

The Evolving Spectrum of Pediatric Non-Type 1 Diabetes: A Clinical and Genetic Study

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Abstract

Purpose

This study aimed to characterize the clinical and genetic spectrum of non-type 1 diabetes in a tertiary pediatric endocrinology center and to evaluate temporal trends and factors associated with different diabetes subtypes.

Methods

This retrospective observational study included children and adolescents aged < 18 years diagnosed with non-type 1 diabetes at the Pediatric Endocrinology and Diabetes Unit, between 2011 and 2026. Patients were classified according to their final clinical and, when available, molecular diagnosis. Clinical, anthropometric, and biochemical characteristics were compared among diabetes subtypes.

Results

A total of 82 patients with non-type 1 diabetes were included. Type 2 diabetes was the most common subtype (38/82, 46.3%), followed by MODY (36/82, 43.9%) and other forms of non-type 1 diabetes (8/82, 9.8%). Eight different MODY-associated genes were identified, with *GCK*, *HNF1A*, *ABCC8* and *HNF4A* accounting for the majority of genetically confirmed cases. BMI SDS was significantly higher in patients with type 2 diabetes than in those with MODY or other non-type 1 diabetes ($P < 0.001$). C-peptide and insulin concentrations were also higher in type 2 diabetes than in MODY ($P = 0.006$ and $P = 0.003$, respectively). The distribution of diabetes subtypes did not differ significantly according to HbA1c category at diagnosis ($P = 0.227$).

Conclusion

Type 2 diabetes and MODY constituted the predominant forms of pediatric non-type 1 diabetes in this tertiary-center cohort. Clinical characteristics such as BMI and endogenous insulin secretion may provide useful supportive information for differentiating diabetes subtypes; however, HbA1c at diagnosis alone did not distinguish the major subtypes.

What is Known

- Pediatric non-type 1 diabetes is etiologically heterogeneous, with substantial clinical overlap between type 2 and monogenic diabetes.
- This overlap may complicate etiological classification in children and adolescents.

What is New

- The number of children diagnosed with type 2 diabetes increased over the study period.
- Molecular testing revealed substantial genetic heterogeneity among patients with MODY.

Introduction

Diabetes mellitus in childhood comprises a heterogeneous group of disorders with distinct etiologies, pathophysiological mechanisms, treatment strategies, and long-term outcomes. Although type 1 diabetes remains the predominant form of diabetes in children and adolescents, the epidemiology of pediatric diabetes has changed considerably over the past two decades. The increasing prevalence of childhood obesity has been accompanied by a rising incidence of youth-onset type 2 diabetes, while advances in molecular genetic testing have substantially improved the recognition of monogenic diabetes, resulting in an increasingly diverse spectrum of non-type 1 diabetes encountered in pediatric practice [1-3].

Non-type 1 diabetes includes type 2 diabetes, maturity-onset diabetes of the young (MODY), syndromic diabetes, and other rare monogenic or secondary forms of diabetes. Although these disorders may share overlapping clinical features, they differ markedly in their genetic basis, disease progression, therapeutic requirements, risk of complications, and implications for genetic counseling. Consequently, accurate etiological classification has become an essential component of pediatric diabetes care, enabling personalized treatment and appropriate long-term follow-up [2-4].

Monogenic diabetes represents a small but clinically important proportion of pediatric diabetes and results from pathogenic variants affecting genes involved in pancreatic β -cell development, insulin secretion, or insulin action [2,3]. Establishing the correct molecular diagnosis is clinically important because it may alter treatment, predict associated extra-pancreatic manifestations, facilitate family screening, and improve genetic counseling. The widespread implementation of next-generation sequencing has further expanded the spectrum of recognized monogenic diabetes, including several recently identified disease-causing genes [2].

Previous pediatric studies have primarily focused on the overall distribution of diabetes, including type 1 diabetes, whereas data specifically addressing the clinical and genetic characteristics of children with non-type 1 diabetes remain limited. A Turkish single-center study demonstrated an increasing frequency of pediatric type 2 diabetes over time and highlighted the growing recognition of MODY; however, genetic confirmation was available in only a subset of clinically suspected patients and comprehensive characterization of rare monogenic and syndromic diabetes was lacking [5].

Therefore, the present study aimed to describe the etiologic distribution, clinical characteristics, temporal trends, and genetic spectrum of pediatric non-type 1 diabetes diagnosed at a tertiary referral center. We also sought to compare the clinical features of different non-type 1 diabetes subtypes and to summarize the phenotypic and molecular characteristics of patients with genetically confirmed

monogenic diabetes, thereby emphasizing the clinical value of careful phenotypic assessment and targeted genetic testing.

