MODERN TECHNOLOGIES IN CONTROL OF NON-TUBERCULOSIS MYCOBACTERIA IN CYSTIC FIBROSIS PATIENTS

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Background

Non-tuberculosis mycobacterium (NTM) is opportunistic infection with difficult eradication for the cystic fibrosis (CF) patients. NTM can be acquired at an early age and, also after lung transplantation. Accurate identification is a key point of successful treatment, and prevention of severe complications. The aim of the present study was to elaborate molecular-genetic approaches to culture-independent identification of NTM and to eradication control.

Methods

Four CF patients (13-36 years old) were under the long-term monitoring. Sputum of the patients was collected, and analyzed by hsp65 gene amplification and sequencing. Microbiome was identified by high-throughput sequencing of 16S rDNA amplicons (Fig. 1)

Results

NTM species identification demonstrated that two patients were infected with *M. abscessus*, the third patient – with *M. avium*, and the fourth – with *M. chelonae*.

Fig. 1 Scheme of 16S rDNA gene: variable and conservative regions

Fig. 2 Bacterial phyla detected in samples during the treatment

Fig. 3 Mycobacteriaceae representatives detected in samples during the treatment

One patient with *M. abscessus* has died at the age of 19. The second patient was successfully treated, however shortly thereafter he was infected with *Pseudomonas aeruginosa* (Fig. 2) Two last patients received multi-component therapy resulted in NTM eradication, it was confirmed by high-throughput sequencing of microbiome. These two patients have *cftr* gene mutations subjected to Ivacaftor treatment, which improved lung function significantly. Several weeks late microbiome analysis revealed the increase in the proportion of different Proteobacteria, especially Sphingomonadaceae representatives, and the trace amount of *Mycobacteria*. It was the result of the improved lung drainage by Ivacaftor. (Fig. 2-3)

Conclusions

The use of the two genes (16S rDNA and hsp65) together improves the NTM species identification. High-throughput sequencing of 16S rDNA amplicons can be useful for monitoring patient's microbiome and treatment outcomes