Influence of cytokines on Dmt1 iron transporter and ferritin expression in insulin-secreting cells

S Lortz, S Schröter†, V Stückemann‡, I Mehmeti and S Lenzen

Hannover Medical School, Institute of Clinical Biochemistry, 30623 Hannover, Germany
(†S Schröter is now at Department of Neurobiology, Max Planck Institute for Biophysical Chemistry, 37077 Göttingen, Germany)
(‡V Stückemann is now at Twincore Centre for Experimental and Clinical Infection Research, 30625 Hannover, Germany and Department of Gastroenterology, Hepatology and Endocrinology, Hannover Medical School, 30623 Hannover, Germany)

Abstract
Free intracellular ferrous iron (Fe²⁺) is essential for the generation of the extremely toxic hydroxyl radicals, which contribute to β-cell destruction by cytokines. Therefore the expression of the different divalent metal transporter 1 (Dmt1) isoforms and ferritin (Ft) subunits, responsible for iron import and chelation, was analyzed under pro-inflammatory conditions (IL1b alone or together with TNFα + IFNγ). The Dmt1 isoforms (1A/1B and +IRE/−IRE) and the total Dmt1 expression in insulin-producing cells (RINm5F and INS-1E), in primary rat islets and, for comparison, in the neuroendocrine PC12 cell line were quantified by qRT-PCR. In addition, the expression of the light (L-Ft) and heavy Ft (H-Ft) subunits and the mitochondrial Ft isoform (Mtft) in insulin-producing cells under control conditions and after cytokine treatment was estimated. The 1B isoform was the predominant Dmt1 mRNA in all insulin-producing cells, accounting for almost 100% of the 1A/1B isoform expression. For the IRE variants, +IRE expression was higher than −IRE expression. Pro-inflammatory cytokines accelerated the expression of Dmt1 isoforms significantly with an overall 2.5- to 3-fold increase in the total Dmt1 expression. In contrast, the expression of the iron-buffering ferritin subunits L- and H-Ft was unaffected by IL1β and only slightly induced by the cytokine mixture. Mtft expression was also not increased. Dmt1 expression was significantly elevated through pro-inflammatory cytokines, whereas Ft expression was marginally increased. This imbalance between the increased iron transport capacity and the almost unaffected iron storage capacity can foster cytokine-mediated formation of hydroxyl radicals and thus pro-inflammatory cytokine toxicity through elevated free iron concentrations.

Key Words
- insulin-secreting cells
- iron transport and storage
- Dmt1
- ferritin
- reactive oxygen species
- pro-inflammatory cytokines
- Haber–Weiss reaction

Introduction
The destruction of insulin-secreting β-cells by infiltrating immune cells is mediated via soluble pro-inflammatory cytokines, in particular interleukin 1β (IL1β), tumor necrosis factor-α (TNFα), and interferon-γ (IFNγ) (Jörns et al. 2005, Thomas et al. 2009). Activation of the respective receptors initiates the intracellular signaling cascades leading ultimately to β-cell dysfunction and apoptosis (Cnop et al. 2005, Novotny et al. 2012).
One major component of this process is the oxidative destruction of cellular structures by an increased generation of reactive oxygen species (ROS), especially of highly toxic hydroxyl radicals (Gurgul-Convey et al. 2011, Mehmeti et al. 2011a). Hydroxyl radicals are formed in the Haber–Weiss reaction in the presence of catalytically active free ferrous iron (Fe2+) from intracellular hydrogen peroxide (Halliwell & Gutteridge 2007).

Circulating iron is sequestered by transferrin within the bloodstream. Through interaction with the transferrin receptors this transferrin-bound iron can enter the cell by endocytosis. The subsequent transport step from the endosome to the cytosol is mediated by the divalent metal transporter 1 (Dmt1), which is expressed in four known isoforms, resulting from two different 5'-variants, called 1A and 1B, and two 3'-variants, which are different in their 3'-translated and UTR, containing or not an iron-responsive element (+IRE/−IRE; Gunshin et al. 1997, Hubert & Hentze 2002, MacKenzie et al. 2008). These elements are important for the regulation of the Dmt1 expression by influencing mRNA stability (Galy et al. 2008) and each of these 3'-variants can occur with both 5'-types of RNA. Due to the central role of iron for the synthesis of heme prosthetic groups and iron-sulfur clusters, a high ratio of H:L subunits, the apoferritin molecule (Harrison & Arosio 1996). At variance from the cytosolic Ft molecule, the mitochondrial Ft (Mtft) molecule has a homopolymeric structure with a high homology to the Ft-H molecule (Levi et al. 2001).

