Incidence of Pediatric Celiac Disease Varies by Region

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INTRODUCTION: **The Environmental Determinants of Diabetes in the Young study follows an HLA risk selected birth cohort for celiac disease (CD) development using a uniform protocol. Children under investigation come from 6 different regions within Europe and the United States. Our aim was to identify regional differences in CD autoimmunity and CD cumulative incidence for children born between 2004 and 2010.**

METHODS: **Children (n = 6,628) with DQ2.5 and/or DQ8.1 were enrolled prospectively from birth in Georgia, Washington, Colorado, Finland, Germany, and Sweden. Children underwent periodic study screening for tissue transglutaminase antibodies and then CD evaluation per clinical care. Population-specific estimates were calculated by weighting the study-specific cumulative incidence with the population-specific haplogenotype frequencies obtained from large stem cell registries from each site.**

RESULTS: **Individual haplogenotype risks for CD autoimmunity and CD varied by region and affected the cumulative incidence within that region. The CD incidence by age 10 years was highest in Swedish children at 3%. Within the United States, the incidence by age 10 years in Colorado was 2.4%. In the model adjusted for HLA, sex, and family history, Colorado children had a 2.5-fold higher risk of CD compared to Washington. Likewise, Swedish children had a 1.4-fold and 1.8-fold higher risk of CD compared with those in Finland and Germany, respectively.**

DISCUSSION: **There is high regional variability in cumulative incidence of CD, which suggests differential environmental, genetic, and epigenetic influences even within the United States. The overall high incidence warrants a low threshold for screening and further research on region-specific CD triggers.**

SUPPLEMENTARY MATERIAL accompanies this paper at http://links.lww.com/AJG/C731, http://links.lww.com/AJG/C732

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INTRODUCTION

Determining the true incidence of celiac disease (CD) is not possible without nonbiased screening for the disease (1). This is because many cases occur with neither a family history nor with classic symptoms (2,3). A recent meta-analysis of studies reporting population-based incidence estimates concluded that the pediatric incidence of biopsy-proven CD remains on the rise (1). However, these estimates are highly dependent on the regional diagnostic practices. The prospective Diabetes Autoimmunity Study in the Young (DAISY) cohort study in Colorado estimated the 15-year cumulative incidence of biopsy-proven CD in the general pediatric population to be a remarkable 1.9% for children born between 1993 and 2004 (4). This estimate was an even higher 3.1% when accounting for those with high and persistent autoantibody levels who did not undergo a biopsy.

The Environmental Determinants of Diabetes in the Young (TEDDY) study prospectively follows children born between

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2004 and 2010 at genetic risk for both type 1 diabetes (T1D) and CD at 6 separate clinical sites in 4 countries. Children are longitudinally monitored for CD autoimmunity (CDA) with autoantibodies to tissue transglutaminase (tTGA), and the protocol is therefore designed for timely and thorough ascertainment of the development of persistent tTGA positivity or CDA and subsequent CD. Individuals may have CDA without experiencing CD if they have transient or fluctuating antibody levels, low antibody levels without biopsy evaluation, dietary modification influencing further evaluation, or potential CD. The population contains various DQ2.5 and DQ8.1 combinations representing the highest risk HLA-DQ haplogenotypes for CD (5). While prior publications have stratified CD risk by HLA-DQ haplogenotype and country, incidence could not be extrapolated to the general population due to the enrichment of CD-permissive HLA-DQ haplogenotypes. In this study, we identified regional differences in population-wide CD cumulative incidence in the United States and European countries using a highly unique cohort of children selected for close monitoring based on specific "high-risk" HLA-DQ haplogenotypes.

METHODS

Study design and population

TEDDY study examines environmental risk factors for the development of T1D and CD in individuals at high underlying genetic risk followed up from birth to age 15 years at 6 clinical research centers: Colorado, Georgia, Washington, Finland, Germany, and Sweden, as previously described (2,5–7).

From September 2004 to February 2010, 424,788 newborns were screened for specific human leukocyte antigen (HLA) haplogenotypes and 8,676 children were enrolled in TEDDY study (see Supplementary Figure 1, http://links.lww.com/AJG/C731). TEDDY study eligible haplogenotypes include DQ2.5/DQ2.5, DQ2.5/DQ8.1, DQ8.1/DQ8.1, and DQ8.1/DQ4.2 (see Supplementary Table 1, http://links.lww.com/AJG/C732). Participants were screened annually for tTGA starting at 2 years of age, as described further. With the first tTGA positive result, all previous collected samples were then tested for tTGA to determine the earliest time point of autoimmunity. Sex and family history of CD and T1D were self-reported (see Supplementary Table 2, http://links.lww.com/AJG/C732).

