Ins2 Deficiency Augments Spontaneous HLA-A*0201–Restricted T Cell Responses to Insulin

Irene Jarchum and Teresa P. DiLorenzo

_J Immunol_ 2010; 184:658-665; Prepublished online 4 December 2009; doi: 10.4049/jimmunol.0903414

http://www.jimmunol.org/content/184/2/658

**References**

This article _cites 48 articles_, 24 of which you can access for free at: http://www.jimmunol.org/content/184/2/658.full#ref-list-1

**Subscription**

Information about subscribing to _The Journal of Immunology_ is online at: http://jimmunol.org/subscription

**Permissions**

Submit copyright permission requests at: http://www.aai.org/About/Publications/JI/copyright.html

**Email Alerts**

Receive free email-alerts when new articles cite this article. Sign up at: http://jimmunol.org/alerts
Ins2 Deficiency Augments Spontaneous HLA-A*0201–Restricted T Cell Responses to Insulin

Irene Jarchum* and Teresa P. DiLorenzo*,†

Type 1 diabetes results from the autoimmune destruction of insulin-producing β cells by T cells specific for β cell Ags, including insulin. In humans, the non-MHC locus conferring the strongest disease susceptibility is the insulin gene, and alleles yielding lower thymic insulin expression are predisposing. We sought to incorporate this characteristic into an HLA-transgenic model of the disease and to determine the influence of reduced thymic insulin expression on CD8+ T cell responses to preproinsulin. We examined NOD.Ins2−/− mice, which do not express insulin in the thymus and show accelerated disease, to determine whether they exhibit quantitative or qualitative differences in CD8+ T cell responses to preproinsulin. We also generated NOD.Ins2−/− mice expressing type 1 diabetes-associated HLA-A*0201 (designated NOD.β2m−/−.HHD.Ins2−/−) in an effort to obtain an improved humanized disease model. We found that CD8+ T cell reactivity to certain insulin peptides was more readily detected in NOD.Ins2−/− mice than in NOD mice. Furthermore, the proportion of insulin-reactive CD8+ T cells infiltrating the islets of NOD.Ins2−/− mice was increased. NOD.β2m−/−.HHD.Ins2−/− mice exhibited rapid onset of disease and had an increased proportion of HLA-A*0201–restricted insulin-reactive T cells, including those targeting the clinically relevant epitope Ins B10–18. Our results suggest that insulin alleles that predispose to type 1 diabetes in humans do so, at least in part, by facilitating CD8+ T cell responses to the protein. We propose the NOD.β2m−/−.HHD.Ins2−/− strain as an improved humanized disease model, in particular for studies seeking to develop therapeutic strategies targeting insulin-specific T cells. The Journal of Immunology, 2010, 184: 658–665.

*Department of Microbiology and Immunology and †Department of Medicine, Division of Endocrinology, Albert Einstein College of Medicine, Bronx, NY 10461

Received for publication October 20, 2009. Accepted for publication November 12, 2009.

This work was supported by National Institutes of Health Grants R01 DK064315, P01 DK052956, and P60 DK020541 (Albert Einstein College of Medicine’s Diabetes Research and Training Center) and by grants from the Juvenile Diabetes Research Foundation and the Irma T. Hirschl/Monique Weill-Caulier Trust. The flow cytometry facility at Albert Einstein College of Medicine is supported by National Institutes of Health Cancer Center Grant P30 CA013330.

Address correspondence and reprint requests to Dr. Teresa P. DiLorenzo, Department of Microbiology and Immunology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461. E-mail address: teresa.dilorenzo@einstein.yu.edu

Abbreviations used in this paper: IGRP, islet-specific glucose-6-phosphatase catalytic subunit-related protein; MFI, mean fluorescence intensity; VNTR, variable number of tandem repeats.

