

Immunology in the clinic review series; focus on type 1 diabetes and viruses: the enterovirus link to type 1 diabetes: critical review of human studies

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Summary

The hypothesis that under some circumstances enteroviral infections can lead to type 1 diabetes (T1D) was proposed several decades ago, based initially on evidence from animal studies and sero-epidemiology. Subsequently, enterovirus RNA has been detected more frequently in serum of patients than in control subjects, but such studies are susceptible to selection bias and reverse causality. Here, we review critically recent evidence from human studies, focusing on longitudinal studies with potential to demonstrate temporal association. Among seven longitudinal birth cohort studies, the evidence that enterovirus infections predict islet autoimmunity is quite inconsistent in our interpretation, due partially, perhaps, to heterogeneity in study design and a limited number of subjects studied. An association between enterovirus and rapid progression from autoimmunity to T1D was reported by one longitudinal study, but although consistent with evidence from animal models, this novel observation awaits replication. It is possible that a potential association with initiation and/or progression of islet autoimmunity can be ascribed to a subgroup of the many enterovirus serotypes, but this has still not been investigated properly. There is a need for larger studies with frequent sample intervals and collection of specimens of sufficient quality and quantity for detailed characterization of enterovirus. More research into the molecular epidemiology of enteroviruses and enterovirus immunity in human populations is also warranted. Ultimately, this knowledge may be used to devise strategies to reduce the risk of T1D in humans.

Keywords: aetiology, autoimmunity, enterovirus, infection, T1D

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Introduction

Type 1 diabetes (T1D) results from a selective immune-mediated destruction of the pancreatic beta cells in subjects carrying permissive human leucocyte antigen (HLA) genotypes. Rapidly increasing incidence, sometimes with epidemic patterns, and other evidence suggest that non-genetic factors are involved in the aetiology [1]. Enteroviruses have been the primary candidate since Gamble reported high titres of neutralizing antibodies to Coxsackie B virus in recent-onset T1D patients [2], and Yoon isolated a

Coxsackie B4 virus from a child with T1D and established several lines of evidence for causality [3]. Despite a number of impressive investigations using different approaches, the nature of the relationship between enterovirus and T1D remains controversial. In most cases, diagnosis of T1D follows a long period of preclinical islet autoimmunity [4]. The latter is essential for interpretation of aetiological studies, as viruses present at diagnosis may have infected the host late in the disease process, or aetiological infections may have been cleared at the time of diagnosis. Enterovirus infections may contribute potentially to initiation of

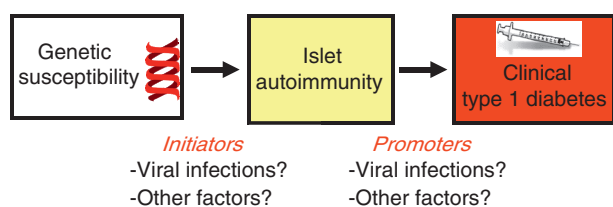


Fig. 1. Illustration of the two-stage process leading to type 1 diabetes. Enterovirus may influence initiation of autoimmunity, progression from islet autoimmunity to clinical disease, or both. It is also possible that enterovirus influences the risk of developing atypical type 1 diabetes not preceded by islet autoimmunity, such as fulminant type 1 diabetes seen in some cases in Japan [5].

autoimmunity, modulating progression from islet autoimmunity to clinical T1D or both (Fig. 1) [6,7]. Enterovirus infections can probably also precipitate diagnosis non-specifically in those with advanced preclinical disease.

Experiments in rodent models suggest that enteroviral infection accelerates the disease process when occurring after the accumulation of immune cells in the pancreatic islets [8–11]. A recent report has suggested a similar effect in humans [12]. Prospective studies in humans pose a number of challenges in study design and interpretation, which we will discuss in this review. Potential mechanisms and other aspects of importance for understanding the potential link between enterovirus and T1D are covered by others in this issue (see reviews by Lind *et al.*, Jaidane *et al.*, Hober *et al.* and Grieco *et al.*), or have been reviewed elsewhere (e.g. [13–19]).

Enteroviruses: epidemiology and methods of detection

Enteroviruses are ubiquitous, single-stranded non-enveloped RNA viruses, transmitted generally through the faecal–oral route, and replicating primarily in the gut. There are more than 100 defined human enterovirus serotypes (<http://www.picornaviridae.com>), and many more strains have been defined by sequencing. Much of the knowledge about the biology of enteroviruses is derived from poliovirus and a few prototypic strains of other enteroviruses. Many properties may differ across serotypes, and even across isolates within serotypes [20,21]. Most enterovirus infections are asymptomatic, but some serotypes are associated with severe clinical symptoms in a small proportion of those infected [20,22–24]. While most children encounter an enterovirus by the age of 2 years, infection with a given serotype is obviously not as common [25,26]. Co-infections with two serotypes may occur [25,26]. Epidemic outbreaks often follow natural circulation of the same serotype, and it is not entirely clear why outbreaks of enterovirus-associated disease sometimes occur. As spontaneous mutations and recombination are common among enteroviruses [27], it is

speculated that virulent strains may emerge spontaneously during an infection.

