UNIVERSITI TEKNOLOGI MARA

Amplification of microRNA-17 and microRNA-18 sequence from HepG2 Cancer Cell Line

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ABSTRACT

PCR is a rapid and modern technique for amplifying DNA sequences, which is based on the principle of enzymatic replication of the nucleic acids (Staněk, 2013). HepG2 is a human liver cancer cell which develop from chronic diffuse liver disease, other disease like Hepatitis B or Hepatitis C or from other triggers like chronic alcohol consumption, environment or by any harmful chemical.

In HepG2 cancer cell, there is an over expression of miRNA-17 and miRNA-18 which enhance the migration and proliferation of the liver cancer cell (Sun et al., 2013). The present study was conducted to determine whether the sequence of the miRNA-17 and miRNA-18 in the HepG2 cancer cell line can be amplified by using the specific primer. The sequence alignment of miRNA-17 and miRNA-18 could be seen clearly by using BOXSHADED software even though there are two base pair in sequence of miRNA-18 that are different from the original sequence. This is due to the substitution of G to C and point mutation of N. In conclusion, the sequence of miRNA-17 and miRNA-18 of HepG2 cancer cell line can be amplified by using the specific forward and reverse primer.

CHAPTER 1

INTRODUCTION

1.1 Background of study

Over the past few year , many reports showed that miRNAs was differentially expressed in cancer with several studies have shown that miRNAs profiling was highly accurate to classify tumors and predict outcome (Garzon, Fabbri, Cimmino, Calin, & Croce, 2006). Approximately, 500 miRNAs gene identified in human genome important in biological process which have important roles in growth, development , homeostasis and disease (Blenkiron & Miska, 2007). MiRNAs are endogenously expressed, functional RNAs that interact with native coding mRNAs to cleave mRNA or repress translation (Wang & Zhang, 2008).

MiRNAs is small non-coding protein that inhibits gene expression post-transcriptionly. MiRNAs expression profile demonstrated miRNAs deregulated in human cancer which regulate oncogenes, tumor suppressor and number of cancer-related gene controlling cell cycle, apoptasis, cell migration & angiogenesis. MicroRNA-17-92 has oncogenic potential and may act as tumor suppressor some miRNAs & their target site to be mutated in cancer. So, miRNAs has great diagnostic potential for human cancer (Zhang, An, & Teng, 2009).

Most effort is engaged in identifying and investigating the target genes of miRNAs, miRNA gene promoter methylation or transcriptional regulation is another important field of investigation, since these two main mechanisms can form a