Medical Biochemistry

Integrative pipeline to identify potential long non coding RNA-Associated competing endogenous RNA and its implication in hepatocellular carcinoma cells
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Background: Circulating transcriptome plays a crucial role in hepatocellular carcinoma (HCC) development and progression.

Method: First, utilizing bioinformatics tools, we selected an HCC-specific RNA-based biomarker panel including; glucose autophagy-associated (SOGA1) mRNA with long non-coding RNA antisense for X-inactive-specific transcript (lncRNA-TSIX) and microRNA-548-a-3p. Second, we attempted to validate these biomarkers using the sera of HCC versus control by qPCR.

Results: The RNA-based biomarker panel exhibited excellent sensitivity and specificity in differentiating HCC patients from controls.

Conclusion: The chosen circulatory RNA-based biomarker panel has potential role in HCC pathogenesis.

CRISPR: a promising tool for treatment of cancer
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CRISPR (clustered regularly interspaced short palindromic repeats) are specific repeated bacterial DNA sequences that originally identified in bacteria and archaea. CRISPR systems are involved in bacterial adaptive immunity against invading viruses. Natural and engineered CRISPR systems are recently utilized as gene-editing tools. Based on CRISPR RNA/target DNA interaction, it is highly-specific, flexible gene-editing tool. In addition, it is relatively fast and cheap and does not require special expertise. Optimizing of several technical parameters including custom design of guide RNA and delivery method of the system is, however, essential for increasing the efficiency of CRISPR system and solving the notable limitation of off-target DNA cut.

Promising CRISPR application’s list is rapidly expanding including but not limited to performing cutting-edge biomedical research, treatment of genetic diseases, and treatment of cancers. There is an actively running clinical trial for treatment of lung cancer in China and a US-approved clinical trial for treatment of multiple myeloma, sarcoma and melanoma to be conducted soon during early 2018.

There is an urgent need to establish and regularly update the legal and ethical standards for basic and preclinical CRISPR-based research on the expression of human genes, and the use of the technique in somatic cells for clinical applications; and with some restrictions, in germ-line cells or embryos, at least until adequate information would be available on its safety.

Applied bioinformatics in medical research
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Large and fast steps had been moved on through the area of Bioinformatics “the use of computers to collect, analyze, and interpret biological information at the molecular level”. In this presentation, we will focus on how to use bioinformatics tools to develop a project for Medical research, based on an integrative approach of using several bioinformatics resources together with experimental laboratory validations of the interplay of the genomic information. We will learn How to retrieve Disease related genes and their regulatory noncoding-RNAs from different databases, which represent an organized collection of tremendous amount of stored sequence information accumulating worldwide. Such in silico data; is based on previous microarray studies that integrated both the information gained from microarray gene expression profiling of protein-coding genes and the noncoding RNAs profiling.

The presentation is concerned of Liver cancer which represents nearly 6% of the global cancer incidence and represents the second most common cause of cancer related death worldwide. Novel accurate strategies for early detection of hepatocellular carcinoma (HCC) and hence better treatment are strongly needed. This could rely on studying the cancer transcriptome (coding and non-coding) which plays a critical role in HCC.

First, we will retrieve HCC related genes from different data bases as; Oncogenic database of HCC. OncoDB.HCC, CellMinerHCC are databases of microarray expression profiles of different HCC cell lines. To enhance the data reliability, we will verify the expression of the chosen gene in HCC by searching the Cancer Genetic web, The Cancer Genome Atlas (TCGA), Gene Atlas, Protein Atlas and Gene atlas databases.

This will be followed by a pathway enrichment analysis of the chosen genes using the Reactome Pathway database, the KEGG pathway and the Genemania database to explore the role of the target gene in special biological process categories involved in carcinogenesis, e.g. enrichment for cell cycle, angiogenesis, apoptosis, cell proliferation and cell adhesion. Finally, we will start to identify the target gene and its regulatory noncoding RNAs association, first, miRNA-Target interactions; by retrieving data from microRNA.org - Targets and Expression, mir2disease.org and mirWalk databases. As regard the identification of lncRNAs that act as epigenetic regulator of the Target gene we will access the database of lncRNA acting as competing endogenous RNA (Inceldb), IncRNA and disease database and for more verification we will search the IncRNome knowledge database. Furthermore, for circular RNAs associated with the chosen gene we will go through the CircInteractome database and Cancer specific circular RNA data base: a database for cancer-specific circular RNAs.