

Prevalence of monogenic diabetes in the Lithuanian pediatric and young adult population

Valerie M. Schwitzgebel¹, Mirjam Dirlewanger¹, Philippe Klee¹, Federico Santoni², Jean-Louis Blouin, Dovile Razanskaite-Virbickiene³, Evalda Danyte³, Rimante Dobrovolskiene³, Dalia Marciulionyte³, Ingrida Stankute³ and Rasa Verkauskiene³

¹Pediatric Endocrinology and Diabetology Unit, University Hospitals of Geneva, 1211 Geneva, Diabetes Center, Faculty of Medicine, University of Geneva, Geneva, Switzerland.

²Department of Genetic Medicine, University Hospitals of Geneva, 1211 Geneva, Switzerland.

³Department and Institute of Endocrinology, Medical Academy, Lithuanian, University of Health Sciences, Eiveniu 2, LT-50161 Kaunas, Lithuania.

Introduction

Monogenic diabetes is a heterogeneous group of metabolic disorders resulting from defects in single genes. Over 80% of the subjects remain undiagnosed, mainly because of lack of access to genetic testing. The aim of our study was to do a comprehensive genetic analysis of the whole pediatric and young adult autoimmune antibody negative diabetes population of Lithuania.

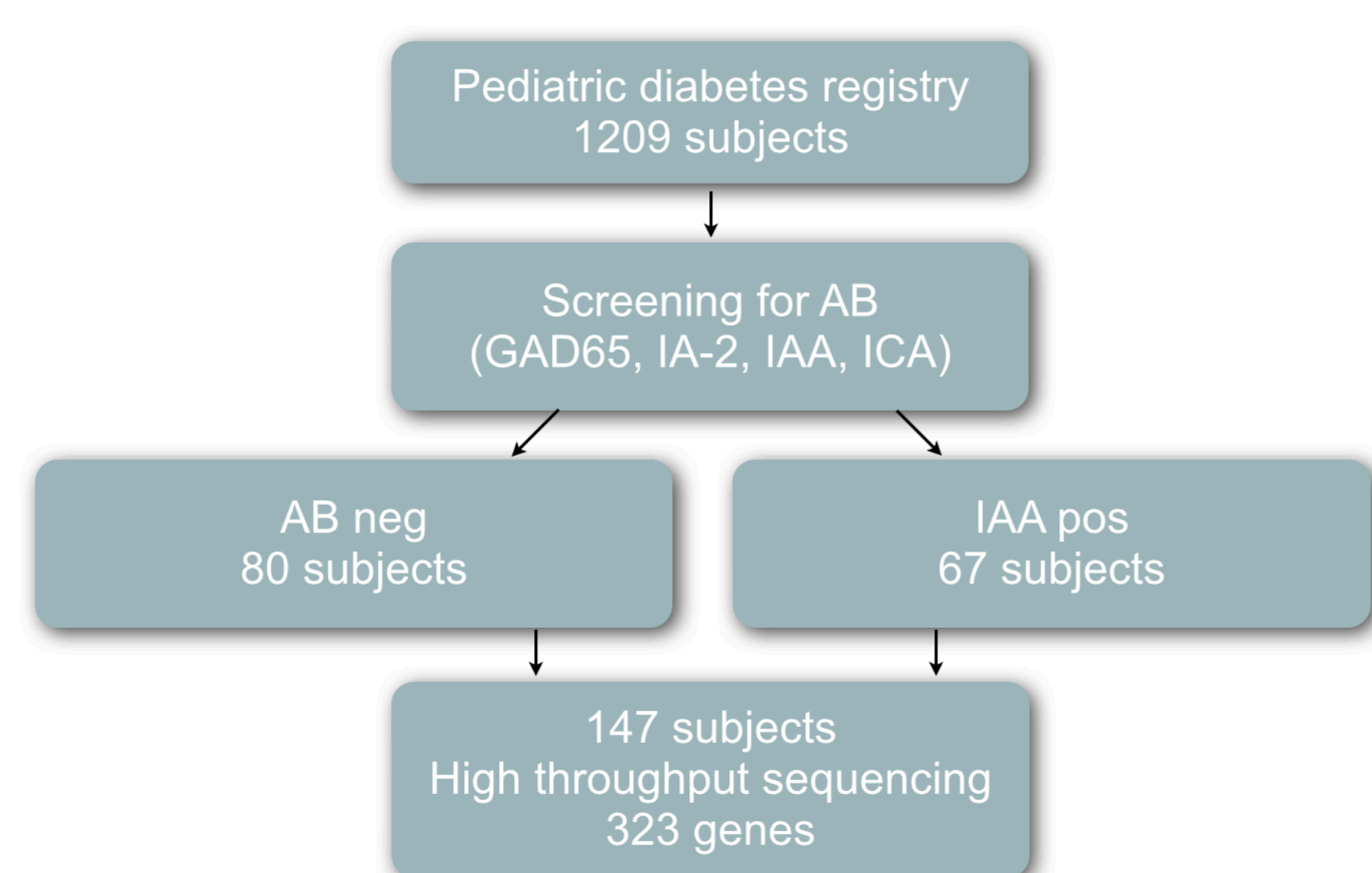
Methods

Overall 1209 diabetic subjects, including 860 children (age 0-18 years) and 349 young adults (age >18-25 years), were screened for the presence of islet autoimmune antibodies (GAD65A, IA-2, ICA and IAA). **Genetic analysis** was performed by high throughput sequencing from DNA selected for all