For clinical or epidemiological studies, enterovirus can be detected in various types of biological specimens from humans. Traditional cell culture methods are quite sensitive for detection, except for some species A serotypes which cannot be grown in culture [24,26]. Enterovirus is detectable most readily in faeces, where it is usually detectable for 3–4 weeks, but rarely more than 2–3 months [12,25,26,28]. In a proportion of gut infections, enterovirus is also detectable in blood, usually for a few days in immunocompetent hosts [24]. It has been suggested that enterovirus is detectable more readily in peripheral blood mononuclear cells (PBMC) than in serum, but few studies have evaluated this systematically [29,30].

Systemic infection may, in some instances, lead to dissemination to other target organs, and enterovirus RNA or protein can sometimes be detected in intestinal, heart or pancreatic tissue by reverse transcription–polymerase chain reaction (RT–PCR), immunohistochemistry or *in-situ* hybridization. Interesting studies of pancreatic tissue from T1D patients and controls have appeared in recent years [31–33]. Other studies of pancreatic tissue have not found enterovirus or found a similar proportion of positives in controls [34,35]. It appears that a number of methodological factors may profoundly influence the results of such studies, as discussed in [33,36]. This was also suggested in an as yet unpublished study presented in abstract form by Tauriainen and co-workers, including the Network for Pancreatic Organ Donors (nPOD) group (<http://www.jdrfnpod.org>). This and similar projects focusing on optimizing specimen handling and standardizing and validating methodology is likely to bring this field forward. Below, we focus on methods of enterovirus detection that are more feasible in large-scale prospective studies.

RT–PCR for enterovirus RNA detection

RT–PCR is a relatively simple and very sensitive method of detection and a number of different assay formulations have been used, including conventional, nested or seminested and real-time RT–PCR. Most RT–PCR primer sets used target the highly conserved 5′ non-coding region (NCR) of the enterovirus genome, which should detect essentially all serotypes. Even among primer sets targeting conserved regions of the 5′ NCR, the exact primer sequences have varied between studies. For instance, two related primer sets used in a single study produced very different results [37], suggesting that validity varied by primer sequence. Continued optimization and validation seem to improve the methodology but each assay has certain advantages and some drawbacks, depending on the application [38–41]. Detailed characterization of positive samples requires sequencing of variable parts of the genome, particularly the VP1 region.

Enterovirus serology

Many different formulations of serological assays have been used in studies of T1D, including neutralization tests and various forms of immunoassay [42]. There is a general problem with cross-reactivity between serotypes, which may be exploited when aiming to cover all serotypes. Using mixes of different heat-treated antigens and synthetic peptides based on consensus sequences are strategies employed towards this end [43,44]. Serological assays were developed and validated with appropriately timed acute and convalescent sera from patients with aseptic meningitis confirmed by enterovirus isolation (see, e.g. [43] and references therein). There may thus be some bias towards serotypes prevalent in aseptic meningitis and which grows in culture. An important drawback is that it is difficult to define an appropriate cut-off for positivity when appropriately timed paired samples are not available. Some immunoglobulin (Ig)M enzyme assays have demonstrated high sensitivity with paired sera, usually at the cost of some reduction in specificity [45]. When applied in prospective studies with approximately 3–6-month sample intervals, the frequency of serologically defined infections are several-fold higher than the frequency of enterovirus detected by RT–PCT in serum [12,46,47].

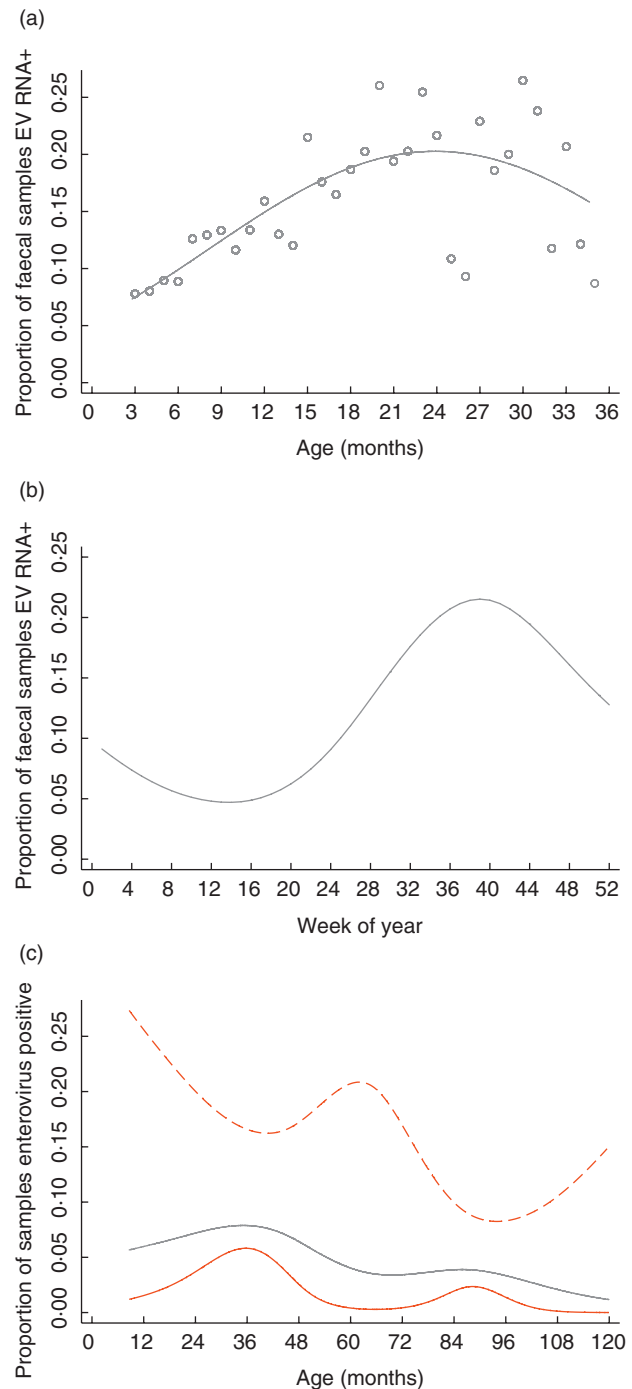
How common are enterovirus infections in the population?