Ethical considerations

Informed consent was obtained for all studied children from a parent or legal guardian for HLA screening and participation in prospective follow-up. The study was approved at each site by its local Institutional Review Board and was monitored by a National Institutes of Health External Evaluation Committee, as previously described (8).

tTGA autoantibody measurements

tTGA autoantibodies (tTGA-IgA and tTGA-IgG combined) were measured by radiobinding assays in 2 separate laboratories, as previously described (5). Blood samples were obtained and stored for TEDDY study participants every 3 months until age 48 months and then at least every 6 months thereafter. Starting at the 2-year visit, tTGA was routinely tested and tested annually thereafter. If tTGA was positive at the annual screening, the child's samples collected before this positive result were tested for tTGA to determine the timing of seroconversion.

Definitions of CD and CDA

CDA was defined as positivity (>99th percentile of healthy control sera) in 2 consecutive tTGA tests at least 3 months apart. This was a primary study outcome. In seropositive children, CD was defined based on a duodenal biopsy with Marsh score ≥2 (9). The decision whether to biopsy was determined by the clinical gastroenterologist and was outside of the formal study protocol. When biopsy was not performed, individuals with an average tTGA of ≥100 units from 2 consecutive positive sera were considered to have CD for study purposes (10). A post hoc sensitivity analysis was performed including children with an average tTGA of ≥ 67.4 units from 2 consecutive positive sera in the outcome of CD. This lower cutoff was selected based on the findings of a receiver operating characteristic curve (data not shown).

Stem cell registries

Stem Cell Donor Registries record the phased HLA-DQ genotypes of possible bone marrow transplant donors worldwide. The stem cell donor registries of the United States (National Marrow Donor Program), Finland (Finnish Stem Cell Registry), Germany (Zentrales Knochenmarkspender-Register Deutschland and Dusseldorf Blood Bank), and Sweden (Tobias Registry) were used to determine the major celiac risk–associated HLA-DQ haplogenotypes at each TEDDY site. For the United States, region-specific haplogenotype frequencies were used to weight the TEDDY proxy haplogenotype cumulative incidence. The HLA-DQ haplogenotypes (at 2-field resolution) included in the population risk estimates along with corresponding proxy haplogenotypes from TEDDY study, are shown in the Supplementary Digital Content (see Table 3, http://links.lww.com/AJG/C732). For the purposes of describing registry haplotypes, any non-DQ2.5 and non-DQ8.1 haplotype are referred as "X" throughout this article. Of note, TEDDY study did not enroll individuals with the DQ2.5/X or DQ2.2/DQ7.5 haplogenotypes. Because these each have 1 DQA1*05 allele and 1 DQB1*02 allele, TEDDY DQ2.5/8.1 incidence was used as a proxy for these haplogenotypes. Because the DQB1*02 has been shown to have a dose-dependent effect, the DQ2.5/DQ2.2 frequency in the stem cell registry was included with the DQ2.5/2.5 frequency because these haplogenotypes confer similar risk (11).

Statistical methods

In TEDDY, cumulative risk for CDA (or CD) was estimated from the Breslow cumulative baseline hazard estimates at the event times of each stratum by TEDDY sites and HLA haplogenotypes. Risk of CDA (or CD) was compared between sites using hazard ratios from a Cox proportional hazard model, adjusting for HLA, sex, and family history of CD (5). To estimate the general population cumulative incidence in each region, the risk per clinical site and HLA haplogenotype by age was first multiplied by the corresponding HLA haplogenotype frequency obtained from the regional stem cell donor registries and then summed over a total of 4 TEDDY-defined haplogenotypes, as indicated in the Supplementary Digital Content (see Table 3, http://links.lww.com/AJG/C732). SAS, version 9.4 (Cary, NC) was used for statistical analysis, and R (4.0.5) package ggplot2 was used to generate figures.

