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### **IFN $\beta$ Accelerates Autoimmune Type 1 Diabetes in Nonobese Diabetic Mice and Breaks the Tolerance to $\beta$ Cells in Nondiabetes-Prone Mice<sup>1</sup>**

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# IFN $\beta$ Accelerates Autoimmune Type 1 Diabetes in Nonobese Diabetic Mice and Breaks the Tolerance to $\beta$ Cells in Nondiabetes-Prone Mice<sup>1</sup>

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Genetic and environmental factors are decisive in the etiology of type 1 diabetes. Viruses have been proposed as a triggering environmental event and some evidences have been reported: type I IFNs exist in the pancreata of diabetic patients and transgenic mice expressing these cytokines in  $\beta$  cells develop diabetes. To determine the role of IFN $\beta$  in diabetes, we studied transgenic mice expressing human IFN $\beta$  in the  $\beta$  cells. Autoimmune features were found: MHC class I islet hyperexpression, T and B cells infiltrating the islets and transfer of the disease by lymphocytes. Moreover, the expression of  $\beta_2$ -microglobulin, preproinsulin, and glucagon in the thymus was not altered by IFN $\beta$ , thus suggesting that the disease is caused by a local effect of IFN $\beta$ , strong enough to break the peripheral tolerance to  $\beta$  cells. This is the first report of the generation of NOD (a model of spontaneous autoimmune diabetes) and nonobese-resistant (its homologous resistant) transgenic mice expressing a type I IFN in the islets: transgenic NOD and nonobese-resistant mice developed accelerated autoimmune diabetes with a high incidence of the disease. These results indicate that the antiviral cytokine IFN $\beta$  breaks peripheral tolerance to  $\beta$  cells, influences the insulinitis progression and contributes to autoimmunity in diabetes and nondiabetes-prone mice. *The Journal of Immunology*, 2004, 173: 6667–6675.

Type 1 diabetes (T1D)<sup>3</sup> is an autoimmune disease of unknown etiology caused by the selective destruction of pancreatic  $\beta$  cells as a consequence of the complex interaction between genetic and environmental factors (1). Genetic susceptibility to the development of the disease has been described. At the present, more than 20 putative diabetes predisposing genes have been identified in the mouse and human genome, but only MHC genes are related to the disease (2–4). Studies on identical twins showed a concordance rate of diabetes lower than 50%, suggesting an important role for the environmental factors, e.g., viral infections (5). Viruses might be involved in the pathogenesis of the disease through exposure to sequestered Ags released by damaged  $\beta$  cells, by altering some mechanisms of peripheral tolerance, by

molecular mimicry, or by a direct destruction of the insulin-producing cells (6, 7).

Type I IFNs (IFN $\alpha$ ,  $\beta$ ,  $\epsilon$ ,  $\kappa$ ,  $\lambda$ , and  $\omega$ ) provide the first line of defense against viral infection but their mechanisms of action are only partially understood. Among other effects, type I IFNs increase the expression of MHC class I molecules and induce the activity of NK and CTLs and the production of cytokines. For years, an abnormal expression of type I IFNs has been reported in the sera of patients affected with autoimmune diseases (8). In previous studies, other scientists and we have detected type I IFNs in the pancreata of patients with a recent onset of diabetes (9–11). The expression of type I IFNs, IFN $\alpha$  and IFN $\kappa$ , by the  $\beta$  cells induces autoimmune diabetes in nondiabetes-prone transgenic mice (12, 13). These mice developed insulinitis and hypoinsulinemic diabetes with a cumulative incidence of ~50%. Transgenic mice expressing human IFN $\beta$  under the control of rat insulin promoter (RIP-HuIFN $\beta$ ) were created (14) to avoid the sterility observed in mice expressing high levels of mouse IFN $\beta$  (15). HuIFN $\beta$  is active in mouse cells although its efficacy is ~1000 times lower than that of mouse IFN $\beta$  (14). The transgenic mice in a C57BL/6SJL background showed features of a prediabetic state, with peri-insulinitis but without spontaneous diabetes. When these mice were backcrossed to the outbred albino CD-1 mice, they spontaneously developed diabetes with an incidence of 11%. Since type I IFN induction takes place in cells infected mainly by viruses, this model suggests that the initial  $\beta$  cell damage may induce the production of IFN $\beta$  by  $\beta$  cells, thus triggering inflammation and cell-mediated autoimmunity.

Because IFNs act as both antiviral factors and inflammatory mediators, the aim of this study was to characterize the immunology of diabetes in the RIP-HuIFN $\beta$  transgenic mice and to evaluate the role of IFN $\beta$  in animal models with different susceptibility to diabetes: a spontaneous model of diabetes, the NOD mice (16) and a diabetes-free, MHC-matched, homologous strain, the Nonobese-resistant mice (NOR) (17). NOR/LTJ is an insulinitis-resistant

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<sup>3</sup> Abbreviations used in this paper: T1D, type 1 diabetes; RIP, rat insulin promoter; HuIFN $\beta$ , human IFN $\beta$ ; NOR, nonobese resistant;  $\beta_2$ m,  $\beta_2$ -microglobulin; ICA, islet cell Ab.

and diabetes-free strain where limited regions of the NOD/LtJ genome have been replaced by genome from the C57BLKS/J strain. In this study, we provide evidence that diabetes in RIP-HuIFN $\beta$  transgenic mice is autoimmune. The expression of this cytokine in  $\beta$  cells accelerates diabetes in NOD mice and breaks the tolerance to insulin-producing cells in NOR mice. This type I IFN is a functional mediator for the development of autoimmunity to  $\beta$  cells.

## Materials and Methods

### Mice

Transgenic mice expressing HuIFN $\beta$  under the control of the rat insulin I promoter (18) in outbred albino CD-1 background (CD-1 RIP-HuIFN $\beta$ ) were generated by backcrossing the original C57BL6/SJL RIP-HuIFN $\beta$  transgenic mice to CD-1 mice (14). NOD mice, NOR mice, and NOD-SCID mice, unable to produce mature T and B lymphocytes (19), were obtained from The Jackson Laboratory (Bar Harbor, ME). Mice were kept in our facility under specific pathogen-free conditions in a 12-h light-dark cycle with free access to a standard diet. The Guidelines for the Use and Care of Laboratory Animals of the Generalitat de Catalunya were followed and animal studies have been approved by the Hospital Germans Trias i Pujol Review Board. To generate inbred NOD RIP-HuIFN $\beta$  and NOR RIP-HuIFN $\beta$ , the CD-1 RIP-HuIFN $\beta$  outbred mice were backcrossed at least six times onto the NOD or NOR strains. The acquisition of the genetic background was controlled by the analysis of microsatellites. NOD RIP-HuIFN $\beta$  mice were backcrossed twice onto the NOD-SCID strain to generate NOD-SCID RIP-HuIFN $\beta$ . Nontransgenic littermates were used as controls for each strain of mice.