Pro-inflammatory cytokines, however, favor pro-oxidative conditions and the generation of hydroxyl radicals in insulin-secreting cells (Lortz et al. 2000). The extremely low expression of the hydrogen peroxide-inactivating enzymes catalase and glutathione peroxidase, together with a relatively high superoxide dismutase expression (Lenzen et al. 1996, Tiedge et al. 1997, Lenzen 2008), leads to an accumulation of hydrogen peroxide under the influence of pro-inflammatory cytokines (Gurgul-Convey et al. 2011). Although catalase expression in human islets (Welsh et al. 1995) is somewhat higher than that in rodent islets (Lenzen et al. 1996, Tiedge et al. 1997, Lenzen 2008), the catalase activity of human β-cells is, when compared with other tissues, very low (for discussion see Lenzen (2008)) and therefore similar damaging effects of ROS could be observed in human islets (Benhamou et al. 1998).

Together with an induction of iron import via Dmt1 through pro-inflammatory cytokines (Hansen et al. 2012), this would support hydroxyl radical formation, promoting serious damage to many cellular structures (Mehmeti et al. 2011b, Hansen et al. 2014). We therefore characterized the influence of pro-inflammatory cytokines on the expression of the different Dmt1 isoforms and whether enhanced Dmt1 expression could be compensated, probably by increased expression of the iron-chelating protein Ft.

Materials and methods

Tissue culture of insulin-producing cells

Insulin-producing RINm5F tissue culture cells were cultured in RPMI-1640 medium supplemented with 10 mM glucose, 10% (v/v) FCS, penicillin, and streptomycin as described previously (Lenzen et al. 1996, Tiedge et al. 1997). Insulin-secreting INS-1E cells (kindly provided by Prof. C Wollheim) were cultured as previously described (Asfari et al. 1992). The neuroendocrine PC12 cells were cultured in RPMI-1640 medium supplemented with 10 mM glucose, 5% (v/v) FCS, 10% (v/v) horse serum, penicillin, and streptomycin (Greene & Tischler 1976). All cell lines were cultured at 37 °C in a humidified atmosphere of 5% CO2.

Rat islet isolation

Pancreatic islets were isolated from 250 to 300 g adult male Lewis rats by collagenase digestion, separated by Ficoll gradient, and handpicked under a stereo microscope (Tiedge et al. 1997). Isolated islets were cultured overnight in RPMI-1640 medium supplemented with 5 mM glucose, 10% FCS, penicillin, and streptomycin at 37 °C in a humidified atmosphere of 5% CO2.

Exposure to pro-inflammatory cytokines

The cells were seeded in 6 cm tissue culture plates at a density of 1×10⁶ cells and allowed to attach for a period of 24 h. Thereafter the cells were exposed to
600 U/ml human IL1β or a combination of cytokines (cytokine mixture) consisting of 60 U/ml IL1β, 185 U/ml human TNFa, and 14 U/ml IFNγ (PromoCell, Heidelberg, Germany) for the indicated incubation times.

Hypoxic incubation

For incubation under hypoxic conditions, the cells were cultured 24 h after seeding at 37 °C in a humidified atmosphere of 1% O2 balanced with N2 for hypoxia for the indicated incubation times (6 and 24 h hypoxia or 24 h hypoxia followed by 6 h normoxia). Hypoxia was generated in an oxygen-regulated incubator (CB210 incubator with O2 control option, Binder, Tuttlingen, Germany). After incubation, total RNA was isolated immediately.