Methods

Study Design and Study Population

This retrospective observational study included children and adolescents aged <18 years who presented to the Division of Pediatric Endocrinology, Suleyman Demirel University Faculty of Medicine, between 2011 and 2026 and were diagnosed with diabetes mellitus other than type 1 diabetes. Patients with a diagnosis of non-type 1 diabetes during the study period were identified from the medical records and included in the study.

Patients were classified according to their final clinical and, when available, molecular diagnosis. The study population included patients with maturity-onset diabetes of the young (MODY), type 2 diabetes, syndromic diabetes, other monogenic forms of diabetes, and secondary diabetes.

Diabetes mellitus was diagnosed according to standard pediatric diagnostic criteria based on fasting or random plasma glucose, HbA1c or oral glucose tolerance testing, as applicable [6].

Classification of Diabetes Subtypes

MODY was clinically suspected based on a combination of features suggestive of monogenic diabetes, including a multigenerational family history of diabetes, absence of typical features of insulin resistance, relatively preserved endogenous insulin secretion, and/or a clinical course atypical for type 1 or type 2 diabetes. Patients with clinical suspicion of MODY generally underwent a MODY gene panel, and those with an identified causative variant were classified as genetically confirmed MODY [2].

Variants classified as pathogenic or likely pathogenic according to established variant interpretation criteria were considered causative. Variants of uncertain significance were not considered diagnostic.

Type 2 diabetes was diagnosed based on overweight or obesity, clinical features of insulin resistance, family history of type 2 diabetes, and the clinical course and treatment response [1].

Syndromic diabetes was defined as diabetes occurring as part of a recognized genetic syndrome, whereas other monogenic diabetes included genetically confirmed monogenic forms that did not meet the definition of MODY or syndromic diabetes. Secondary diabetes was defined as diabetes associated with an underlying condition or recognized secondary cause.

Diabetes-related autoantibody results, including glutamic acid decarboxylase antibodies (GAD), islet cell antibodies (ICA), and insulin autoantibodies (IAA), were obtained from the medical records; these three

antibodies constituted the routine autoantibody panel throughout the study period. Positivity for ≥ 1 diabetes-related autoantibody was defined as positivity for at least one of GAD, ICA, or IAA.

Statistical Analysis

Continuous variables were expressed as median (interquartile range [IQR]), and categorical variables as number and percentage. Comparisons of continuous variables among the three diabetes subtypes were performed using the Kruskal–Wallis test. When the overall comparison was statistically significant, pairwise comparisons were performed using Dunn’s post-hoc test with Bonferroni correction. Categorical variables were compared using the chi-square test or Fisher’s exact test, as appropriate. For statistically significant overall comparisons, pairwise categorical comparisons were performed with Bonferroni correction. Comparisons across HbA1c categories were performed using the Kruskal–Wallis test for continuous variables and the chi-square test or Fisher’s exact test for categorical variables, as appropriate. A two-sided P value of <0.05 was considered statistically significant. Statistical analyses were performed using IBM SPSS Statistics version 29.0 (IBM Corp., Armonk, NY, USA).

Ethics

This study was performed in accordance with the principles of the Declaration of Helsinki. The study protocol was approved by the Health Sciences Ethics Committee of Suleyman Demirel University (Meeting No. 129, Decision No. 28; August 25, 2026).

Results

Study population and distribution of diabetes subtypes

A total of 82 children and adolescents with non-type 1 diabetes were included in the study. Type 2 diabetes was the most common subtype, comprising 38 patients (46.3%), followed by MODY in 36 patients (43.9%). The remaining eight patients (9.8%) had other forms of non-type 1 diabetes, including syndromic diabetes, other monogenic diabetes, and secondary diabetes. The baseline demographic, clinical, anthropometric, and laboratory characteristics of the study population according to diabetes subtype are presented in **Table 1**.

The median age at diagnosis was 13.0 years (IQR, 9.8–16.0) in patients with MODY, 15.0 years (IQR, 13.0–16.0) in those with type 2 diabetes, and 13.5 years (IQR, 9.0–15.5) in patients with other non-type 1 diabetes ($P=0.068$). Female sex was similarly distributed among the three groups ($P=0.774$).

Clinical and biochemical characteristics

Anthropometric characteristics differed significantly among diabetes subtypes. Height SDS differed significantly among the groups ($P=0.002$), with lower values observed in patients with other non-type 1

diabetes compared with both MODY and type 2 diabetes. BMI SDS was significantly higher in patients with type 2 diabetes than in both MODY and other non-type 1 diabetes ($P<0.001$).

