

Research Article

# The Value of IL-13, IL-4, ADRB2, Fce1b Non-Invasive Gene Test for Early Diagnosis of Children's Asthma in Zhuhai

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## Abstract

**Objective:** To explore the value of IL-13, IL-4, ADRB2, and Fce1b non-invasive gene test for early diagnosis of children's asthma in Zhuhai. **Methods:** Children under the age of 6 who were treated in the pediatric clinic and ward of Zhuhai People's Hospital from July 2022 to December 2023 with asthma symptoms were selected as the research objects, and the sample collection and genetic testing were completed. According to the asthma gene prediction model, the detected gene loci were divided into high-risk genome (study group 1) and low-risk genome (study group 2), and the two groups of children were followed up for one year, and the number of children diagnosed with asthma in study group 1 and study group 2 was statistically analyzed. **Results:** There was a difference between the number of confirmed asthma cases in high-risk genome and the number of API positive cases in all confirmed asthma cases ( $P < 0.05$ ). The number of confirmed asthma cases in high-risk genome was higher than that in all confirmed asthma cases, and the number of confirmed asthma cases in low-risk genome was lower, with the  $\chi^2$  value of 6.402 ( $P < 0.05$ ). **Conclusion:** The genetic model of childhood asthma has predictive value in children with asthma in Zhuhai, and can identify high-risk children with childhood asthma at an early stage.

## Keywords

IL-13, IL-4, ADRB2, FcER1B, Children Asthma Gene

## 1. Introduction

The proportion of children with asthma symptoms worldwide is 14.2%, and the mortality rate is 0-0.7 per 100,000 population, which is higher than that of adults, and the lifetime prevalence of children is as high as 14% [1]. According to research data, the prevalence of childhood asthma is on the rise, and the etiology of childhood asthma is complex, involving environmental, immune, genetic and other factors [2]. The cause of children's asthma is complicated, involving many factors such as environmental, immunity, and genetic. How to identify high-risk groups of children's asthma in the early days and make early intervention on the crowd, which is of great

significance to preventing children's asthma. After more than 10 years of continuous research and development, Professor Bao Yixiao's team created the first asthma gene prediction model in many asthma susceptible genes [3-5], but the model was mainly monitored in East China [6]. Zhuhai is located in the coastal area of the Pearl River Delta south of the Yangtze River. It is an immigrant city and a humid climate. The main ingredients of residents are seafood with allergens. This study will apply asthma gene prediction model Verification provides reference for early diagnosis and personalized therapy for children's asthma.

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## 2. Methods

### 2.1. General Information

Collection from July 2022 to July 2023, the 6-year-old and 6-year-old of Zhuhai City People's Hospital, which is in line with 80 children with symptoms of asthma and asthma symptoms in the "Guidelines for the Diagnosis and Prevention of Children's bronchial asthma" [7, 8]. Among them, it contains includes Children who have clearly diagnosed asthma and asthma symptoms but have not reached the standard of asthma diagnostic standards. After genetic testing, the genetic testing model is divided into 45 high-risk genome and 35 low-risk genome. All participants have the consent of this study, and this study has been approved by the Ethical Committee of the Zhuhai Municipal People's Hospital.

### 2.2. Method

(1) Specimen collection: According to the principle of informed consent, oral and buccal mucosa swabs were collected. (2) SNP typing of target gene: The SNP loci of four susceptible genes, IL-13 rs20541, IL-4 rs2243250, ADRB2 rs1042713 and FcER1B rs569108, were detected by Taqman probe method.

### 2.3. Indicator Monitoring

(1) Count the cases of asthma diagnosed in the past or in the follow-up in the high-risk genome; (2) Counting the cases of asthma diagnosed in the low-risk genome in the past or in the follow-up; (3) Use the asthma prediction index to evaluate the children who have been diagnosed with asthma and the chil-

dren who have been diagnosed with asthma during follow-up, and count the positive cases of asthma prediction index (API).

### 2.4. Statistical Processing

Analysis with SPSS26.0 statistical software. Counting data is expressed by the number of cases (%), and the comparison between the two groups of data is made by  $\chi^2$  test, with a statistical difference of  $P < 0.05$ .

## 3. Results

### 3.1. Distribution of Basic Data of Two Groups of Children

There was no significant difference in general data between the two groups ( $P > 0.05$ ). The distribution of basic data of two groups of children are shown in Table 1.

### 3.2. The Number and Proportion of Confirmed Asthma Cases and API Positive Cases in the Two Groups

The proportion of confirmed asthma cases in high-risk genome in all confirmed asthma cases is different from that of API positive cases in all confirmed asthma cases ( $P < 0.05$ ), and the former is higher than the latter, as shown in Table 2. The number of confirmed asthma cases in the high-risk genome accounts for a high proportion of all confirmed asthma cases, while the number of confirmed asthma cases in the low-risk genome accounts for a low proportion of all confirmed asthma cases, with the  $\chi^2$  value of 6.402 ( $P < 0.05$ ). The specific values are shown in Table 2.

**Table 1.** Distribution of basic data of two groups of children.

Variable	High-risk genome Group	Low-risk genome Group	P value
Total	45	35	/
Boy	27 (60.00%)	23 (65.71%)	0.61
Girl	18 (40.00%)	12 (34.29%)	0.60
Age	4.24±1.67	4.02±1.58	0.42

**Table 2.** The number and proportion of confirmed asthma cases and API positive cases in the two groups.

	High-risk genome Group	Low-risk genome Group	API positive	$\chi^2$ value	P value
Previously diagnosed asthma	33	15	11	6.402	0.006
Follow-up diagnosis of asthma	15	7	7		

## 4. Discussion

Asthma is still an incurable chronic respiratory disease, and its prognosis is still a challenge in today's scientific research [9-12]. With the in-depth study of the complex phenotype of asthma, our understanding of asthma is no longer limited to controlling the disease, uncovering the risk factors that affect the persistence or recurrence of asthma, and it is particularly important to intervene the occurrence and development of asthma from the source.

Asthma is a common chronic disease in children, which seriously threatens children's growth and health. In recent years, the incidence and mortality of asthma have been on the rise, and the prevalence of asthma in children has also increased significantly [13-15]. At present, the diagnosis of asthma in children needs to be based on respiratory symptoms, signs and lung function tests to confirm the existence of variable expiratory airflow restriction, and to exclude other diseases that can cause related symptoms, and it needs long-term follow-up observation, so the diagnosis is lagging behind. It is of great significance to identify the high-risk groups of asthma early and intervene them early.

This study found that the number of confirmed asthma cases in the high-risk genome accounts for a relatively high proportion of all confirmed asthma cases, and the number of positive asthma cases in the low-risk genome accounts for a low proportion of all confirmed asthma cases, indicating that the childhood asthma gene model has predictive value in children with asthma in Zhuhai, and can identify high-risk children with childhood asthma at an early stage. Early intervention for high-risk children to achieve primary prevention of childhood asthma.

## 5. Conclusion

The genetic model of childhood asthma has predictive value in children with asthma in Zhuhai, and can identify high-risk children with childhood asthma at an early stage.

## Abbreviations

GINA    Global Initiative for Asthma  
API     Asthma Prediction Index

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## Conflicts of Interest

The author of this article declares no conflicts of interest.

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