Tong Zhang, J Proteomics Bioinform 2013, 6:7
http://dx.doi.org/10.4172/0974-276X.S1.069

OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference on
Proteomics & Bioinformatics
July 15-17, 2013 Courtyard by Marriott Philadelphia Downtown, USA

The applications of metagenomics and metatranscriptomics in biological wastewater treatment

Tong Zhang
The University of Hong Kong, China

High-throughput sequencing is being widely applied in various biological studies, including wastewater treatment. This presentation mainly summarizes its applications in multiple aspects of biological wastewater treatment using the case studies conducted at Environmental Biotechnology Laboratory in Department of Civil Engineering, The University of Hong Kong. Section I introduces bacterial diversity of activated sludge taken from 14 wastewater treatment plants (WWTPs), profile of major functional groups, and primer evaluation, based on 454 pyrosequencing platform. Section II presents the major nitrification groups and processes revealed using Illumina metagenomics approaches. Section III discusses the antibiotics resistance genes identified using high-throughput sequencing. Section IV reveals seasonal variation of microbial communities for 4 years in a WWTP and the correlations of bacterial populations with operational and environmental factors. Section V shows expression of nitrification/denitrification genes using the combined metagenomic and metatranscriptomic approaches. Section VI demonstrates mining of cellulose-conversion genes from the assembled ORFs from metagenomic data. Section VII displays the draft genome of an isolated Bacillus species assembled from metagenomic data.

Biography

The researches of Zhang (Associate Professor) are mainly on applications of environmental bioinformatics, including metagenomics, metatranscriptomics, proteomics, etc., in studies of biological wastewater treatment (N removal and P recovery), bioenergy from wastewater/wastes (cellulosic biomass, sludge, kitchen waste), biodegradation of emerging pollutants (antibiotics, PPCP and EDCs), antibiotic and heavy metal resistance genes, and environmental toxicology of nanoparticles and metals to microorganisms. He has an H Index of 23 with >110 SCI journal publications and 1700 citations. He serves as Advisor for BGI (Beijing Genomics Institute) on Environmental Microbiology and Biotechnology, and ASM (American Society of Microbiology) Country Liaison to China.