It should be clear from the above that the reported occurrence of enterovirus infections depends critically on methodology. Figure 2 shows examples of prevalence of

enterovirus infections in serial samples from the Diabetes and Autoimmunity Study in the Young (DAISY) and MIDIA (Diabetes Autoimmunity Study in the Young, described below) by season, age and method of detection. In addition to variation over these established factors, there appears to be substantial random variation even when several hundreds of samples are analysed (Fig. 2a).

Regardless of the definition of enterovirus infection, human studies attempting to capture the infection history are limited by low sampling frequency. The age and

Fig. 2. Variation of enterovirus prevalence by age, season and method of detection in two longitudinal birth cohort studies [Environmental Triggers of Type 1 Diabetes (MIDIA) and Diabetes and Autoimmunity Study in the Young (DAISY)]. (a) Prevalence of enterovirus RNA by age in nearly 8000 monthly faecal samples from nearly 800 children in MIDIA (unpublished data from ref. [48]). Circles are observed prevalence in age groups, and the line represent smoothed predictions from logistic regression model with a second-degree polynomial. (b) Prevalence of enterovirus RNA in monthly faecal samples from MIDIA children aged 3–36 months, by season [smoothed as in (a), but with restricted cubic splines]. (c) Prevalence of enterovirus infection by age and type of sample in DAISY (data from ref. [12]). Subjects with autoimmunity ($n = 140$) were tested for enterovirus RNA in rectal swabs (grey line) and serum (red solid line), and enterovirus serology (red dashed line) in samples collected every 3–6 months (serology only in subset of samples, all enterovirus assays conducted in Heikki Hyöty’s laboratory). Infections were defined serologically as a doubling or more in optical density in one or more of five immunoglobulin (Ig)M, IgG and IgG enzyme immunoassays (see [12] for details). All curves were smoothed using restricted cubic splines in logistic regression models. Curves must be interpreted with caution because of relatively few positive samples and substantial random variation, cf. (a).



frequency of sample collection, type of samples and assays will influence the ability to detect an association between enterovirus and risk of islet autoimmunity or T1D.

Enterovirus in T1D patients and healthy control subjects

Enterovirus serology

Green [42] systematically reviewed studies of Coxsackie B serology and T1D up to 2002, some of which included patients who were not recent-onset cases. Among 13 studies using positivity for any Coxsackie B antibody as a marker of infection, there were indications of a possible relationship, but the authors concluded that the heterogeneity in assays, study design and results did not allow a conclusion or calculation of a pooled estimate [42]. Also, the smaller studies tended to have larger estimated odds ratios, suggestive of publication bias [42]. Separate analyses were also performed for antibodies specific for Coxsackieviruses B3, 4 and 5 (for 11, 17 and 11 studies, respectively), with little or no suggestion of any relationship overall, and with similar heterogeneity. Few serology studies have been published since. A few studies HLA-typed cases but no study genotyped controls, and statistical adjustment for the HLA genotype as a potential confounder was thus not possible. The latter is also the case for similar studies using RT-PCR for enterovirus detection, discussed below.

Enterovirus RNA in blood samples

Yeung provided a very useful overview of studies using molecular methods of enterovirus detection [34], but calculated pooled estimates across all studies despite recommendations not to do so in the presence of large heterogeneity in results and study design [49]. For instance, results based on *in-situ* hybridization or immunohistochemistry on pancreatic tissue were pooled with those based on RT-PCR on blood samples or combined methods of detection [34]. In our judgement, a joint analysis of studies of enterovirus RNA by RT-PCR on serum, plasma or whole blood among newly diagnosed T1D patients and matched controls would be reasonable (Fig. 3). The overall result in Fig. 3a is consistent with an odds ratio of approximately 10–12, which was also obtained by Yeung *et al.* [34]. Note, however, that the *I*-square estimate of statistical heterogeneity was drastically lower (0.0%) compared to that among studies of newly diagnosed T1D patients and controls presented by Yeung *et al.* (*I*-square = 59%). While there was limited variation between studies in the frequency of enterovirus RNA in serum from healthy controls (Fig. 3b), there was wide variation between studies in the frequency of enterovirus RNA in serum from newly diagnosed T1D patients (Fig. 3c). There is an impression that the earliest studies showed a higher frequency among patients than did the more recent ones. Conversely,

data so far presented only as conference abstracts in 2010 and 2011 by Antonio Toniolo's group from Italy have shown enterovirus positivity in the large majority of T1D patients.

It is notable (Fig. 3c) that one laboratory reported no enterovirus RNA in any sample from T1D patients at or near diagnosis in three independent data sets [12,54,58]. This is the Finnish laboratory that has reported many positive samples from prediabetic individuals in longitudinal studies [12,58]. Thus, lack of assay sensitivity would be unlikely. Finally, a recent study larger than all previous ones reported a threefold higher proportion of enterovirus RNA in serum from T1D patients compared to controls, but the majority of patients were unfortunately not recent-onset cases [61].

