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ECG sequence analysis using pseudo-DNA structure

Yan Ji
Yunnan University, China

ECG signal is the important basis of clinical detection of cardiovascular disease. Technology by ECG measurement equipment to get the ECG data for a long period of time has been formed specification but analysis method of the mass ECG data is still the research front and it has actual demand. Model of introduced in this report using pseudo-DNA structure to deal with ECG data can transform the time series of 1D into of the visualize result of 2D. Using the normal and abnormal ECG signal from the different measuring profile can be compared formation distribution differences between normal ECG and abnormal ECG sequence intuitively and reached to show the distribution state of normal ECG and abnormal ECG from the macro graphical distribution level.

kunmingjy@sina.com

Assessment of circulating microRNAs biomarkers for colorectal adenocarcinomas in Saudi patents by next-generation sequencing

Mourad A M Aboul-Soud, Yazeed Al-Sheikh, Khaled K Al-Harbi, Hazem K Ghneim and Alaa Al-Bzour
King Saud University, Saudi Arabia

Colorectal Cancer (CRC) is the third most common cancer disease worldwide. In the year 2005, the population of the Kingdom of Saudi Arabia was estimated at 16,945,484, composed mostly of native Saudis (62%). In that same year, the Saudi Cancer Registry, reported that CRC was the second most common malignancy among Saudis for all ages (10.3%) and the number one malignancy in males (11.8%). It has been predicted that by the year 2030, that the CRC incidence in Saudi Arabia would increase fourfold in both genders. Hence, more in-depth efforts on the molecular basis of CRC are warranted. MicroRNAs (miRNAs), a novel class of small non-coding RNAs, are effective post-transcriptional regulators of gene expression with a critical regulatory function acting as an oncogene or a tumor-suppressor gene. However, the diagnostic value of miRNAs has not been fully explored. This study is aimed at the discovery of novel miRNA biomarkers via the use of a high-throughput Next-Gen Illumina-based sequencing strategy; thus enabling a comprehensive survey of all novel and differentially-expressed miRNAs in CRC tissues and plasma as compared to healthy controls. Subsequently, the level of expression of potential miRNA markers will be validated by real-time PCR and their key miRNA target genes will be identified by gene the ontology analysis. Next, miRNAs that are significantly dysregulated (i.e. down-regulated and up-regulated) will be identified, whereby enabling the identification of some of the bonafide miRNAs regulators in colorectal adenocarcinomas. The outcome of this study will extend our current knowledge on miRNA dysregulation in the CRC. As such, the results will pave the road towards the robust validation of potentially novel circulating miRNAs biomarkers for early and minimally-invasive diagnosis of CRC.

maboulsoud@ksu.edu.sa