Copyright © 2010 by The American Association of Immunologists, Inc. 0022-1767/10/$16.00 www.jimmunol.org/cgi/doi/10.4049/jimmunol.0903414

The Journal of Immunology

Downloaded from http://www.jimmunol.org/ by guest on October 3, 2017
(31–33) and no murine class I MHC molecules, to identify β cell peptides targeted by T cells in the context of HLA-A*0201 (34, 35). Importantly, several of these peptides have also been shown to be recognized by T cells from patients with type 1 diabetes (25, 36, 37).

In this study, we show that NOD.β2m−/−.HHD.Ins2−/− mice exhibit rapid onset of disease and have an increased proportion of HLA-A*0201–restricted insulin-reactive T cells, including those targeting the clinically relevant epitope Ins B10–18 (25–27, 29). Taken together, our findings suggest that insulin alleles that pre-dispose to type 1 diabetes in humans do so, at least in part, by augmenting CD8+ T cell responses to the protein. We propose the NOD.β2m−/−.HHD.Ins2−/− strain as an improved humanized disease model, in particular for epitope mapping experiments and for studies seeking to develop therapeutic strategies targeting insulin-specific T cells.

Materials and Methods

Animals

NOD and NOD.Ins2−/− mice (14) were originally obtained from The Jackson Laboratory (Bar Harbor, ME). NOD and NOD.Ins2−/− mice are maintained by brother-sister mating at the Albert Einstein College of Medicine. For breeding of NOD.Ins2−/− mice, the females were always heterozygous for Ins2, NOD.β2m−/− (18) and NOD.β2m−/−.HHD mice (35) have been previously described and are maintained by brother-sister mating at Albert Einstein College of Medicine. NOD.β2m−/−.HHD mice express a monochain chimeric HLA-A*0201 molecule consisting of human β2-microglobulin covalently linked to the α1 and α2 domains of HLA-A*0201, followed by the α3, transmembrane, and cytoplasmic portions of H-2Dβ. All animal experiments were approved by the Institutional Animal Care and Use Committee at Albert Einstein College of Medicine.

Type 1 diabetes assessment

Type 1 diabetes was assessed by the presence of glucosuria as measured with Diastrix reagent strips (Bayer, Elkhart, IN). Mice were considered diabetic after two consecutive positive measurements.

Assessment of insulitis by histopathology

As previously described (38), pancreata were fixed in Bouin’s solution and sectioned. Tissue was stained with aldehyde fuchsin for visualization of islets and with an H&E counterstain for identification of leukocytes. Islets (at least 20/mouse in most cases) were individually scored as follows: 0, no lesions; 1, peri-insular leukocytic aggregates, usually periductal infiltrates but no islet destruction; 2, 25% islet destruction; 3, >25–75% islet destruction; and 4, >75% islet destruction. An insulitis index was calculated by the formula: insulitis index = (total score for all islets)/(4 × number of islets examined). Diabetic mice or animals that died after becoming diabetic were assigned an insulitis index of 1, because these mice usually had <20 remaining islets, and all examined islets were score 4.

Peptides

A peptide library containing all of the 8-mer, 9-mer, 10-mer, and 11-mer peptides that can be derived from murine preproinsulin I was synthesized by Mimotopes (Raleigh, NC) using their proprietary Truncated PepSet technology. Each mixture in the libraries contained four peptides with a common C terminus, but having a length of 8, 9, 10, or 11 residues. The four peptides in each mixture were present in approximately equimolar amounts. Concentrated peptide stocks (2.75 mM) were prepared in 50% acetonitrile/H2O, and 40 mM (i.e., ~10 mM for each peptide in the mixture) working stocks were obtained by serial dilution in PBS (pH 6.5). Individual peptides, having a purity of ≥90%, were obtained from Mimotopes. Concentrated stocks (10 mM) were prepared in DMSO, and 10 mM working stocks were obtained by dilution in PBS.

Islet isolation

Islet isolation by collagenase perfusion of the common bile duct was performed as previously described (39). Briefly, the common bile duct was cannulated and the pancreas perfused with 1.5 ml of 0.625 mg/ml cold collagenase P (Roche, Indianapolis, IN). The inflated pancreas was removed, placed in a 50-ml conical tube with 0.5 ml collagenase P, and incubated for 14 min at 37°C to digest exocrine tissue. Islets were then washed and handpicked using a micromanipulator under a dissecting microscope. Islets were handpicked again and counted and placed in culture as described below.

