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Journal of Pharmacogenomics & Pharmacoproteomics

Bioinformatics approach to profile oral and gut microbiome in colitis

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Abstract

Advances in bioinformatics and high-throughput sequencing technologies have significantly increased our capability to explore the human microbiome. 16S ribosomal RNA (rRNA) is sequenced to understand the taxonomic composition of the human microbiome. In this study, bioinformatics analysis of 16S rRNA sequenced data from diseased (Crohn's Colitis (CC) or Ulcerative Colitis (UC)) and adjacent healthy colon samples was performed by using Quantitative Insights Into Microbial Ecology (QIIME). Further, considering the race-specific information for these samples, a comparison of colon microbiome differences between African-Americans and Caucasians was performed. As a result, two hundred-eight different bacterial species were characterized. However, only fifty-three bacteria were described at the species level. The fraction of non-detrimental bacteria in diseased CC and UC samples was different from adjacent healthy colon samples. Additionally, the microbiome of diseased samples was dominated by oral bacteria belonging to the Phyla Firmicutes (Streptococcus, Staphylococcus, Peptostreptococcus) and Fusobacteria (Fusobacterium). The results also showed differences in the microbiome between African-Americans and Caucasians, indicating potential research focus on health disparities.

Biography

Sammed Mandape build bioinformatics solutions that drive scientific research. Currently, he is invested in analyzing massive human genome data, both nuclear and mitochondrial, to identify unique DNA fingerprinting markers to help advance forensic science. His bioinformatics experience includes analyzing and interpreting NGS/ MPS data, developing bioinformatics tools, administering system architecture that support bioinformatics operations and everything else in between. Areas he works in: Forensic Bioinformatics, Cancer Research, Infectious Diseases, Human Microbiome Profiling, Metabolomics.