A family history of diabetes was present in 77.8% of patients with MODY, 78.9% of those with type 2 diabetes, and 50.0% of those with other non-type 1 diabetes ($P=0.205$). Obesity was more frequent in patients with type 2 diabetes than in those with MODY ($P=0.015$). Weight loss at diagnosis was also more common in the type 2 diabetes group than in the MODY group ($P=0.042$). In contrast, incidental hyperglycemia was more frequent in patients with MODY and other non-type 1 diabetes than in those with type 2 diabetes ($P=0.004$ and $P=0.002$, respectively).

Diabetes-related autoantibody positivity was observed in 12 of 36 patients with MODY (33.3%), compared with 5 of 38 patients with type 2 diabetes (13.2%) and none of the patients with other non-type 1 diabetes ($P=0.032$). GAD antibody positivity was detected in 2 patients with MODY (5.6%), 3 patients with type 2 diabetes (7.9%), and none of the patients with other non-type 1 diabetes ($P=0.686$).

Median fasting plasma glucose and HbA1c levels did not differ significantly among the three groups ($P=0.217$ and $P=0.079$, respectively). C-peptide concentrations differed significantly among the groups ($P=0.008$), with higher levels in patients with type 2 diabetes than in those with MODY ($P=0.006$). Insulin concentrations were also significantly different among the groups ($P=0.005$), with higher levels in patients with type 2 diabetes than in those with MODY ($P=0.003$).

HbA1c levels at diagnosis

Patients were categorized into three groups according to HbA1c level at diagnosis: $<7\%$, $7\text{--}10\%$, and $\geq 10\%$. Thirty patients were classified into the $<7\%$ group, 28 into the $7\text{--}10\%$ group, and 24 into the $\geq 10\%$ group (Table 2). The distribution of HbA1c levels at diagnosis according to diabetes subtype is shown in Figure 1.

MODY accounted for 60.0%, 35.7%, and 33.3% of patients in the $<7\%$, $7\text{--}10\%$, and $\geq 10\%$ HbA1c groups, respectively. Type 2 diabetes accounted for 36.7%, 50.0%, and 54.2% of patients in the corresponding groups. The distribution of diabetes subtypes did not differ significantly across HbA1c categories ($P=0.227$).

Fasting plasma glucose increased significantly across the HbA1c categories, with median values of 115.0 mg/dL (IQR, 100.5–126.3), 157.0 mg/dL (IQR, 123.5–235.5), and 295.5 mg/dL (IQR, 255.5–380.3) in the $<7\%$, $7\text{--}10\%$, and $\geq 10\%$ groups, respectively ($P<0.001$). BMI SDS, C-peptide, and insulin concentrations did not differ significantly across HbA1c categories.

Genetic spectrum of MODY

Among the 36 patients classified as MODY, 31 had a genetically confirmed causative variant and were included in the genotype-specific analysis. Eight different causative genes were identified (Table 3). *GCK* was the most frequently identified gene (n=9), followed by *HNF1A* (n=8), *ABCC8* (n=5) and *HNF4A* (n=5). *BLK*, *PDX1*, *CEL* and *HNF1B* variants were each identified in one patient.

The clinical characteristics of genetically confirmed MODY patients according to the causative gene are summarized in **Table 3**.

Other forms of non-type 1 diabetes

Eight patients (9.8%) had other forms of non-type 1 diabetes. These included three patients with Wolfram syndrome (DIDMOAD), two patients with *TRMT10A*-related diabetes, one patient with Rabson–Mendenhall syndrome, one patient with cystic fibrosis-related diabetes, and one patient with post-dumping hyperglycemia.

Temporal distribution of diabetes subtypes

The number of patients diagnosed with non-type 1 diabetes increased across the study periods. Among patients with an available diagnosis year, 12 were diagnosed during 2011–2015, 29 during 2016–2020, and 41 during 2021–2026 (Figure 2). The number of patients with type 2 diabetes increased from 3 in 2011–2015 to 12 in 2016–2020 and 23 in 2021–2026, whereas the number of patients with MODY was 7, 15 and 14 across the three periods, respectively.

Discussion

The present study characterizes the clinical and genetic spectrum of pediatric non-type 1 diabetes in a tertiary pediatric endocrinology center over a 15-year period. Type 2 diabetes was the most common subtype, accounting for 46.3% of the cohort, followed closely by MODY (43.9%). Patients with type 2 diabetes had significantly higher BMI SDS and a higher frequency of obesity, whereas patients with MODY had lower C-peptide and insulin concentrations. Importantly, a causative genetic variant was identified in 31 of 36 patients clinically classified as MODY, with *GCK*, *HNF1A*, *ABCC8* and *HNF4A* accounting for the majority of genetically confirmed cases. These findings emphasize the marked clinical and genetic heterogeneity of pediatric non-type 1 diabetes and the importance of appropriate etiological classification.

