conferenceseries.com

conferenceseries.com
1406th Conference

3rd International Conference on

Transcriptomics

October 30-31, 2017 Bangkok, Thailand

e-posters

Walid Tawfik et al., Transcriptomics 2017, 5:3 (Suppl)
DOI: 10.4172/2329-8936-C1-016

Laser spectroscopic applications in cancer nanotechnology

Walid Tawfik and Yehia Badr
Cairo University, Egypt

In recent years, several techniques have been applied since the "war on cancer" was pronounced. Advanced laser spectroscopic methods for creating and controlling specific nanoparticles have been performed to treat and diagnose cancer cells. Numerous laser based spectroscopic methods have been applied to identify breast cancer like; Laser-induced fluorescence, laser Raman scattering and laser photoacoustic spectroscopy. Aside from individual differences that result in normal variations in lipids and glycogen, a clear distinction between normal and malignant tissues can be observed. The obtained absorption spectra were observed using FTIR-Raman Spectrometer technique from different samples of breast tumors with normal spectra reveals very important features that can be applied as diagnostic techniques. The results of the applied methods are comparable with the conventional techniques like biopsy etc. Laser irradiation methods were applied to sensitize and control nanoparticles propertied which are needed for treatment of cancers. The observed results will be used to improve the prospective methods to study how nanoparticles can be used as molecular imaging agents to detect and monitor cancer progression in future.

Recent Publications

References

1. Husseiny M I, M Abd El-Aziz, Y Badr and M A Mahmoud (2007) Biosynthesis of gold nanoparticles using Pseudomonas aeruginosa. Spectrochimica Acta Part A: Molecular and Biomolecular Spectroscopy; 67(3): 1003-1006.

2. Badr Yehia A and Salah Eldin I HassabElnaby (2004) Raman, mid and NIR FTIR absorption spectra of breast cancer reveal a good diagnosis tool. Biomedical Optics; 78-88.

Biography

Walid Tawfik, is Egyptian associate Professor, in laser spectroscopy and ultrafast lasers at the National Institute of Laser (NILES), Cairo University, Cairo, Egypt. In 1994 he joined NILES as staff member and promoted as assistant lecturer, assistant professor and associate Professor in 1996, 2000 and 2008, respectively. He has received the BSC, Master and PhD degrees in physics, laser physics and laser spectroscopy in 1992, 1996, 2000, respectively, from Cairo University, Egypt. He is interested in the field of ultrafast lasers and ultrafast phenomenon.

walid_tawfik@hotmail.com

Notes:

Zainab Khanum et al., Transcriptomics 2017, 5:3 (Suppl)
DOI: 10.4172/2329-8936-C1-016

Analysis of up-regulated gene families during Langra mango (*Mangifera indica L.*) fruit development

Zainab Khanum, Atta-ur-Rahman, M Iqbal Choudhary and M Kamran Azim
University of Karachi, Pakistan

Langra mango fruit is the export quality variety of Pakistan. This variety is well known for its taste and aroma. Much of the transcriptomics work has been conducted on the ripening physiology of the mango fruit but there has been less focus on the mango organogenesis. To better understand the temporal and spatial dynamics during the mango fruit's development, the plant's developmental genetics approach was followed. This approach involved mRNA sequencing by using the SOLiD 5500™ Genetic Analyzer platform. De novo transcriptome assembly and de novo transcript quantification was carried out for eight different developmental stages of a Langra mango fruit by using SATRAP assembler pipeline and RSEM, respectively. BLASTx program for NCBI nr-database, KAAS and BlastKOALA tools were used for gene functional annotation and metabolic pathways identification. Simple sequence repeats in transcripts were identified by GMATA software. This revealed a repertoire of up-regulated gene families during development with no prior literature support. Around ten gene families are enriched during the Langra mango fruit's development. Up-regulated genes involved in plant's development, embryogenesis and immune response were classified, especially the GIGANTEA (GI) nuclear protein gene. GI gene is climate and photoperiod regulated and is a key player in plant's circadian clock control, flowering time regulation, drought tolerance and salt tolerance. Up-regulated gene products were also classified which are responsible for ROS control and have nutraceutical properties including defense against cancers and human pathogens. The Langra mango fruit's developmental transcriptome was also compared with the mango transcriptomes from Pakistan, China and Mexico.

Recent Publications

References

1. Azim MK, Khan IA, Zhang Y (2014) Characterization of Mango (Mangifera indica. L) transcriptome and chloroplast genome. Plant Molecular Biology; 85 (1-2):193-208.