RESULTS

Cohort characteristics

As of July 31, 2020, there were 6,628 HLA-typed eligible children carrying the DQ2.5, DQ8.1, or both haplotypes, who had undergone 1 or more tTGA tests and were thus included in this analysis. The median follow-up was 11.5 years (interquartile range 10.0–13.1 years). Altogether, 580 children (9%) had a first-degree relative with T1D, and 317 (5%) reported a first-degree

relative with CD (see Supplementary Table 2, http://links.lww.com/AJG/C732).

Of the 6,628 HLA-eligible screened children, 1,299 (20%) children met the CDA outcome and 529 (8%) met the study diagnostic criteria for CD based on biopsy or persistently high tTGA levels. The median age at CDA across all sites was 41 months (interquartile range 27–66 months). Symptom distribution in TEDDY study has previously been reported and is notable for the fact that most children with CDA were asymptomatic (2).

Cumulative risks according to site and haplogenotype

The observed regional cumulative risks for CDA and CD at each TEDDY site were compared according to the 3 highest risk HLA-DQ haplogenotypes (Figure 1). These observed cumulative risks are more completely detailed in the Supplementary Digital Content (see Table 4, http://links.lww.com/AJG/C732). Overall, Sweden continues to demonstrate the highest risk, with 63.1% and 28.3% of DQ2.5 individuals developing CDA and CD by age 10 years, respectively. This high rate of CD mirrors what was reported in earlier TEDDY publications (5). Finland consistently had a higher incidence of CDA than Colorado, for example, 60.4% vs 50.9% for DQ2.5 individuals, respectively, but had a lower incidence of CD when compared with Colorado (20.3% vs 22.6% for DQ2.5 individuals, respectively). CDA and CD risk varied substantially by haplogenotype and by clinical center, but the relative risk by region was preserved regardless of the haplogenotype. For example, the disease burden for each region remained highest in Sweden and lowest in Washington state for all haplogenotypes.

Comparing site-specific risk for CDA and CD

Differences in site-specific CDA and CD risk are summarized in Table 1. Adjusting for HLA, sex, and family history, children enrolled at the Colorado site were 2.5 times more likely (95% confidence interval [CI] = 1.7–3.5) to develop CD as those enrolled in Washington state. Finnish children were 0.70 times less likely (95% CI = 0.55–0.89) than their Swedish counterparts to develop CD. Compared with the US sites, Swedish children were 1.3 times more likely to develop CDA (95% CI = 1.2–1.5) and 1.7 times more likely to develop CD (95% CI = 1.4–2.0). Finnish children were 1.2 times as likely to develop CDA as those in the United States (95% CI = 1.1–1.4) but were not at a higher risk of CD (hazard ratio [HR] = 1.2 95% CI = 0.91–1.5). Swedish children were at a higher CD risk than those in Finland and Germany (HR = 1.4 and HR = 1.8; 95% CI = 1.1–1.8 and 95% CI = 1.2–2.8, respectively).