### Genotyping

The presence of the transgene was determined by standard PCR using genomic DNA obtained from mice tails and specific primers to HuIFN $\beta$ : HuIFN $\beta$  sense (5'-TCACCAGGGGAAACTC-3') and HuIFN $\beta$  antisense (5'-CAGTCACTTAAACAGCATCT-3'). The PCR products were resolved by 2% agarose gel and ethidium bromide staining. The genotyping for the microsatellite markers linked to *Idd* loci (*Idd1-Idd15*) was performed using genomic DNA from the fourth generation of mice from the aforementioned NOD and NOR backcrosses (20, 21), with a set of 11 primers specific for polymorphic loci between NOD/CD-1 and NOR/CD-1: *D6Mit52*, *D3Nds36*, *D2Mit107*, *D4Mit202*, *D1Mit24*, *D5Mit69*, *D11Mit320*, *D7Mit20*, *D7Nds3*, *D14Nds3*, and *D3Nds6*. The chosen markers were evenly spaced along the genome. PCR products were electrophoresed in 4% agarose gel and stained with ethidium bromide. Homozygous

mice for *Idd* NOD or NOR alleles (including *Idd1* for H-2g<sup>7</sup>) were selected for the following backcross.

### Insulin and glycemia assays

Blood glucose levels were measured weekly in CD-1 RIP-HuIFN $\beta$  mice and nontransgenic littermates between weeks 4 and 20 using Glucocard strips (Menarini, Barcelona, Spain). Mice with either successive blood glucose levels higher than 200 mg/dl or with a measure higher than 360 mg/dl were considered diabetic ( $n = 10$  per condition). Starting at day 21, all CD-1, NOD, and NOR transgenic mice, after N6 backcross onto NOD or NOR background, were monitored daily for glycosuria using Chroma 1 Glucose test strips (Menarini). Insulin levels were determined in both CD-1 RIP-HuIFN $\beta$  mice and nontransgenic littermates. Nonfasting insulinemia was determined in sera and pancreatic insulin content was measured in total pancreas homogenized in HCl/ethanol by RIA (Linco Research, St. Charles, MO). The i.p. glucose tolerance test was performed in fasting conditions in control (NOR and NOD-SCID) and transgenic (NOR RIP-HuIFN $\beta$  and NOD-SCID RIP-HuIFN $\beta$ ) adult mice. First, a blood sample was obtained from the tail vein to measure the basal level of glucose. Mice were subsequently given an i.p. injection of 2 mg of glucose per g of body weight. Blood glucose levels were measured at 15, 30, 60, 120, and 210 min after the injection.

### Assessment of HuIFN $\beta$ in the sera of transgenic mice

The amount of HuIFN $\beta$  in the sera of CD-1 RIP-HuIFN $\beta$  transgenic mice was determined by ELISA (Fujirebio, Tokyo, Japan). The ELISA test showed no cross-reactivity with murine IFN $\beta$  (range of detection, 2.5–200 IU/ml).

### Effect of HuIFN $\beta$ on the pancreas and the thymus expression profile

Real-time RT-PCR was performed to quantify the specific mRNA for preproinsulins I and II, glucagon and  $\beta_2$ -microglobulin ( $\beta_2m$ ). Total RNA was extracted from pancreas, thymus, and liver from CD-1 RIP-HuIFN $\beta$  using TRIzol reagent (Invitrogen Life Technologies, Gaithersburg, MD) according to the manufacturer's instructions. RNA was then DNase treated (DNA-free kit; Ambion, Houston, TX). After denaturation, 3  $\mu$ g of total RNA was reverse transcribed in a 20- $\mu$ l volume using a Promega Reverse Transcriptase kit (Promega, Southampton, U.K.) for 1 h at 42°C in a solution containing 20 U of RNasin inhibitor (Promega), 4  $\mu$ l of 5 $\times$  reverse transcriptase buffer, 1 mM dNTPs, 5  $\mu$ M oligo(dT), and 100 U of Moloney murine leukemia virus. Real-time PCR was performed in a Light Cycler (Roche Diagnostic, Mannheim, Germany), using the FastStart DNA Master SYBR Green kit and specific primers (Table I). The results were analyzed

Table I. List of primers used for the detection of  $\beta$ -actin, preproinsulin I, preproinsulin II, HuIFN $\beta$ ,  $\beta_2m$ , and glucagon in real-time RT-PCR and list of Abs used on frozen sections and cell suspensions

Gene	Primer Sense	Primer Antisense	Amplicon Size (bp)
$\beta$ -Actin	GTTACCAACTGGGACGACA	TGGCCATCTCTGCTCGAA	459
Preproinsulin I	ACTTCCCTACCCTGCT	CCAAGTCTGAAGGTCC	218
Preproinsulin II	CCCTGCTGGCCCTGCTCTT	CTGCTCCCGGGCTCCAC	197
Glucagon	CAGACAGAAGCGCATG	TGGCCCTCCAAGTAAGA	233
HuIFN $\beta$	TCACCAGGGGAAACTC	CAGTCACTTAAACAGCATCT	238
$\beta_2m$	CCGGAGAAATGGGAAGC	GTAGACGGTCTTGGGC	240

Ab/hybridoma	Marker	Source
M18/2	Mouse CD18	BD Pharmingen (San Jose, CA)
17A2	Mouse CD3	BD Pharmingen
RM4-5 FITC	Mouse CD4 (L3T4)	BD Pharmingen
53-6.7 PE	Mouse CD8a (Ly-2)	BD Pharmingen
1D3 PE	Mouse CD19	BD Pharmingen
GK1.5/TIB-207	Mouse CD4 (L3T4 Ag)	American Type Culture Collection (ATCC, Manassas, VA)
53-6.72/TIB-105	Mouse CD8 (Ly-2)	ATCC
RA3-3A1/6.1/TIB-146	Mouse B220 (B cell Ag)	ATCC
F4/80/HB-198	Macrophages	ATCC
N418/HB-224	Mouse CD11c	ATCC
Dx5 PE	Mouse CD49b (NK cell Ag)	BD Pharmingen
N-19	Mouse CD49b (NK cell Ag)	Santa Cruz Biotechnology (Santa Cruz, CA)
M1/42.3.9.8.HLK/TIB-126	H-2 (nonpolymorphic MHC class I)	ATCC
NIMR-4	I-A (nonpolymorphic MHC class II)	Southern Biotechnology Associates
Sheep to human IFN $\beta$	HuIFN $\beta$	BioSource International (Camarillo, CA)
Guinea pig to insulin	Insulin	Biogenesis

using the LDCA software supplied with the machine. A PCR with  $\beta$ -actin-specific primers was performed as control. A standard curve was produced for  $\beta$ -actin, preproinsulins I and II, glucagon, HuIFN $\beta$ , and  $\beta_2$ m with serial dilutions of the corresponding quantified cDNAs using a densitometric method (Quantity One, Huntington Station, NY). The real-time PCR was performed with an annealing temperature of 65°C. The results were expressed as the ratio between the level of relevant gene expression and the level of  $\beta$ -actin expression.