Culture of islet-infiltrating T cells

Culture medium for islet-infiltrating cells consisted of RPMI 1640 medium supplemented with 10% FBS (HyClone, Logan, UT), 1 mM sodium pyruvate, nonessential amino acids, 28 μM β-mercaptoethanol (designated RPMI-10), and 50 U/ml recombinant human IL-2 (ProproTech, Rocky Hill, NJ). Approximately 50 islets/well were cultured in 24-well tissue culture plates at 37°C, 5% CO2 for 7 d. As previously reported (39), in most cultures, the majority of the cells were CD8+ after this time period (e.g., for NOD mice at 7–8 wk of age, percentage of CD8+ T cells = 65.5 ± 17.3; range, 39.2–85.4).

IFN-γ ELISPOT assay

ELISPOT plates (MAHA S45 10; Millipore, Billerica, MA) were precoated with anti-mouse IFN-γ mAb (BD Biosciences, San Jose, CA) and blocked with 1% BSA (Fraction V; Sigma-Aldrich, St. Louis, MO). Mitomycin C-treated APCs (RMA-S/Kd for NOD and NOD.Ins2−/− mice and T2 for NOD.β2m−/−.HHD and NOD.β2m−/−.HHD.Ins2−/− mice) were added at 2 × 105 cells/well and pulsed with 1 μM peptide. Cultured islet-infiltrating T cells were added at 2 × 105 cells/well, and plates were incubated at 37°C for 40 h. IFN-γ secretion was detected with a second, biotinylated anti-mouse IFN-γ mAb (BD Biosciences), and spots were developed using streptavidin-alkaline phosphatase (Zymed Laboratories, Carlsbad, CA) and 5-bromo-4-chloro-3-indolyl-phosphate/NBT substrate (Sigma-Aldrich). Spots with a minimum size of 0.01 mm2 were counted using an automated ELISPOT reader system (Autoimmun Diagnostika, Strassberg, Germany). Spot counts shown are background (PBS)-subtracted.

MHC stabilization assay

Peptide binding to Db or Kd was determined as described (40). Briefly, following overnight incubation at 26°C, RMA-S/Kd cells were incubated with peptide or PBS and human β2-microglobulin (Sigma-Aldrich, St. Louis, MO) for 20 h at 37°C. Cells were stained with anti-Dβ (clone 34-2-12) or anti-Kβ mAb (clone SF11.1, both from BD Biosciences, San Jose, CA), and analyzed by flow cytometry. The positive control peptide for Db was Misc2 (YAIENYEL) and for Kβ NRP-V7 (KYNKANVFL). The fluorescence index was calculated as the ratio of the average mean fluorescence intensity (MFI) in the presence of peptide divided by the average MFI in the presence of solvent alone.

Statistical analysis

The Mann-Whitney U test was used throughout the study to determine the statistical significance of the data, except for analysis of survival curves, for which the log-rank (Mantel-Cox) test was used.

Results

Accelerated insulitis and diabetes in NOD.Ins2−/− mice

Disease development in our female NOD.Ins2−/− and NOD mice agree with the incidence of diabetes previously reported by others (14, 15). As shown in Fig. 1A, 100% of NOD.Ins2−/− mice and 20% of NOD mice became diabetic by 16 wk of age. In addition, we found that islets of young (4–5 wk of age) and older (10–11 wk of age) female NOD.Ins2−/− mice were more heavily infiltrated than those from female NOD mice of similar age (Fig. 1B).