coding and splicing regions of 323 genes involved in diabetes and pancreas development (including the 13 MODY genes). Raw sequencing data was analyzed using a locally developed pipeline. The most prominent variants were selected according to the score of prediction of damaging effects on the respective proteins using SIFT, Polyphen-2, MutationTester-2 and confirmed by Sanger sequencing.

Results

We screened 1209 subjects from the pediatric diabetes registry. The results are depicted in Fig 1.

Figure 1: Diagram of the screened subjects



Genetic analyses were performed in a total of 147 subjects with suspected monogenic diabetes. We included the IAA positive probands under insulin treatment, because the antibodies were tested after introduction of insulin. The clinical characteristics at diabetes onset are summarized in table 1, the genetic results are depicted in Fig. 2.

Table 1: Clinical characteristics at diabetes onset

	Diabetes onset <0.5 yrs	Diabetes onset 0.5-18 yrs	Diabetes onset >18-25 yrs
Number of patients (total 147)	4	133	10
% of collection	2.7	90.5	6.8
% of female	50	52	30
Age at onset (years)	0.3	7.8	21.3
% Pos FHx	50	44.4	60
HbA1c (mmol/mol (%))	83.6 (9.8)	66.1 (8.2)	78 (9.25)
Initial BG (mmol/l)	37.3 ±24.6	15.7 ±8.4	14.94 ±6.1
Ketosis %	50	52	33

Figure 2: The genetic results of the 147 subjects with suspicion of monogenic diabetes. Genetic analysis revealed mutations/variants in known MODY genes in 25.9% of the probands.