The increasing number of patients identified with non-type 1 diabetes over the study period may reflect changes in referral patterns, disease recognition, and the increasing prevalence of youth-onset type 2 diabetes. In our study, type 2 diabetes accounted for 46.3% of non-type 1 diabetes cases, while MODY accounted for 43.9%. When patients with type 1 diabetes were excluded from the cohort reported by Haliloğlu et al., type 2 diabetes and clinical MODY accounted for 48 of 134 (35.8%) and 44 of 134 (32.8%) non-type 1 diabetes cases, respectively [5]. Similarly, after excluding type 1 diabetes from the cohort reported by Kim et al., type 2 diabetes accounted for 49 of 70 (70.0%) non-type 1 diabetes cases,

whereas clinical MODY accounted for 8 of 70 (11.4%) [7]. These differences may reflect variations in referral patterns, population characteristics, diagnostic approaches, and access to genetic testing across centers.

The significantly higher BMI SDS and greater frequency of obesity observed in our type 2 diabetes group support the clinical value of anthropometric assessment in the initial etiological evaluation of pediatric diabetes. However, obesity alone cannot reliably distinguish type 2 diabetes from monogenic diabetes, particularly in populations with increasing childhood obesity. The clinical overlap between these entities may lead to diagnostic uncertainty, particularly in children with a strong family history of diabetes. Previous studies have similarly emphasized the difficulty of distinguishing type 2 diabetes from MODY based solely on clinical characteristics [5,8]. In our cohort, the relatively high proportion of MODY may be related to the tertiary referral setting and the use of MODY gene panels in patients with clinical suspicion of monogenic diabetes. Among the 36 patients clinically classified as MODY, 31 had a genetically confirmed causative variant, indicating a high diagnostic yield in this clinically selected population. This finding emphasizes that the high proportion of MODY observed in our cohort should not be interpreted as a population prevalence estimate, but rather as a reflection of the selected nature of a tertiary pediatric endocrinology cohort.

Interestingly, the distribution of diabetes subtypes did not differ significantly according to HbA1c category at diagnosis. Although MODY accounted for a greater proportion of patients with HbA1c <7%, the overall distribution across HbA1c categories was not statistically different. This finding suggests that HbA1c level at presentation alone is insufficient for etiological classification of non-type 1 diabetes. The marked increase in fasting plasma glucose across HbA1c categories, despite the absence of a significant difference in diabetes subtype distribution, further supports the concept that the degree of hyperglycemia at presentation reflects glycemic severity rather than the underlying etiology of diabetes. Therefore, clinical phenotype and glycemic severity at diagnosis should be considered as complementary rather than definitive features, and molecular testing remains essential when monogenic diabetes is suspected.

The genetic spectrum observed in our cohort was dominated by *GCK* and *HNF1A*, followed by *ABCC8* and *HNF4A*. These four genes accounted for the majority of genetically confirmed MODY cases, whereas *BLK*, *PDX1*, *CEL* and *HNF1B* were each identified in a single patient. Previous studies have demonstrated considerable variation in the distribution of MODY-associated genes between populations. *GCK*, *HNF1A* and *HNF4A* are among the most frequently recognized causes of MODY, although the relative contribution of individual genes varies according to genetic background, referral patterns, and access to molecular testing [2,8-10,13]. The identification of several less common genes in our cohort supports the use of multigene testing rather than restricting molecular evaluation to the most common MODY genes.

An important finding of our study was the difference in endogenous insulin secretion between diabetes subtypes. C-peptide and insulin concentrations were significantly higher in patients with type 2 diabetes than in those with MODY, consistent with greater insulin resistance and preserved endogenous insulin

secretion in type 2 diabetes. Conversely, the lower C-peptide concentrations observed in MODY are compatible with impaired β -cell function. Similar differences in C-peptide concentrations between pediatric type 2 diabetes and MODY have been reported previously [5,7]. These findings suggest that C-peptide may provide useful supportive information when distinguishing monogenic diabetes from type 2 diabetes, although it should not be used as a stand-alone diagnostic criterion.