#### Adoptive transfer of diabetes

Adoptive transfer experiments were performed transferring splenocytes or pancreatic-infiltrating cells from NOD RIP-HuIFN $\beta$  and NOR RIP-HuIFN $\beta$  diabetic mice into adult NOD-SCID mice. NOD-SCID mice were transferred only with splenocytes from NOR nontransgenic littermates because they are insulinitis free. As positive control, splenocytes from wild-type NOD diabetic mice were injected in NOD-SCID mice. As negative control, NOD-SCID mice were sham transferred with physiological serum. Splenocytes or pancreatic-infiltrating cells from recent-onset diabetic NOD RIP-HuIFN $\beta$  mice were transferred into adult nondiabetic NOD RIP-HuIFN $\beta$  mice to assess the acceleration of the disease. The different transfer experiments were performed in a minimum of three recipients per condition ( $n = 3-6$ ). To obtain splenocytes, a mechanically disrupted spleen was incubated in a hypotonic solution to remove erythrocytes. After washing, the cells were counted and injected into the tail vein. Pancreata from recent-onset diabetic animals were digested with collagenase P (Worthington Biochemical, Lakewood, NJ) and total digest was mechanically disrupted. Islet infiltrating lymphocytes were obtained by discontinuous density gradient using a lymphocyte isolation solution (Rafer, Barcelona, Spain). Lymphocytes were recovered from the interphase, washed twice, and transferred as above. In both cases, the cells to transfer were examined for viability by trypan blue exclusion and only the preparations with a viability  $>80\%$  were transferred. Adult NOD-SCID males were injected i.v. with  $2 \times 10^7$  splenocytes or  $10^6$  islet infiltrating cells resuspended in 200  $\mu$ l of sterile physiological serum. After the transfer, the mice were monitored for assessment of diabetes every 2 days for 15 wk. Pancreata from mice that developed diabetes after the transfer were extracted and frozen for immunohistological analysis.

#### Autoantibodies

Five-micrometer mouse pancreatic cryosections were air dried and incubated with the sera from control (CD-1, NOD, and NOR nontransgenic littermates) and nondiabetic transgenic animals (CD-1 RIP-HuIFN $\beta$ , NOD RIP-HuIFN $\beta$ , and NOR RIP-HuIFN $\beta$ ). The secondary Ab was a FITC-labeled goat anti-mouse Ig (Southern Biotechnology Associates, Birmingham, AL). All sections were blindly evaluated for the presence of autoantibodies to islet cells by two independent observers under an UV microscope and an image analyzer (OpenLab 2.0; Improvision, Coventry, U.K.).

#### Flow cytometric analysis

Splenocytes from transgenic mice (CD-1 RIP-HuIFN $\beta$ , NOD RIP-HuIFN $\beta$ , and NOR RIP-HuIFN $\beta$ ) and nontransgenic littermates were isolated by mechanical disruption, and erythrocytes were lysed with a hypotonic solution. Cell clumps were allowed to sediment and the supernatant was centrifuged at  $548 \times g$  for 5 min. Aliquots of  $10^5$  spleen cells were stained with specific Abs (Table I) conjugated to FITC and PE for 30 min to detect T CD4 and CD8 subsets, respectively. A PE-labeled CD19 Ab was used to stain B cells. The controls included unstained cells (autofluorescence control) and cells stained with an irrelevant isotype-matched control PE/FITC. Dead cells were excluded by propidium iodide staining. The analysis was conducted in a FACScan Cell Analyzer (BD Biosciences, San Jose, CA) and the data were analyzed using CellQuest software (BD Biosciences).

#### Insulinitis development

To determine the degree of islet infiltration, pancreata from transgenic mice in different genetic backgrounds were snap frozen in an isopentane/cold acetone bath and stored at  $-70^\circ\text{C}$ . Five-micrometer cryostat sections were obtained at five nonoverlapping levels. The sections were stained with H&E. Groups of mice ( $n = 6$ ) were analyzed at different ages (6, 9, and 12 wk), assessing 40–100 islets per animal. Insulinitis was scored on a 0–4 scale as described elsewhere (22).

#### Immunohistological analysis

Consecutive pancreatic cryostat sections (5  $\mu$ m) from different mice were air dried as described above. To block nonspecific binding, 2% FCS was

added to the PBS used to dilute the Abs. The sections were sequentially incubated with 1) Ab to specific marker (Table I), 2) FITC-labeled goat anti-rat IgGs (Southern Biotechnology Associates) or FITC-labeled rabbit anti-sheep FITC (Zymed Laboratories, San Francisco, CA), 3) guinea pig anti-insulin, and 4) tetramethylrhodamine isothiocyanate-labeled goat anti-guinea pig Ab (Biogenesis, Eschwege, Germany). The preparations were assessed with a fluorescence UV microscope and an image analyzer (OpenLab 2.0; Improvision).

#### Statistical analysis

Statistical analyses to compare independent groups were performed using the  $t$  test when groups passed normality and showed equal variance tests. When these tests failed, Mann-Whitney  $U$  test was performed. Differences were considered significant when a value of  $p < 0.05$  was reached.

## Results

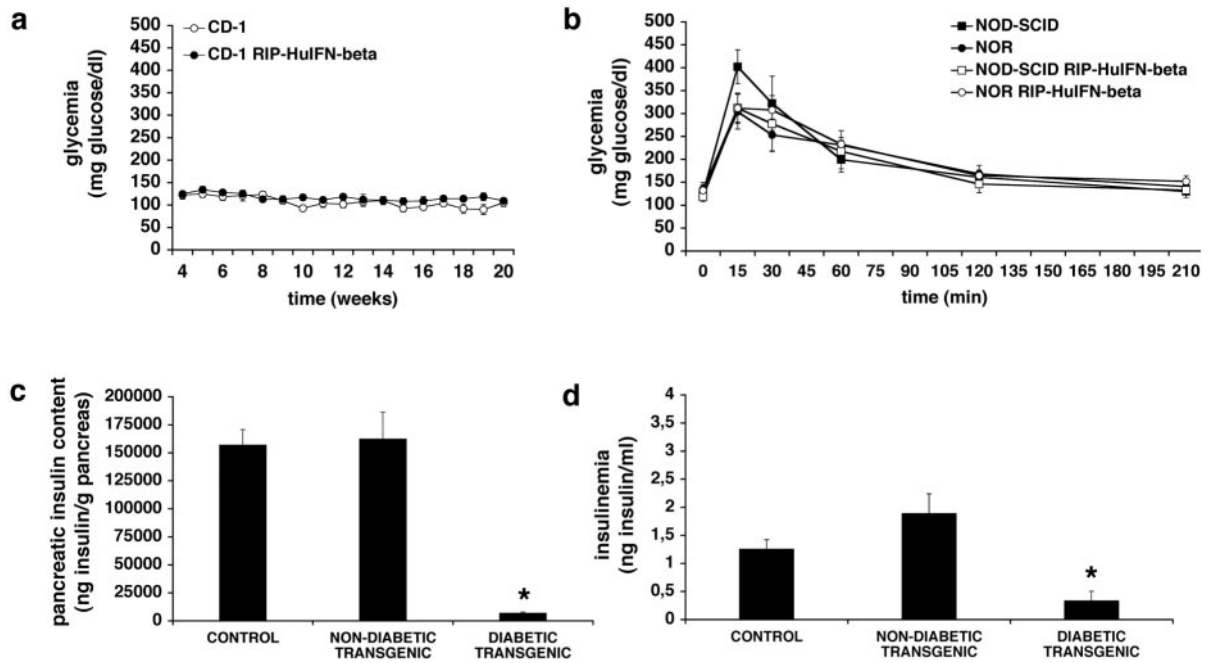
### *Diabetes is not caused by a dysfunction of $\beta$ cells in transgenic mice*

