Cutting Edge: Type 1 Diabetes Occurs despite Robust Anergy among Endogenous Insulin-Specific CD4 T Cells in NOD Mice

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Insulin-specific CD4+ T cells are required for type 1 diabetes. How these cells are regulated and how tolerance breaks down are poorly understood because of a lack of reagents. Therefore, we used an enrichment method and tetramer reagents to track insulin-specific CD4+ T cells in diabetes-susceptible NOD and resistant B6 mice expressing I-A^g7. Insulin-specific cells were detected in both strains, but they only became activated, produced IFN-γ, and infiltrated the pancreas in NOD mice. Unexpectedly, the majority of Ag-experienced cells in NOD mice displayed an anergic phenotype, but this population decreased with age as tolerance was lost. B6 mice expressing I-A^g7 were protected because insulin-specific cells did not become effector or anergic T cells but remained naive. These data suggest that NOD mice promote tolerance through anergy induction, but a small proportion of autoreactive T cells escape anergy to provoke type 1 diabetes. The Journal of Immunology, 2013, 191: 4913–4917.

Insulin is an immunodominant Ag during type 1 diabetes (T1D) (1–4). In NOD mice, >90% of insulin-specific CD4+ T cells in the pancreas are specific for the insulin B chain (InsB) peptide 9–23 (InsB9–23) (3), and these cells are required for T1D (5). In addition, tolerogenic immunization with InsB9–23 peptide delays or prevents T1D (6, 7). Despite the well-established role of insulin-specific CD4+ T cells during T1D, little is known about how this immune response develops because these cells have been difficult to track. There has not been an in-depth analysis of this critical CD4+ T cell population to understand how peripheral tolerance fails and T1D develops.

MHC class II tetramers are powerful reagents to track Ag-specific CD4+ T cells. When coupled with magnetic enrichment, rare cells can be tracked with high precision (8, 9). However, a major challenge in generating MHC class II tetramers is determining the peptide-binding register. The relevant binding register for the InsB10–23 epitope is debated (10–13). However, there is evidence that the majority of InsB10–23-reactive CD4+ T cells recognize the 14–22 core segment ALYLVCGER (register 3) when mutated to optimize binding to I-A^g7 (11, 12). Therefore, we constructed a tetramer reagent containing the modified register 3 epitope bound to I-A^g7 to define the dynamics of the insulin-specific CD4+ T cell response in diabetes-susceptible NOD mice, as well as resistant B6 mice expressing the I-A^g7 allele (B6.g7) (14). Our results led to the surprising conclusion that most InsB10–23r3: I-A^g7-specific T cells are anergic in NOD mice but are naive in B6.g7 mice.

Materials and Methods

Mice

NOD mice were purchased from Taconic. B6.g7 mice were generated by Zucchielli et al. (14). NOD.BDC2.5 mice were purchased from The Jackson Laboratory. NOD.BDC2.5 cells were isolated, as described (15), and 7500 naïve T cells were transferred i.v. to 7–12-wk-old prediabetic NOD mice. Blood glucose ≥ 250 mg/dl indicated diabetes (LifeScan). All animal experiments were approved by the Institutional Animal Care and Use Committee of the University of Minnesota.

Insulin tetramer

The InsB10–23r3:I-A^g7 tetramer was constructed similarly as described (8). Briefly, I-A^g7 monomer containing the peptide HLYERLYLVCGEEG was produced and biotinylated in Drosophila S2 cells. Biotinylated monomer was purified on a monomeric avidin column (Thermo Scientific) and combined with streptavidin (SA)-PE and SA-allophycocyanin (Prozyme) to produce the tetramers. The National Institutes of Health tetramer core provided I-A^g7 hen egg lysozyme (HEL)11–25 tetramer (AMKRHGLDNYRGYS).
Flow cytometry

Single-cell suspensions were generated, as described (15). Tetramer-binding cells were enriched from the spleen and non-draining lymph nodes (non-dLNs; periaortica, inguinal, brachial, cervical, axillary, and mesenteric lymph nodes) by incubation with 10 nM PE- or allophycocyanin-tetramer for 1 h at 25°C, followed by anti-PE and anti-allophycocyanin MicroBeads for 30 min at 4°C and prior to elution over magnetic columns (Miltenyi Biotec).

Samples were collected using a BD LSR II and Fortessa (BD Biosciences). Data were analyzed using FlowJo software (TreeStar). Cells were enumerated using AccuCheck Counting Beads (Life Technologies).

Cytokine stimulation and priming

Cytokines from insulin-specific CD4+ T cells were assessed in vitro in complete DMEM containing 100 ng/ml PMA, 1000 ng/ml ionomycin, and 10 μg/ml brefeldin A (Sigma) for 4 h (15). For BDC2.5 T cells, 500 ng acetylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected i.v. for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenously for 4 h. The modified InsB10–23 peptide (11) or HEL 11–25 (Genemedylated p31 peptide (YVRPLWVRME) (Genemed Synthesis) was injected intravenous...
T cells encounter Ag and differentiate into pathogenic Th1 cells in NOD mice, whereas failure to encounter autoantigen in B6.g7 mice leads to a lack of Th1 differentiation. Insulin-specific CD4+ T cells can differentiate into Foxp3+ regulatory T cells

Previous reports demonstrated that regulatory T cells (Tregs) influence the development of T1D (20). We examined the possibility that NOD mice had a decreased frequency of insulin-specific Tregs. However, Foxp3+ Tregs developed in both strains, and we did not measure a significant difference between NOD and B6.g7 mice (Fig. 3B). Therefore, we speculate that Ag-specific Tregs alone are not the main mechanism for diabetes resistance in the B6.g7 mouse. In fact, it appears that there are more Tregs in NOD mice compared with B6.g7 mice; however, this difference is not statistically significant.

