

Research Article

CHARACTERISTICS OF THE GLCCI1 RS37973 POLYMORPHISM AMONG CHILDREN WITH BRONCHIAL ASTHMA AGED 6–16 YEARS AT CAN THO CHILDREN'S HOSPITAL, 2024–2026

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ABSTRACT

Genetic factors may influence asthma characteristics and treatment response in paediatric patients. This study aimed to describe the distribution of the GLCCI1 rs37973 polymorphism in children with bronchial asthma at Can Tho Children's Hospital. A cross-sectional descriptive study was conducted on 81 children aged 6–16 years diagnosed with bronchial asthma from June 2024 to May 2026. Clinical characteristics and GLCCI1 rs37973 genotypes were analyzed using PCR-based genetic testing. Most participants were aged 6–11 years (82.7%) and male (63.0%), with a mean age of 9.05 ± 2.36 years. Genotype analysis showed that the AG genotype was the most common (51.9%), followed by GG (25.9%) and AA (22.2%). The G allele frequency (51.9%) was slightly higher than the A allele frequency (48.1%). No significant associations were identified between rs37973 genotypes and most demographic or clinical characteristics. However, a statistically significant association was observed between genotype distribution and history of COVID-19 infection ($p < 0.05$). In conclusion, the AG genotype and G allele were predominant among Vietnamese children with bronchial asthma. These findings provide preliminary data for future studies investigating genetic factors associated with asthma management and corticosteroid responsiveness.

Keywords: bronchial asthma, children, GLCCI1, polymorphism, rs37973.

INTRODUCTION

Bronchial asthma is a common chronic inflammatory respiratory disease in children and remains an important public health concern worldwide. In Vietnam, the prevalence of childhood asthma has increased in recent years (Ministry of Health, 2020). According to the Global Initiative for Asthma guidelines, inhaled corticosteroids (ICS) are the cornerstone of long-term asthma management because of their anti-inflammatory effects and ability to improve asthma control (GINA, 2025).

Genetic factors may contribute to differences in asthma characteristics and treatment response among patients. Among candidate genes related to corticosteroid response, the *glucocorticoid-induced transcript 1* (GLCCI1) gene has attracted increasing attention. Previous studies have reported that the rs37973 polymorphism of the GLCCI1 gene may be associated with asthma susceptibility and responsiveness to inhaled corticosteroids in several populations (Tantisira *et al.*, 2011; Hu *et al.*, 2016; Salhi *et al.*, 2019).

Several studies in Asian pediatric populations have shown that the AG genotype is frequently the predominant genotype of the GLCCI1 rs37973 polymorphism (Huang *et al.*, 2020; Xu *et al.*, 2017). In addition, environmental and infectious factors may influence asthma manifestations and inflammatory responses in children (Filippatos *et al.*, 2023). However, studies evaluating the GLCCI1 rs37973 polymorphism in Vietnamese children with bronchial asthma remain limited. Therefore, this study was conducted to describe the characteristics of the GLCCI1 rs37973 polymorphism in children aged 6–16 years with bronchial asthma at Can Tho Children's Hospital.

MATERIALS AND METHODS

Materials: The study population consisted of children aged 6–16 years diagnosed with bronchial asthma at Can Tho Children's Hospital from June 2024 to May 2026.

Inclusion criteria: Pediatric patients aged 6–16 years who were newly diagnosed with bronchial asthma for the first time according to the Global Initiative for Asthma (GINA, 2025) guidelines, based on clinical manifestations and spirometry findings, were eligible for inclusion. Only patients indicated for preventive treatment (Step 2 or higher), with no prior history of asthma preventive therapy, and managed within the first three months after diagnosis were included. In addition, all participants were required to have complete medical records fully evaluated by physicians. The study was conducted with informed consent from parents or legal guardians.

Exclusion criteria: Asthmatic children with other chronic pulmonary conditions (bronchiectasis, cystic fibrosis, tuberculosis, bronchopulmonary dysplasia, etc.) or extrapulmonary diseases (heart, liver, or kidney failure), immunodeficiency, malnutrition, or those currently taking medications for other diseases.

