Potential microRNAs for early diagnostics of hepatocellular carcinoma (HCC) in human

Nguyen Bao Quoc[1*], Nguyen Thai Anh Thu[1], Nguyen Doan Nguyen Phuong[1],
and Nguyen Ngoc Bao Chau[2]

[1]Research Institute for Biotechnology and Environment, Nong Lam University,
Ho Chi Minh City, Vietnam
[2]Faculty of Biotechnology, Ho Chi Minh City Open University, Vietnam
[*]Corresponding author, E-mail: baoquoc@gmail.com

Abstract

In the present, studies of the roles of microRNAs (miRNAs) in hepatocellular carcinoma (HCC) have either focused on specific individual miRNA and a few suspected targets or simply reported a list of potential miRNAs based on expression profiling. In this study, the authors investigated a more in-depth understanding of the roles of miRNAs and their targets by using bioinformatic tools to screen miRNAs as potential biomarkers for early diagnosis of HCC. Datasets were collected from Gene Expression Omnibus (GEO database) by keywords: "human hepatocellular carcinoma microRNA." There were four datasets selected, including GSE62044 (combine GSE62007 and GSE62043), GSE74618, GSE21362, and GSE10694. The authors assessed the level of mature miRNAs in all datasets with more than 1,000 miRNAs and 937 HCC samples of patients in many countries. Statistical analysis indicated that twelve of these miRNAs, which present in all of the datasets, had a significant alteration in the expression level. Seven of these miRNAs (miRNA-221, miRNA-222, miRNA- 224, miRNA-93, miRNA-25, miRNA-106b, and miRNA-155) were up-regulated in HCC while the other five miRNAs (miRNA-34a, miRNA-99a, miRNA-139-5p, miRNA-422a và miRNA-214) were down-regulated. All of them had a relevance to the hallmarks of cancer, such as cell proliferation, differentiation, invasion, metastasis, angiogenesis, metabolism, and immune system. In HCC patients, the portion of surviving and month surviving in query genes, which have modified, is lower than in the case of those not modified. These were evidence supporting the correlation between the levels of miRNA expression and HCC; therefore, they may be considered as biomarkers for early diagnosis of HCC. Furthermore, this could be a list of potential miRNAs to carry out further dept-studies in wet-laboratory.

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