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# **Brief report:**

# Next generation sequencing for viruses in children with rapid onset type 1 diabetes

# Short running title: Viruses in type 1 diabetes

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#### Abstract

Viruses are candidate causal agents in the pathogenesis of type 1 diabetes. We hypothesized that children with a rapid onset of type 1 diabetes may have been exposed to strong causal infectious agents shortly before the initiation of islet autoimmunity and could be particularly helpful for the identification of causal agents of autoimmune diabetes. We used next generation sequencing to search for viruses in plasma samples and examined history of infections and fever in children from The Environmental Determinants of Diabetes in the Young (TEDDY) study who progressed to type 1 diabetes within 6 months from the appearance of islet autoimmunity, and in matched islet autoantibody negative controls. Viruses were infrequently detected in the period surrounding seroconversion in cases as well as controls. Moreover, infection history was similar between the children with rapid onset type 1 diabetes. These findings do not support a major role for viruses in the pathogenesis of early rapid onset autoimmune diabetes in childhood.

Type 1 diabetes is an autoimmune disorder where disease onset is preceded by a pre-clinical period of islet autoimmunity (1). Check points in the pre-clinical pathogenesis include the initiation of islet autoimmunity, and progression to type 1 diabetes, and the rate of this process is variable (2). Although the majority of children who develop type 1 diabetes take years to progress from islet autoimmunity to diabetes, some children have a rapid or fulminant disease progression where clinical diabetes occurs within months from the appearance of islet autoantibodies. These cases appear to have uncontrolled beta cell destruction and could be particularly helpful for the identification of causal agents of autoimmune diabetes. We hypothesized that such children may have been exposed to strong causal agents shortly before the appearance of islet autoantibodies. Infections in infancy are candidate causal agents of islet autoimmunity and type 1 diabetes (3-5). We therefore examined history of documented infections and fever as well as plasma samples for virus by unbiased deep sequencing in the period surrounding the initiation of islet autoimmunity in children who transitioned rapidly between autoimmunity and disease in The Environmental Determinants of Diabetes in the Young (TEDDY) study (6).

# Methods

#### The Environmental Determinants of Diabetes in the Young (TEDDY)

TEDDY is a prospective cohort study with the primary objective of identifying environmental factors that are associated with increased risk of islet autoimmunity and type 1 diabetes. It includes six clinical research centers in the US (Colorado, Georgia/Florida, Washington) and Europe (Finland, Germany, and Sweden). Infants were eligible if they were younger than 4.5 months and had high-risk human leukocyte antigen alleles (*HLA-DR, DQ*). From 2004-2010, TEDDY screened over 420,000 newborns and identified 21,589 children with high-risk HLA-DR, DQ genotypes. Of those, 8,677 (932 with first-degree family history of type 1 diabetes) were enrolled into prospective follow-up. Participants were seen every 3 months up to 4 years of age, and every 6 months after age 4 years. Blood samples were collected at each visit. Written informed consent was obtained from the parents. The Study was approved by the ethical committee of each site (6).

#### Study outcomes

The first primary outcome was the appearance of confirmed persistent islet autoimmunity, defined as positive for at least one autoantibody (GAD65A, IA-2A, or IAA) in both TEDDY core laboratories (Barbara Davis Center, Aurora, Colorado and the University of Bristol Laboratory, Bristol, UK) in two consecutive samples or in one sample in children who developed diabetes before a follow-up sample was available for autoantibody testing (7). Families were notified of the child's autoantibody results at their next study visit (i.e. after 3 months). The study endpoint was the development of type 1 diabetes as defined by the American Diabetes Association criteria (8).

# Study subject and study design

Of the 8,677 enrolled children, 355 had islet autoimmunity, and 86 of these progressed to type 1 diabetes by July 2011 when this analysis was designed. Twenty-four of the 86 children with progression to type 1 diabetes developed type 1 diabetes within 6 months from the appearance of islet autoimmunity and were defined as rapidly progressed type 1 diabetes cases (Figure 1 A).