Study design and sampling method: A cross-sectional descriptive study was conducted on 81 children aged 6–16 years diagnosed with bronchial asthma at Can Tho Children's Hospital from June 2024 to May 2026. The diagnosis of bronchial asthma was established according to the Global Initiative for Asthma (GINA, 2024) and the Vietnamese Ministry of Health guidelines for asthma diagnosis and management (Ministry of Health, 2020). Convenience sampling was applied during the study period, and patients who met the inclusion criteria and whose parents or guardians provided written informed consent were consecutively enrolled in the study.

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Baseline demographic characteristics included age group, age at asthma onset, sex, and residential area. Clinical risk factors and asthma-related exposures were collected through medical records and interviews with patients or caregivers, including BMI, personal and family history of allergies, history of COVID-19 infection, vaccination history, secondhand smoke exposure, weather changes, air pollution exposure, and exercise-related asthma symptoms.

Genetic analysis included determination of *GLCC11* rs37973 genotype frequencies (AA, AG, and GG) and allele frequencies (A and G). Genotype and allele distributions were further evaluated according to demographic and clinical characteristics.

Data collection and statistical analysis

Data were collected through face-to-face interviews, clinical examinations, and asthma assessments according to the Global Initiative for Asthma (GINA, 2025) guidelines. Spirometry was performed using the MostGraph-02 system (Japan) and the Koko® Spirometer (nSpire Health, Inc., USA) at Can Tho Children’s Hospital. Peripheral blood samples were collected in EDTA tubes and transferred to the Molecular Biology Laboratory of Can Tho University of Medicine and Pharmacy for genetic analysis.

Genomic DNA was extracted from whole blood samples using the GeneJET Genomic DNA Purification Kit (Thermo Scientific) according to the manufacturer’s instructions. DNA concentration and purity were evaluated using a NanoDrop spectrophotometer before amplification. The *GLCC11* rs37973 polymorphism was analyzed using Real-Time PCR with TaqMan™ SNP Genotyping Assays (Applied Biosystems, USA) on the SaCycler-96 Real-Time PCR system. The PCR reaction mixture included TaqMan Genotyping Master Mix, sequence-specific primers, fluorescent probes, template DNA, and nuclease-free water in a total reaction volume of 20 µL. Thermal cycling conditions consisted of an initial denaturation step followed by 40 amplification cycles according to the manufacturer’s protocol. Laboratory procedures were performed using the GYROZEN MINI centrifuge, DKT200-1 dry bath incubator, Rotofix 32A centrifuge, and vortex mixer. Genotype determination was conducted automatically based on fluorescence signal analysis.

Collected data were coded, entered, and analyzed using SPSS version 20.0 software. Descriptive statistics and comparative analyses were performed, with a p-value < 0.05 considered statistically significant.

III. RESULTS

A total of 81 children aged 6–16 years diagnosed with bronchial asthma were included in this study. The mean age of the study population was 9.05 ± 2.36 years, and male patients accounted for the majority of cases.

Baseline demographic and clinical characteristics of the study population are summarized in Table 1. Most participants were in the 6–11-year age group and resided outside Can Tho City. Histories of allergy, allergic rhinitis, and secondhand smoke exposure were commonly observed among the study subjects. In addition, weather changes and air pollution exposure were frequently reported as asthma-triggering factors.

Table 1. Baseline demographic and clinical characteristics of children with bronchial asthma

Features		Frequency (n)	Percentage (%)
Body mass index (BMI)	Thinness	9	11,1
	Normal	39	48,1
	Overweight/Obesity	33	40,7
Personal history of allergic diseases	Yes	37	45,7
	No	44	54,3
History of food allergies	Yes	19	23,5
	No	62	76,5
History of allergic rhinitis	Yes	25	30,9
	No	56	69,1
History of COVID-19 infection	Yes	33	40,7
	No	48	59,3
Weather changes as asthma triggers	Yes	42	51,9
	No	39	48,1
Exposure to air pollution	Yes	23	28,4
	No	58	71,6
Exercise-induced symptoms	Yes	35	43,2
	No	46	56,8
Exposure to secondhand smoke	Yes	27	33,3
	No	54	66,7
Family history of allergic diseases	Yes	24	29,6
	No	57	70,4
Routine vaccination status	Yes	33	40,7
	No	48	59,3

The distribution of *GLCC11* rs37973 genotypes is illustrated in Figure1. The heterozygous AG genotype was the predominant genotype in the study population, whereas the AA genotype was the least frequently observed.

