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Impact of next generation sequencing formats on microbial genomics

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Abstract

The availability of multiple, massively parallel, high throughput sequencing systems has revolutionized the field of microbial genomics. The capability to rapidly sequence whole genomes at low cost has had a tremendous impact on rapid identification of novel emerging pathogens, on tracking disease outbreaks and in fostering new discovery.

In this presentation we will present data on the sequencing of multiple organisms that (i) led to the rapid detection of strain specific polymorphisms in *Bacillus anthracis* and *Yersinia pestis,* (ii) enabled comparative genomic analysis and defined genome evolution in *Listeria spp*, and *Cronobacter spp,* (iii) revealed the diversification of virulence factor content and host adaptation in subpopulations of *Salmonella spp.,* (iv) helped in tracing outbreaks, (v) enabled the study of parallel acquisition of bacteriophage at Shiga toxin phage insertion sites during the evolution of the E.coli O157:H7 lineage and (vi) resulted in rapid assay development to monitor novel pathogen outbreaks potentially enabling better patient management and health outcomes.

These data sets strongly support the need to introduce NGS systems into the study of comparative genomics, outbreak investigations and diagnostics.

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