Longitudinal studies of enterovirus and islet autoimmunity

Virus detected in patients at or after diagnosis may well have infected the host after disease onset, whether the virus is detected in tissues, blood or faeces. Furthermore, lack of virus at diagnosis does not exclude a role of virus in the aetiology, as 'hit-and-run'-type mechanisms may have been involved. Prospective studies with frequent sampling of biological specimens and a sufficient number of cases with end-point are necessary to document statistically significant associations between infections and later risk of islet autoimmunity or T1D. The available longitudinal studies investigating the potential link between serial postnatal measures of enterovirus infections and islet autoimmunity (or T1D) are presented in Table 1.

They include the three Finnish studies DIPP (Diabetes Prediction and Prevention Study), DiMe (Childhood Diabetes In Finland) and TRIGR (Trial to Reduce IDDM in the Genetically at Risk), the DAISY in Colorado, MIDIA in Norway (Environmental Triggers of Type 1 Diabetes) and the German BABYDIAB and Babydiet studies. Preliminary data from a study in Australia called Viral Etiology of type 1 Diabetes (VIGR) have been presented only in abstract form at the time of writing, and results shown in the review by Yeung *et al.* [34], but details on methodology have not yet been published in full. All these studies include children with increased risk of T1D, defined by a first-degree family history, HLA susceptibility genes or both. Seven studies have published data from a total of 176 cases of islet autoimmunity, and one study (DiMe) followed subjects with islet autoimmunity for T1D as end-point. Sample frequency and method of detection varied between these studies (Table 1).

Challenges in statistical analysis of longitudinal data

Available studies varied in how data were presented and analysed. There is always a trade-off between carrying out the different types of analyses needed to detect relevant patterns, and 'data dredging'. The latter can potentially lead to false-positive associations due to multiple testing. Samples

