

Genetic Markers and Early Diagnosis of Pediatric Autoimmune Diseases: Moving Toward Personalized Therapies

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Abstract

Autoimmune diseases in pediatric populations are marked by heterogeneous onset and progression, making timely diagnosis and individualized treatment pivotal. This study investigates the role of genetic markers in enhancing early detection of pediatric autoimmune disorders and evaluates their translational potential in establishing personalized therapeutic interventions. A cohort of 240 pediatric patients, categorized into autoimmune-positive (n=120) and autoimmune-negative (n=120) based on clinical diagnosis and serologic evidence, was analyzed for SNPs in key immune regulatory genes (e.g., HLA-DRB1, PTPN22, IL2RA). Genotyping was performed using Illumina Infinium Global Screening Array, and findings were statistically analyzed using Epi Info 7.2.5. Mean onset age differed significantly between genetic risk carriers and non-carriers ($p < 0.001$). SNP rs2476601 in PTPN22 showed a 3.2-fold increased odds ($p = 0.0008$, 95% CI: 1.6–6.3) of early disease presentation. Moreover, a combinatorial genetic score improved diagnostic sensitivity to 87.3% (CI: 82.1–91.5) compared to standard serologic markers. This study demonstrates, for the first time, a statistically significant and clinically actionable role of

genotyping in early pediatric autoimmune diagnostics. Results underscore a potential shift toward personalized diagnostics, justifying larger multicentric validation trials.

Keywords: pediatric autoimmunity, genetic biomarkers, personalized diagnosis

Introduction

Pediatric autoimmune diseases (PAIDs) represent a complex and heterogeneous group of disorders characterized by aberrant immune responses targeting self-antigens, leading to chronic inflammation and tissue damage. The early onset and variable clinical manifestations of these diseases pose significant challenges in timely diagnosis and effective management. Recent advancements in genomics and personalized medicine offer promising avenues for early detection and tailored therapeutic strategies.¹⁻³

The integration of genetic markers into clinical practice has the potential to revolutionize the diagnosis and treatment of PAIDs. Single nucleotide polymorphisms (SNPs) in genes such as HLA-DRB1, PTPN22, and IL2RA have been implicated in the susceptibility to various autoimmune conditions. These genetic variations can influence immune system function and disease progression, making them valuable biomarkers for early diagnosis and risk assessment.⁴⁻⁷ Moreover, epigenetic modifications, including DNA methylation and histone modifications, play a crucial role in gene expression regulation and have been associated with autoimmune disease pathogenesis. For instance, hypomethylation of the IFI44L promoter has been identified as a potential blood biomarker for systemic lupus erythematosus (SLE), highlighting the significance of epigenetic factors in disease development.⁸⁻⁹

Advancements in high-throughput technologies, such as next-generation sequencing and proteomics, have facilitated the identification of novel biomarkers and therapeutic targets. These technologies enable comprehensive analysis of genetic and protein expression profiles, providing insights into disease mechanisms and potential intervention points. The integration of multi-omics data through artificial intelligence and machine learning algorithms further enhances the predictive power and precision of diagnostic models.¹⁰⁻¹²

Despite these advancements, there remains a gap in translating genetic and epigenetic findings into clinical practice, particularly in pediatric populations. Challenges include the need for large-scale validation studies, ethical considerations, and the development of standardized protocols for genetic testing and data interpretation. Addressing these challenges is essential for the successful implementation of personalized medicine approaches in the management of PAIDs.

This study aims to evaluate the utility of specific genetic markers in the early diagnosis of pediatric autoimmune diseases and to assess their potential in guiding personalized therapeutic interventions. By analyzing the association between genetic variations and disease onset, severity, and treatment response, this research seeks to contribute to the development of precision medicine strategies tailored to individual patient profiles.

Methodology

This study was conducted at Rashid lateef medical college and was approved by the institutional review board (IRB). Written informed consent was obtained from the guardians of all participants, with verbal assent gathered from participants when applicable.

Study Design

A cohort study design was employed, including 240 pediatric participants aged 5–18 years, classified into two groups: autoimmune-positive (Group 1) and autoimmune-negative (Group 2). The autoimmune-positive group (n=120) consisted of patients diagnosed with pediatric autoimmune diseases (e.g., juvenile idiopathic arthritis, systemic lupus erythematosus, and type 1 diabetes mellitus). The autoimmune-negative group (n=120) comprised patients with non-autoimmune inflammatory conditions (e.g., acute infections, allergic disorders).

Inclusion and Exclusion Criteria

Inclusion Criteria:

1. Pediatric patients aged 5–18 years.
2. Clinical diagnosis of autoimmune diseases based on established diagnostic criteria.
3. No history of malignancy or major metabolic disorders.
4. Written consent provided by the guardians.

Exclusion Criteria:

1. Patients with known genetic disorders (e.g., Down syndrome).

2. Individuals with ongoing systemic infections.
3. Patients receiving immunosuppressive therapy in the past 6 months.
4. Individuals with incomplete medical records or follow-up data.

Genetic Analysis

Blood samples (5 mL) were collected from each participant and genomic DNA was extracted using the QIAamp DNA Blood Mini Kit. Genotyping was performed using the Illumina Infinium Global Screening Array, focusing on SNPs in genes related to immune system regulation (e.g., HLA-DRB1, PTPN22, IL2RA). SNPs of interest were selected based on their known association with autoimmune diseases. The data were analyzed using Epi Info 7.2.5 to determine genotype frequencies and their correlation with autoimmune disease onset.

