Journal of Computational Intelligence in Bioinformatics
ISSN 0973-385X Volume 7, Number 1 (2014) pp. 13-21

http://www.ripublication.com

MicroRNA Profiling for Tuberculosis in Human

Vinupriya, Tanusree Chaudhuri* and Kusum Paul

Department of Biotechnology, The Oxford College of Engineering, Bommanahalli, Hosur Road. Bangalore -560068 Karnataka, India.
E mail: tanushreebioinformaticsoxford@gmail.com
Mobile: 9945122040, 9480739846
Tel.: 080 - 3021 9601 / 02, 3021 9701 / 02 Fax: 080 - 3021 9629
** Corresponding author.*

ABSTRACT

The role of microRNA in the pathogenesis of tuberculosis is the interesting topic in medicine at present. It was proposed that the microRNA can be a useful biomarker for monitoring of tuberculosis and might be the important part in pathogenesis of disease. The identification of new biomarker is one of the most important task in the field of clinical and pharmaceutical research, for the first time we identified the novel marker by doing analysis of microRNA profiling for tuberculosis in Human. In TargetScan database for 57 human gene 135 miRNA for vertebrate, 88 miRNA for mammals and 1186 miRNA for poorly conserved were found and identified, around 1408 miRNA after statistical analysis, the miRNA was divided into three groups high(10 and more then10), medium(3-9) and low(1-2) the graphs (figure 1 to 3) were plotted according to the range. Based on the high range from mammal miRNA we can say more confidently 12 genes (Table1) with high score was identified from miRNA analysis, these are the genes GPR180, GSTM3, RAB6B, WISP1, IGFBP5, FLT1, PALM2-AKAP2, RTN4RL1, TSPYL5, UCHL5, DCK, QSOX2 which can be a good biomarker for tuberculosis. The microRNA part can be detected and this can be important key information in further study of the pathogenesis of tuberculosis.

Keywords: miRNA, tuberculosis, biomarker, TargetScan, vertebrate, mammals, poorly conserved.

1. INTRODUCTION

A microRNA is a small non-coding RNA molecule (containing about 22 nucleotides) found in viruses, which functions in transcriptional and post-transcriptional regulation of gene expression. Encoded by eukaryotic nuclear DNA in animals and plants and by viral DNA in certain viruses whose genome is based on DNA, miRNAs function base-pairing with complementary sequences within mRNA molecules. As a result, these mRNA strands are silenced because they can no longer be translated into proteins by ribosomes, and such complexes are often actively disassembled by the cell ("target degradation"). The human genome may encode over 1000 miRNAs, which may target about 60% of mammalian genes and are abundant in many human cell types [10].

Pulmonary tuberculosis is an important infectious disease. This disease has been known for many years. However, there is no success in control of this disease despite there is a long history of BCG vaccine. The exact molecular pathogenesis of pulmonary tuberculosis is not completely clarified and this is still the myth in medicine. Based on the advanced molecular laboratory at present, some new researches report the importance of microRNA in the pathogenesis of pulmonary tuberculosis. The microRNA could be detected in blood of the patients with pulmonary tuberculosis (1). Li et al. reported that there is a genetic association between pulmonary tuberculosis and SNPs within the corresponding miRNAs (2). Ma et al. found that microRNA helped control innate and adaptive immune responses to tuberculosis by targeting interferon-γ (3). The detected microRNA is relating to the clinical manifestation of disease and can be the biomarker for pulmonary tuberculosis [9].

The first success in clarification that microRNA takes role in pulmonary tuberculosis pathogenesis was published in 2011 (4). Hence, the knowledge on microRNA in pulmonary tuberculosis is very limited. Although it is no doubt that microRNA might be detectable in blood of the patients, it is still not known about its origin. The microRNA might come from the host or pathogen and this is a topic for further studies. The microRNA part can be detected and this can be important key information in further study of the pathogenesis of pulmonary tuberculosis [9].

A bioinformatics study to assess the microRNA within known tuberculosis RNA.