To discard a reduced capacity to produce insulin by the  $\beta$  cells of transgenic mice, the glycemia, the insulinemia, and the pancreatic insulin content were determined in healthy CD-1 transgenic mice. No significant differences in glycemia were observed between CD-1 RIP-HuIFN $\beta$  mice and nontransgenic littermates at weeks 4–20 (Fig. 1*a*), except in animals progressing toward diabetes. The blood glucose concentration was  $116.4 \pm 6.4$  mg/dl (mean  $\pm$  SEM) in transgenic animals ( $133.2 \pm 2.1$ , male and  $96.7 \pm 16$ , female, respectively) and  $106.7 \pm 8.7$  mg/dl in the control group ( $120.6 \pm 2.4$ , male and  $94.4 \pm 1.9$ , female, respectively). Two weeks before the clinical onset of the disease, diabetic-prone transgenic animals showed progressively increasing blood glucose levels. To rule out the possibility that  $\beta$  cell destruction was caused by the deleterious effects of HuIFN $\beta$ , we backcrossed NOD RIP-HuIFN $\beta$  mice onto the NOD-SCID strain twice. No significant differences were observed in glycemia between NOD-SCID RIP-HuIFN $\beta$  mice ( $119.4 \pm 2.4$  mg/dl, mean  $\pm$  SEM) and nontransgenic littermates ( $123.9 \pm 3.7$  mg/dl). In addition, to assess whether the transgene could influence  $\beta$  cell metabolism, we tested the response of transgenic (NOD-SCID and NOR) and control animals to an acute increase of blood glucose levels (Fig. 1*b*). Glycemia of transgenic and control animals reached the highest value 15 min after glucose administration and decreased to basal values at 120 min in all groups. No significant differences were found between transgenic and control mice at any time, demonstrating that insulin production and secretion was unaffected by the transgene.

The pancreatic insulin content was normal in CD-1 RIP-HuIFN $\beta$  ( $156.9 \pm 13.7$   $\mu$ g of insulin/g of pancreas, mean  $\pm$  SEM) when compared with that of the controls ( $162.2 \pm 23.8$   $\mu$ g of insulin/g of pancreas) except in recent-onset diabetic subjects ( $p < 0.05$ ; Fig. 1*c*). Insulinemia was not altered in CD-1 transgenic animals ( $1.9 \pm 0.3$  ng/ml) compared with controls ( $1.3 \pm 0.2$  ng/ml) and, as expected, diabetic mice showed a significant decrease in the insulin levels in serum ( $0.3 \pm 0.04$  ng/ml,  $p < 0.05$ ; Fig. 1*d*). In addition, no significant differences were observed in the levels of preproinsulin or glucagon RNA when compared to transgenic mice and nontransgenic littermates (see below). Apoptotic cells (TUNEL) were not detected in the noninfiltrated islets of healthy mice (data not shown). All of these data suggest that the development of diabetes is not a consequence of  $\beta$  cell dysfunction caused by the effect of the transgene or its product.

### *HuIFN $\beta$ affects the islets but not the thymic environment*

HuIFN $\beta$  was detected in the sera from CD-1 RIP-HuIFN $\beta$  transgenic animals. The amount of this cytokine in sera was  $49.2 \pm 12.7$  IU/ml in transgenic animals, statistically different from  $5.6 \pm$



**FIGURE 1.** RIP-HuIFN $\beta$  transgenic mice developed hypoinsulinemic diabetes, but it is not caused by a dysfunction of  $\beta$  cells in transgenic mice. *a*, No significant differences in glycemia (mg/dl) in nonfasting conditions (mean  $\pm$  SEM) were observed between CD-1 RIP-HuIFN $\beta$  mice and nontransgenic littermates. *b*, Intraperitoneal glucose tolerance test was not altered in transgenic mice. Glycemia (mg/dl, mean  $\pm$  SEM) after i.p. administration of glucose in fasting conditions in control (NOR and NOD-SCID) and transgenic (NOR RIP-HuIFN $\beta$  and NOD-SCID RIP-HuIFN $\beta$ ) adult mice. Glycemia of transgenic and control animals returned to basal levels 120 min after glucose administration. No significant differences were found when compared groups of transgenic and control mice. *c*, Pancreatic insulin content decreased only in diabetic mice. Insulin concentration (ng/g pancreas) in control and transgenic mice did not show significant differences. Diabetic transgenic mice decreased its pancreatic insulin levels ( $p < 0.05$ ) compared with healthy groups. *d*, Insulinemia (ng/ml serum) is not altered by transgenic expression of HuIFN $\beta$ . Significant differences in insulin concentration were found between healthy and diabetic animals.

1.6 IU/ml in nontransgenic littermates ( $p < 0.01$ ). These data indicate a systemic distribution of HuIFN $\beta$ .

To assess the effects of circulating HuIFN $\beta$  on the molecular pattern expression in the thymus (primary lymphoid organ) and in the liver (control tissue), we determined the mRNA levels for preproinsulins I and II, glucagon, and  $\beta_2m$  in CD-1 RIP-HuIFN $\beta$  transgenic mice. In addition to the presence of protein (HuIFN $\beta$ ) in the sera, we confirmed the transcription of HuIFN $\beta$  mRNA in the pancreas and the thymus of transgenic mice (Table II). HuIFN $\beta$  did not alter the level of expression of preproinsulin I, which was only detected in the pancreas but not in the thymus or in the liver. However, preproinsulin II was detected in the pancreas, thymus, and liver but the differences between transgenic animals and controls were not significant, thus confirming that the transgene did not affect the transcription of insulin. Glucagon was

detected in the pancreas and the thymus but not in the liver, and no significant differences were found when comparing transgenic and control animals. The amount of  $\beta_2m$  mRNA was higher in the pancreata of transgenic mice than in the control group ( $p < 0.05$ ), showing an enhanced transcription of MHC class I, due to the effect of HuIFN $\beta$  (these data were confirmed by immunofluorescence staining of the islets with Abs to MHC class I). By contrast, no significant differences were found in the levels of  $\beta_2m$  in the thymus of transgenic and control mice. These data confirmed that the islets of Langerhans of transgenic animals have a normal expression profile of insulin I, insulin II, and glucagon and an increased MHC class I hyperexpression caused by the local release of HuIFN $\beta$ . Moreover, the expression of  $\beta_2m$ , preproinsulin, and glucagon in the thymus of transgenic mice was unaffected by the expression of the transgene. These results suggests that, in terms of

Table II. Quantification of the expression of genes related to diabetes in the CD-1 RIP-HuIFN $\beta$  mice and controls (CD-1 nontransgenic littermates) by real-time RT-PCR<sup>a</sup>