Real-time quantitative RT-PCR

Total RNA was isolated as previously described (Chomczynski & Sacchi 1987). For cDNA synthesis, random hexamers were used to prime the reaction of the RevertAid H- M-MuLV reverse transcriptase (Fermentas, St Leon-Rot, Germany). QuantiTect SYBR Green technology (Qiagen), which uses a fluorescent dye that only binds double-stranded DNA, was employed. The reactions were carried out using the Opticon Realtime-PCR-System (Bio-Rad). The samples were first denatured at 94 °C for 3 min, followed by 40 PCR cycles comprising a melting step at 94 °C for 30 s, an annealing step at 62 °C for 30 s, and an extension step at 72 °C for 30 s. Optimal parameters for the PCRs were empirically defined and the purity and specificity of the amplified PCR product for each experiment was verified by melting curve analysis. All transcripts showed C_t-values, which were at least ten C_t-values lower than the values for blanks. Each PCR amplification was carried out in triplicate. The primer sequences are listed in Supplementary Table 1, see section on supplementary data given at the end of this article. Data are expressed as relative gene expression after normalization to the housekeeping gene β-actin using the Qgene96 (Institute of Biochemistry and Genetics, Research Group Cardiovascular Genetics, University of Basel, Switzerland) and LineRegPCR (Heart Failure Research Center, Amsterdam, the Netherlands) software.

Western blot analyses

After 48 h of incubation, whole-cell extracts were sonified in ice-cold PBS on ice for 15 s at 60 W with a Braun-Sonic 125 sonifier. Protein content was determined by the BCA assay (Pierce, Rockford, IL, USA). 20 μg protein per lane was fractionated by 12.5% SDS–PAGE and transferred to polyvinylidene fluoride membranes. Nonspecific binding sites of the membranes were blocked by 5% non-fat dry milk for 1 h at room temperature. Then the membranes were incubated overnight at 4 °C with the specific primary antibody (Dmt1, sc-30120, diluted 1:200; actin, sc-1615, 1:250, Santa Cruz Biotechnology). The excess of primary antibody was removed by three washes with wash buffer (PBS, 0.1% Tween 20, 0.1% BSA), subsequently the membrane was incubated with the peroxidase-labeled secondary antibodies at a dilution of 1:20,000 at room temperature for 1 h. The protein bands were visualized by chemiluminescence using the ECL detection system (GE Life Sciences, Freiburg, Germany). The intensity of the bands was quantified through densitometry with the Gel-Pro Analyzer 6.0 program (Media Cybernetics, Silver Spring, MD, USA).

Statistical analyses

Data are expressed as mean ± S.E.M. Statistical analyses were performed using ANOVA plus Bonferroni’s test for multiple comparisons (Graphpad, San Diego, CA, USA).

Results

Expression of the different Dmt1 isoforms in insulin-producing cells and primary rat islets

For the quantification of the four characterized Dmt1 isoforms in different insulin-producing cell lines and primary rat islets, qRT-PCR analyses with isoform-specific primers were carried out. The 1B transporter isoform was the predominately expressed Dmt1 isoform in all insulin-producing cell lines and rat pancreatic islets, responsible for almost 100% of total Dmt1 expression (Fig. 1). In contrast to this, expression of the 1A isoform was extremely low in all investigated insulin-producing cells and accounted for <1% of the total Dmt1 expression. Regarding the +/− IRE splice variants, the expression level of +IRE variant was markedly higher than that of −IRE in both RINm5F and INS-1E cells (approximately 40–60% +IRE and 20% −IRE). However, in primary rat islets both variants were expressed equally approximately 30% each, (Fig. 1), which probably results from a different expression pattern of Dmt1 in non-beta islet cells.

Investigation of the neuroendocrine PC12 cell line showed a completely different Dmt1 expression profile. Although the expression of the 1B variant was also predominant in PC12 cells, the expression of the 1A transcript represented up to 40% of the total Dmt1 isoform expression profile.
expression, a multiple of that in insulin-producing cells. The proportion of the CIRE transcript of total DMT1 expression was nearly 80% and therefore twofold higher than in islets or INS-1E cells, whereas the -IRE proportion of total DMT1 expression was !20% (Fig. 1).