Novel CD8+ T cell epitopes targeted in NOD.Ins2−/− mice

We studied islet-infiltrating CD8+ T cells from NOD and NOD.Ins2−/− mice and tested them by IFN-γ ELISPOT assay, screening an exhaustive peptide library that spans the preproinsulin 1 molecule. As shown in Fig. 2A, the only epitope for which we were able to reliably demonstrate reactivity in NOD mice was the previously described NOD epitope Ins1/2 B15–23 (23). Not surprisingly, reactivity to Ins1/2 B15–23 was also observed in NOD.Ins2−/− mice. However, in NOD.Ins2−/− mice, we also found reactivity to a novel epitope cluster shared between preproinsulin 1 and 2, designated “99–101 cluster” (mixes 99, 100, and 101) (Fig. 2A, 2D). As shown in Fig. 2B, we found that the 99–101 cluster contained two novel epitopes from the prepro- and mature Ins1 and Ins2 molecules, Ins1/2 A11–19 (the 9-mer peptide in mix
99) and Ins1/2 A13–21 (the 9-mer peptide in mix 101), defining a novel epitope hot spot in the insulin molecule.

We next sought to determine the MHC restriction of the two novel epitopes by performing IFN-\(\gamma\) ELISPOT with APCs that express either Db or K\(\delta\) and which were washed of excess peptide to prevent T cells from presenting peptide to each other. However, we only observed a response to the peptides when excess peptide was present during the assay (data not shown). This suggests that the peptides have low affinity for MHC and/or that the cysteines in the peptides allow them to dimerize or become otherwise modified in ways that reduce their binding to MHC. We therefore tested variants of Ins1/2 A11–19 and Ins1/2 A13–21 where the anchor position 9 was mutated to a preferred residue (methionine and isoleucine for Db and isoleucine for K\(\delta\)) (41), or where the cysteines were mutated to serines. As shown in Fig. 2C, using a cell-based MHC stabilization assay, we confirmed that the natural versions of the epitopes have very low binding affinity, and, importantly, we demonstrated that both epitopes are presented in the context of Db when the anchor position 9 is mutated to a preferred residue. Of note, the I9 variant (an anchor residue for both K\(\delta\) and Db) of Ins1/2 A11–19, the weakest-binding of the two novel epitopes, shows no detectable affinity for K\(\delta\) (Fig. 2C). In this assay, peptide variants containing serines instead of cysteines did not show improved binding to the MHC.

Higher frequency of insulin-reactive CD8\(^+\) T cells in NOD.Ins2\(^{−/−}\) mice

After finding that they target novel epitopes, we investigated whether CD8\(^+\) T cells recognizing insulin peptides were also quantitatively increased in NOD.Ins2\(^{−/−}\) compared with NOD mice.
mice. The average reactivity to Ins1/2 B15–23 and the novel A11–19 and A13–21 insulin epitopes was six times higher in young NOD.Ins2−/− mice (7–8 wk of age) compared with wild-type animals (Fig. 3A). In addition, in this age group, we obtained 4.7-fold more CD8+ T cells after culturing islet infiltrates from NOD. Ins2−/− mice as compared with wild-type littermates (data not shown). Therefore, the average number of insulin-reactive CD8+ T cells was 28 times higher in NOD.Ins2−/− than in standard NOD female mice (Fig. 3D). This marked difference in insulin reactivity was not observed in older or diabetic mice (Fig. 3A), suggesting that it likely reflects a difference in the precursor frequency of insulin-specific CD8+ T cells and is not a result of a more advanced disease stage in NOD.Ins2−/− versus NOD mice. This is further supported by our finding that reactivity to islet-specific glucose-6-phosphatase catalytic subunit-related protein (IGRP) 206–214, a major CD8+ T cell epitope in NOD mice (22, 42), did not differ significantly between NOD.Ins2−/− and wild-type females at 7–8 wk of age (Fig. 3B).

We investigated whether the difference in insulin-reactive CD8+ T cells in young mice was due to the difference in reactivity to any particular insulin epitope. Even though there was higher reactivity to each of the three insulin epitopes in NOD.Ins2−/− than in NOD mice, these differences were not on their own statistically significant (Fig. 3C). (There was, however, a trend for Ins1/2 B15–23; p = 0.083.) Therefore, the quantitative difference observed in overall insulin reactivity is due to CD8+ T cells specific for all three epitopes studied.

