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THE DNA SEQUENCING REVOLUTION AND ITS' IMPACT ON CLINICAL ONCOLOGY

David I Smith

Mayo Clinic Center, USA

Advances in DNA sequencing have improved dramatically over the past 10 years. In 2000 the first draft of the human genome was developed using Sanger sequencing technology. This technology required individual DNA molecules to be cloned into E. coli, and then the resulting amplified fragments were sequenced in microliter sized reactions. The cost for the generation of the first draft sequence of the human genome cost almost three billion dollars. The advent of next generation sequencing based upon massively parallel sequencing utilized PCR-based methodologies to amplify DNA fragments and dramatically decreased reaction volumes into the picoliter range. While the first next generation sequencer was capable of 20 million base pairs of sequence per run subsequent sequence technologies were capable of much greater sequence outputs. The Illumina DNA sequencers have now increased sequence output from one billion base pairs to over 6 trillion base pairs of sequence per run. In my presentation I will describe the different next generation sequencing platforms and discuss their strengths and weaknesses. I will further describe the different types of sequencing that can be performed on these platforms and how this will totally transform clinical oncology in just the next few years. These technologies enable true personalized cancer treatment and this will completely change how we can prevent cancers, detect them earlier and also treat each individual patient with cancer.

Recent Publications

1. Gao G and Smith D I (2015) Mate-pair sequencing as a powerful clinical tool for the characterization of cancers with a DNA viral etiology. Viruses 7(8):4507-4528.
2. Gao G and Smith D I (2016) Role of the common fragile sites in cancers with a human papillomavirus etiology. Cytogenetic and Genome Research 150(3-4):217-226.
3. Gao G and Smith D I (2016) Human papillomavirus and the development of different cancers. Cytogenetic and Genome Research 150(3-4):185-193.
4. Gao G and Smith D I (2015) WWOX, large common fragile site genes, and cancer. Experimental Biology and Medicine (Maywood) 240(3):285-295.

Biography

David I Smith received his PhD in Biochemistry from the University of Wisconsin in Madison in 1978. His first academic position was at Wayne State University School of Medicine and in 1996 he moved to the Mayo Clinic as a Professor in the Department of Laboratory Medicine and Pathology. He is also the Chairman of the Technology Assessment Group for the Mayo Clinic Center for Individualized Medicine. His laboratory utilizes next generation sequencing to study the different ways that human papillomavirus can cancer in different tissues. His group also studies the common fragile sites which are regions of profound instability found in all individuals.

smith.david@mayo.edu