

# 2<sup>nd</sup> International Conference on **Oceanography**

July 21-23, 2014 Hampton Inn Tropicana, Las Vegas, USA

## Single-cell gene expression analysis: Technologies and application

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Recent studies showed even isogenic populations of exponentially growing microorganisms carrying substantial cell-to-cell heterogeneities at both cellular and molecular levels that are an order of magnitude greater than previously thought. It is increasingly recognized that by using averaged molecular or phenotypic measurements of a whole population for describing cell behaviors, conclusions could be biased as the unique patterns related to specific or distinct functional sub-populations cannot be revealed. Recent progress in developing single-cell based technologies for gene expression analysis in single cells, including the first bacterial single-cell RNA-seq method for the whole transcriptome of single cyanobacterium cells which contain 5~7 femtogram total RNA per cell will be reported. The results provided evidences for significant gene-expression heterogeneity between single cells, and that the heterogeneity seems affected by the environmental stress conditions.

### Biography

Weiwen Zhang is a Professor of Microbiology and Biochemical Engineering, Head of Laboratory of Synthetic Microbiology in the School of Chemical Engineering and Technology of Tianjin University in China. Prior to joining Tianjin University, he was a faculty with Biodesign Institute and the School of Life Science of Arizona State University for 2007-2011 and a senior scientist at Microbiology Department with the Pacific Northwest National Laboratory of the U.S. Department of Energy (DOE) for 2002-2007. He has broad research experience in microbial genetics, physiology and synthetic biology, has authored more than 110 peer-reviewed scientific papers. His recent research focuses on synthetic biology of photosynthetic microorganisms and analysis of microbial consortia.

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