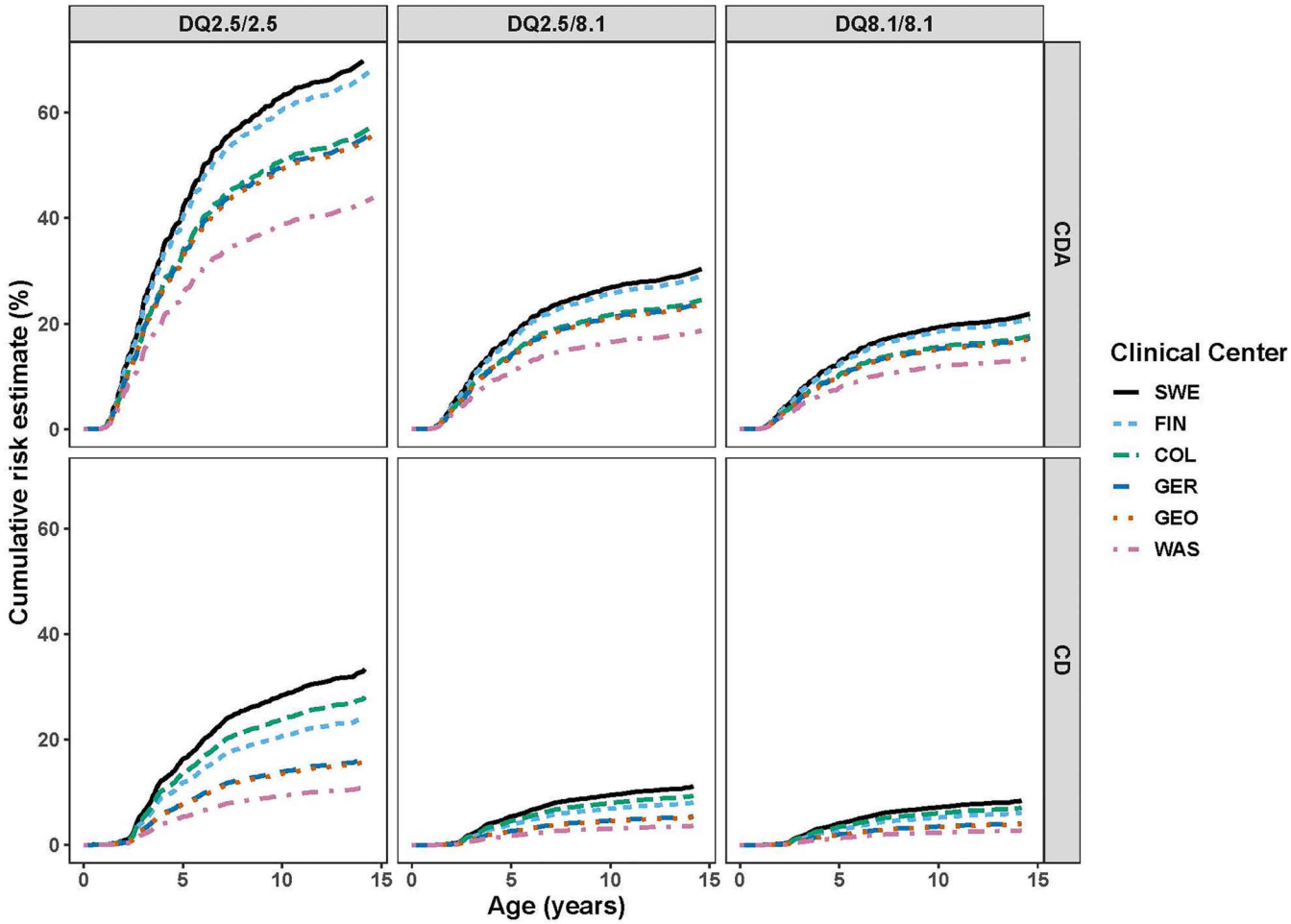

Figure 1. TEDDY population cumulative risk of CDA and CD among DQ2.5/2.5, DQ2.5/8.1, and DQ8.1/8.1 by site. The cumulative risk of CDA and CD stratified by site and HLA-DQ haplogenotype. The y axis shows the cumulative risk (%), and the x axis shows the age (months). The figure legend is ordered from the highest to lowest cumulative risk. The y axis scales were adjusted for each panel based on the range of data. CD, celiac disease; CDA, CD autoimmunity; COL, Colorado; FIN, Finland; GEO, Georgia; GER, Germany; SWE, Sweden; TEDDY, The Environmental Determinants of Diabetes in the Young; WAS, Washington.

Table 1. TEDDY hazard ratios for CDA and CD

Site	CDA		CD	
	Hazard ratio[a] (95% CI)	*P* value	Hazard ratio[a] (95% CI)	*P* value
Washington[b]	1.0		1.0	
Georgia	1.3 (1.0–1.6)	0.05	1.4 (0.92–2.3)	0.11
Colorado	1.3 (1.0–1.6)	**0.02**	2.5 (1.7–3.5)	<**0.001**
Finland	1.4 (1.2–1.8)	<**0.001**	1.9 (1.3–2.8)	<**0.001**
Germany	1.3 (0.99–1.7)	0.06	1.6 (0.93–2.6)	0.09
Sweden	1.5 (1.3–1.9)	<**0.001**	2.8 (2.0–3.9)	<**0.001**

Bolded values indicate *P* value <0.05.
CD, celiac disease; CDA, CD autoimmunity; CI, confidence interval; TEDDY, The Environmental Determinants of Diabetes in the Young.
[a]Model adjusted for HLA, haplogenotype, sex, and family history of CD.
[b]Washington was selected as the reference site because it had the lowest incidence of CDA and CD.

