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The DNA sequencing revolution as an important singularity

Advances in DNA sequencing, based upon massively parallel sequencing, has resulted in dramatic advances in DNA sequence output in the past few years. It is now possible to generate tera-bases of accurate DNA sequence with a single run on several DNA sequencing platforms. This has then made it possible to characterize alterations that occur during cancer development. Genomic alterations can be characterized by targeted sequencing of genes that are frequently altered during cancer development, by sequencing of the entire exome, transcriptome sequencing, and even by whole genome sequencing. Each of these has their own inherent strengths and weaknesses. This talk will describe why I believe that the best strategy for moving forward for the management of cancer patients is whole genome sequencing (WGS). This can currently be done reliably and inexpensively on two competing platforms. The first is the Illumina sequencing platform and the second is from BGI. WGS is a comprehensive technology that can detect all the alterations in a cancer genome and will also describe how and why this may prove to be the best approach for the management of cancer patients.

Biography

David I Smith is the Chairman of the Technology Assessment Group for the Mayo Clinic Center for Individualized Medicine. He is an expert of advanced DNA sequencing methodologies and how to use these to study the molecular alterations that occur during cancer development. His research focuses on the different roles that *Human papillomavirus* plays in the development of different cancers. His group also studies genome instability during cancer development and the role that the common fragile sites plays in this.

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