Sequencing study. This study investigated whether virus sequences were detectable in plasma samples at two time points: 1. the '*last islet autoantibody negative sample*' prior to islet autoantibody seroconversion, and 2. the '*seroconversion sample*' (Figure 1B). Fourteen of the 24 cases had samples with sufficient volume available at both time points. For each of these 14 cases, 1 control child was selected. Controls were children who participated in the TEDDY study but remained negative for all three diabetes associated islet autoantibodies and for type 1 diabetes for at least 12 months after the respective event in cases. Controls were matched by clinical sites where the case child was enrolled and the family history of type 1 diabetes (yes or no), and were selected to have available plasma sample at the respective time points (Table 1). Controls were randomly selected from the pool of potential controls after being matched and conditioned.

*TEDDY book study*: This study investigated whether infections or fever were associated with early rapid progression to type 1 diabetes. All 24 cases, and for each case 3 controls were examined. Controls were selected by the same procedure as for the sequencing study. Three time points were examined in the 96 children (Figure 1B): 1. *Autoantibody negative period*, from birth to the last islet autoantibody negative sample, 2. *Seroconversion period*, from the last islet autoantibody negative sample to the first islet autoantibody positive sample, and 3. *Progression period*: from the first islet autoantibody positive sample to the date of type 1 diabetes diagnosis.

# Nucleic acid sequencing

Total nucleic acids were extracted from 250 µl plasma samples. Nucleic acid quantity and quality were assessed (Bioanalyzer) and samples were prepared for unbiased RT-PCR amplification using random octamer primer pools optimized for amplification of non-human sequences, and linked to an arbitrary 17-mer primer sequence. cDNA was then randomly amplified by PCR with the octamer-linked 17-mer primer in conjunction with the 17-mer primer sequence without the random octamer tail in a 1:9 ratio (9). Products of >70 bp were selected by column purification (MinElute, Qiagen, Hilden, Germany) and ligated to barcoded linkers for sequencing on the 454 Genome Sequencer FLX (454 Life Sciences, Branford, CT, USA) without fragmentation of the products (10). Raw sequence reads were trimmed to remove sequences derived from amplification primers and linkers, and filtered to eliminate highly repetitive sequences. Sequences were then clustered into non-redundant sets and unique reads assembled into contiguous sequences, which were compared to the non-redundant GenBank database at the nucleotide and the translated amino acid level.

#### TEDDY book data

Acute infections or illnesses experienced between study visits were collected with the corresponding dates from interviewing parents and provided every 3 months starting from age 6 months. Acute infections or illnesses were recorded using the International Classification of Disease (ICD)-10 codes, and categorized as respiratory tract, gastrointestinal or other infection. Fever was documented using one of the following ICD-10 codes; R50, R50.9, R50.8 or R56, and was assessed when reported with or without infection. Fever with a measured temperature  $\geq$ 38°C (101°F) was considered high fever.

# Statistical analysis

Findings from the sequencing study were summarized. Overall infections and fever reports before type 1 diabetes onset were analyzed and then assessed according to the three periods of disease progression in the study design. Infections and fever reported during each period of interest were examined as the count of all reports or the indicator of any report. Number of observations with the proportion or the mean with standard deviation (SD) was reported depending on the type of data. Conditional logistic regression adjusted for maternal age at delivery was used to obtain the estimate of odds ratio of the factor of interest in comparison of the matched case and controls.

*P*-values less than 0.05 were used to indicate statistical significance. All reported *p*-values are two-sided without adjustment for multiple testing. All statistical analyses were performed using SAS 9.2 (SAS Institute, Cary, NC).

# Results

# Sequencing study

Unbiased sequencing identified viruses in 6 of 56 plasma samples (Table 1). Virus positive samples were from 4 (1 case, 3 control children) of the 28 children analysed. The human rhinovirus C was found in one case in the last islet autoantibody negative sample. This case did not experience fever and reported respiratory infections 3 times during the autoantibody negative period. Of the 3 control children with viruses in their plasma samples, one child had the GB virus C/Hepatitis virus G in both samples, one child had the Human Herpesvirus 6 in both samples, and one child had the human parvovirus B19 in the seroconversion sample. No virus sequences were identified in all other samples.