Stem cell donor registries for haplogenotype frequencies

According to stem cell donor registry data, DQ2.5/X and DQ8.1/X were the most common HLA-DQ haplogenotypes in the general population (see Supplementary Table 5, http://links.lww.com/AJG/C732). Sweden had the highest frequency of celiac-permissive HLA-DQ haplogenotypes (41.6%) and Georgia the lowest (34.4%). It should be noted that for the DQ2.5/DQ2.5, DQ2.5/DQ8.1, and DQ8.1/8.1 haplogenotypes, which were directly detected in TEDDY study, the Donor Registry frequencies in the Supplementary Digital Content (see Table 5, http://links.lww.com/AJG/C732) roughly match the frequencies observed in the general population newborns screened in TEDDY study, especially the pattern of more frequent risk haplotypes in Sweden and to a lesser extent in Colorado (12).

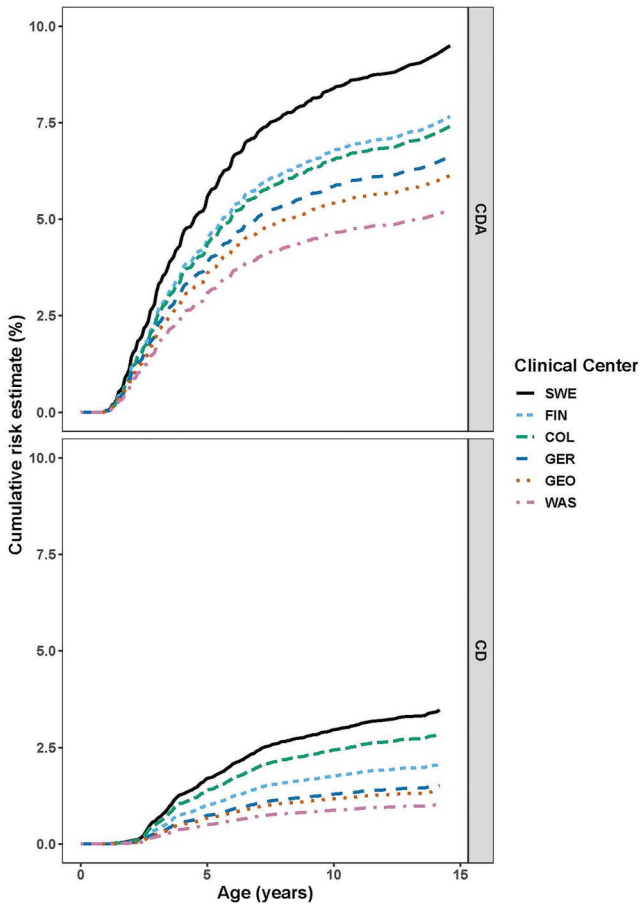

Figure 2. Estimated general population cumulative incidence of CDA and CD by site. The cumulative incidence of CDA and CD stratified by TEDDY site. Observed incidences were weighted with the HLA-DQ haplogenotype frequencies from regional stem cell donor registries to obtain regional estimates. CD, celiac disease; CDA, CD autoimmunity; COL, Colorado; FIN, Finland; GEO, Georgia; GER, Germany; SWE, Sweden; TEDDY, The Environmental Determinants of Diabetes in the Young; WAS, Washington.

Site-specific population cumulative incidence adjusted by regional frequencies of haplogenotypes

While DQ2.5 homozygosity conferred the highest risk of CDA and CD, DQ2.5 heterozygotes contributed most to the cumulative incidence. In this cohort born between 2004 and 2010, the 10-year cumulative incidence was highest in Sweden (CDA 8.4%, CD 3.0%). Within the United States, Colorado had the highest cumulative incidence for both endpoints (CDA 6.5%; CD 2.4%) (Figure 2 and Table 2).

Sensitivity analyses with lower nonbiopsy tTGA threshold for CD

A post hoc sensitivity analysis using a lower tTGA cutoff to define CD serologically (based on receiver operator curve data) was performed to reduce bias in site differences for biopsy referral and to increase the sensitivity of our definition of CD for incidence estimation. The original study strict serologic definition of CD of tTGA ≥100 avoids an overdiagnosis of CD, but at the risk of missing some potential cases that did not receive biopsy. When the tTGA cutoff to define CD was lowered to average 2-visit tTGA≥ 67.4, more children met study serologic criteria for CD. Even with this lower cutoff, the differences in the risk of CD between clinical sites and countries were still observed with statistical significance (data not shown). This indicates that the regional differences in CD incidence could not be solely attributed to detection biases posed by differential biopsy rates.