Gene Expression	Tissue					
	Thymus		Pancreas		Liver	
	CD-1 RIP-HuIFN $\beta$	CD-1	CD-1 RIP-HuIFN $\beta$	CD-1	CD-1 RIP-HuIFN $\beta$	CD-1
Preproinsulin I	—	—	4.17 $\pm$ 1.32	3.81 $\pm$ 0.35	—	—
Preproinsulin II	0.1 $\pm$ 0.01	0.11 $\pm$ 0.008	10.67 $\pm$ 1.7	13.79 $\pm$ 2.29	0.52 $\pm$ 0.06	0.41 $\pm$ 0.1
Glucagon	0.01 $\pm$ 0.001	0.01 $\pm$ 0.002	1.99 $\pm$ 0.37	2.25 $\pm$ 0.57	—	—
HuIFN $\beta$	0.001 $\pm$ 0.0002	—	0.09 $\pm$ 0.01	—	—	—
$\beta_2m$	1 $\pm$ 0.16	0.9 $\pm$ 0.12	3.19 $\pm$ 0.55*	1.21 $\pm$ 0.2*	6.22 $\pm$ 0.52	8.04 $\pm$ 1.34

<sup>a</sup> Results are expressed as the ratio between the level of expression of the gene of interest and a constitutively expressed gene ( $\beta$ -actin)  $\pm$  SE.  $p < 0.05$ .

T cell development, no differences exist between transgenic and wild-type mice.

#### Genetic background influences the onset and the incidence of diabetes in RIP-HuIFN $\beta$ -transgenic mice

The incidence of the disease varies according to the genetic background (Fig. 2). In CD-1 RIP-HuIFN $\beta$  mice, 22% of males and 0% of females developed diabetes. The onset of the disease starts after 7 wk of age (Fig. 2*a*). The analysis of the progeny resulting from F6 backcross with NOR strain onward showed not only a spontaneous development of diabetes but also a significant acceleration of the onset of the disease and an increase of the incidence: Fifty-seven percent of male and 22% of female NOR RIP-HuIFN $\beta$  mice became diabetic. The onset of diabetes started at 3 wk of age (Fig. 2*b*). Mice resulting from F6 backcross with NOD strain (NOD RIP-HuIFN $\beta$ ) onward showed a diabetes incidence of 53% in male and 51% in female mice, starting diabetes at 3 wk of age. The

incidence of diabetes in NOD nontransgenic littermates was identical to that in wild-type NOD: 27% in males and 66% in females (Fig. 2*c*). As expected, neither CD-1 nor NOR nontransgenic mice developed diabetes during the study. Moreover, NOD-SCID RIP-HuIFN $\beta$  mice did not become diabetic.

Most of the NOD and NOR transgenic mice became diabetic just after weaning (3 wk of age), showing a considerable acceleration of the onset of the disease compared with the CD-1 RIP-HuIFN $\beta$  mice that started diabetes at 7 wk of age. These data, along with the variation in the incidence of the disease in the three groups of transgenic mice, suggest that the genetic background influences the start point and the percentage of diabetes in mice expressing this transgene.

#### The development of diabetes is lymphocyte dependent: evidence of autoimmunity

NOD-SCID RIP-HuIFN $\beta$  mice showed no signs of diabetes nor insulinitis, thus indicating that the destruction of islet cells in transgenic mice is not caused by the presence of HuIFN $\beta$  per se and that it is essential they share immunocompetent T and B cells.

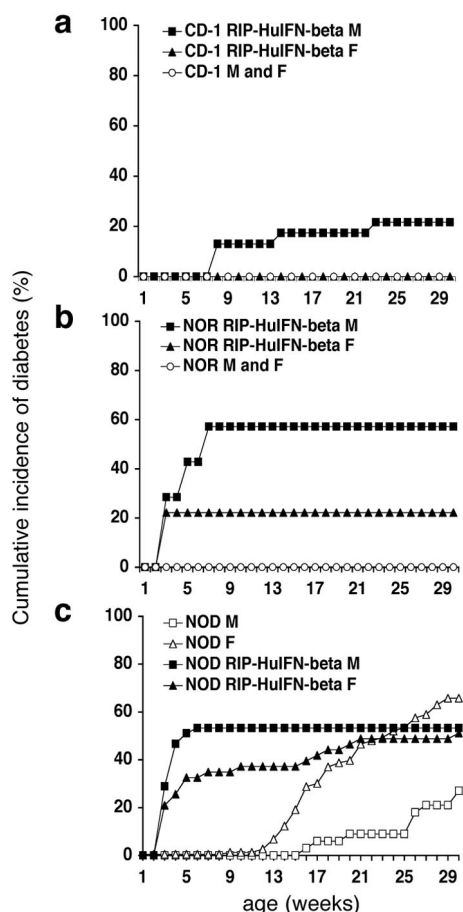
All NOD-SCID mice (four of four) transferred with splenocytes from diabetic nontransgenic NOD mice (positive control), become diabetic after 4–9 wk, as expected (23). All NOD-SCID mice (five of five) transferred with splenocytes or islets infiltrating lymphocytes from diabetic NOD RIP-HuIFN $\beta$  mice developed type 1 diabetes after 4–15 wk after transfer. NOR RIP-HuIFN $\beta$  mice were also able to transfer diabetes in most (three of four) treated NOD-SCID mice at 8–9 wk, starting 4 wk later than littermates that received cells from diabetic NOD RIP-HuIFN $\beta$ . NOD-SCID mice transferred with splenocytes from NOR nontransgenic littermates were insulinitis free 3 wk after the injection and at the end of the follow up (15 wk) none of the animals (zero of six) developed diabetes. All NOD RIP-HuIFN $\beta$  mice (three of three) transferred with autologous splenocytes or pancreatic-infiltrating lymphocytes from diabetic mice developed diabetes in 3–6 days. As expected, sham-transplanted mice did not develop diabetes nor insulinitis. Histological examination of pancreata from transferred diabetic mice showed a high degree of insulinitis, confirming that development of the disease is lymphocyte dependent.

#### Islet cell Abs (ICA) are present in transgenic mice

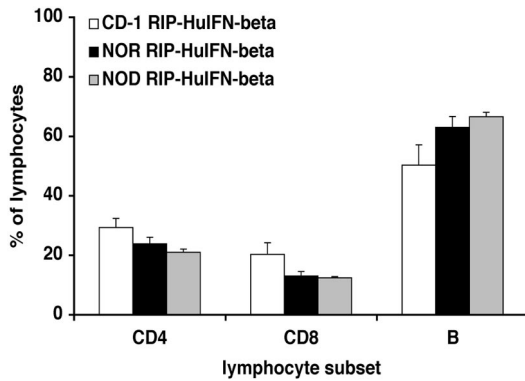
ICA were detected in mice from all of the study groups, including diabetic and healthy animals: CD-1 RIP-HuIFN $\beta$ , NOD RIP-HuIFN $\beta$ , NOR RIP-HuIFN $\beta$ , and also their nontransgenic littermates. The expression of the transgene did not result in a disappearance of or significant increase of ICA. The ICA-positive staining pattern was weak. Occasionally, ICA were associated with antinuclear autoantibodies in endocrine and exocrine tissues. However, the autoantibodies to islet Ags are not a prerequisite for the subsequent emergence of the disease (24).

