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XIVe Congrès international de bactériologie and Applied Microbiology | XIVth Congrès international de mycologie et microbiologie eukaryote | XVIth Congrès international de virologie

ABSTRACTS
RÉSUMÉS

CSM SCM Canadian Society of Microbiologists / Société canadienne des microbiologistes

NRC·CNRC

Organized with the Canadian Society of Microbiologists and the National Research Council of Canada
Organisé avec la Société canadienne des microbiologistes et le Conseil national de recherches du Canada

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Poster Session

MEM-PM3007 - Prostate microbiome analysis using unbiased high-throughput sequencing

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Recent advances in prostate cancer research indicate that a fastidious fungus could be infecting the prostate and causing prostate cancer (Sutcliffe, Sfanos, De Marzo et Laurence, 2014). Many medically important fastidious fungus species remain to be discovered (Ghannoum et al, 2010; Paulino et al, 2008; Findley et al, 2013), and substantial evidence indicates that one such species is causing the chronic prostate inflammation which affects over 80% of American men by age 75. Detecting medically important fastidious fungi such as Pneumocystis jiroveci or Encephalitozoon cuniculi in clinical specimens is very challenging. These two species asymptomatically infect a substantial fraction of the population; they do not grow in commonly used culture media, and commonly used consensus PCR primers fail to amplify their ribosomal DNA. The advent of high-throughput sequencing technology has enabled a new microbe detection technique coined “unbiased high-throughput sequencing” (Lipkin 2010). This technique does not use consensus PCR primers, thus can detect all microbes in clinical specimens, including those whose ribosomal DNA region has substantially diverged from related species. We applied this technique to prostate specimens using the Illumina HiSeq 2500 sequencer and the Leif bioinformatics Toolkit, revealing novel sequences which may be originating from a microbe etiologically related to prostate cancer. This systematic microbe detection technique can be applied to other types of clinical specimens, and can detect both known and novel species of bacteria, fungi, protists and viruses. As high-throughput sequencing becomes more affordable, this technique will be widely used in the detection of microbes in clinical specimens. Most importantly, this technique may reveal an infectious etiology for idiopathic chronic inflammatory diseases such as benign prostatic hyperplasia (BPH), chronic prostatitis (CP/CPPS), non-specific urethritis (NSU), reactive arthritis (ReA), ankylosing spondylitis (AS) and prostate cancer.