The distribution of diabetes-related autoantibodies in our cohort also warrants consideration. Autoantibody positivity was observed in 5 of 38 patients with type 2 diabetes (13.2%), which is consistent with previous reports indicating that pancreatic autoimmunity may be detected in approximately 10–15% of adolescents clinically diagnosed with type 2 diabetes [12]. In contrast, 12 of 36 patients clinically classified as MODY (33.3%) had at least one diabetes-related autoantibody, and autoantibody positivity was present in 9 of 31 genetically confirmed MODY patients (29.0%). This proportion is considerably higher than that reported in previous MODY cohorts. In the large multicenter Turkish study by Özsü et al., diabetes-associated autoantibodies were detected in 11% of 224 genetically diagnosed MODY patients, including anti-GAD, anti-islet, and anti-insulin antibodies [13]. Similarly, a recent pediatric tertiary-center study reported islet autoantibody positivity in 2 of 39 patients with genetically confirmed MODY (5.1%) [14]. In contrast, McDonald et al. reported GAD and/or IA-2 antibodies in fewer than 1% of 508 patients with MODY [15]. These differences should be interpreted cautiously because antibody panels, assays, patient selection, and diagnostic criteria varied across studies. Nevertheless, our findings, together with recent reports, suggest that the presence of diabetes-related autoantibodies should not be regarded as an absolute exclusion criterion for monogenic diabetes when the clinical phenotype and molecular findings support a MODY diagnosis.

Our study also demonstrated the clinical heterogeneity of rare non-type 1 diabetes. Three patients had Wolfram syndrome, while other monogenic diabetes included *TRMT10A*-related diabetes and Rabson–Mendenhall syndrome. Secondary diabetes was represented by cystic fibrosis-related diabetes and post-dumping hyperglycemia. Previous tertiary-center studies have emphasized that syndromic and rare monogenic diabetes may initially be difficult to distinguish from more common diabetes subtypes and that extra-pancreatic manifestations may provide important diagnostic clues [2,7]. The recognition of these conditions is clinically important because the underlying genetic or systemic diagnosis may influence treatment, surveillance, prognosis, and genetic counseling.

The clinical importance of establishing a molecular diagnosis extends beyond diagnostic classification. Specific monogenic diabetes subtypes may have substantially different therapeutic approaches. For example, patients with diabetes caused by *HNF1A*, *HNF4A*, *ABCC8* and related defects may respond particularly well to sulfonylureas, allowing treatment modification in selected patients who might otherwise be treated with insulin [2,11]. Molecular diagnosis also enables identification of affected relatives and facilitates appropriate genetic counseling [7,11]. Thus, the relatively high diagnostic yield of genetic testing in our clinically selected MODY population supports the incorporation of molecular testing into the diagnostic evaluation of children and adolescents whose clinical phenotype is not typical for type 1 or type 2 diabetes.

Strengths and limitations

The major strengths of our study are the relatively long observation period, the focus specifically on non-type 1 diabetes, and the detailed characterization of genetically confirmed MODY. The inclusion of both common and rare forms of non-type 1 diabetes also provides a broad overview of the etiological spectrum encountered in a tertiary pediatric endocrinology center.

Several limitations should be acknowledged. First, the retrospective, single-center design limits the generalizability of our findings. Second, genetic testing was primarily performed in patients with clinical suspicion of MODY rather than systematically in all patients with non-type 1 diabetes; therefore, selection bias may have influenced the observed genetic spectrum and diagnostic yield. Third, the number of patients with rare syndromic and monogenic forms was small, limiting meaningful statistical comparisons within these subgroups.

Conclusion

In conclusion, pediatric non-type 1 diabetes encompasses a broad and clinically heterogeneous spectrum, with type 2 diabetes and MODY representing the predominant subtypes in our tertiary-center cohort. The high proportion of genetically confirmed MODY among clinically suspected cases and the identification of diverse causative genes underscore the importance of considering monogenic diabetes in children and adolescents who do not fit the typical phenotype of type 1 or type 2 diabetes. An integrated approach combining clinical assessment, biochemical evaluation, and appropriately selected genetic testing may facilitate accurate diagnosis, individualized treatment, and appropriate genetic counseling.

Abbreviations

BMI
body mass index
GAD
glutamic acid decarboxylase
HbA1c
glycated hemoglobin
IQR
interquartile range
MODY
maturity-onset diabetes of the young
SDS
standard deviation score.

Declarations

Ethics Approval

This study was performed in accordance with the principles of the Declaration of Helsinki. The study protocol was approved by the Health Sciences Ethics Committee of Suleyman Demirel University (Meeting No. 129, Decision No. 28; August 25, 2026).

Consent to Participate

The study was conducted in accordance with the protocol approved by the institutional ethics committee.

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Competing Interests

The authors have no relevant financial or non-financial interests to disclose.

Data Availability

The datasets generated and/or analyzed during the current study are available from the corresponding author on reasonable request.

Author Contributions

Ozgur Pirgon conceived and designed the study.

Mehmet Izzet Acar collected and analyzed the data, interpreted the findings, evaluated the genetic data, and drafted the manuscript.

Kubra Boztepe contributed to data collection.

Nurten Zarif Ozkan performed the statistical analyses.

Nesibe Kubra Gol contributed to manuscript preparation and revision.

All authors critically reviewed and revised the manuscript and read and approved the final version.