#### Peripheral lymphocyte subsets in transgenic mice

It has been described that type I IFNs have an important effect on the proliferation of different cell types, including lymphocyte subsets (25). To assess the effect of circulating HuIFN $\beta$  in lymphocyte subpopulations, we determined the percentages of splenic lymphocyte subsets in transgenic mice. Mice expressing the transgene in different genetic backgrounds (CD-1, NOR, and NOD) had normal percentages (26) of splenic B and T (CD4 and CD8) lymphocyte subsets (Fig. 3).



**FIGURE 2.** The transgenic expression of HuIFN $\beta$  in islet  $\beta$  cells contributes to the development of diabetes in nondiabetes-prone strains (CD-1 and NOR) and accelerates the onset of the disease in NOD transgenic mice. Cumulative incidence of diabetes (percentage) in RIP-HuIFN $\beta$  transgenic mice in different genetic backgrounds during 30 wk of follow-up ( $n > 40$ ). *a*, Twenty-two percent of CD-1 RIP-HuIFN $\beta$  males (M) developed diabetes after 7 wk of age. CD-1 RIP-HuIFN $\beta$  females (F) and nontransgenic littermates did not develop the disease. *b*, NOR RIP-HuIFN $\beta$  became diabetic after 3 wk of age; the incidence was higher in males (57%) than in females (22%). Nontransgenic littermates did not develop the disease. *c*, NOD RIP-HuIFN $\beta$  mice developed early diabetes, after 3 wk of age, when compared with NOD wild-type mice, after 12 wk. The incidence of the disease in transgenic NOD mice was similar in males (53%) and females (61%); as expected, wild-type NOD mice showed a higher incidence of the disease in females (66%) than in males (27%).



**FIGURE 3.** Peripheral lymphocyte subsets are not altered in transgenic mice. Histogram of percentages corresponding to splenic lymphocyte subsets: T (CD4 and CD8) and B lymphocytes in CD-1 RIP-HuIFN $\beta$ , NOR RIP-HuIFN $\beta$ , and NOD RIP-HuIFN $\beta$  determined by FACS analysis. No significant differences were found between groups.

#### *Expression of HuIFN $\beta$ in islet $\beta$ cells increases the intensity of insulinitis in different genetic backgrounds*

The sequential histological examination of the pancreata of nondiabetic RIP-HuIFN $\beta$  transgenic mice reveals that the intensity of the insulinitis depends on the genetic background. CD-1 RIP-HuIFN $\beta$  mice showed normal islets or just weak insulinitis at 3 wk of age. Ten percent of the islets of 4-wk-old CD-1 RIP-HuIFN $\beta$  mice were weakly infiltrated with mononuclear cells around or inside the islets (peri-insulinitis or mild insulinitis); this pattern was maintained in adult mice in which 15% of the islets were weakly infiltrated (Table III). The insulinitis score (Fig. 4a) was very low due to the lack of moderately and severely infiltrated islets and to the absence of infiltrated islets in some subjects. Only at 12 wk of age the intensity of the insulinitis was significantly higher than that of controls ( $p < 0.05$ ). As expected, the inflammation was more marked and the insulinitis score significantly increased in transgenic mice developing diabetes (Fig. 4c).

The pancreata from nondiabetic NOR RIP-HuIFN $\beta$  mice showed severe infiltration compared with wild-type NOR mice and nontransgenic littermates ( $p < 0.01$ ). In contrast to the pancreata from CD-1 RIP-HuIFN $\beta$  nondiabetic mice, in which most islets were not infiltrated (Table III), NOR transgenic mice showed mononuclear cells infiltrating most islets at 3 wk of age. Adult mice showed 86% of the islets infiltrated (43% moderately or severely). The insulinitis score (Fig. 4b) was significantly higher ( $p < 0.01$ ) in NOR RIP-HuIFN $\beta$  than in CD-1 transgenic mice. Both diabetic NOD and NOR RIP-HuIFN $\beta$  mice showed an insulinitis score higher than transgenic CD-1 diabetic subjects ( $p < 0.05$ ) and similar between them (Fig. 4c). A weak insulinitis is enough to cause the disease in the CD-1 transgenic colony, whereas NOD and NOR transgenic strains require massive infiltration.

#### *HuIFN $\beta$ in the islets causes MHC class I hyperexpression and recruits lymphomononuclear cells*

As expected, HuIFN $\beta$  staining was only positive in  $\beta$  cells of transgenic animals. The islets from CD-1 RIP-HuIFN $\beta$  healthy mice were predominantly noninfiltrated, peri-infiltrated, or poorly infiltrated. The phenotypic characterization of insulinitis (Fig. 5b) showed that most mononuclear islet-infiltrating cells were CD4 and CD8 T lymphocytes (ratio 3:1); B cells were only occasionally detected. A few macrophages were also detected surrounding the endocrine islet cells. Dendritic cells were only observed inside the noninfiltrated islets. MHC class I molecules were hyperexpressed in the endocrine cells of all islets, correlating well with molecular data; no MHC class II hyperexpression was observed in islet cells. Diabetic mice showed normal, peri-infiltrated, and mildly infiltrated islets and a stronger infiltration (peri and poorly) than that observed in nondiabetic mice was detected (Fig. 5a). The composition of the insulinitis in diabetic mice was almost the same as that in healthy animals except for a remarkable increase of B cell clusters in the periphery of the islets.

Most islets from NOR RIP-HuIFN $\beta$  nondiabetic mice were moderately or severely infiltrated by CD18-positive cells (leukocytes). As expected, MHC class I, but not MHC class II, was highly hyperexpressed in endocrine islet cells from all of the islets. The insulinitis mainly consisted of T and B cells (Fig. 5a). We observed B cells, T cells, more CD4 than CD8 cells (ratio 4:1), and few NK cells. B and CD4 cells, but not CD8 cells or NK cells, were distributed in clusters around the islets. These data were confirmed by flow cytometry of pancreatic-infiltrating mononuclear cells (data not shown). Only a few macrophages were observed in the periphery or inside the islets; no dendritic cells were found in the infiltrated islets. The islets from NOR RIP-HuIFN $\beta$  diabetic mice (Fig. 5b) were almost devoid of  $\beta$  cells and showed a higher intensity of insulinitis than healthy mice, but no differences in the composition of the infiltrate were observed. The islets from NOD RIP-HuIFN $\beta$  diabetic mice were almost devoid of  $\beta$  cells and showed a high intensity of insulinitis, but no differences in the infiltrate composition were observed when compared with NOR RIP-HuIFN $\beta$  diabetic mice.

Nontransgenic littermates did not show infiltrating leukocytes or MHC class I hyperexpression (Fig. 5c). Histological examination of pancreata from NOD-SCID RIP-HuIFN $\beta$  revealed that MHC class I was hyperexpressed in the islets due to the effect of HuIFN $\beta$  but, as expected, immunofluorescence staining revealed the lack of insulinitis because SCID mice are unable to produce mature T and B cells (Fig. 5c).

