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The history and future of massively parallel sequencing

David I Smith

Mayo Clinic, USA

Abstract

The present study was undertaken to develop Vitamin D and Calcium rich products using different cooking techniques. Products were prepared using Sundried Mushroom Powder; Ragi Flour, The development of technologies to sequence millions and ultimately billions of individual DNA molecules simultaneously has been called next generation sequencing (NGS). A much better term, however, would be to call it what it is, which is massively parallel sequencing (MPS). The advances in MPS have been phenomenal and in the past 13 years the output on MPS platforms has increased from 20 megabases per run to now over 7 terrabases. First generation MPS is based upon the amplification of individual molecules prior to sequence interrogation. The output and accuracy of these platforms has been outstanding, at the sacrifice that only short DNA molecules could be analyzed. Second generation MPS is based upon sequencing individual molecules which is now capable of analyzing molecules that are hundreds of thousands of base pairs long. However, this comes at the sacrifice of output and sequence accuracy. With both first and generation MPS platforms it is now possible to sequence entire genomes, exomes, targeted genomic regions, and even genome-wide methylation. In my talk I will summarize the history of different MPS platforms and then discuss where we are today and where we should be in the next few years. MPS technologies have the capability of changing how we both look at genomes and ourselves.

Biography:

David I Smith completed his Ph.D. at the age of 23 from the University of Wisconsin in Biochemistry, and had postdoctoral training at the University of California, Irvine. He is a Professor in the Department of Laboratory Medicine and Pathology at the Mayo Clinic and the Chairman of the Technology Assessment Group. He has published over 200 papers in peer reviewed journals. He works on studying the different ways that HPV is involved in the development of cancers.

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