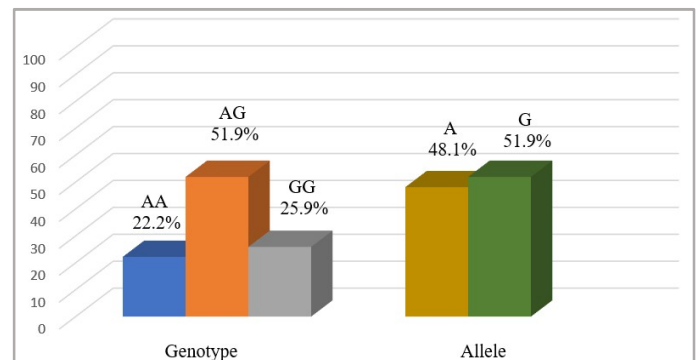


Figure 1. Distribution of *GLCC11* rs37973 genotypes in children with bronchial asthma

(AA: homozygous wild-type genotype; AG: heterozygous genotype; GG: homozygous variant genotype; A: wild-type allele; G: variant allele)

The distribution of *GLCC11* rs37973 genotypes and alleles according to sex is presented in Table 2. The AG genotype was the most frequently observed genotype in both male and female patients, accounting for 69.0% and 31.0% of AG carriers, respectively. Similarly, the G allele was more common than the A allele in both sexes. However, no statistically significant differences were identified in genotype (p = 0.373) or allele (p = 0.492) distributions between male and female patients.

Table 2. Distribution of *GLCC1* rs37973 genotypes and allele frequencies in children with bronchial asthma

rs37973	Male n (%)	Female n (%)	p
Genotype			
AA	9 (50,0)	9 (50,0)	0,373
AG	29 (69,0)	13 (31,0)	
GG	13 (61,9)	8 (38,1)	
Allele			
A	47 (60,3)	31 (39,7)	0,492
G	55 (65,5)	29 (34,5)	

Associations between *GLCC1* rs37973 genotypes and clinical characteristics are shown in Table 3. No significant associations were observed between genotype distribution and overweight/obesity, personal history of allergic diseases, food allergy, allergic rhinitis, secondhand smoke exposure, or family history of allergic diseases (all $p > 0.05$). However, a statistically significant association was identified between rs37973 genotype distribution and history of COVID-19 infection ($p = 0.009$), with the AG genotype accounting for the majority of children with a previous COVID-19 infection.

Table3.Association between *GLCC1* rs37973 genotypes and demographic-clinical characteristics in children with bronchial asthma

Clinical Features	Genotype n (%)			p
	AA	AG	GG	
Overweight/obesity	7 (21,2)	14 (42,4)	12 (36,4)	0,416*
Personal history of allergic diseases	7 (18,9)	20 (54,1)	10 (27,0)	0,807
History of food allergies	4 (21,1)	11 (57,9)	4 (21,1)	0,939*
History of allergic rhinitis	6 (24,0)	12 (48,0)	7 (28,0)	0,898
History of COVID-19 infection	7 (21,2)	23 (69,7)	3 (9,1)	0,009
Exposure to secondhand smoke	5 (18,5)	17 (63,0)	5 (18,5)	0,355
Family history of allergic diseases	5 (20,8)	12 (50,0)	7 (29,2)	0,909

χ^2 Test; * Fisher's Exact test

Associations between *GLCC1* rs37973 genotypes and clinical characteristics are presented in Table 4. A statistically significant association was observed between genotype distribution and history of COVID-19 infection. However, no significant associations were identified between rs37973 genotypes and obesity, personal history of allergies, allergic rhinitis, food allergy, secondhand smoke exposure, vaccination history, or other asthma-triggering factors.