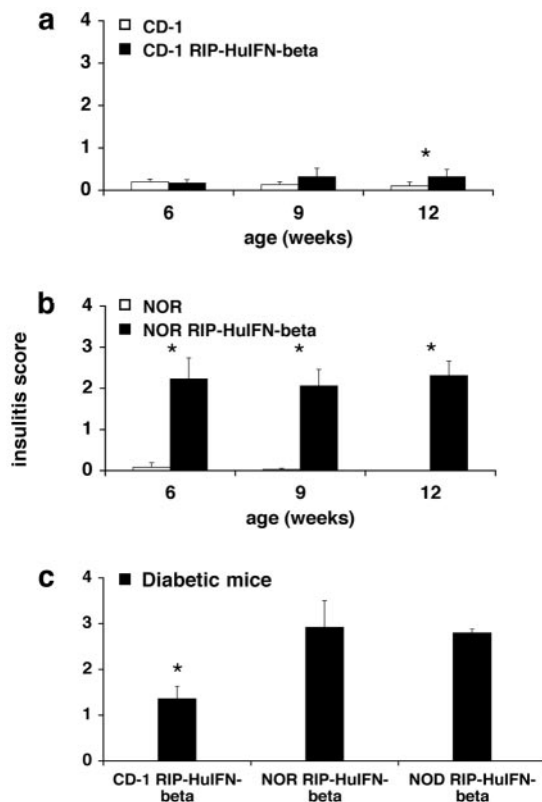
Transgenic mice in the three analyzed genetic backgrounds showed a HuIFN $\beta$  staining pattern that correlates well with the MHC class I hyperexpression in the islets and it is independent of the presence of infiltrating cells.

## Discussion

Type I IFNs have been associated with T1D because they have been detected in the islets of diabetic patients (8, 9, 12), thus suggesting that a viral infection and its consequences may be related

Table III. Percentage of islets of each degree of infiltration in CD-1, CD-1 RIP-HuIFN $\beta$ , NOR RIP-HuIFN $\beta$  nontransgenic littermates, and NOR RIP-HuIFN $\beta$  mice

Genetic Background	Noninfiltrated	peri-Insulinitis	Mild Insulinitis	Moderate Insulinitis	Severe Insulinitis	Insulinitis Score
CD-1	85.34	13.62	1.03	0	0	0.14
CD-1 RIP-HuIFN $\beta$	75.51	21.76	2.15	0.34	0.22	0.27
NOR RIP-HuIFN $\beta$ (-)	97	3	0	0	0	0.04
NOR RIP-HuIFN $\beta$ (+)	14.09	18.79	23.71	26.84	16.55	2.18



**FIGURE 4.** Lymphocytic infiltration increases in the islets from mice expressing HuIFN $\beta$  in the  $\beta$  cells. *a*, Nondiabetic CD-1 RIP-HuIFN $\beta$  colony and nontransgenic littermates at 6, 9, and 12 wk of age. Differences were found at 12 wk of age. *b*, Nondiabetic NOR RIP-HuIFN $\beta$  and nontransgenic littermates at 6, 9, and 12 wk of age showed significant differences. *c*, Insulinitis score in diabetic CD-1 transgenic mice was lower than that observed in NOR and NOD RIP-HuIFN $\beta$  transgenic mice. Insulinitis was scored on a 0–4 scale in groups of six animals per condition. Scoring system: 0, no infiltration; 1, some peri-insular infiltration; 2, heavy peri-insular infiltration and <25% of the insular area infiltrated; 3, between 25 and 75% of the insular area infiltrated; and 4, total islet infiltration. The mean score was obtained by division of the sum of all individual islet infiltration scores by the total number of islets analyzed.

to the development of the disease. Furthermore, during the treatment with type I IFNs a small but significant proportion of patients develop autoimmune diabetes (27, 28). Apart from antiviral activities, type I IFNs are also potent immunomodulators: they are involved in the increase of the expression of MHC class I, in the enhancement of T and NK cell cytotoxicity, in the production of proinflammatory cytokines, and other activities (29, 30). Transgenic mice expressing IFN $\alpha$ ,  $\beta$ , and  $\kappa$  (12–14) in  $\beta$  cells developed type 1 diabetes, with T and B cells infiltrating the islets. These data suggest a local proinflammatory role for these type I IFNs and their ability to induce T1D.

In this study, we provide evidence that the local expression of HuIFN $\beta$  is involved in the development of autoimmune diabetes: 1) the islets from transgenic mice hyperexpress MHC class I molecules, 2) the islets are infiltrated by T and B lymphocytes, 3) the transfer of lymphocytes from a diabetic transgenic animal causes the disease in NOD-SCID recipient mice and accelerates the onset of diabetes in prediabetic recipient mice, and 4) transgenic NOD-SCID RIP-HuIFN $\beta$  mice do not develop diabetes. Moreover, systemic HuIFN $\beta$  does not alter the expression of analyzed pancreatic hormones or  $\beta_2$ m in the thymus, thus supporting the idea that the disease could be caused by a local effect of IFN $\beta$  strong enough to

break the peripheral tolerance to  $\beta$  cells rather than by a change in central tolerance. Preliminary results show that HuIFN $\beta$  could modulate the expression of adhesion molecules, cytokines, and chemokines in the islets (data not shown). Therefore, we conclude that in this transgenic model, the disease is lymphocyte dependent since transgenic animals lacking functional T and B cells cannot develop diabetes or insulinitis, although they increase the expression of MHC class I in the islets.