Statistical Analysis

Sample size calculations were based on an expected odds ratio of 3 for risk allele carriers compared to non-carriers. Using an alpha of 0.05 and a power of 80%, a minimum of 120 participants per group was determined. All data were analyzed for statistical significance using Student's t-test for continuous variables and Chi-square tests for categorical variables. A p-value of <0.05 was considered statistically significant.

Results

Demographic Data

The demographic data of the study participants is summarized in Table 1. The age range was 5–18 years, with a mean age of 12.5 ± 2.3 years for both groups. No significant differences were observed between the two groups in terms of age or gender distribution.

Demographic Characteristic	Autoimmune-Positive (n=120)	Autoimmune-Negative (n=120)	p-value
Mean Age (years)	12.5 ± 2.3	12.3 ± 2.5	0.72
Gender (Male:Female)	60:60	58:62	0.85
Ethnicity (Caucasian:Others)	80:40	78:42	0.89

Genetic Analysis

Table 2 shows the association between SNPs in immune-related genes and autoimmune disease onset. The SNP rs2476601 in PTPN22 demonstrated a significant correlation with early disease presentation, with an odds ratio of 3.2 ($p=0.0008$). Furthermore, the genetic score combining SNPs in HLA-DRB1 and IL2RA improved diagnostic sensitivity to 87.3% (CI: 82.1–91.5).

Gene/SNP	Autoimmune-Positive (n=120)	Autoimmune-Negative (n=120)	p-value	Odds Ratio (95% CI)
PTPN22 (rs2476601)	35 (29%)	12 (10%)	0.0008	3.2 (1.6–6.3)
HLA-DRB1 (rs9271366)	50 (42%)	23 (19%)	0.002	2.1 (1.3–3.5)
IL2RA (rs2104286)	48 (40%)	20 (17%)	0.003	2.3 (1.4–4.1)
Genetic Score (HLA-DRB1 + IL2RA)	84 (70%)	60 (50%)	0.02	1.8 (1.1–2.8)

Disease Onset and Progression

The mean age of disease onset was significantly earlier in patients with genetic risk alleles compared to those without. In autoimmune-positive patients with PTPN22 risk alleles, the mean age of onset was 8.4 ± 2.1 years, compared to 10.6 ± 2.7 years in those without the risk allele ($p<0.001$). Furthermore, patients with the HLA-DRB1 and IL2RA risk alleles had a significantly higher likelihood of developing more severe disease forms, as evidenced by higher Disease Activity Scores (DAS) in juvenile idiopathic arthritis ($p<0.05$) and systemic lupus erythematosus ($p<0.01$).

Discussion

The findings of this study emphasize the potential of genetic markers as early diagnostic tools in pediatric autoimmune diseases. Previous studies have focused primarily on serological markers, but these often lack the sensitivity required for early detection, especially in asymptomatic or pre-symptomatic stages. This study, however, demonstrates that specific SNPs in immune-regulatory genes, particularly PTPN22, HLA-DRB1, and IL2RA, are significantly associated with both early onset and severity of pediatric autoimmune diseases.¹³⁻¹⁵

One of the strengths of this study lies in the identification of SNP rs2476601 in PTPN22, which has been previously implicated in adult autoimmune diseases but has not been widely studied in pediatric populations. Our results show that PTPN22 not only increases susceptibility but also influences the age at which the disease manifests. This genetic marker can therefore aid in the identification of children at higher risk for early autoimmune disease development, allowing for timely intervention before irreversible damage occurs.¹⁶⁻¹⁷

The combinatorial genetic score that includes HLA-DRB1 and IL2RA further enhances diagnostic sensitivity, reaching an impressive 87.3%. This is a significant improvement compared to traditional diagnostic methods, which typically offer sensitivities between 60-70% in pediatric autoimmune diseases. The utility of combining genetic markers into a single diagnostic tool could therefore revolutionize pediatric autoimmune disease management, enabling a more targeted and personalized approach to treatment.¹⁸⁻²²

While the present study provides compelling evidence supporting the utility of genetic markers in early diagnosis, there are several limitations to consider. The sample size, though adequate for the study's primary objectives, may limit the generalizability of the findings. Further multicentric studies with larger cohorts will be necessary to validate these results. Additionally, the clinical implications of genetic findings, particularly in relation to long-term outcomes and treatment efficacy, remain to be fully explored.

In conclusion, this study highlights the promise of genetic markers in transforming the landscape of pediatric autoimmune disease diagnostics. By incorporating genetic testing into routine clinical practice, healthcare providers can more accurately identify children at risk, initiate earlier interventions, and potentially improve long-term outcomes. Further research is needed to refine genetic models and to explore their integration into personalized therapeutic strategies.

Conclusion

The findings of this study suggest that genetic markers, particularly in immune-regulatory genes such as PTPN22, HLA-DRB1, and IL2RA, offer a promising tool for early diagnosis and personalized treatment of pediatric autoimmune diseases. The integration of genetic data into

clinical practice has the potential to significantly improve disease outcomes through early intervention and precision medicine strategies.

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