DISCUSSION

In this study, the general population cumulative incidence of CD by age 10 years is highly variable, ranging between 0.9% (Washington) and 2.4% (Colorado) within the United States and as high as 3% (Sweden). The rates of CDA are even higher, indicating that not all who develop autoimmunity have progressed to CD. These differences remain after adjusting for key factors, including HLA haplogenotypes,

Table 2. Estimated general population cumulative incidence of CDA and CD by site

CDA	Colorado, %	Georgia, %	Washington, %	Finland, %	Germany, %	Sweden, %
5 yr age	4.4 (4.0–4.8)[a]	3.6 (3.2–4.1)	3.1 (2.8–3.4)	4.5 (4.1–5.0)	3.9 (3.3–4.5)	5.6 (5.2–6.0)
10 yr age	6.5 (6.0–7.2)	5.4 (4.8–6.1)	4.6 (4.2–5.2)	6.8 (6.2–7.4)	5.9 (5.0–6.8)	8.4 (7.8–9.0)
CD	**Colorado**	**Georgia**	**Washington**	**Finland**	**Germany**	**Sweden**
5 yr age	1.4 (1.2–1.6)	0.7 (0.5–0.8)	0.5 (0.4–0.6)	1.0 (0.9–1.2)	0.7 (0.6–1.0)	1.7 (1.5–1.9)
10 yr age	2.4 (2.1–2.8)	1.2 (0.9–1.5)	0.9 (0.7–1.1)	1.8 (1.5–2.1)	1.3 (1.0–1.7)	3.0 (2.7–3.3)

CD, celiac disease; CDA, CD autoimmunity.
[a]Brackets represent the 95% confidence interval.

sex, and family history. Our findings overall are consistent with a recent meta-analysis of worldwide incidence data that suggested that CD incidence continues to rise and is highest among children, but is region dependent (1). Our study specifically finds disparities in cumulative incidence even within the US participating sites and confirms dissimilarities between the United States and Europe through a prospective and uniform screening program (5,13,14).

Notably, each specific HLA-DQ haplogenotype was associated with consistently lower disease burden in Washington state vs Colorado and similarly with lower disease burden in Germany vs Sweden and Finland, regardless of the specific HLA haplogenotype. This indicates that any specific HLA haplogenotype risk does not convey the same risk for disease from region to region. Finland consistently had a higher cumulative incidence of CDA, but not CD when compared with Colorado, suggesting that Finland may have higher rates of low level or transient autoimmunity or differing environmental factors that ameliorate progression to CD such as higher rates of probiotic supplementation in the first year of life (15).

Multiple environmental factors likely account for the marked differences in autoimmunity among regions, such as diet, chemical exposures, vaccination patterns, gastrointestinal infections, or more likely an interaction of all of these exposures. There are also likely non-HLA and epigenetic influences that moderate the development of CDA and CD. The effect of some of these factors on CDA and CD has been well described in other studies (16–21), although the field still lacks a full understanding of the interplay of environment on the development of CDA and CD. Other publications from TEDDY cohort have highlighted differences in gluten intake (22), rotavirus vaccination rates (23), and early-life gastrointestinal infections and season of birth (23,24) at the respective sites. For example, Sweden, the site with the highest CD and CDA incidence, has previously been observed to have the lowest rotavirus vaccination rates and the highest median gluten intake among TEDDY sites. Capturing environmental, genetic, and epigenetic exposures such as detailed dietary intake and detailed genetic identification of the stool virome and microbiome remains a primary focus of the TEDDY study. Future prospective studies isolating these modifiable factors should also be planned to assess causal pathways and plan for preventive strategies.

There are several limitations to this study. The self-reported nature of family history does pose the potential for information bias, but it would not have been feasible to have all family members of study participants screened as well. Because the decision to proceed to biopsy is outside of the study protocol, differences in biopsy rates between sites may introduce bias when estimating the incidence of CD. The inclusion of individuals with only very high tTGA levels helps capture additional cases with CD but could be too stringent. However, when a lower threshold was used for TEDDY serologic criteria for CD to account for this, the differences in regional risk were preserved. Furthermore, similar regional differences were seen for the outcome of CDA, which is not affected by these differential biopsy rates. However, it cannot be excluded that the observed regional differences resulted from random variation or differences in regional follow-up and testing. Because initial screening for tTGA in the United States is performed by a laboratory that only measures the immunoglobulin A (IgA) isotype (as opposed to in Europe, which measures both IgA and immunoglobulin G [IgG] isotypes), it is possible that a very small number of individuals in the United States would be missed because of IgA deficiency. By using the less stringent definition of CDA and the more stringent definition of CD, we provide a range for estimated cumulative incidence for which the actual value of CD incidence likely falls within (4,25).