In TargetScan database for 57 human gene 135 miRNA for vertebrate, 88 miRNA for mammals and 1186 miRNA for poorly conserved were found. Around 1408 miRNA were identified after screening, the miRNA was divided into three groups high (10 and more then10), medium (3-9) and low (1-2) the standard graphs were plotted according to the range and there were no overlap found and the high range from mammals miRNA, 240 gene was found and screened . so more confidently we can say that 12 gene (Table 1) with high score was identified. Based on the miRNA analysis these are the genes GPR180, GSTM3, RAB6B, WISP1, IGFBP5, FLT1, PALM2-AKAP2, RTN4RL1, TSPYL5, UCHL5, DCK, QSOX2 which can be a good biomarker for tuberculosis.

2. MATERIALS AND METHODS

2.1. Identification of Human Tuberculosis target: The target genes for human tuberculosis were identified from the Mouse Tumor Biology database having url: http://www.informatics.jax.org/mtbwi/orthologySearch.do;jsessionid=5F45AEEB7E9CCEDFC16D3D81522509F9?sortBy=HumanGS&compare=Equals&reference=94720&asList=true

In this database a total 57 no of genes were reported.

2.2. Identification of human miRNA: The miRNAs were identified from TasgetScanS database having url: http://www.targetscan.org/

2.3. Identification of miRNA for human TB targets: The miRNAs for human tuberculosis target genes were identified by self written perl script. By our method for a total set of 57 no of human genes a total 1408 no of miRNAs were identified.

2.4. Statistical estimation: Different statistical parameter estimation and standard graph were plotted through microsoft excel worksheets.

3. Results And Discussion

3.1. Factors guiding miRNA targeting: From a total set of 57 genes in human we have identified the respective miRNAs from TargetScanS database. In that gene set 57 human gene 135 miRNAs were identified those are reported to be present in vertebrate, 88

miRNAs were identified those are reported to be present in mammals and 1186 miRNA for poorly conserved were found.

The miRNAs which were reported to be present in all three groups when checked throughly, it was found that the miRNAs were repeating most of the time from one gene to other. This repeating pattern of miRNAs indicates that one miRNA can target more than one gene at a time and at the same time one gene can be targeted by many miRNAs. So, we decided to reveal the most important miRNA through the repeating nature of miRNA. For our further study we have taken the three groups separately and studied it throughly.

The identification of new biomarker is one of the most important task in the field of clinical and pharmaceutical research, We for the first time identified the novel marker by doing analysis of microRNA profiling for tuberculosis in Human and identified 1408 miRNA after statistical analysis, the miRNA was divided into three groups high(10 and more then10), medium(3-9) and low(1-2) the graphs (figure 1 to 3) were plotted according to the range. Based on high range from mammal miRNA we can say more confidently 12 genes (Table1) with high score was identified from miRNA analysis, these are the genes GPR180, GSTM3, RAB6B, WISP1, IGFBP5, FLT1, PALM2-AKAP2, RTN4RL1, TSPYL5, UCHL5, DCK, QSOX2 **which can be a good biomarker for tuberculosis**.

4. Acknowledgements

We extend my sincere thanks to the management of The Oxford College of Engineering for their support. We thank our principal Dr. Nagaraj and our HOD Dr. Kusum Paul, Department of Biotechnology for providing necessary resources.

.

5. References:

[1] Guo W, Li JT, Pan X, et al. Candidate Mycobacterium tuberculosis genes targeted by human microRNAs. Protein Cell 2010;1:419-21.

[2] Ma F, Xu S, Liu X, et al. The microRNA miR-29 controls innate and adaptive immune responses to intracellular bacterial infection by targeting interferon-γ. Nat Immunol 2011;12:861-9.

[3] Fu Y, Yi Z, Wu X, et al. Circulating microRNAs in patients with active pulmonary tuberculosis. J Clin Microbiol 2011;49:4246-51.

