

## MicroRNA from tuberculosis RNA: A bioinformatics study

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### ABSTRACT

The role of microRNA in the pathogenesis of pulmonary tuberculosis is the interesting topic in chest medicine at present. Recently, it was proposed that the microRNA can be a useful biomarker for monitoring of pulmonary tuberculosis and might be the important part in pathogenesis of disease. Here, the authors perform a bioinformatics study to assess the microRNA within known tuberculosis RNA. The microRNA part can be detected and this can be important key information in further study of the pathogenesis of pulmonary tuberculosis.

### KEY WORDS

Pulmonary; tuberculosis; microRNA; RNA

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### Introduction

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 chest 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 miR-29 helped control innate and adaptive immune responses to tuberculosis by targeting interferon- $\gamma$  (3). The detected microRNA is relating to the clinical manifestation of disease and can be the biomarker for pulmonary tuberculosis.

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. Here, the authors perform a bioinformatics study to assess the microRNA within known tuberculosis RNA. The microRNA part can be detected and this can be important key information in further study of the pathogenesis of pulmonary tuberculosis.

### Materials and methods

This is a bioinformatics study. The assessment of the RNA of the Mycobacterium tuberculosis RNA was performed using a standard computational bioinformatics method, Mireval (5). Briefly, this technique makes use of basic comparative structural bioinformatics approach. The similarity comparison was done based on structural clustering technique (6). Blast was done against mirBase (7). Finally, an ab initio prediction method was used for judging the detected microRNA (8). In this work, the RNA codon of strain AIIMS/LM/SS/TB-2132/06/SP (JQ012998.1), which is the longest available RNA codon in PubMed database at present were used as a primary template.

### Results

According to the study, there is a detected microRNA region within the studied RNA. The position is at 500 to 580. The figure showing this part is presented in Figure 1. The repeat analysis showed the consistency of the results implying the precision and accuracy of the analysis.

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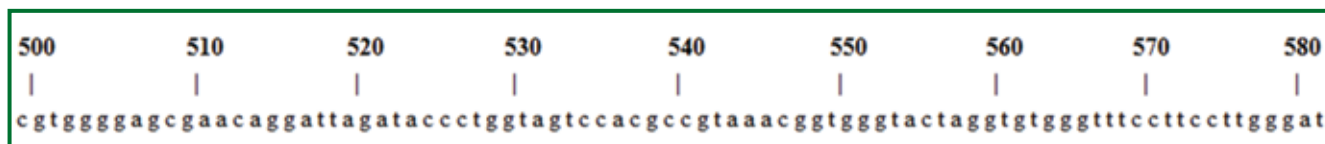


Figure 1. Showing the section that act as microRNA (picture directly generated by computational analysis based on Mireval).

## Discussion

MicroRNA is the specific kind of RNA that is the focus in the study of pathogenesis of disease at present. Based on the advancement in clinical molecular biology, the study of the MicroRNA is possible. Also, it is accepted that the diagnostic tool based on microRNA is the most sensitive diagnostic tool at present. For pulmonary tuberculosis, Wu *et al.* noted that microRNA expression profiling identifies, miR-155 and miR-155\* could be good potential diagnostic markers for active tuberculosis (9). Another study by Fu *et al.* noted for the possible use of miR-29 as biomarker for active pulmonary tuberculosis (4). Also, a recent study noted that miR-21 has important role in streptomycin treatment of pulmonary tuberculosis (10).

The study on microRNA in pulmonary tuberculosis is useful. The analysis of the RNA of pathogen is an interest aspect. Based on this report, it can conclude that some detected microRNA in the collected sample from the patient with tuberculosis come from the RNA of the tuberculosis pathogen. This means that microRNA can come from either pathogen or patient. The determination of the detected microRNA in this work can be the new diagnostic approach. Conclusively, the finding of microRNA can confirm that a part of microRNAs that play role in the complex pathogenesis of pulmonary tuberculosis might come from the pathogen. Further studies are required for assessment the exact role of microRNAs in pathogenesis of disease.

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