David L Perkins, Transcriptomics 2016, 4:2(Suppl)
http://dx.doi.org/10.4172/2329-8936.C1.008

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Microbiome functions identified by the metatranscriptome

The human microbiome plays an important role in regulating human health and disease. Previous studies have relied on 16S rRNA amplicon and shotgun metagenome sequencing to investigate the bacterial composition of the microbiome. These approaches provide a taxonomic assignment that is used to predict microbial functions based on known genome sequences. Here we report an extremely deep shotgun sequencing and comparative analysis of the human fecal microbiome using metatranscriptomics and metagenomics. In our previous study, we analyzed the human fecal microbiome using a shotgun metagenomic approach, and in the present study we compiled a total of 139.6 million reads using multiple sequencing methods and platforms. Specifically, after establishing the reproducibility of our methods with extensive multiplexing, we compared the metagenome and metatranscriptome with following parameters: 1) the Illumina HiSeq versus MiSeq platforms, 2) the sequence reads versus *de novo* assembled contigs, and 3) the effect of shorter versus longer reads. Interestingly, our analysis identified differential expression of bacterial genes indicating over- and under-represented bacterial functions in the fecal microbiome.

Biography

David L Perkins is a MD, PhD who is currently a Professor of Medicine at University of Illinois at Chicago. He obtained his PhD in Immunology and is also a Practicing Kidney Transplant Nephrologist. His current research focuses on the role of the microbiome in immunosuppressed subjects. He has published more than 100 papers in reputed journals, serves on numerous editorial boards and has been a standing member of a NIH study section.

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