# **TEDDY** book study

All cases and 70 of 72 controls reported at least one infection prior to the onset of type 1 diabetes (Table 2). A similar proportion of cases and controls reported infections in the islet autoantibody negative period (75% vs 74%), seroconversion period (71% vs 72%), and progression period (71% vs 67%). Moreover, the number of infections per child during each of these periods was similar between cases and controls (Table 3). Respiratory infections were the most commonly reported infections in both cases and controls.

In contrast to the reported infections, reported fever differed between the cases and controls (Table 2). Fever was reported less frequently in cases as compared to controls in the whole period to type 1 diabetes (p=0.032). Of interest, this difference was only seen in the seroconversion period (p=0.030) and progression period (p=0.033), and not seen in the autoantibody negative period. This difference appeared to be due to decreased episodes of fever during reported infections.

# Discussion

Infectious agents are frequently, but inconclusively discussed candidate causal agents in the pathogenesis of type 1 diabetes (11-16). Here, using state-of-the-art methods for virus detection, we report that viruses are infrequently detected in the period surrounding seroconversion in children who progress to diabetes rapidly after developing islet autoimmunity. Moreover, children who developed type 1 diabetes rapidly in early childhood did not have more or different infections than matched islet autoantibody negative control children. Of potential interest, episodes of fever associated with infection were decreased in the children with rapid progression to diabetes. The findings do not support a prominent role for viruses in the pathogenesis of early rapid onset autoimmune diabetes in childhood.

The findings were generated on a subset of type 1 diabetes cases within the TEDDY study. For the infection history data, they represent all children in whom diabetes was diagnosed within 6 months of islet autoantibody in the study, and for the deep sequencing data, around 60% of such cases. In both analyses, controls from the TEDDY study that were well matched to cases were used as the comparator. Both children with and without a family history of type 1 diabetes were represented. Limitations include the relatively small numbers of cases studied, and the sampling which although is at 3 month intervals, may be too wide to identify virus.

Findings with respect to virus and infection history in type 1 diabetes have been controversial. Although the literature repeatedly reports associations between type 1 diabetes and viral infections (14-18), in particular enterovirus infections, there are also substantial reports that fail to confirm the findings (11-13). We had expected that the cases examined in this study would provide a best-case scenario for the identification of viruses if they were causal, but failed to detect virus in plasma from all but one of the 14 cases studied. We conclude either that a recent virus infection is not a frequent cause of type 1 diabetes in children with a rapid diabetes onset or that we lack the sensitivity to detect virus infection. Deep sequencing techniques are currently state of the art and have been used to identify viral cause of disease (19). Within the cohort, viruses were consistently identified in both samples in 2 children suggesting that the methodology can reproducibly detect infection at 3 monthly intervals in plasma. Moreover, if we assume that virus is only present for 2 weeks, the deep sequencing technique is 100% sensitive, and sampling was random, then we would expect to be able to identify virus in around one quarter of actual cases where virus was present for two weeks. Under these assumptions, the one case identified would therefore correspond to less than half the cases analysed. The infection history data also does not support a prominent role of virus in these cases. Although infections were reported frequently in the children, their frequency was similar in cases and controls. Of potential interest, fever was infrequent in the cases, despite similar frequencies of infections in the cases and controls, suggesting that fever may provide protection in the disease pathogenesis and warrants further investigation.

In conclusion, in depth examination of cases of rapidly developing autoimmune diabetes in early childhood failed to find evidence for a viral cause of islet autoimmunity and progression to diabetes.

Conflict of interest statement: We declare that we have no conflict of interest.

#### **Author Contributions**

AZ, EB, and JK designed this project within the TEDDY study. HL reviewed the data and undertook statistical analysis, interpretation of the results, and contributed to the writing of the manuscript. TB performed virus sequencing and critically reviewed the manuscript for intellectual content. CW and MP acquired and reviewed the data and contributed to writing the manuscript and critically reviewed the manuscript for intellectual content. HH was involved in the interpretation of the results. AZ, MR, OS, JXS; BH and AK are principal investigator of the TEDDY study, designed the study, and acquired and reviewed the data, and critically reviewed the manuscript for intellectual content. AZ and EB contributed to the statistical analysis, were involved in the interpretation of the results, and wrote the manuscript.