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Tables

Table 1

Baseline demographic, clinical, anthropometric, and laboratory characteristics of children with non-type 1 diabetes according to diabetes subtype

Variable	MODY (n = 36)	Type 2 diabetes (n = 38)	Other non-type 1 diabetes (n = 8)	P
Demographic Characteristics				
Age at diagnosis, years	13.0 (9.8–16.0)	15.0 (13.0–16.0)	13.5 (9.0–15.5)	0.068
Female sex, n (%)	23 (63.9)	27 (71.1)	5 (62.5)	0.774
Anthropometric Characteristics				
Height SDS	0.10 (– 0.54–0.67)	0.27 (– 0.41–0.53)	–1.44 (– 1.94 to – 1.01)	*0.002
BMI SDS	0.44 (– 0.27–1.35)	3.03 (2.14–3.68)	–1.80 (– 2.04–1.16)	*<0.001
Clinical Presentation				
Family history of diabetes, n (%)	28 (77.8)	30 (78.9)	4 (50.0)	0.205
Obesity, n (%)	3 (8.3)	14 (36.8)	0 (0)	*0.003
Polyuria, n (%)	13 (36.1)	9 (23.7)	2 (25.0)	0.483
Polydipsia, n (%)	12 (33.3)	8 (21.1)	1 (12.5)	0.323
Polyphagia, n (%)	4 (11.1)	1 (2.6)	0 (0)	0.235
Weight loss, n (%)	4 (11.1)	14 (36.8)	0 (0)	*0.008
Incidental hyperglycemia, n (%)	16 (44.4)	4 (10.5)	6 (75.0)	*<0.001
Laboratory Findings at Diagnosis				
Fasting plasma glucose, mg/dL	127 (113–256)	159 (118–245)	269 (221–301)	0.217
Footnote. Continuous variables are presented as median (interquartile range [IQR]) and categorical variables as n (%). Continuous variables were compared using the Kruskal–Wallis test and categorical variables using the chi-square test or Fisher's exact test, as appropriate. For statistically significant overall comparisons, pairwise comparisons were performed with Bonferroni correction; significant pairwise P values are reported in the text.				
Abbreviations: BMI SDS, body mass index standard deviation score; GAD, glutamic acid decarboxylase; IQR, interquartile range; SDS, standard deviation score.				

Variable	MODY (n = 36)	Type 2 diabetes (n = 38)	Other non-type 1 diabetes (n = 8)	P
Demographic Characteristics				
HbA1c, %	6.9 (6.4–9.8)	8.6 (6.9–11.08)	7.6 (7.15–12.58)	0.079
C-peptide, ng/mL	1.53 (1.21–2.79)	3.72 (2.38–4.57)	3.36 (1.23–5.44)	*0.008
Insulin, µIU/mL	15.0 (6.39–29.05)	28.0 (23.15–45.35)	20.13 (14.60–41.17)	*0.005
Autoantibody Status				
GAD positivity, n (%)	2 (5.6)	3 (7.9)	0 (0)	0.686
≥ 1 diabetes-related autoantibody positivity, n (%)	12 (33.3%)	5 (13.2%)	0 (0%)	*0.032
Footnote. Continuous variables are presented as median (interquartile range [IQR]) and categorical variables as n (%). Continuous variables were compared using the Kruskal–Wallis test and categorical variables using the chi-square test or Fisher’s exact test, as appropriate. For statistically significant overall comparisons, pairwise comparisons were performed with Bonferroni correction; significant pairwise P values are reported in the text.				
Abbreviations: BMI SDS, body mass index standard deviation score; GAD, glutamic acid decarboxylase; IQR, interquartile range; SDS, standard deviation score.				

Table 2
Clinical characteristics according to HbA1c level at diagnosis

Variable	< 7%	7–10%	≥ 10%	P
Number of patients, n	30	28	24	—
MODY, n (%)	18 (60.0)	10 (35.7)	8 (33.3)	0.082
Syndromic diabetes, n (%)	0 (0)	2 (7.1)	1 (4.1)	0.686
Other monogenic diabetes, n (%)	0 (0)	1 (3.5)	2 (8.3)	0.530
Type 2 diabetes, n (%)	11 (36.7)	14 (50.0)	13 (54.2)	0.392
Secondary diabetes, n (%)	1 (3.3)	1 (3.5)	0 (0)	0.651
Age at diagnosis (years)	13.0 (11.3–15.8)	15.0 (12.0–16.0)	14.5 (12.0–16.0)	0.395
BMI SDS	0.55 (– 0.24–2.66)	2.00 (0.90–2.82)	2.33 (0.71–3.33)	0.170
Fasting plasma glucose (mg/dL)	115.0 (100.5–126.3)	157 (123.5–235.5)	295.5 (255.5–380.3)	*<0.001
C-peptide (ng/mL)	1.67 (1.29–3.82)	3.34 (2.28–4.03)	2.30 (1.40–4.35)	0.338
Insulin (μIU/mL)	24.10 (12.61–42.58)	27.10 (14.70–36.10)	21.52 (9.15–34.35)	0.633
Diabetes subtype distribution, overall				0.227
Footnote. Continuous variables are presented as median (interquartile range [IQR]) and categorical variables as n (%). Continuous variables were compared using the Kruskal–Wallis test and categorical variables using the chi-square test or Fisher’s exact test, as appropriate.				