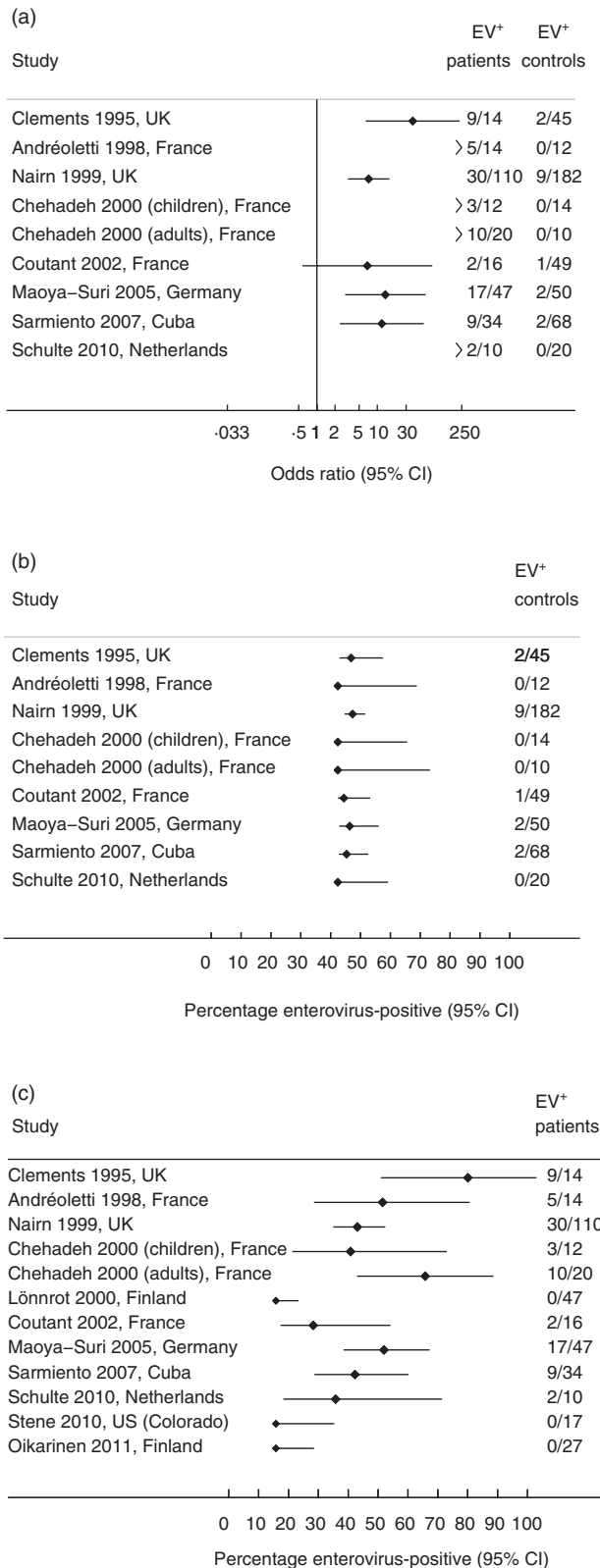


Fig. 3. Studies of enterovirus RNA in serum or plasma from patients with type 1 diabetes diagnosed within 1 month and from healthy controls. (a) Odds ratio for association between enterovirus and type 1 diabetes. Odds ratio estimates had to be calculated using Woolf's formula, as information for matched analysis was not provided in original publications. The *I*-squared estimate of statistical between study heterogeneity was 0.0%. Odds ratio estimates cannot be calculated from studies with zero observed controls with enterovirus. Overall results (association and heterogeneity) were similar after adding 0.5 to all four cells in the 2 × 2 table for studies with zero observed controls with enterovirus RNA-positive serum (data not shown). (b) Percentage of enterovirus-positive age-matched healthy controls (with exact 95% confidence intervals). (c) Percentage of enterovirus positive type 1 diabetes (T1D) patients. Note that three studies of patients with newly diagnosed T1D did not include matched controls, and are thus not included in panels (a) and (b). References cited (first author and publication year indicated) are [12,30,50–58]. Data from Oikarinen 2011 [58] include data not presented in original publication, obtained by personal communication from H. Hyöty and S. Oikarinen, Tampere, Finland. Not included are data based on enterovirus detection in peripheral blood mononuclear cells, which were available from Schulte [30], and also by two other studies [37,59]. Other studies not included were Craig [60], who did not provide separate data on results based on serum samples (only for positivity in serum and/or faecal samples), and a few studies of type 1 diabetes patients who were not newly diagnosed.

when islet autoantibodies first appear the exact time order cannot be determined, as both occur in an interval, usually of 3–12 months. The potential effect of enterovirus infections could, theoretically, be cumulative, reflecting multiple 'hits' over time. Alternatively, it could be argued that infections should occur just before islet autoimmunity to be implicated plausibly in the aetiology. The latter can be investigated by restricting analysis to narrow time-intervals [46,64], or the frequency of infections just before islet autoimmunity can be compared with other time-intervals in the same individual in so-called case 'cross-over analysis' [72]. The latter is appealing because each subject is his/her own control, but our experience from MIDIA suggests that seasonal variation in enterovirus infection makes it difficult to obtain unbiased results (unpublished observation). Intra-individual correlation among repeated samples within subjects must also be taken into account in the analysis when enterovirus frequency is the dependent variable. This is frequently ignored (see Table 2). 'Per-subject analysis' (see Table 2) is simpler, but important information in the repeated samples is lost.

The time-varying nature of enterovirus infection history in each individual can be modelled with time to event (autoimmunity or T1D) analysis. The type of mechanism operating may profoundly influence the ability to detect an association, and the interpretation of such analyses is complex [73], but ignoring the truly time-varying nature of enterovirus infection history is probably not a better option.

collected before islet autoimmunity (or T1D) and during the corresponding period in matched controls should be distinguished from other samples, but this has not always been carried out. If an infection is detected in the sample interval

Table 1. Longitudinal studies of enterovirus and islet autoimmunity or type 1 diabetes (T1D).

Study	Subjects included	Age (month) at sample collection	Definition of islet autoimmunity/no. of case subjects tested for enterovirus	Type of sample and enterovirus assay	Relevant publications
DiMe	Siblings of newly diagnosed children with T1D in Finland	6-month intervals from T1D in sib	≥1 of ICA, IAA, GADA, IA2A*/I1 cases progressed to T1D	Serum, serology and RT-PCR†	[54,74]
DIPP	Newborns with moderate- or high-risk HLA genes in Finland	Cord,(3),6,(9),12,(15),18,(21), 24 (30),36, . . . ‡	ICA (IAA, GADA, IA2A measured if ICA-positive)/up to 41 cases§	Serum (plus faecal samples‡), serology and RT-PCR†	[28,46,58,75,76]
Second pilot of TRIGR	Newborns with family history of T1D in Finland	Cord, 3,6,9,12,18,24	≥1 of IAA, GADA, IA2A, ICA*/I19 cases	Serum, serology and RT-PCR†	[47]
German BABYDIAB	Offspring of patients with T1D in Germany	Cord, 9, 24,36,60,96	≥1 of IAA, GADA, IA2A, ICA*/I28 cases	Serum, Coxsackievirus serology	[65]
DAISY	Relatives of T1D and newborns with moderate or high-risk HLA genes in Colorado‡	9,12,15,24,36,48, . . .	≥1 of IAA, GADA, IA2A on ≥2 consecutive occasions/up to 26 cases	Serum, rectal swabs, saliva, RT-PCR**	[66]
DAISY ('progression cohort')	As above	3–6-month intervals from islet autoimmunity	140 cases of islet autoimmunity tested, of which up to 50 progressed to T1D	Serum, rectal swabs, RT-PCR† (serology in subsample)	[12]
MIDIA	Newborns with the high-risk HLA genes in Norway	3,4,5,6,7,8,9, . . .,36††	≥2 of IAA, GADA, IA2-A on ≥2 consecutive occasions/27 cases	Faecal samples, RT-PCR‡‡	[64]
Babydiät	Relatives of T1D and newborns with moderate or high-risk HLA genes in Germany	3,6,9,12§§	≥1 of IAA, GADA, IA2A, Zn-T8A/22 cases	Faecal samples, RT-PCR , cell culture	[41]
VIGR	Newborns with family history of T1D in Australia	6, 12, 18, 24, 30, . . .	≥2 of IAA, GADA, IA2-A/I13 cases¶¶	Serum, RT-PCR***	***

