Late breaking abstract

MEM : New Topic Name (Workshops name)
Microbiomes

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Advantages of RNA-Seq over DNA-Seq in Microbiome Analysis

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Objectives: Antibodies against fungi are associated with many idiopathic chronic conditions including psoriasis, Crohn's disease, multiple sclerosis, ankylosing spondylitis, and reactive arthritis. These conditions also exhibit elevated IL-17, a cytokine necessary for the control and clearance of fungal infections (Delsing, 2012). Minute amounts of fungal antigens induce a robust Th17 immune response (Marijnissen, 2012). For testing the hypothesis that these conditions could be caused by a fungal infection, the detection of low abundance fungal cells in clinical specimens is therefore of critical importance.

Methods: Although consensus PCR of ribosomal DNA has traditionally been used for this purpose, next-generation sequencing of Total DNA and RNA provides a more sensitive low-bias assessment of the human microbiome. As a proof of concept, we applied this technique to prostate specimens using the Illumina HiSeq 4000 sequencer and the Leif bioinformatics toolkit (Laurence, 2014).

Results: Genbank sequences annotated with the wrong taxonomic label required significant manual curation (Laurence, 2014), especially for the RNA-Seq results. Though the sensitivity of DNA-Seq and RNA-Seq was similar, only RNA-Seq allowed the taxonomic classification of novel species present in these specimens: DNA-Seq reads from novel species were too divergent to be aligned with reference nucleotide sequences, whereas RNA-Seq reads were much less divergent, especially ribosomal RNA reads.

Conlusion: Total RNA-Seq is an excellent microbiome analysis technique for human clinical specimens. Unlike Total DNA-Seq, it allows taxonomic classification of reads from novel or unknown microbes, a critical feature for microbiome research projects. Unlike consensus PCR, it can detect all microbes, not only those matching the chosen consensus primer sequences.

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