

Lung microbiota and genetical component of human organism

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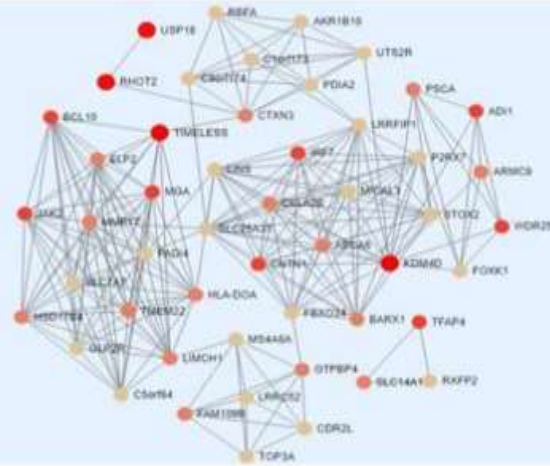
Introduction

Material and Methods

At present time a contribution of lung microbiota components in many lung disorders is actively studied. It is important to reveal interaction between lung taxa and genetical component of human organism.

The MicrobiomeAnalyst integrated with R language was used for current analysis. TSEA method was applied for detection of association between lung taxa with human genetics. Accordingly to Pubmed data in this analysis were used taxa that can make significant contribution to lung cancer

Results



Via TSEA analysis gene network was constructed. It was composed by factors that have significant association with lung microbiota

Using Pubmed data, lung microbiota taxa that can influence lung cancer development were selected for current analysis

The lung taxa list was composed of Acidovorax, Klebsella, Moraxella catarrhalis, Mycobacterium tuberculosis, Granulicatella adiacens, Veillonella, Megasphaera, Acidivorax, Granulicatella adiacens, Streptococcus intermedius, Capnocytophaga, Selenomonas, Neisseria

FDR and p-value parameters were used for selection of genes that have strongest linkage with lung taxa.

KDM4D encodes demethylase 4D and has association with such lung taxa like Veillonella and Megasphaera

Gen	p-value	FDR	Таксоны
<i>KDM4D</i>	0,00215	1,0	<i>Veillonella</i> <i>Megasphaera</i>

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THANK YOU FOR YOUR ATTENTION