[4] Ritchie W, Théodule FX, Gautheret D. Mireval: a web tool for simple microRNA prediction in genome sequences. Bioinformatics 2008;24:1394-6.

[5] Ritchie W, Legendre M, Gautheret D. RNA stem-loops: to be or not to be cleaved by RNAse III. RNA 2007;13:457-62.

[6] Griffiths-Jones S, Grocock RJ, van Dongen S, et al. miRBase: microRNA sequences, targets and gene nomenclature. Nucleic Acids Res 2006;34:D140-4.

[7] Sewer A, Paul N, Landgraf P, et al. Identification of clustered microRNAs using an ab initio prediction method. BMC Bioinformatics 2005;6:267.

[8] Wu J, Lu C, Diao N, et al. Analysis of microRNA expression profiling identifies miR-155 and miR-155* as potential diagnostic markers for active tuberculosis: a preliminary study. Hum Immunol 2012;73:31-7.

[9] Somsri Wiwanitkit, Viroj Wiwanitkit. MicroRNA from tuberculosis RNA: A bioinformatics study. J Thorac Dis 2012; 4(3):296-297

[10] Homo sapiens miRNAs in the miRBase at Manchester University

Figures:

Number of miRNA families broadly conserved among vertebrate :

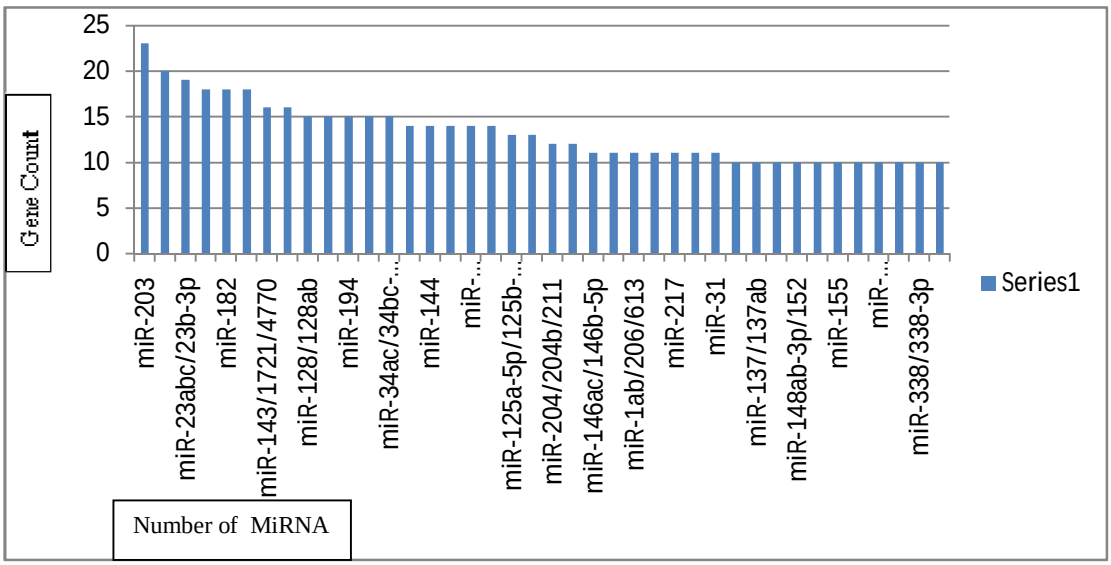

Figure1. The graph shows around 135 miRNA were identified by all the studies, 40 miRNA identified with high score.