Table 3

Clinical characteristics of genetically confirmed MODY according to the disease-causing gene

Causative gene	Patients, n (%)	Female, n (%)	Age at diagnosis (years)	Family history of diabetes, n (%)	HbA1c at diagnosis (%)	C-peptide (ng/mL)
GCK	9 (29.0)	6 (66.7)	12.0 (8.0–14.0)	9 (100)	6.4 (6.3–6.5)	1.53 (0.70–2.79)
HNF1A	8 (25.8)	5 (62.5)	13.5 (11.5–14.8)	8 (100)	6.55 (6.43–8.23)	1.77 (1.23–2.24)
ABCC8	5 (16.1)	4 (80.0)	16.0 (13.3–18.3)	1 (20.0)	9.7 (7.8–11.4)	2.06 (1.37–3.52)
HNF4A	5 (16.1)	3 (60.0)	7.0 (6.0–12.0)	4 (80.0)	10.2 (8.6–11.1)	1.21 (0.37–1.21)
BLK	1 (3.2)	1 (100)	17	0 (0)	6.8	—
PDX1	1 (3.2)	1 (100)	2	0 (0)	11.0	0.21
CEL	1 (3.2)	1 (100)	16	1 (100)	15.4	2.10
HNF1B	1 (3.2)	0 (0)	8	1 (100)	5.8	—
Total	31 (100)	—	—	—	—	—
Footnote. Continuous variables are presented as median (interquartile range [IQR]). For genes represented by a single patient, individual values are reported.						

