

# The relationship between the microbes in the lower respiratory tract and allergic respiratory diseases in children

<b>Submission date</b> 30/09/2020	<b>Recruitment status</b> No longer recruiting	<input type="checkbox"/> Prospectively registered <input type="checkbox"/> Protocol
<b>Registration date</b> 06/10/2020	<b>Overall study status</b> Completed	<input type="checkbox"/> Statistical analysis plan <input checked="" type="checkbox"/> Results
<b>Last Edited</b> 07/01/2022	<b>Condition category</b> Respiratory	<input type="checkbox"/> Individual participant data

## Plain English summary of protocol

### Background and study aims

With the development of DNA sequencing technologies, it has been found that there are microbes similar to those in the upper respiratory tract (the nose and nasal cavity, the pharynx, and the larynx) present in the healthy human lower respiratory tract (LRT), including the lungs and bronchi. The aim of this study is to analyse the LRT microbiome and evaluate the relationship between this microbiome and allergic respiratory diseases in children.

### Who can participate?

Children who visit the respiratory department and undergo bronchoscopy (a procedure where a tube is inserted through the nose or mouth, down the throat and into the windpipe, bronchi and bronchioles of the lungs)

### What does the study involve?

Total IgE (antibody) levels are detected using a special protein analyser. The peripheral blood cell count is measured using an automatic blood analyser. DNA is extracted from samples of fluid taken during bronchoscopy and the microbiome is sequenced and analysed.

### What are the possible benefits and risks of participating?

There are no benefits and risks of participating.

### Where is the study run from?

The affiliated hospital of the Capital Institute of Pediatrics (China)

### When is the study starting and how long is it expected to run for?

January 2018 to May 2020

### Who is funding the study?

Beijing Medical Research Institute (China)

Who is the main contact?  
Jinghua Cui  
cuijinghua7910@hotmail.com

## Contact information

**Type(s)**  
Scientific

**Contact name**  
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## Additional identifiers

**EudraCT/CTIS number**  
Nil known

**IRAS number**

**ClinicalTrials.gov number**  
Nil known

**Secondary identifying numbers**  
704209958

## Study information

**Scientific Title**  
The relationship between the lower respiratory tract microbiome and allergic respiratory tract diseases in children

**Study objectives**  
A decrease in microbial diversity and change in composition could lead to an increase in allergic symptoms. The colonised microbiota of the lower respiratory tract (LRT) in children, especially that of Bacteroidetes and Streptococcus, show a certain correlation with early respiratory allergic diseases.

**Ethics approval required**  
Old ethics approval format

**Ethics approval(s)**

Approved 20/06/2019, the medical ethics committee of the Capital Institute of Pediatrics (Beijing, China. +86 (0)8569 5535; shouerkyb@sina.com), ref: SHERLLM2019006

**Study design**

Single-centre cross-sectional cohort study

**Primary study design**

Observational

**Secondary study design**

Cross sectional study

**Study setting(s)**

Hospital

**Study type(s)**

Other

**Participant information sheet**

No participant information sheet available

**Health condition(s) or problem(s) studied**

Allergic respiratory tract diseases in children

**Interventions**

Nucleic acid is extracted from samples of bronchoalveolar lavage fluid (BALF) of children taken during bronchoscopy treatment and the 16S rDNA gene is sequenced and analysed.

**Intervention Type**

Other

**Primary outcome measure**

The microbiome in BAFL measured using 16S rDNA sequenced on a MiSeq instrument (Illumina, Inc.) using a Miseq v2 reagent kit (Illumina, Inc.) at a single timepoint

**Secondary outcome measures**

There are no secondary outcome measures

**Overall study start date**

01/01/2018

**Completion date**

01/05/2020

**Eligibility****Key inclusion criteria**

Children who visit the respiratory department and undergo bronchoscopy

**Participant type(s)**

Patient

**Age group**

Child

**Sex**

Both

**Target number of participants**

68

**Total final enrolment**

68

**Key exclusion criteria**

1. Diagnosis of pneumonia with specific pathogen infection such as fungus, virus, or mycoplasma
2. History of mechanical ventilation

**Date of first enrolment**

01/01/2018

**Date of final enrolment**

31/12/2018

**Locations****Countries of recruitment**

China

**Study participating centre**

The affiliated hospital of the Capital Institute of Pediatrics

Beijing

China

10020

**Sponsor information****Organisation**

Capital Institute of Pediatrics

**Sponsor details**

2 Yabao Road

Chaoyang District

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shouerkyb@sina.com

### **Sponsor type**

Research organisation

### **Website**

<http://www.shouer.com.cn/en/web/detail.aspx?menuID=515&contentID=3536>

### **ROR**

<https://ror.org/00zw6et16>

## **Funder(s)**

### **Funder type**

Research organisation

### **Funder Name**

Beijing Medical Research Institute (BMR2019-11)

## **Results and Publications**

### **Publication and dissemination plan**

Planned publication in a peer-reviewed journal and sharing data on the National Genomics Data Center of the China National Center for Bioinformation (CNCB-NGDC).

### **Intention to publish date**

01/01/2021

### **Individual participant data (IPD) sharing plan**

The datasets generated during and/or analysed during the current study are/will be available upon request from Jinghua Cui (cuijinghua7910@ hotmail.com). After the paper and the data are published, if consent is obtained from the author, the data can be shared with all who are interested in this study.

### **IPD sharing plan summary**

Available on request

### **Study outputs**

Output type	Details	Date created	Date added	Peer reviewed?	Patient-facing?
<a href="#">Results article</a>		14/05/2021	07/01/2022	Yes	No