Number of miRNA families conserved only among mammals:

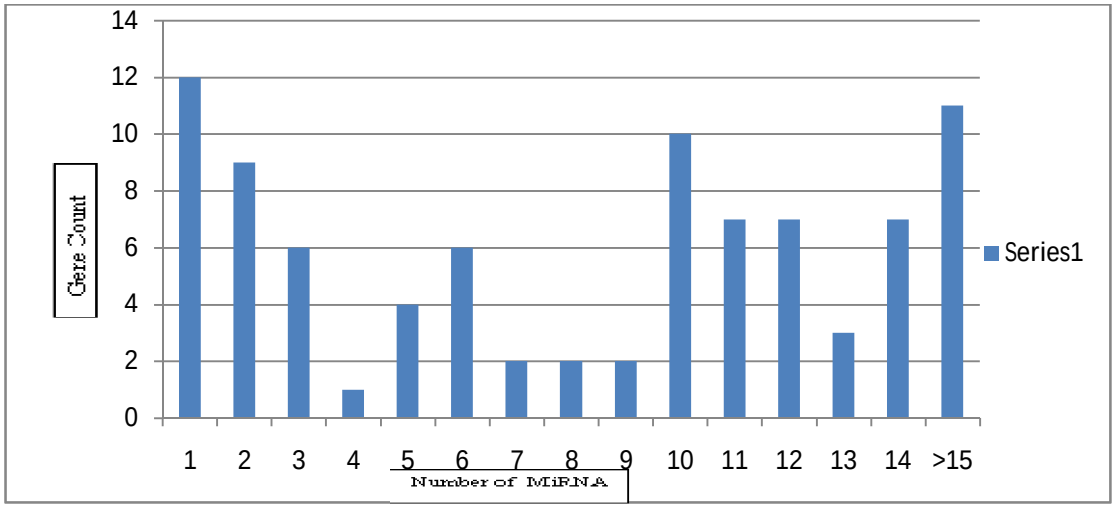

Figure 2. The graph shows around 88 miRNA were identified by all the studies, 44 miRNA identified with high score.

Number of miRNA Poorly conserved miRNA Families:

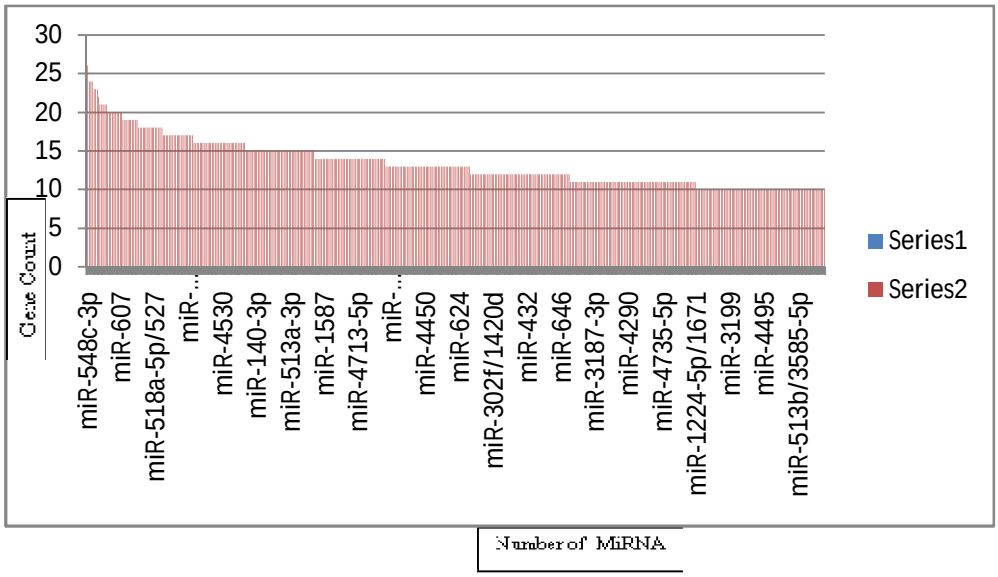

Figure 3. The graph shows around 1186 miRNA were identified by all the studies, 480 proteins identified with high score.

Table 1: This table shows the details of 47 gene from which 12 gene can be good potential biomarker for tuberculosis.

Gene names	Count
GPR180	17
GSTM3	15
RAB6B	14
WISP1	14
IGFBP5	13
FLT1	12
PALM2-AKAP2	11
RTN4RL1	11
TSPYL5	11
UCHL5	11
DCK	10
QSOX2	10