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Altered Airway Microbiota Composition in Patients With Pulmonary Hypertension¹

Abstract
Alteration in microbiota composition of respiratory tract has been reported in the progression of many chronic lung diseases; yet, the correlation and causal link between respiratory tract microbiota and the disease development of pulmonary hypertension (PH) remain largely unknown. This study aims to define and compare the respiratory

Predictive Value of Pulmonary Arterial Compliance in Systemic Lupus Erythematosus Patients With Pulmonary Arterial Hypertension¹

Abstract
Pulmonary arterial hypertension is a serious complication of systemic lupus erythematosus. It is characterized by increased right ventricular afterload, which mainly comprises pulmonary arterial compliance (PAC) and pulmonary vascular resistance. The role of PAC in predicting the outcome of systemic lupus

CAR (CARSKNKDC) Peptide Modified ReNcell-Derived Extracellular Vesicles as a Novel Therapeutic Agent for Targeted Pulmonary Hypertension Therapy⁴

Abstract
In recent years, mesenchymal stem cell (MSC)-derived extracellular vesicles (EVs) are emerging as a potential therapeutic agent for pulmonary hypertension (PH). However, the full realization of MSC-derived EV therapy has been hampered by the absence of standardization

人体体表和体内存在种类繁多、数量巨大的微生物群，受到复杂的人体内外因素影响。人体微生态系统是一个非常复杂的系统，正常菌群在宿主的生命活动中发挥至关重要的作用。咽部是连接口腔、鼻咽与下呼吸道、食道等的生理部位，与外界环境相通，是很多细菌侵入下呼吸道并引起肺部感染的重要通道。咽部微生态环境的动态平衡在多种人类疾病的发生发展中发挥重要作用。因此，系统研究肺动脉高压疾病状态下咽部微生态的组成和分布对进一步理解肺动脉高压的表型和机制具有潜在的重要意义。

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Altered Airway Microbiota Composition in Patients With Pulmonary Hypertension

Chenting Zhang, Tingling Zhang, Wenju Lu, Xin Duan, Xiaoyun Luo, Shiyun Liu, Yuqin Chen, Yi Li, Jiyuan Chen, Jing Liao, Dansha Zhou, Xu Chen, Huazhuo Feng, Guoping Gu, Tao Wang, Haiyang Tang, Ayako Makino, Nanshan Zhong, Jason X.-J. Yuan, Kai Yang, Jian Wang

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English

本研究收集了118例肺动脉高压患者和79例健康对照的咽拭子，通过16S ribosomal RNA基因测序手段首次动脉高压患者和健康对照组咽部菌群的组成存在差异。与健康对照组相比，肺动脉高压患者咽部的菌群丰富度升高、多样性下降，其中链球菌属、劳特罗普氏菌属、雷尔氏菌属三种菌丰度明显高于健康对照组，且组间差异显著分析和LDFSe多级物种差异分析提示，这三种菌在咽部的差异表达有望成为肺动脉高压无创诊断的一组新型、潜在的生物标记物。而进一步功能预测分析提示，肺动脉高压患者咽部富集菌群与细菌侵袭上皮细胞、细菌内毒素等信号通路的激活密切相关。

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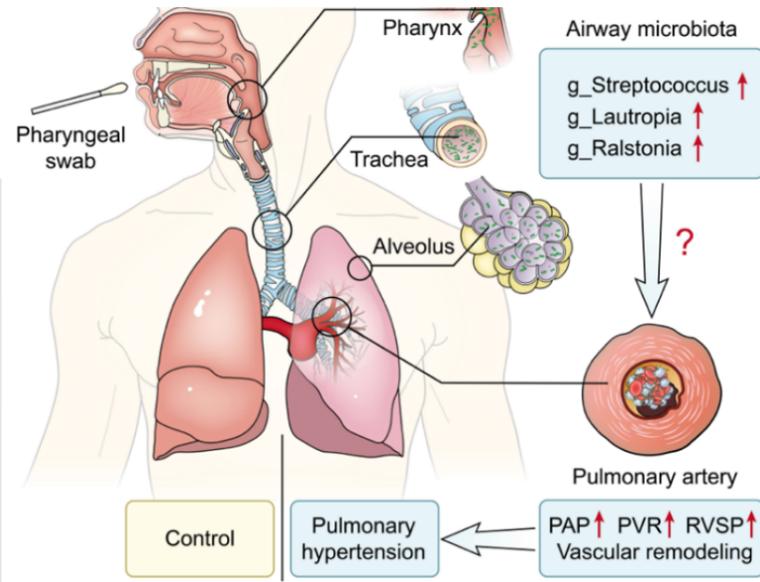
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