**FIGURE 3.** CD8+ T cell reactivity to insulin epitopes in the islet infiltrates of NOD and NOD.Ins2−/− mice. A, Female NOD.Ins1−/− (filled circles) and NOD mice (open circles) of different ages (7–8 and 10–11 wk of age) or diabetic were studied for reactivity to insulin epitopes by IFN-γ ELISPOT. The numbers of spot-forming cells in response to three insulin epitopes (Ins1/2 B15–23, A11–19, and A13–21) in each culture of islet-infiltrating cells were subtracted for PBS, normalized to the percent of CD8+ T cells (determined by flow cytometric analysis of an aliquot of each culture), and averaged. The data are expressed as the number of spot-forming cells per 2 × 10^6 CD8+ T cells. Each data point represents one mouse or the pooled islets of multiple mice. B, Reactivity to IGRP 206–214 is shown. In A and B, the group of NOD.Ins2−/− mice at 10–11 wk of age includes mice that were diabetic. C, Reactivity of mice at 7–8 wk of age for the individual insulin epitopes is shown. These data are normalized as in A to the percent of CD8+ T cells in each culture. D, The total number of islet-infiltrating CD8+ T cells reactive to insulin (the added reactivity to the three insulin epitopes) or to IGRP 206–214 is shown for NOD.Ins2−/− (black bars) and NOD mice (white bars) at 7–8 wk of age.

**Disease acceleration in NOD.β2m−/−.HHD.Ins2−/− mice**

To translate our findings of the CD8+ T cell population in NOD.Ins2−/− mice more directly to human patients, we generated NOD.β2m−/−.HHD.Ins2−/− mice expressing the human class I MHC molecule HLA-A*0201, but no murine class I MHC molecules, and also lacking Ins2 expression. Introduction of the Ins2 deficiency markedly accelerated diabetes development in NOD.β2m−/−.HHD mice (Fig. 4A; p < 0.001). Although NOD.β2m−/−.HHD mice in our colony began developing diabetes at 16 wk of age, disease onset was as early as 5 wk of age in the NOD.β2m−/−.HHD.Ins2−/− stock. Further, 90% of NOD.β2m−/−.HHD.Ins2−/− mice developed diabetes by 10 wk of age. Interestingly, the onset of diabetes in NOD.β2m−/−.HHD.Ins2−/− mice was also accelerated with respect to NOD.Ins2−/− mice (Fig. 4A; p < 0.001). This suggested that the HLA-A*0201–restricted T cell response is affected to a greater degree than the Db and Kd response by the lack of thymic insulin expression, establishing the NOD.β2m−/−.HHD.Ins2−/− mouse as an improved model of type 1 diabetes.

**Identification of insulin epitopes targeted in NOD.β2m−/−.HHD.Ins2−/− mice**

To identify the insulin epitopes targeted in NOD.β2m−/−.HHD.Ins2−/− mice, we tested islet-infiltrating cells for reactivity to our exhaustive library of preproinsulin 1 peptides by IFN-γ ELISPOT. CD8+ T cells from NOD.β2m−/−.HHD.Ins2−/− mice recognized insulin epitopes previously described by us to be targeted in the context of HLA-A*0201 in NOD.β2m−/−.HHD mice (34) (Figs. 4B, 5B). However, we also identified responses to two other epitopes that were not previously demonstrated to be targets of islet-infiltrating CD8+ T cells from NOD.β2m−/−.HHD mice (Fig. 4B). These reactivities were named the “35–37 cluster” and Ins A10–20. The 35–37 cluster contained Ins1/2 B10–18 (Fig. 4C), a peptide completely conserved between mice and humans, and reported to be a particular insulin epitope. Even though there was higher reactivity by the lack of thymic insulin expression, establishing the NOD.β2m−/−.HHD.Ins2−/− model of type 1 diabetes (25).