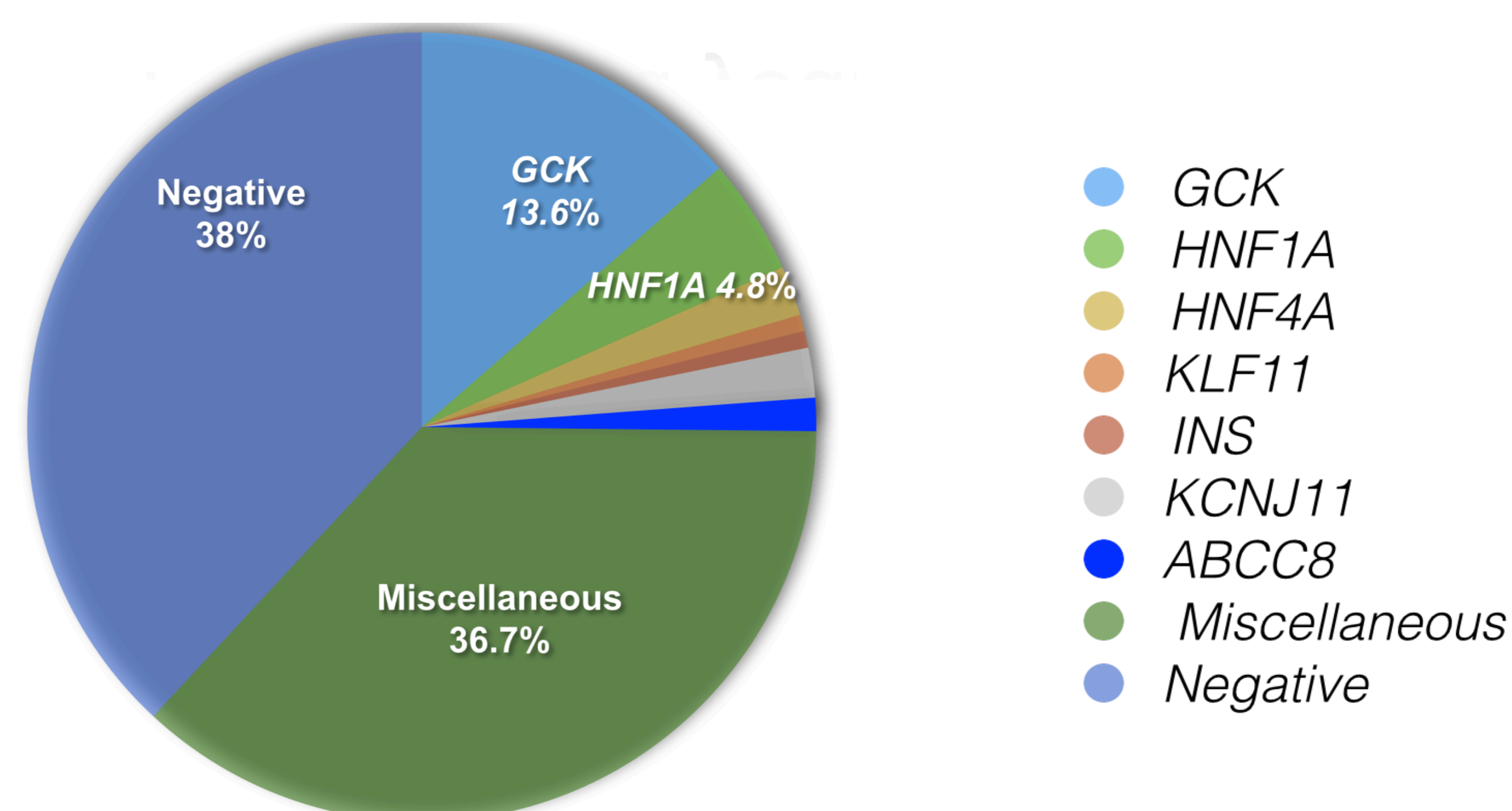


Table 2: The clinical characteristics of the different groups according to the gene defect are depicted.

Characteristics at study entry	GCK	HNF1A	HNF4A	INS	KCNJ11	ABCC8	KLF11
Number of patients (total 38)	20	7	3	1	4	2	1
Age (yrs)	12.48	18.28	23.3	17	11.72	22	1.5
HbA1c (mmol/mol (%))	43 (6.1)	45 (6.3)	72 (8.7)	93 (10.7)	73 (8.83)	113 (12.25)	55 (7.2)
Treatment							
Insulin (%)	0	57.1	100	100	100	100	100
Oral agent (%)	5	28.6					
None (%)	95						
Complications (%)							
Nephropathy (%)	0	0	33.3	0	66.67		0
Retinopathy (%)			33.3		33.3		
Polyneuropathy (%)			33.3			100	

Table 3: Prevalence of monogenic diabetes

	Subjects	Diabetes onset		
		<0.5 yrs	0.5-18 yrs	>18-25 yrs
Number of patients	1209	4	1191	14
AB neg cohort (except IAA)	147	4	133	10
MODY genes	38	4	31	3
Prevalence total cohort (%)	3.1	0.3	2.6	0.2
Prevalence AB neg cohort (%)	25.9	2.7	21.1	2.0
Prevalence AB neg cohort according to age (%)		100	23.3	30

Discussion and Conclusion

This testing approach yields a high rate of positive results. In the whole Lithuanian pediatric diabetic and young adult population (1209 probands), GCK mutations are found in 1.65%, HNF1A mutations in 0.6% and HNF4A mutations in 0.25% of the patients.

Authors have no conflict of interest