T cell anergy develops in the pLNs of NOD mice

It is thought that T1D develops as the result of the loss of peripheral tolerance. However, tolerance induction in the endogenous insulin-specific CD4+ T cell population has never been tested. We predicted that the majority of insulin-reactive T cells would escape tolerance and cause diabetes. However, we found that only a small subset of insulin-reactive T cells produced IFN-γ and infiltrated the pancreas (Figs. 2, 3). We speculated that Ag-experienced insulin-specific T cells might become anergized and be retained in the SLOs. To test this in T1D, we used our recently characterized adoptive-transfer model to study islet-specific CD4+ T cells (15). In this model, a low number of naive T cells from the BDC2.5 mouse were transferred into prediabetic NOD mice to mimic the endogenous population (15). By 3 wk posttransfer, the BDC2.5 CD4+ T cells developed an anergic phenotype (Foxp3−FR4−CD73−) (Fig. 4A, 4B). Surprisingly, more BDC2.5 CD4+ T cells in the pLNs were anergic (Fig. 4A, 4B) than were effector phenotype cells (FR4−CD73−CD44−Foxp3−). In contrast, anergic phenotype cells were largely absent from the spleen and pancreas (Fig. 4A, 4B). To validate that coexpression of FR4 and CD73 correlated with functional anergy in diabeticogenic
T cells, we assessed IFN-γ in the pLNs. Following peptide challenge, IFN-γ was not produced by CD73+FR4+BDC2.5 T cells in the pLNs, and these cells were largely absent from the spleen and non-dLNs (Fig. 4E, 4F). It was difficult to assess cytokine production from the insulin-specific population because of low cell numbers; however, anergic polyclonal CD4+ cells were functionally impaired compared with effector cells, similarly to BDC2.5 cells (Supplemental Fig. 1E). We speculate that the small population of effector cells in the pLNs have escaped tolerance and participate in T1D pathogenesis. The frequency of anergic phenotype insulin-specific T cells was significantly higher in the pLNs of young NOD mice (5 wk) compared with older NOD mice (20–26 wk), consistent with the idea that as mice age, more cells break tolerance. These data support a model in which anergy is induced in a large fraction of insulin-specific CD4+ T cells in the pLNs early in life. However, insulin-specific cells can be detected in the pancreas at this age (Fig. 2), demonstrating that tolerance is incomplete, and progression to T1D may require only a small fraction of self-reactive T cells escaping peripheral tolerance. Furthermore, these data suggest that anergy is not sustained as NOD mice age, which may contribute to enhanced infiltration of the pancreas, ultimately causing diabetes.

We next compared the frequency of anergic cells to ascertain whether anergic cells dominated the B6.g7 mice. B6.g7 mice did not have a significant population of anergic insulin-specific cells (Fig. 4F). These data suggest that B6.g7 mice are protected from T1D because insulin-specific cells do not become effector T cells and retain a naïve phenotype rather than become anergic cells.

Although the mechanisms that limit autoimmunity in B6.g7 mice but fail in NOD mice remain to be fully elucidated, our data suggest that there is a substantial difference in the presentation of InsB10–23/MHC class II between these mouse strains. Our findings suggest that, in NOD mice, insulin-specific CD4+ T cells encountered Ag in the pLNs between weeks 3 and 5 of life, and a small subset differentiated into IFNγ+ effector cells and infiltrated the pancreas, whereas another larger subset became anergic. Despite the induction of anergy in a large fraction of cells in the pLNs, insulin-specific CD4+ T cells in young NOD mice are capable of driving disease. Therefore, we speculate that only a small number of activated effector cells are responsible for T1D in NOD mice. We further speculate that B6.g7 mice are diabetes resistant because these cells fail to encounter autoantigen and remain naïve.

In conclusion, we developed an MHC class II tetramer that allows tracking of InsB10–23/MHC class II CD4+ T cells. Despite the presence of pathogenic CD4+ T cells in NOD mice, an anergic population emerged specifically in the pLNs. This population diminished over time and was absent from the pancreas. In B6.g7 mice, insulin-specific cells remained naïve, suggesting an absence of Ag encounter. Studying how insulin-specific CD4+ T cells become activated in NOD mice, but not in B6.g7 mice, may provide new insight into how tolerance is breached during T1D. It would be interesting to determine whether other InsB9–23 registers have the same bias toward anergy induction or whether these cells are more pathogenic (12, 24). Understanding how peptide/MHC binding impacts the effector potential of diabetogenic CD4+ T cells may aid in our therapeutic efforts to restore tolerance in T1D patients.
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Disclosures
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References