**Higher frequency of insulin-reactive CD8+ T cells in NOD.β2m−/−.HHD.Ins2−/− mice**

We tested cultured islet-infiltrating cells from mice at 7–8 wk of age against our panel of peptides, which included Ins1 L3–11, Ins1 B5–14, Ins1/2 A2–10 (previously identified in our laboratory (34)), as well as Ins1/2 B10–18 and Ins1/2 A10–20. As shown in Fig. 5A, NOD.β2m−/−.HHD.Ins2−/− mice had a much higher frequency of insulin-reactive CD8+ T cells infiltrating their islets (p = 0.0005). The average proportion of insulin-specific CD8+ T cells in the islet infiltrate of NOD.β2m−/−.HHD.Ins2−/− mice was almost 8 times higher than in the NOD.β2m−/−.HHD stock. There was a higher proportion of both Ins1/2 A10–18-specific and Ins1/2 B10–18-specific cells in NOD.β2m−/−.HHD.Ins2−/− compared with NOD.β2m−/−.HHD mice (Fig. 5B; p = 0.0003 and p = 0.015, respectively). These differences were observed even when older NOD.β2m−/−.HHD mice were examined (Fig. 5B), confirming that they were not simply due to the altered kinetics of diabetes development in the two strains (Fig. 4A). The response to
IGRP epitopes tended to be greater in NOD.β2m−/−.HHD than NOD.β2m−/−.HHD.INS2−/− mice, and analysis of the response to individual IGRP epitopes revealed a significant difference in the response to IGRP 228–236 (Fig. 5C; p = 0.02), the immunodominant IGRP epitope in NOD.β2m−/−.HHD mice (35).

Discussion

Defects in central tolerance, particularly in the thymic expression of autoantigens, are known to play a crucial role in the development of autoimmune (6, 7, 43, 44). Intrathymic injection of insulin and other autoantigens targeted by T cells in mouse models of type 1 diabetes leads to protection from autoimmune disease (45, 46). Ins2 deficiency has been previously studied to model the genetic association of alleles at the insulin promoter, leading to low thymic expression of insulin and susceptibility to type 1 diabetes in humans (10–12, 14, 15). Chentoufi and Polychronakos (10) demonstrated that Ins2−/− mice do not have decreased insulin expression in the pancreas and that these mice have higher T cell responses to insulin as compared with Ins1−/− mice. Recently, Ins2 was specifically deleted in the medullary thymic epithelial cells of mice. When these animals were also rendered Ins1−/− deficient to eliminate residual thymic insulin expression, autoimmune diabetes was induced (13). Although these studies were not performed in the NOD background, they helped to solidify the Ins2−/− phenotype as a result of the absence of Ins2 expression in the thymus and not the islet. However, careful analysis of changes in the specificity of T cells infiltrating the pancreatic islets of NOD.INS2−/− mice, particularly CD8+ T cells, has been lacking. We hypothesized that such insights would provide opportunities for further translation to human patients carrying class I VNR alleles.

We chose to examine the peptide specificity of islet-infiltrating T cells, rather than those at other sites, because the largest proportion of islet-specific T cells is found within the islets themselves (24). Furthermore, studies in NOD-based models of autoimmune diabetes have revealed that similar epitope hierarchies are found in the islets, spleen, pancreatic lymph nodes, and blood (24). Our approach, examining the peptide specificity of islet-infiltrating T cells, led us to demonstrate for the first time here that Ins1/2 A11–19 and Ins1/2 A13–21 are targeted by CD8+ T cells in NOD. INS2−/− mice in addition to the KE-restricted Ins1/2 B15–23 epitope (23). When assessing overall reactivity to insulin epitopes, there was a significantly higher proportion of insulin-reactive CD8+ T cells in the islets of NOD.INS2−/− compared with NOD mice. Therefore, in addition to targeting novel epitopes, the frequency of insulin-reactive CD8+ T cells at 7–8 wk of age is six times higher in NOD.INS2−/− than NOD mice. In fact, the absolute number of T cells recognizing the KE and DI insulin epitopes is 28 times higher in NOD.INS2−/− mice as compared with NOD. Despite differences in the degree to which tolerance is achieved for particular insulin epitopes, lack of insulin expression in the thymus leads to overall greater levels of insulin-reactive CD8+ T cells, which correlate with exacerbated disease. The pathogenicity of insulin-specific CD8+ T cells is further indicated by our previous work in which we used an in vivo cytotoxicity assay to show that CD8+ T cells specific for Ins B15–23/H-2Kb, Ins A2–10/HLA-A2, and Ins B5–14/HLA-A2 can all kill peptide-bearing targets in vivo (34).