Table 4. Association between *GLCC1* rs37973 genotypes and clinical characteristics in children with bronchial asthma

Clinical Characteristics	Allele n (%)		p
	A	G	
Overweight/ obesity	28 (42,4)	38 (57,6)	0,372
Personal history of allergies	34 (45,9)	40 (54,1)	0,607
History of food allergy	19 (50,0)	19 (50,0)	0,794
History of allergic rhinitis	24 (48,0)	26 (52,0)	0,980
History of COVID-19 infection	37 (56,1)	29 (43,9)	0,095
Secondhand smoke exposure	27 (50,0)	27 (50,0)	0,739
Family history	22 (45,8)	26 (54,2)	0,702

χ^2 Test

Overall, the results demonstrated that the *GLCC1* rs37973 AG genotype and G allele were predominant among children with bronchial asthma in this study population. Most demographic and clinical characteristics showed no significant association with rs37973 genotype distribution, except for a history of COVID-19 infection.

DISCUSSION

In the present study, most children with bronchial asthma were aged 6–11 years, with a predominance of male patients. These findings are generally comparable to the epidemiological characteristics of childhood asthma reported in previous studies and current asthma guidelines, which indicate that asthma commonly develops during childhood and is more frequently observed in boys before adolescence (GINA, 2025; Ministry of Health, 2020).

Histories of allergy, allergic rhinitis, and secondhand smoke exposure were commonly observed among the study subjects. Environmental triggers such as weather changes and air pollution exposure were also frequently reported. Similar observations have been described in previous studies suggesting that environmental exposure and allergic comorbidities may contribute to asthma symptoms and exacerbations in children (Filippatos *et al.*, 2023). In addition, obesity and environmental pollution have been suggested as potential factors influencing asthma control and airway inflammation in pediatric patients (Keskin *et al.*, 2019).

Genetic analysis in the present study showed that the AG genotype was the most frequently observed genotype of the *GLCC1* rs37973 polymorphism, followed by GG and AA genotypes. The G allele frequency was slightly higher than that of the A allele. These findings are relatively similar to previous studies evaluating *GLCC1* polymorphisms in asthma patients, particularly in Asian populations (Hu *et al.*, 2016; Huang *et al.*, 2020). Tantisira *et al.*, (2011) previously reported that variants of the *GLCC1* gene may be associated with variability in corticosteroid responsiveness among asthma patients. Other studies in Chinese and Tunisian populations also suggested possible associations between the rs37973 polymorphism and response to inhaled corticosteroids (Salhi *et al.*, 2019; Xu *et al.*, 2017). However, differences in genotype frequencies among studies may be related to ethnicity, environmental exposure, study population characteristics, and sample size.

No statistically significant associations were identified between rs37973 genotype distribution and most demographic characteristics, including sex, age group, residential area, and age at asthma onset. Similar findings have been reported in previous studies, suggesting that the *GLCC1* rs37973 polymorphism may not be strongly associated with baseline demographic characteristics in asthma patients (Hu *et al.*, 2016; Keskin *et al.*, 2019).

In the present study, a statistically significant association was observed between rs37973 genotype distribution and history of COVID-19 infection. Although the underlying mechanism remains unclear, respiratory viral infections may influence airway inflammatory responses differently according to genetic background. Previous reports have suggested that viral infections can contribute to airway inflammation and immune dysregulation in children with asthma (Filippatos *et al.*, 2023). Nevertheless, this finding should be interpreted cautiously because of the relatively small sample size and the limited number of patients in some subgroups.

Several limitations should be considered when interpreting the findings of this study. The relatively small sample size and single-center design may limit the generalizability of the results. In addition,

the study focused only on the *GLCC11* rs37973 polymorphism and did not directly evaluate treatment outcomes or corticosteroid responsiveness. Other related genetic variants and inflammatory biomarkers were also not investigated. Despite these limitations, the present study provides preliminary descriptive data regarding the distribution of the *GLCC11* rs37973 polymorphism in Vietnamese children with bronchial asthma and may contribute to future studies investigating genetic factors related to asthma management and corticosteroid responsiveness.

CONCLUSION

The *GLCC11* rs37973 AG genotype and G allele were the predominant genetic characteristics observed among children with bronchial asthma in this study. Most demographic and clinical characteristics were not significantly associated with rs37973 genotype distribution, except for a history of COVID-19 infection. These findings provide preliminary data on the distribution of the *GLCC11* rs37973 polymorphism in Vietnamese pediatric asthma patients and may contribute to future studies investigating genetic factors related to asthma management and corticosteroid responsiveness.

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