TEDDY study enrolled only 4 of the described at-risk HLA-DQ haplogenotypes, and therefore, several assumptions were necessary to estimate the general population cumulative incidence. First, because TEDDY study did not enroll DQ2.5/X individuals from the general population, this study used DQ2.5/DQ8.1 risk as a proxy for the calculation of the DQ2.5/X estimated cumulative incidence. While DQ8.1 is a risk haplotype on its own, it does not add to DQ2.5 risk when present in a DQ2.5/DQ8.1 haplogenotype (4). Because DQ4.2 is not known to affect CD risk, this study also uses DQ8.1/DQ4.2 risk as a proxy for DQ8.1/X risk. Another minor caveat to this estimate is that the additional risk incurred by having DQ2.2 alone was not included in the risk assessment, except when inherited with DQ7.5 or DQ2.5 (26–28). When considering DQ2.2/DQ7.5, the celiac literature indicates that the DQA1*05-DQB1*02 heterodimer confers similar disease risk in trans as in cis and was therefore accounted for accordingly (29). Participation in stem cell registries may pose selection bias. However, the HLA-DQ frequency data from newborn HLA screening from TEDDY and other birth cohort studies mirrors the data from the stem cell registries, suggesting that these registries are representative (4). Finally, some stem cell registries excluded participants based on a medical history of autoimmune diseases such as CD, and some children with CDA may have started a gluten-free diet before diagnostic confirmation of CD. However, these additional limitations would each only result in a further slight underestimation of the general population CD cumulative incidence. By contrast, our higher estimates are consistent with the previous DAISY cohort in Colorado including adolescents born before 2004. This study's

current estimate at 10 years of 2.4% in Colorado is similar to DAISY's estimated cumulative incidence of 2.1%–3.6% by 10 years (4). Taken together, these findings indicate that pediatric CD incidence is currently extremely high in some regions and may continue to manifest in rising rates of CD in adults (1,29). It also emphasizes the notion that CD remains underascertained in the general population and current screening recommendations based on high-risk characteristics or symptoms may leave many cases unidentified.

In conclusion, there is a high cumulative incidence of CD that varies from country to country and even from state to state. From a policy standpoint, this informs future screening practices and supports efforts toward mass screening, at least in some areas. In the clinical setting, this points to the importance for clinicians to have a low threshold for CD screening in the appropriate clinical scenario. The ongoing high incidence of CD in the pediatric population suggests that there are still active environmental and non-HLA drivers of disease at least in some regions. These differences cannot be explained simply by the proportion of HLA-DQ haplogenotype risk found within the various regional background populations, sex, or family history. Ongoing analyses of environmental, genetic, and epigenetic exposures in TEDDY birth cohort will aid in the understanding of these marked differences in regional CDA and CD. Future analyses will focus on the interplay of these potential mediators and moderators in the development of CDA and CD.

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CONFLICTS OF INTEREST

Guarantor of the article: Edwin Liu, MD.

Specific author contributions: W.H., M.G.S., and E.L. were involved in study concept and design, analysis, and interpretation of the data; drafted the manuscript; critically revised the manuscript for important intellectual content, and approved the final manuscript submitted and authorship list. Q.L. was involved in study concept and design, analyzed, and interpreted the data, did the statistical analysis, critically revised the manuscript for important intellectual content and approved the final manuscript submitted and authorship list. P.M., L.G. C.A.A., K.L., S.K., J.I., J.K., B.A., A.-G.Z, J.T., M.J.R., and D.A. were involved in study concept and design, analyzed, and interpreted the data, critically revised the manuscript for important intellectual content and approved the final manuscript submitted and the authorship list.

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Study Highlights

WHAT IS KNOWN

- ✓ Celiac disease (CD) is common, and reported incidence differs by study and by region.
- ✓ Birth cohort studies suggest nongenetic factors may explain the observed differences.

WHAT IS NEW HERE

- ✓ There is a high rate of new CD cases up to age 10 years, suggesting that there are still active drivers of disease.
- ✓ Regional variation of CD exists even within the United States.
- ✓ CD was common in all studied regions, and clinicians should have a low threshold to screen in the appropriate clinical scenario.

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