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Table 1. Viruses detection in 56 plasma samples at the two time points in the sequencing study:  $1^{st}$  sample: the 'last islet autoantibody negative sample' prior to islet autoantibody seroconversion, and  $2^{nd}$  sample: the 'seroconversion sample' of 14 cases and controls pairs

Pair		Clinical Site*	family history of type 1 diabetes	Age at 1 <sup>st</sup> sample (months)	Virus detection at 1 <sup>st</sup> sample	Age at 2 <sup>nd</sup> sample (months)	Virus detection at 2 <sup>nd</sup> sample	Age at diagnosis of type 1 diabetes (months)
1	Case	FIN	no	19	NEG	22	NEG	27
1	Control	FIN	no	18	NEG	21	NEG	-
					Human			
2	Case	COL	yes	9	rhinovirus C	11	NEG	15
					(HRVNEGC)			
							Human	
2	Control	COL	yes	9	NEG	12	parvovirus	-
							B19 (B19V)	

3	Case	COL	no	17	NEG	21	NEG	21
3	Control	COL	no	18	NEG	21	NEG	-
4	Case	GER	yes	16	NEG	22	NEG	28
4	Control	GER	yes	19	NEG	22	NEG	-
5	Case	GER	yes	7	NEG	9	NEG	12
5	Control	GER	yes	6	NEG	10	NEG	-
6	Case	COL	no	15	NEG	18	NEG	20
6	Control	COL	no	14	NEG	18	NEG	-
7	Case	GER	yes	7	NEG	9	NEG	13
7	Control	GER	yes	6	NEG	10	NEG	-
8	Case	WAS	no	6	NEG	9	NEG	10
8	Control	WAS	no	5	NEG	8	NEG	-
9	Case	WAS	yes	24	NEG	27	NEG	33
9	Control	WAS	yes	24	NEG	27	NEG	-
10	Case	GER	no	7	NEG	10	NEG	12
10	Control	GER	no	6	NEG	9	NEG	-

11	Case	GEO	yes	6	NEG	9	NEG	14
					Human		Human	
11	Control	GEO	yes	7	herpesvirus 6	10	herpesvirus 6	-
					(HHVNEG6)		(HHVNEG6)	
12	Case	SWE	yes	6	NEG	9	NEG	15
12	Control	SWE	yes	6	NEG	8	NEG	-
13	Case	COL	no	9	NEG	12	NEG	18
13	Control	COL	no	8	NEG	12	NEG	-
14	Case	FIN	no	7	NEG	10	NEG	15
					GB virus C/		GB virus C/	
14	Control	FIN	20	6	Hepatitis	9	Hepatitis	
14	Control	IOI FIIN	no	6	virus G	9	virus G	-
					(GBVNEGC)		(GBVNEGC)	

\* COL: Colorado, FIN: Finland, GER: Germany, GEO: Georgia/Florida, SWE: Sweden, WAS: Washington

NEG: negative

		Case	Control		
		n (%)	n (%)	OR (95% CI)	p-value
	Any infection	24 (100%)	70 (97%)		
	Fever	17 (71%)	62 (86%)	0.22 (0.06-0.88)	0.032
	High fever <sup>†</sup>	15 (63%)	56 (78%)	0.42 (0.14-1.24)	0.116
	Fever without	9 (38%)	22 (31%)	1.21 (0.44-3.30)	0.715
Birth to Type 1	infectious illness	9 (38%)		1.21 (0.44-3.30)	0.715
Diabetes	Fever with any	14 (58%)	56 (78%)	0.36 (0.12-1.10)	0.072
	infectious illness	14 (38%)			0.072
	Respiratory tract	24 (100%)	68 (94%)		
	Gastrointestinal tract	11(46%)	29 (40%)	1.55 (0.50-4.76)	0.447
	Other	5 (21%)	13 (18%)	1.40 (0.36-5.48)	0.630
	Any infection	18 (75%)	53 (74%)	0.94 (0.20-4.52)	0.940
	Fever	13 (54%)	38 (53%)	1.10 (0.31-3.85)	0.882
	High fever†	12 (50%)	30 (42%)	1.54 (0.49-4.81)	0.463
Autoontikedu	Fever without	(250)	8 (11%)	1.95 (0.59-6.50)	0.075
Autoantibody	infectious illness	6 (25%)			0.275
negative period	Fever with any	0 (290/ )	33 (46%)		0 659
	infectious illness	9 (38%)		0.76 (0.22-2.60)	0.658
	Respiratory tract	18 (75%)	49 (68%)	1.89 (0.40-8.89)	0.420
	Gastrointestinal tract	5 (21%)	16 (22%)	0.96 (0.27-3.44)	0.944