*'Persistently positive', but no explicit operational definition in publications. †Reverse transcription–polymerase chain reaction (RT-PCR) [conserved 5' non-coding region (NCR) of enterovirus] in Hytöy's laboratory, details described in [67]. ‡Not all centres in Diabetes Prediction and Prevention Study (DIPP) included blood samples at ages in parenthesis. Faecal samples were collected monthly from ages 3 to 22 months; results reported for 12 cases in Salminen *et al.* 2004 [28]. §A recent publication from DIPP [62] presented data on enterovirus serology [immunoglobulin (Ig)A and IgG enzyme immunoassay (EIA) with heat-treated Coxsackie B4 virus as antigen] in serial samples at ages 3–24 months from 107 cases with islet cell antibodies (ICA) plus at least one of insulin autoantibodies (IAA), glutamic acid decarboxylase autoantibodies (GADA) or insulinoma antigen 2 (IA2) autoantibodies (IA2A) on at least two consecutive occasions; see text. ||Enzyme-linked immunosorbent assay (ELISA) IgG antibodies against a panel of heat-treated antigens from different Coxsackievirus serotypes. Not paired samples. ¶Offspring or siblings of patients with T1D were included regardless of human leucocyte antigen (HLA) genotype, while general population newborns were included if they carried at least one T1D susceptibility haplotype (DR4-DQ8, DR3-DQ2, or both). **RT-PCR in H. A. Rotbart's laboratory, details described in [68]. This study also tested for enterovirus IgM using an ELISA method described by Helfand [63] against 14 non-polio enterovirus serotypes (Coxsackie B1–6, Coxsackie A9, echo 4, 6, 9, 11, 30 and 34, and enterovirus 71), but serology data were not presented in the publication by Graves *et al.* (see text). ††While faecal samples were collected monthly as indicated, blood for islet autoantibody testing were collected at ages 3, 6, 9 and 12 months, then annually. ‡‡Real-time RT-PCR (conserved 5' NCR of enterovirus) in O. Cinek's laboratory, details described in [69], based primarily on primer sequences from [70]. §§Faecal samples also collected later, but enterovirus only tested up to 12 months of age. Blood samples collected every 3 months up to 3 years, then annually, tested for islet autoantibodies. |||Real-time RT-PCR with (panEV) primers and probes described in [39]. Positive samples partial VP1 sequenced to determine serotype. ¶¶According to Yeung *et al.* [34], 13 subjects were positive for two or three islet autoantibodies (requirement of persistence not mentioned explicitly). ***In the review by Yeung *et al.* [34], only serum enterovirus RNA results were reported, while according to the cited conference abstract by Al-Shabeeb other types of specimens were also tested for presence of enterovirus RNA. Apparently, a multiplex PCR method described in [71], with nested primers targeting the conserved 5' NCR of enterovirus, was used for detection of enterovirus. Details of methodology for enterovirus detection and data analysis applied in viral aetiology of type 1 diabetes (VIGR) have not yet been published. ZnT8A: zinc transporter 8 autoantibody; DiMe: Childhood Diabetes in Finland study; HLA: human leucocyte antigen.

Table 2. Postnatal enterovirus infections before islet autoimmunity and the corresponding period for matched controls from longitudinal birth cohort studies.

Study and type of enterovirus (EV) Assay/sample	Per sample results EV ⁺ case samples <i>versus</i> EV ⁺ control samples Odds ratio (95% CI)*	Per subject results Case subjects EV ⁺ at least once <i>versus</i> controls Odds ratio (95% CI)*
RNA in faeces		
DIPP [28]	Not reported	5/12 (42%) <i>versus</i> 15/53 (28%), OR = 1.8 (0.5–6.6)
MIDIA [64] [§]	43/339 (13%) <i>versus</i> 94/692 (14%), OR = 1.0 (0.6–1.7)	18/27 (67%) <i>versus</i> 30/53 (57%), OR = 1.5 (0.6–4.0)
Babydiet [41]	5/72 (7%) <i>versus</i> 27/267 (10%), OR = 0.7 (0.2–2.2)	4/22 (18%) <i>versus</i> 20/82 (24%), OR = 0.7 (0.2–2.3)
RNA in serum		
DIPP [46]	Not reported [†]	Not reported
TRIGR [47]	?/? (14%) <i>versus</i> ?/? (8.4%), OR = 1.8 (?–?)	Not reported
VIGR [‡]	Not reported	5/13 (38%) <i>versus</i> 28/198 (14%), OR = 3.8 (1.2–12) [‡]
Serology		
BABYDIAB [65]	0/62 (0%) <i>versus</i> not reported [‡]	0/28 (0%) <i>versus</i> not reported [‡]
Combination of methods		
DIPP serology and/or serum RNA [46]	33/152 (22%) <i>versus</i> 105/751 (14%), OR = 1.7 (1.1–2.6)	Not reported
TRIGR serology and/or serum RNA [47]	Not reported (but 0.83 <i>versus</i> 0.29 infections per child reported significantly different)	Not reported
DAISY (GP) RNA in rectal swab or saliva [66]**	0/17 (0%) <i>versus</i> 3/35 (9%)	0/10 (0%) <i>versus</i> 3/21 (14%)
DAISY (relatives) EV RNA in serum, rectal swab or saliva [66]**	1/10 (10%) <i>versus</i> 2/8 (25%), OR = 0.3 (0.02–4.6)	1/6 (17%) <i>versus</i> 2/6 (33%), OR = 0.4 (0.03–6.2)