Based on previous studies, we know that CD8+ T cell epitopes identified in HLA-transgenic NOD mice can be excellent candidates for testing in patients, as two of the three IGRP epitopes identified by our laboratory using T cells from HLA-A*0201-transgenic NOD mice (35) were later shown to be targeted in patients with type 1 diabetes (25, 36, 37). This led us to generate the novel NOD.β2m−/−.HHD.INS2−/− mouse strain, in which two factors that contribute to type 1 diabetes in humans (i.e., diminished insulin expression in the thymus and the presence of the MHC class I susceptibility allele HLA-A*0201) [31–33], are represented. The strikingly accelerated onset of disease in NOD.β2m−/−.HHD.INS2−/− mice indicates that the presence of both susceptibility factors in the NOD background may provide a better “humanized” model of type 1 diabetes. Particularly, careful study of the HLA-A*0201-restricted T cell responses in this stock may lead to critical insights into the mechanisms of type 1 diabetes development in humans. Evidence that NOD.β2m−/−.HHD.INS2−/− mice represent an improved model of the disease comes from the finding that they are characterized by CD8+ T cells that frequently target Ins B10–18. Several independent laboratories established the importance of Ins B10–18-specific CD8+ T cells during development of type 1 diabetes in humans. This epitope is processed and presented by cells expressing HLA-A*0201 (47) and specifically targeted by T cells from peripheral
blood of recent-onset and long-standing patients with type 1 diabetes (25, 26, 29). Further, this epitope is targeted by HLA-A*0201–restricted CD8+ T cells from peripheral blood of patients with recurrent autoimmune diabetes after islet transplantation (27). However, extensive analyses failed to identify Ins B10–18-specific T cells infiltrating the islets of NOD (34). The work presented here, demonstrating that this epitope is only targeted in NOD, β2m−/−.HHD mice in the context of Ins2 deficiency, strongly supports the NOD, β2m−/−.HHD. Ins2−/− strain as an improved model of type 1 diabetes.

Islet-infiltrating CD8+ T cells from NOD, β2m−/−.HHD. Ins2−/− mice were also found to target the Ins1/2 A10–20 peptide mixture (mix 100, Fig. 2D). This reactivity can most likely be attributed to Ins A12–20, as this 9-mer peptide was found to be processed and presented by preproinsulin-expressing HLA-A*0201–positive cells (47) and to be recognized by HLA-A*0201–restricted T cells from patients with type 1 diabetes (25). Ins1/2 A10–20 is in the same region of the insulin protein as Ins1/2 A11–19 and Ins1/2 A13–21, the novel epitopes targeted in NOD. Ins2−/− mice in the context of D9. Interestingly, C57BL/6 mice transgenically expressing CD80 on their β cells develop diabetes when immunized with a preproinsulin-encoding plasmid, and the diabetogenic CD8+ T cells target Ins1/2 A12–21 in the context of Kb (48). The fact that several peptides, varying in sequence by very few amino acids, are targeted by islet-infiltrating T cells in the context of three different class I MHC alleles (D9, HLA-A*0201, and Kb) establishes this region of the molecule as an epitope hot spot.

