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Effect of Smoking on Respiratory Flora

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Abstract: Objective to explore the influence of smoking on respiratory microbiota. Methods the traditional bacterial culture method was used to analyze the bacterial colonies qualitatively and quantitatively. The 16SrDNA fragment of characteristic bacterial colonies was amplified by PCR and sequenced, and then compared with the NCBI gene sequence library to analyze the changes of bacterial communities in the secretion of the pharyngeal wall of healthy smokers and non-smokers. Results the bacteria detection rate of smokers was significantly higher than that of non-smokers (P < 0. 05). Conclusion Smoking can increase the amount of bacteria in oropharynx and increase the incidence of pathogenic bacteria, so that the respiratory tract flora imbalance.

1. Introduction

Smoking is a global medical and social problem, which has become one of the health threats to human society. A variety of chemical substances produced in the process of smoking are inhaled into the human body, causing the damage of respiratory mucosa and the change of bacterial flora. In order to study the influence of smoking on respiratory tract bacteria, 50 healthy non-smoking people and 50 long-term smoking people were collected for bacterial culture and colony gene fragment analysis, to analyze the difference of bacterial communities between the two, to understand the influence of smoking on the distribution of respiratory tract bacteria.

2. Objects and Methods

Clinical data From June 2020 to June 2021, 100 students who had a history of smoking and 100 students who had never had a history of smoking were selected. Smokers who smoke more than 1 cigarette a day and have not quit smoking for more than 1 consecutive year. All the selected subjects were those who passed the physical examination in the affiliated hospital of the campus, and there was no statistical difference in age and gender between the two groups.

Specimen collection and identification the oropharyngeal specimen was scraped with a disposable sterile long face tip and put into the culture medium containing brain and heart extract and fetal bovine serum. After shaking and mixing, the obtained specimen suspension was left standing. After standing, the bacterial suspensions were multiplied by 1, 10, 100 and 500 times of dilution, respectively, and then the diluted bacterial suspensions were added into the solid medium for culture. 100ul of each diluted bacterial suspension was added to blood plate culture medium, chocolate culture medium, McConkey culture medium, Sarborough culture medium and anaerobic solid culture medium, and evenly coated with sterile stainless steel coating stick. After coating, the blood plate, McConkey and Sarborg solid medium were incubated in a 37 ℃ temperature box, the

chocolate medium was incubated in a 37 ℃ 5% carbon dioxide environment, and the anaerobic medium was incubated in an anaerobic environment.

Main preparations and instruments and equipment Nutrition AGAR blood plate is provided by Zhengzhou Berite Biotechnology Co., Ltd. The bacteria identification and drug sensitivity analysis system SIEMENS96 is provided by German company. Statistical Processing SPSS 20.0 software was used for statistical analysis of all the test data.

3. Results

AS shown in table 1, the detection rates of Staphylococcus aureus, Streptococcus pneumoniae, Klebsiella pneumoniae, Cattagranhella, Pseudomonas aeruginosa and Escherichia coli in 100 participants in smoking group were significantly higher than those in non-smoking group ($P < 0.05$), the detection rate of Neisseria, Anaerobic coccus, Corynebacterium and other bacteria was significantly decreased ($P < 0.05$).

Table 1 Detection rate of lung bacteria in smokers and non-smokers (cases/percentage)

group	Staphylococcus aureus	Streptococcus pneumoniae	Klebsiella pneumoniae	Catarabranhans	proteus	Pseudomonas aeruginosa	E. coli	Neisseria bacteria	Anaerobic bacteria	Rod bacteria
100 cases of smokers	29 (29)	19 (19)	Twenty-four (24)	Seven (7)	Five (5)	Twelve (12)	Nine (9)	Four (4)	Five (5)	Seven (7)
100 cases of non-smokers	Two (2)	Two (2)	Three (3)	17 (17)	Three (3)	1 (1)	0 (zero)	Twenty-four (24)	Thirty (30)	21 (21)
P values	< 0.05	< 0.05	< 0.05	< 0.05	> 0.05	< 0.05	< 0.05	< 0.05	< 0.05	< 0.05