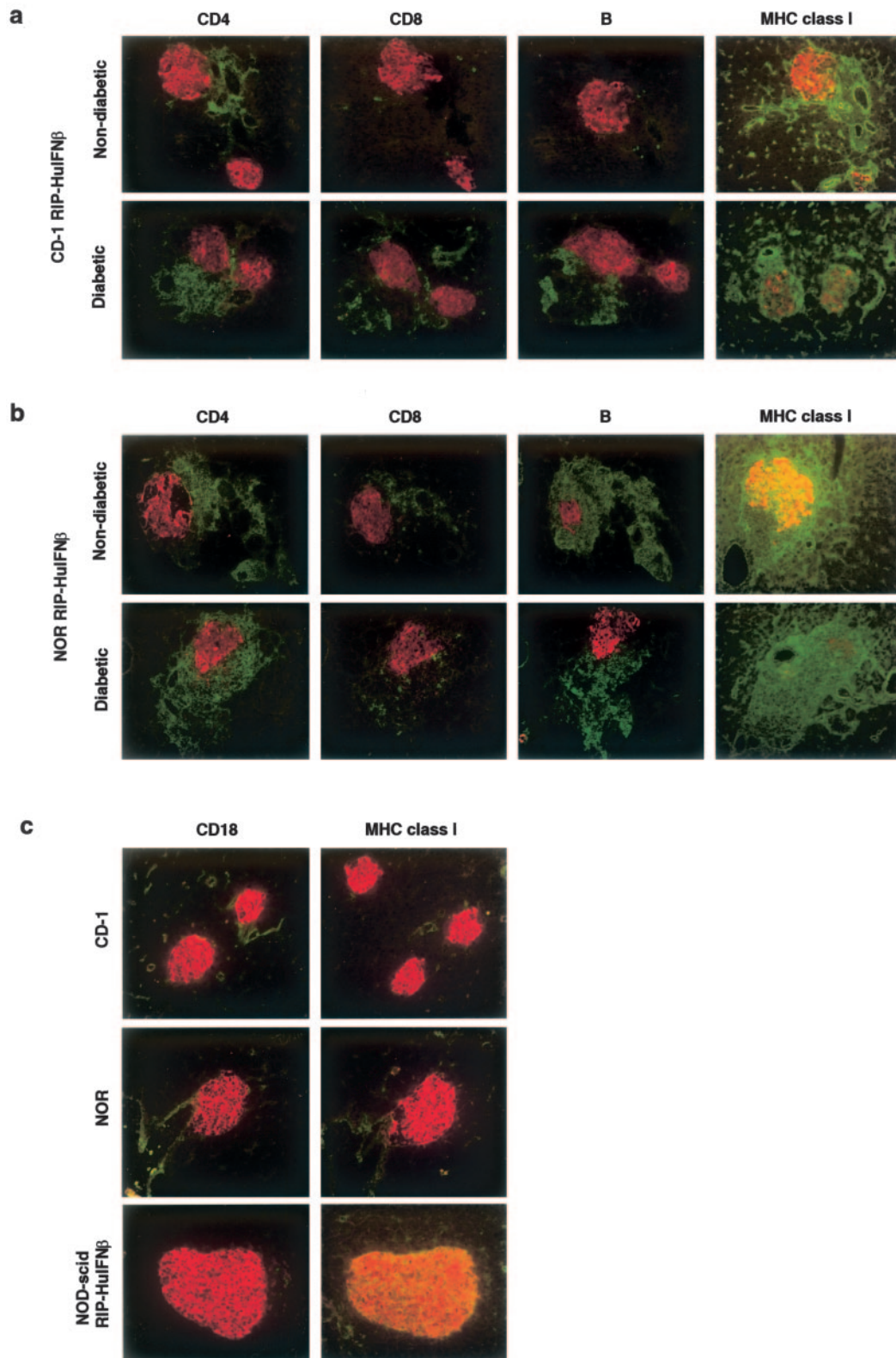
To study the role of IFN $\beta$  in diabetes, we also introduced the RIP-HuIFN $\beta$  transgene in different genetic backgrounds with different susceptibility to T1D. We demonstrated that the genetic background not only determines the onset and the severity of the lesions related to the disease but also that these genetic factors cannot protect individuals from T1D by themselves when an inducing factor triggers the autoimmune process.

It has been previously described that a small percentage of N3 generation obtained from the backcross of C57BL/6/SJL RIP-HuIFN $\beta$  to CD-1 mice spontaneously developed T1D (14). In this study, we showed an increase of the incidence of diabetes in homozygous mice kept under specific pathogen-free conditions. The research in the field of T1D has developed many transgenic mice in nondiabetes-prone strains that were later backcrossed to diabetes-prone NOD mice. This is the first report of the generation of NOD and NOR transgenic mice expressing a type I IFN in the islets. NOD mice expressing HuIFN $\beta$  in  $\beta$  cells showed an acceleration of the disease and, unexpectedly, NOR RIP-HuIFN $\beta$  mice developed early diabetes with a high incidence. The severity of the insulinitis varied according to the genetic background and was correlated with the incidence of diabetes. The three models shared a MHC class I hyperexpression in the islet cells, but whereas diabetic NOD and NOR transgenic mice islets were strongly infiltrated, diabetic CD-1 RIP-HuIFN $\beta$  mice were only mildly infiltrated. These results indicated that the genetic background was not strong enough to protect mice from diabetes when an injury triggered an inflammatory response in the islets. In humans, the lack of concordance of diabetes in identical twins indicates that nongenetic factors determine the development of the disease. These factors might be environmental agents but also random factors such as the generation of the immunological repertoire are subject to complex regulation.

The influence of HuIFN $\beta$  was always stronger in males than in females. It has been described that male mice have more difficulty maintaining glucose homeostasis under conditions of impaired  $\beta$  cell function and that male islets are more susceptible to an autoimmune damage than are female islets but male islet-specific lymphocytes are less aggressive (31). Results similar to ours have been recently described in nondiabetes-prone transgenic mice expressing IFN $\kappa$  in  $\beta$  cells (13), where a higher incidence of the disease in males than in females was observed (G. Vassileva, personal communication). Assuming a viral etiology for T1D in humans, females seem to be less susceptible than males to the environmental infectious influences (32).

To date, 14 different viruses have been reported to be associated with the development of autoimmune diabetes in both humans and animal models (5). The most convincing data include an increased frequency of diabetes in patients with enterovirus infection (33), congenital rubella syndrome, measles (34), and the detection of CMV in the lymphocytes of diabetic patients (35). Viral infections result in an enhancement of the MHC class I expression in a number of cell types which normally do not express these molecules (36). This enhancement may occur by a direct interaction between the viral component and the MHC class I gene or indirectly by virus-induced soluble factors, IFN- $\gamma$ , IFN- $\alpha\beta$ , and TNF- $\alpha$  produced by the infected cells (37). Thus, these viruses induced an





**FIGURE 5.** HuIFN $\beta$  contributes to the recruitment of lymphomononuclear cells to the islets in immunocompetent mice and causes MHC class I hyperexpression in the endocrine cells. Double immunofluorescence staining of 5- $\mu$ m pancreatic cryostat sections, insulin (in red), and specific markers (in green). MHC class I/insulin overlap shown in orange. Original magnification,  $\times 200$ . *a*, CD-1 RIP-HuIFN $\beta$  transgenic mice, nondiabetic (*upper panels*) and recent-onset diabetic (*lower panels*). *b*, NOR RIP-HuIFN $\beta$  transgenic mice, nondiabetic (*upper panels*) and recent-onset diabetic (*lower panels*). *c*, Control animals: CD-1 (*upper*), NOR (*middle*), and NOD-SCID RIP-HuIFN $\beta$  (*lower*).

enhanced display of self-peptides in MHC class I, which led to the temporary activation of autoreactive T cells and autoimmunity (38).

Nevertheless, it is very difficult to connect viruses and T1D: it is well known that development of the disease in humans and animal models is reduced in the presence of high amounts of pathogens.

Recently it has been demonstrated that viral infections could influence the progression of insulinitis beneficially at the preclinical stage if produced at the correct location, time, and intensity, preventing autoimmune diabetes (39), correlating well with some protocols that prevent diabetes in NOD mice by administration of antiviral cytokines in mice (40, 41). The timing of the infection, the viral strain, the antigenic load, and other unknown factors must be crucial in the protection or predisposition to the disease.

The results presented here, along with previous and future studies, will provide a greater understanding on how the production of type I IFNs in the pancreas affects the recruitment of infiltrating cells and accelerates the onset of diabetes. The genetic background by itself does not protect mice from diabetes when damages, stresses, or dangers affect  $\beta$  cells with intensity strong enough to trigger an inflammatory response. Our data indicate that the antiviral cytokine IFN $\beta$  expressed in insulin-producing cells triggers the break of peripheral tolerance to  $\beta$  cells, leading to insulinitis and autoimmunity in diabetes and nondiabetes prone mice.

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