Figures

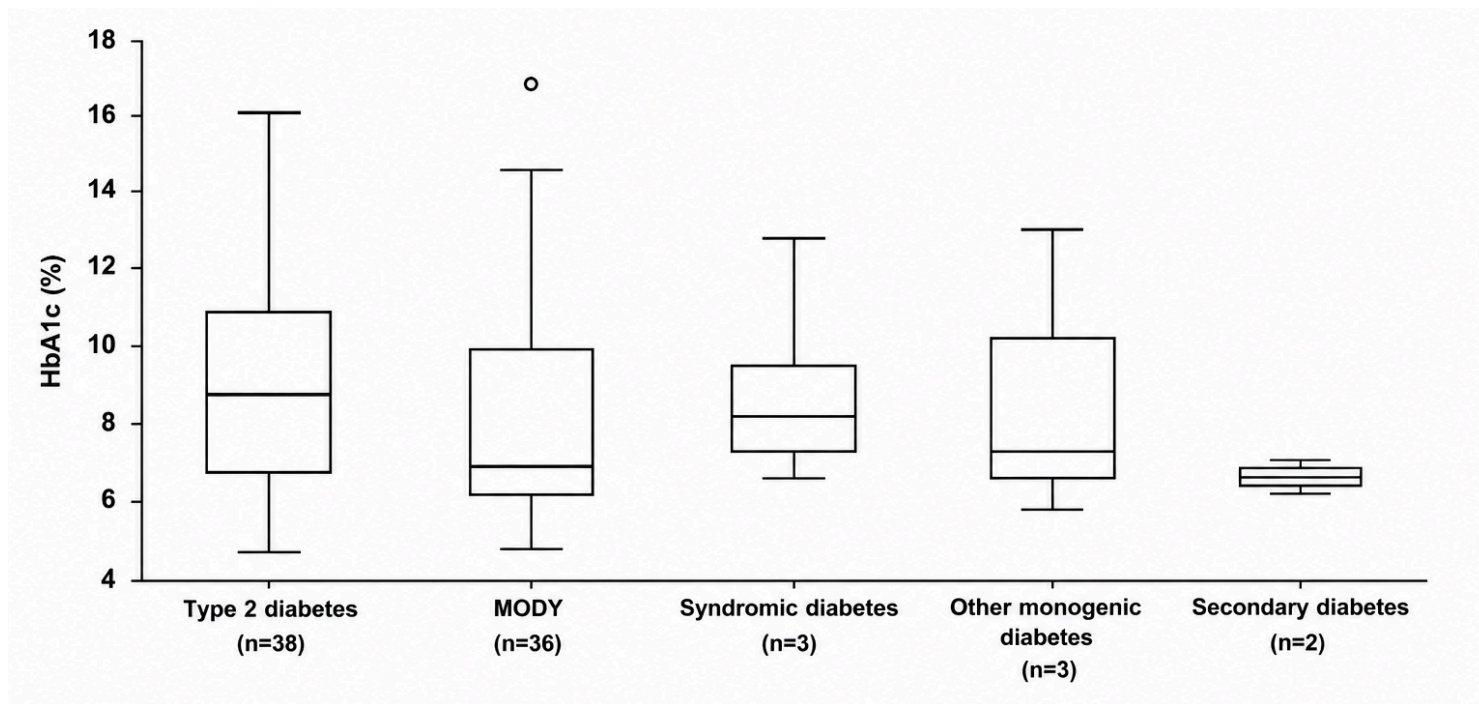


Figure 1

Distribution of HbA1c levels at diagnosis according to diabetes subtype

Boxes represent the interquartile range, horizontal lines indicate the median, and outliers are shown as individual points

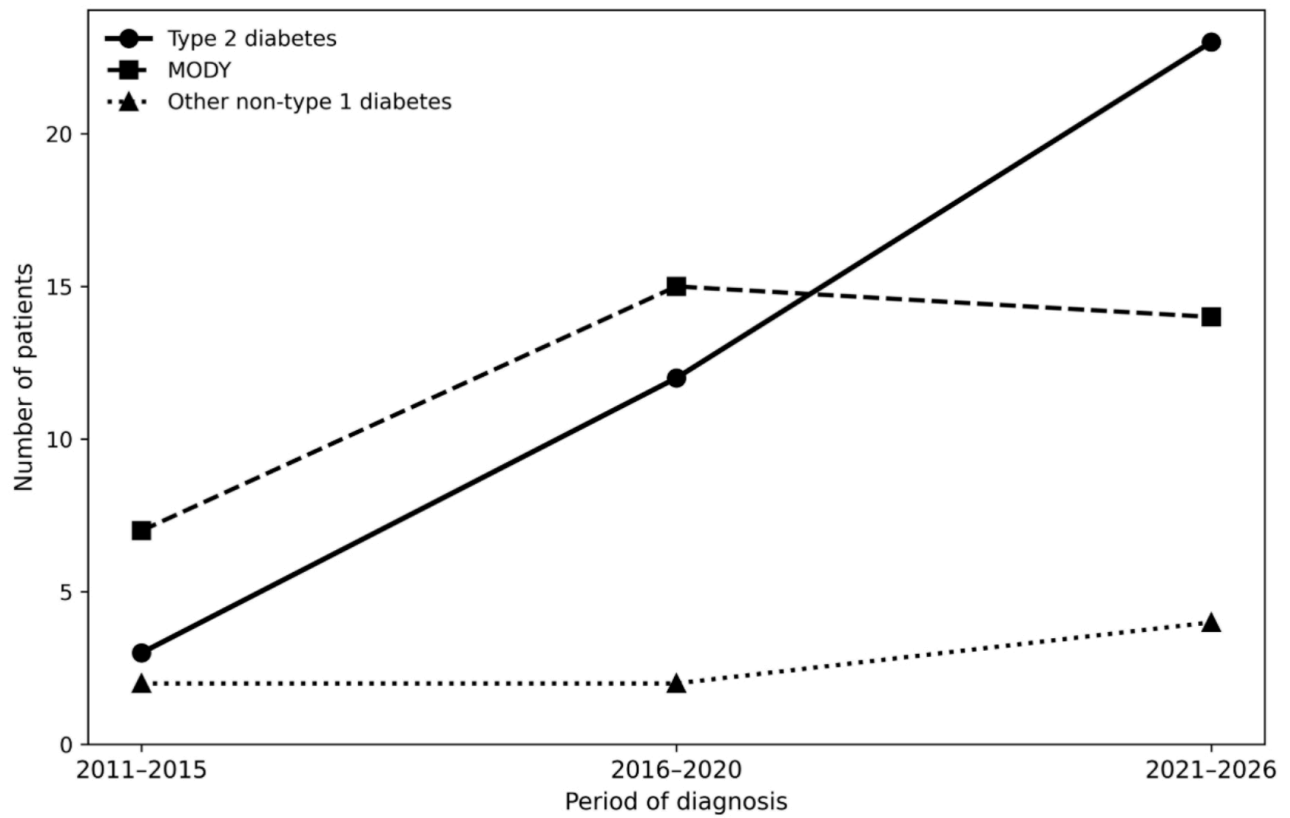


Figure 2

Temporal distribution of diabetes subtypes according to the period of diagnosis