2. Velu Sivankalyani and Noam Alkan et. al. (2016) Transcriptome Dynamics in Mango Fruit Peel Reveals Mechanisms of Chilling Stress. Frontiers in Plant Science.

3. Joanna M, Abril I and Richard D. Emes (2015) Assembly, Assessment, and Availability of De novo Generated Eukaryotic Transcriptomes. Front Genet.; 6: 361.

4. Van Schie CC and Takken FL (2014) Susceptibility genes 101: how to be a good host. Annual Rev Phytopathol; 52:551-81.

5. Kerstin K, Alice P and Gerco C (2010) Regulation of transcription in plants: mechanisms controlling developmental switches. Nature Reviews Gene; DOI:10.1038/nrg2885

Biography

Zainab Khanum has her expertise in transcriptomics. Her research interests include developmental genetics and human cancers related functional genomics. She is a Biotechnology graduate from University of Karachi, Pakistan. She is currently enrolled in PhD program at International Center for Chemical and Biological Sciences, University of Karachi, Pakistan. She has expertise in manual extraction of high quality total RNA, next generation mRNA sequencing and bioinformatics. She looks forward to conduct her future research on projects that will benefit the health sector, agriculture sector and economy of her country.

zainab12khanum@gmail.com

Notes:

conferenceseries.com

conferenceseries.com
1406th Conference

3rd International Conference on

Transcriptomics

October 30-31, 2017 Bangkok, Thailand

Accepted Abstracts

conferenceseries.com

Transcriptomics 2017, 5:3 (Suppl)
DOI: 10.4172/2329-8936-C1-016

RNA-seq data analysis for bacterial transcriptomics

Yahaya Yabo, P Monsieurs and N Leys
Universiteit Brussel, Belgium

The advent of high-throughput sequencing technologies has played a significant role in the transition of biomedical research from *in vivo* to *in silico* approach. RNA-seq has emerged as one of the technologies used in the analysis of all RNA populations found in a cell or group of cells and effectively dominating the existing methods used such as the microarray technology. Several tools have been recommended for the analysis of mostly eukaryotic RNA-seq data to determine differentially expressed genes under varying conditions or treatment groups. However, up until now no consensus has been reached on the best analytical tool/tools to adopt in the analysis, especially for bacterial RNA-seq data analysis. This work systematically compared different combinations of alignment algorithms and differential gene expression analytical tools with the aim of selecting the best alignment and differential gene expression tools that will improve the process of analyzing bacterial RNA-seq data to determine most of the differentially expressed genes under different experimental conditions with high accuracy. As a proof of concept for benchmarking the selected tools, we used real-life, paired-end and RNA-seq reads of 150 nt length obtained from sequenced libraries of *Cupriavidus metallidurans* (NA4 strain) using Illumina HiSeq 2000 platform. The evaluated alignment algorithms showed comparable performance in aligning reads to the reference genome. Among the tested tools for differential gene expression analysis, edgeR detected more number of genes while DESeq2 was found to be more stringent and tends to prevent some low expressed genes with fold changes around the cut-off to be considered as differentially expressed genes, as such lowering the number of false positive detections. We propose base on our benchmarking results a pipeline for the analysis of RNA-seq data for bacterial transcriptomics.

yahaya.yabo@udusok.edu.ng

Transcriptomics 2017, 5:3 (Suppl)
DOI: 10.4172/2329-8936-C1-016

Integrative network analysis reveals novel insights of disease mechanisms

Jun Zhu
School of Medicine at Mount Sinai, USA

There are multiple ways to perturb key pathways leading to disease initiation andprogression. Large scale genetic/genomic studies have been conducted to uncover driver events of diseases such as germline or somatic mutations, gene fusion or translocations, methylation or other epigenetic changes, copy number alterations, gene expression changes. However, molecular mechanisms through which these driver events lead to diseases are not clear in most of cases. We developed methods to leverage multiple data types available in the studies. We previously developed an analytical procedure, Reconstructing Integrative Molecular Bayesian Networks (RIMBANET)

(1), to reveal pathways linkingcausal events to disease phenotypes. This integrative approach has been successfully used in dissecting causal relationships in complex human diseases such as diabetes and obesity, cardiovascular disease, neurodegenerative diseases, and multiple types of cancers including breast cancer, hepatocellular carcinoma, prostate cancers

(2). We showed that integration of diverse types of data with gene expression data can improve network accuracy with the directed network representing biologically meaningful causal relationships as opposed to sheer statistical relationships. We also showed that activities of functional units

(3) (such as subnetworks) are more robust in predicting disease progression (4) or more important in understanding multiple genes and pathways interactions regulating progression of complex diseases.

jun.zhu@mssm.edu

Notes: