic databases broaden our understanding of bacterial population structure and allow better control of circulating pathogens.

Speaker Biography

She is a Polish molecular biologist, currently she is working as a research assistant in the department of teacher training and biodiversity studies Poland.

e: alinagorna@gmail.com