Table 2. Number of children who reported one or more infections and fever reports in the all time points investigated

	Other	2 (8%)	8 (11%)	0.57 (0.08-3.87)	0.564
	Any infection	17 (71%)	52 (72%)	0.95 (0.31-2.86)	0.922
	Fever	4 (17%)	30 (42%)	0.27 (0.08-0.88)	0.030
	High fever†	4 (17%)	25 (35%)	0.39 (0.12-1.23)	0.108
	Fever without	2 (8%)	11 (15%)	0.47 (0.09-2.56)	0.380
Seroconversion	infectious illness	2 (8%)	11 (13%)	0.47 (0.09-2.30)	0.380
period	Fever with any	3 (13%)	26 (36%)	0.23 (0.06-0.88)	0.032
	infectious illness	5 (1570)	20 (30 70)	0.23 (0.00-0.00)	0.052
	Respiratory tract	15 (63%)	49 (68%)	0.71 (0.24-2.15)	0.543
	Gastrointestinal tract	3 (13%)	10 (14%)	1.25 (0.27-5.84)	0.776
	Other	1 (4%)	4 (6%)	1.11 (0.10-11.86)	0.931
	Any infection	17 (71%)	48 (67%)	1.34 (0.30-6.08)	0.706
	Fever	5 (21%)	30 (42%)	0.14 (0.02-0.85)	0.033
	High fever†	3 (13%)	26 (36%)	0.11 (0.01-0.90)	0.040
	Fever without	2 (8%)	8 (11%)	0.76 (0.14-4.13)	0.752
Progression	infectious illness	2 (070)	0 (11/0)	0.70 (0.11 1.13)	0.752
period	Fever with any	5 (21%)	25 (35%)	0.30 (0.07-1.40)	0.126
	infectious illness	0 (21/0)	20 (00 %)	0.00 (0.07 1.10)	0.120
	Respiratory tract	15 (63%)	43 (60%)	1.06 (0.31-3.60)	0.921
	Gastrointestinal tract	6 (25%)	10 (14%)	2.64 (0.70-9.95)	0.153
	Other	2 (8%)	3 (4%)	2.65 (0.33-21.11)	0.358

†high fever indicates a measured temperature  $\geq 38^{\circ}C (101^{\circ}F)$ 

		Case	Control		
		Mean (SD)	Mean (SD)	OR (95 % CI)	p-value
Autoantibody	Any infection	3.5 (3.9)	2.8 (3.6)	1.22 (0.93-1.60)	0.150
negative period	Fever	1.0 (1.2)	1.1 (1.5)	0.97 (0.62-1.53)	0.901
Seroconversion	Any infection	1.7 (2.0)	2.0 (1.9)	0.93 (0.69-1.25)	0.615
period	Fever	0.3 (0.8)	0.8 (1.3)	0.61 (0.33-1.12)	0.108
Progression	Any infection	1.6 (1.5)	1.7 (2.1)	0.95 (0.66-1.37)	0.782
period	Fever	0.4 (0.9)	0.7 (0.9)	0.57 (0.26-1.21)	0.143

Table 3. Number of infections and fever reports in all time points investigated

# **Figure Legends**

**Figure 1:** Flow chart of the study population for the TEDDY book and sequencing study (A), Flow chart of the different time points investigated in the TEDDY book and sequencing study (B).