The proportion of islet-infiltrating CD8+ T cells specific for insulin epitopes is almost eight times higher in NOD, β2m−/−. HHD. Ins2−/− than NOD, β2m−/−.HHD mice. Further, the proportion of islet-infiltrating T cells reactive to Ins1/2 A2–10 is 9 times higher in NOD, β2m−/−.HHD. Ins2−/− compared with NOD, β2m−/−.HHD mice at 7–8 wk of age. Interestingly, this epitope was the immunodominant epitope in NOD, β2m−/−.HHD mice (34). This is perhaps an indication that the precursor frequency of T cells specific for this epitope is high, and whereas some escape tolerance in NOD, β2m−/−.HHD mice, many more do so and expand when insulin expression is lacking in the thymus. Ins1/2 A2–10 is thought to be an important target of the pathogenic process, as we previously reported in vivo cytotoxicity to cells displaying this peptide in NOD, β2m−/−.HHD mice (34). Our finding that the HLA-A*0201–restricted T cell response to IGRP epitopes is repressed in NOD, β2m−/−.HHD. Ins2−/− mice may reflect the complexity of the dynamics of expansion of CD8+ T cell specificities. The inability of IGRP-reactive T cells to expand in the islets of young NOD, β2m−/−.HHD. Ins2−/− mice may be due to competition with insulin-specific CD8+ T cells for interaction with APCs. The markedly higher precursor frequency of CD8+ T cells specific for insulin epitopes may be at a threshold such that expansion of other specificities is limited. Because the insulin-specific CD8+ T cell response is particularly affected in Ins2-deficient mice in the context of HLA-A*0201, this may explain why we observed a decrease in the IGRP-reactive T cell response in NOD, β2m−/−.HHD. Ins2−/− mice but not in the NOD. Ins2−/− strain.

Our results indicate there is epitope dependence in terms of which insulin-reactive T cells undergo negative selection when encountering an antigenic ligand in the thymus. Although tolerance to some T cell specificities is almost complete in the context of thymic insulin expression (e.g., Ins1/2 A10–20 and Ins1/2 B10–18), tolerance to others is clearly only partial (e.g., Ins1/2 A2–10). Differences in the efficiency with which these autoreactive T cells are thymically deleted may be due to several factors, including the preferential processing and presentation of particular regions of the insulin molecule, and the precursor frequency of a specific autoreactive CD8+ T cell population.

All in all, the markedly accelerated incidence of disease in NOD, β2m−/−.HHD. Ins2−/− mice strongly supports the Ins2 deficiency as an excellent model for the association between low thymic expression of insulin and susceptibility to type 1 diabetes development in humans. Our studies of the CD8+ T cell response to insulin and IGRP in the context of the human HLA-A*0201 allele establish the necessary tools that would allow novel therapies to be tested in NOD, β2m−/−.HHD. Ins2−/− mice, as many T cell specificities relevant to disease have been identified and can be monitored. This is particularly exciting in view of recent findings suggesting that insulin therapy in combination with anti-CD3 treatment is a promising strategy to peripherally tolerate insulin-specific T cells (49). Further, it is possible that patients with class I VNTR insulin alleles will respond differently to this therapy compared with patients carrying the dominantly protective class III alleles.

FIGURE 5. Altered frequency of islet-infiltrating cells specific for HLA-A*0201–restricted insulin and IGRP epitopes in NOD, β2m−/−.HHD. Ins2−/− compared with NOD, β2m−/−.HHD. Ins2−/− mice (open symbols) and NOD, β2m−/−.HHD. Ins2−/− mice (filled symbols) at 7–8 wk of age were tested by IFN-γ ELISPOT for reactivity to insulin and IGRP CD8+ T cell epitopes. A. The reactivity to all insulin (Ins A10–20, Ins B10–18, Ins1 L3–11, and Ins1/2 A2–10) or IGRP epitopes (IGRP 228–336, IGRP 265–273, and IGRP 337–345) studied was averaged for each mouse after background subtraction. Reactivity to the individual epitopes is shown for insulin (B) and IGRP (C). The data were normalized to the percentage of CD8+ T cells (determined by flow cytometric analysis of an aliquot of each culture). Each symbol represents an individual mouse. In B, NOD, β2m−/−.HHD mice at 12–13 wk of age were also examined.
Acknowledgments
We thank David V. Serreze for critical reading of the manuscript.

Disclosures
The authors have no financial conflicts of interest.

References