*EV⁺: positivity for enterovirus detectable with given assay (positives/number tested). Unless stated otherwise, odds ratios (ORs) with confidence intervals (CI) were calculated based on Woolf's formula, because information for/from appropriate matched analysis was not presented in most publications. If anything, this tends to slightly underestimate ORs. For 'per sample analysis', this analysis ignores correlation among repeated measurements, and tends to result in too narrow CIs/too low *P*-values. Yeung's reporting [34] of per-subject results from several studies [28,47,66] were inconsistent with our interpretation of the original publications. [†]Results reported for samples including before and after islet autoimmunity [10/248 (4%) *versus* 33/1113 (3%), OR = 1.4, 95% CI: (0.7–2.8)]. [‡]Preliminary result reported in the review by Yeung *et al.* [34], with no details on methodology. Controls were apparently all non-cases in the cohort. It was not stated explicitly that infections were counted only before islet autoimmunity in cases and a corresponding period in controls. Results apparently based on serum enterovirus RNA only. [§]OR for per-subject analysis from random intercept model to account for repeated measurements within individuals. 'Naive' analysis (ignoring repeated measurements), as in the other results provided here, give OR = 0.9 (95% CI: 0.6–1.4). Per-subject results presented here were calculated using Woolf's formula for comparison with other studies, based on raw data available in Supplementary Fig. 1 in [64]. ^{||}Several other studies tested for enterovirus antibodies in serum, but separate results were not reported separately in the publications. A recent publication from Diabetes Prediction and Prevention Study (DIPP) reported no overall association between signs of enterovirus infection detected by serial increase in immunoglobulin (IgA) or IgG enzyme immunoassay (EIA) (with heat-treated Coxsackievirus B4 as antigen) at ages 3–24 months and later risk of islet autoimmunity in 107 cases and 446 islet autoantibody-negative controls [62]. Frequencies of serologically defined infections were not reported, however. Graves *et al.* /Diabetes and Autoimmunity Study in the Young (DAISY) [66] also tested for enterovirus IgM and found no significant differences between the percentage of sera positive for IgM in cases and controls for each of the serotypes examined separately (all *P*-values >0.31), no significant differences between cases and controls in median optical density for each serotype, and no significant difference in proportion of cases and controls with positive IgM for at least one serotype (M. Rewers, *et al.*, unpublished). [¶]Two cases positive for islet autoantibodies at ages 1 and 2 years, respectively, were positive for Coxsackievirus IgG in samples after islet autoimmunity, but one of the two cases was positive for one of the 'secondary' enterovirus antibody assays (CVB4IgG) in a sample collected before islet autoimmunity. **GP: general population newborns with human leucocyte antigen (HLA) susceptibility risk haplotypes; relatives: siblings or offspring of patient with type 1 diabetes, included regardless of HLA genotype. Enterovirus RNA was not tested in serum from the GP cohort because of apparently redundant information in serum, rectal swab and saliva, and some unavailable serum samples. MIDIA: Diabetes Autoimmunity Study in the Young; TRIGR: Trial to Reduce IDDM in the Genetically at Risk; VIGR: viral aetiology of type 1 diabetes.

Systematic analysis of the longitudinal studies of islet autoimmunity

We have attempted to present results from the available studies in a comparable manner across studies, but appropriate information was unfortunately not often available from the original publications (Table 2).

Three studies (DIPP, MIDIA and Babydiet) reported separate data from stool samples, and none showed any significant association with islet autoimmunity [28,41,64]. In MIDIA, the lack of association also remained when restricting to periods just prior to seroconversion, and there was also no difference when counting samples after seroconversion for islet autoantibodies [64]. In DIPP, there was a tendency towards an association, but the result was significant only when combined with enterovirus serology, which rather suggests an association with serology [28]. In the Babydiet study, some infections may have been missed because of sampling every 3 months rather than monthly, and a possible close temporal association could not be investigated as enterovirus was tested only up to 12 months, while most cases seroconverted at a later age (mean 2.6 years, up to 7.9 years) [41].

Separate results for serum enterovirus RNA in the period before islet autoimmunity and the corresponding period in matched controls has not been reported explicitly in any publication we are aware of. Abstracted information suggests no significant association in DIPP or TRIGR [46,47], and only modest differences if anything. There was an apparent association in the new study from Australia (preliminary results from VIGR presented in review by Yeung *et al.* [34]), but detailed information for appropriate interpretation has not yet been published (Table 2). Results from studies of serum enterovirus RNA restricted to cases progressing to T1D are discussed in the next section.

DIPP and TRIGR reported significant associations when combining enterovirus RNA in serum with infections defined serologically based on serial increase in at least one of several assays. The fact that large majority of infections were detected with serology suggests that serology was driving this association [46,47]. BABYDIAB analysed only enterovirus serology [65], but infrequent sampling and in many instances only one or no sample available from before islet autoimmunity suggest limited power to detect any relationship. A recent publication from DIPP describes no significant association between serologically defined infections in serial samples from ages 3–24 months and later risk of islet autoimmunity in 107 cases of autoimmunity and 446 matched controls, but the frequencies of serologically defined infections were not reported [62]. Graves *et al.* [66] also tested for enterovirus serology in DAISY, and found no significant association with islet autoimmunity in DAISY (unpublished observation, M. Rewers). Notably, a uniform finding in the longitudinal studies was that enterovirus RNA was detected rarely, if ever, continuously in the same individual for more than about 3 months.

Does enterovirus influence progression from islet autoimmunity to T1D in humans?