4. Discussion

A large number of aerobes, microaerobes and anaerobes colonized the respiratory tract of healthy people, mainly Proteus, Clostridium, Neisseria, Bacteroidetes, Prevotella, Veronococcus and Haemophilus. Under the influence of external environment, the species and quantity distribution of bacterial population will change [1]. Normal flora can serve as a natural barrier to the human body, and the whole microecology can maintain a balanced state, so that the body is protected from the invasion of pathogens from the outside world. When the living environment of the outside world changes, the micro-ecology that connects with the outside world will also change, and the types and quantities of bacteria in the upper respiratory tract will change, directly affecting human health. The smoke from burning cigarettes contains dozens of substances that are directly carcinogenic, a variety of heavy metals and the addictive nicotine [2]. In addition, smoking leads to changes in respiratory flora, increasing the possibility of various respiratory diseases. Streptococcus pyogenes,

staphylococcus aureus and other pathogenic bacteria replaced the original bacterial colonies, the whole bacterial community succession, a variety of pathogenic microorganisms rapidly increased, the original ecological balance of bacteria was destroyed, unable to antagonize foreign bacteria, resulting in a sharp increase in respiratory tract infections.This study showed that the detection rates of upper respiratory pathogens such as Staphylococcus aureus and Streptococcus pneumoniae in smokers were significantly higher than those in non-smokers ($P < 0.05$), and the detection rates of Neisseria and anaerobe were lower than those in non-smokers. In 100 volunteers, the detection rate of Staphylococcus epidermidis in the pharynx of non-smokers was higher than that of smokers, and the detection rate of Streptococcus pneumoniae and aureus was significantly lower than that of smokers. Based on this, we believe that the substances produced by cigarette burning have changed the upper respiratory tract microecology, the number and species of normal colonization bacteria are reduced, and the increasing number of various pathogenic bacteria leads to an increase in the incidence of respiratory diseases.

At present, there are no obvious effective measures for many respiratory diseases, and new microbial species are constantly emerging, so the research on respiratory flora has not stopped. The normal microflora forms a specific microflora barrier in each cavity and body surface of the host body that communicates with the outside world and plays a defense role against invading pathogenic microorganisms [3]. Infection is a symptom of microbiome disorder, where bacteria reach a certain number or colonize certain areas and cause disease in the host. In the past, infection was considered to be the infection of pathogenic microorganisms, but now it is believed that in addition to the infection of pathogenic microorganisms, a large proportion of patients do not have the infection of pathogenic bacteria, and the inflammation is caused by the disorder of the normal flora in the site. Various chemicals produced by smoking make the respiratory tract flora imbalance, prone to throat discomfort and other respiratory symptoms [4]. Using the method of restoring the normal bacteria in the body rather than using antibiotics to kill a large number of bacteria, can prevent antibiotic resistance caused by the abuse of antibiotics, but also can reduce the cost of treatment to avoid secondary harm. Biological agents regulating the balance of upper respiratory tract flora should be a reasonable combination of normal respiratory tract flora [5]. With the development of biomedical research, the pathological reaction caused by the destruction of the normal flora of the body has become more and more clear, and a variety of microbial agents have been used to regulate and treat diseases, rather than simply resist them. Therefore, it is necessary to improve tobacco to avoid respiratory damage caused by smoking.

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References

[1] Wang, C., Liu, J.Y. (2015) Research progress on the role of cigarette smoke in the pathogenesis of chronic obstructive pulmonary disease. Journal of Applied Medicine, 31(1), 8-9.

[2] Dang, R.Y, Zhao, C.Y, Fan, X, et al. (2018) Effects of cigarette smoke exposure on the distribution of bacteria in the lower respiratory tract of normal mice. Shandong Medicine, 58(20), 9-12.

[3] Pu, J.D., Huang, L.M., Ye, X.Q., et al. (2016) Effects of fine particulate matter in the environment on transdifferentiation of human bronchial epithelial cells. Chinese Journal of Tuberculosis and Respiratory Diseases, 39(10), 784-790.

[4] Simon, C., Daniel, R. (2011) Metagenomic analyses: past and future trends. Appl Environ Microbiol, 77(4), 1153-1161.

[5] Singh, B.K., Macdonald, C.A. (2010) Drug discovery from uncultivable microorganisms. Drug Discov Today, 15(78), 792-799.