The hypotheses that enterovirus infections can initiate islet autoimmunity or enhance progression from islet autoimmunity to T1D are not mutually exclusive, but testing of the two hypotheses requires different study designs. We investigated recently in DAISY whether enterovirus infections can contribute to increased rate of progression from islet autoimmunity to clinical T1D [12], in an attempt to mimic results from mouse models [8,19]. The rate of progression to T1D was significantly higher in sample intervals after detection of enterovirus RNA in serum [12]. The observed association may be interpreted in various ways, but it was remarkable that none of the samples available from the day of T1D diagnosis were positive for enterovirus RNA. This suggests that the observed association was not due to reverse causality.

Recently, Oikarinen reported the frequency of serum enterovirus RNA during follow-up of 38 cases of islet autoimmunity who progressed to T1D and in controls who remained negative for islet autoantibodies [58]. The difference was largest around the time of seroconversion, which suggests a role in initiating islet autoimmunity, as reported previously from the same study. However, interpretation in relation to the hypothesis that enterovirus may accelerate progression is hampered by the fact that this study did not include follow-up samples from individuals with islet autoimmunity who did not progress to T1D [58]. DiMe is the only other longitudinal study of enterovirus with T1D as end-point, and significant associations with enterovirus RNA and serology have been reported [54,74]. This study also included control subjects who were negative for islet autoimmunity throughout follow-up, and no subjects with islet autoimmunity who did not progress.

Perinatal enterovirus infection, the polio model and potential protection by infection

Some studies have suggested a relationship between perinatal infections and risk of T1D in childhood [74,77–79], while a number of others have not found any significant relationship [46,47,65,80]. There are many methodological differences between these studies, and a detailed review of this literature is beyond the scope of this paper.

The analogy between poliomyelitis and the potential enterovirus–T1D link was pointed out a long time ago [14]. It is possible that declining proportions of pregnant women providing their infants with anti-enterovirus antibodies may explain some of the increasing incidence of T1D over time [81], although direct evidence for this in humans is lacking. Interestingly, diabetes induced with selected virus infections in LEW.1WR1 rat offspring could be prevented by infection with the same virus of the mothers prior to pregnancy, suggesting strongly that maternal antibodies could be

involved. Similar findings were observed for Coxsackievirus B3-induced diabetes in a transgenic NOD mouse model (P.G. Larsson and M. Flodström-Tullberg, results presented as conference abstracts in 2010 and 2011). In these models, a single strain of virus was responsible for essentially all cases of diabetes, and although the results are of interest it is questionable whether such a scenario can be extrapolated to human T1D.

A number of potential mechanisms have been proposed to explain the so-called hygiene hypothesis for type 1 diabetes [82–84]. Depending on the timing, enterovirus and other microbial agents may reduce the incidence of autoimmune diabetes in experimental animals [17,19]. Induction of regulatory T cells is among the mechanisms involved [85], but it is unknown whether a similar phenomenon operates in humans.

Some suggestions for future studies

Throughout history, different paradigms have influenced the views on criteria for evaluating causal relationships between virus or other potential aetiological factors and disease, and methodological advances have often led to new discoveries [86]. In the near future, we believe that high-throughput ('next generation') sequencing technology may contribute to human studies of viruses in causation of T1D [87,88]. Applications of this technology in virology are still scarce, and not without problems [89–92]. With proper standardization and validation, this technology has the potential to discover novel viruses and ideally combine detection with detailed characterization of genomes from potentially aetiological viruses.

With larger and higher-quality data sets in the future, such as those expected from the Environmental Determinants of Diabetes in the Young (TEDDY) study [93], we believe that the field can also benefit from more sophisticated statistical analysis and exploration of the impact of the many sources of error. No matter how refined the methods, some bias will always remain in human observational epidemiology. Conversely, the Achilles' heel of mechanistic studies based on experimental studies in rodents or *in-vitro* systems lies in generalization to humans. We hope that potential mechanisms can be discovered or corroborated in experimental models, and that this can be translated into hypotheses testable in humans. An example of a finding in a related field which may have potential relevance in T1D is the interesting data suggesting that a terminally deleted, defective form of Coxsackievirus B3 may persist in the myocardium in mice and perhaps also humans [94].

To have any impact on prevention of T1D, we have to envisage some form of randomized prevention trial in the future, based on vaccination or otherwise. If and when a human trial can be justified, it should be based on a critical and balanced summary of available evidence from human observational studies and experimental studies.

Summary and conclusion

Cross-sectional data suggest a higher prevalence of enterovirus RNA in the blood of newly diagnosed patients with T1D than that among healthy controls, although this was not confirmed by all studies. An association between enterovirus and rapid progression from autoimmunity to T1D was reported by one longitudinal study and awaits replication. Some longitudinal studies have suggested an association of enterovirus infection with the development of islet autoimmunity. On closer inspection, study designs and results were quite heterogeneous and based on a small number of subjects. Observed associations have not been investigated at the viral genotype or serotype level. Available longitudinal studies have not provided evidence for persistence of enterovirus in serum or faeces for more than a few weeks with available methods. Despite 40 years of research, the role of enteroviruses in the aetiology of T1D is far from proven. Large birth cohort studies with frequent sampling of blood and faecal samples and strict follow-up for islet autoimmunity and T1D may help, but ultimately a randomized clinical trial of vaccination or other type of intervention will be necessary.

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Disclosure

No conflict of interest reported.

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