**Effects of hypoxia on Dmt1 gene expression in insulin-producing RINm5F cells**

Under oxygen deprivation, a number of signaling pathways involved in systemic iron transport, cellular iron supply, and metabolism are activated. Therefore, the effects of temporary hypoxia on Dmt1 isoform expression were analyzed.

Incubation of RINm5F cells for 6 h at 1% O2 had no effect on the expression of all investigated Dmt1 isoforms or on total Dmt1 expression (Fig. 2). Although an extension of the incubation time to 24 h resulted in a threefold induction of Dmt1 1A, while the expression of 1B, of C/IRE, and of the total Dmt1 remained unchanged. A transient hypoxic period of 24 h followed by 6 h under normoxic conditions increased Dmt1 1A

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**Figure 1**

Expression of the different Dmt1 isoforms in insulin-producing cells, primary rat islets, and PC12 cells. Total RNA was isolated 24 h after culture under control conditions from RINm5F cells, INS-1 cells, primary rat islets, and PC12 cells. The gene expression of all investigated Dmt1 isoforms was analyzed by qRT-PCR with Dmt1 1A, 1B (grey bars), +IRE and –IRE (white bars)-specific primers and with a primer pair detecting a Dmt1 consensus sequence. The expression levels were normalized to the housekeeping gene β-actin. The gene expression of total Dmt1 in each cell type was set as 100%. Data are mean ± S.E.M. from 6 to 14 individual experiments.

**Figure 2**

Effects of hypoxia on Dmt1 gene expression in insulin-producing RINm5F cells. RINm5F cells were incubated for up to 24 h with 1% O2, for 24 h under hypoxic conditions followed by a 6 h normoxic incubation (24+6 h) or for 24 h under control conditions. After incubation, total RNA was isolated and the Dmt1 isoform expression and total Dmt1 expression was analyzed by qRT-PCR with specific primers. The expression levels were normalized to the housekeeping gene β-actin and the expression level of each Dmt1 isoform or the total Dmt1 expression under control conditions was set as 100%. Data are mean ± S.E.M. from 4 to 14 individual experiments. *P<0.05, **P<0.01 compared with the control incubation.
isoform expression approximately threefold, similar to the induction after 24 h hypoxia alone. The expression of all other investigated isoforms and the total Dmt1 expression were ~30–50% higher after 24 h hypoxia followed by 6 h normoxic incubation, but not significantly different from the control values (Fig. 2).

Effects of pro-inflammatory cytokines on Dmt1 gene expression in insulin-producing RINm5F cells

In earlier studies, we could show that the production of ROS, especially of hydroxyl radicals, is a central element in the cytokine-mediated destruction process of insulin-producing cells (Gurgul-Convey et al. 2011, Mehmeti et al. 2011a). Therefore, the effects of pro-inflammatory cytokines on the different Dmt1 isoforms were investigated. Both, IL1β and a mixture of pro-inflammatory cytokines, consisting of IL1β, TNFα and IFNγ, caused a fivefold induction of the 1A and a 1.5-fold induction of the 1B isoform expression after 6 h incubation. After 24 h, the IL1β- and cytokine mixture-mediated increase in the expression of 1A isoform was already 20-fold and further increased to 40-fold after the 48 h treatment. An increase in the expression of 1B isoform was also observed, although the induction was lower than that of the 1A isoform (threefold after 24 h and fourfold after 48 h incubation; Fig. 3).

Parallel to the changes in expression of the 1B isoform, the IRE-containing mRNA variant showed a 2.5- to 3-fold increase after 6 h incubation with IL1β alone and the cytokine mixture. However, thereafter the gene expression increase was ten- and 14-fold, respectively, after 24 and 48 h incubation with pro-inflammatory cytokines. The expression of the −IRE isoform was enhanced threefold after 6 h, sixfold after 24 h, and eightfold after 48 h incubation with both IL1β alone and the cytokine mixture.

![Graphs showing gene expression changes](http://jme.endocrinology-journals.org)

**Figure 3**

Effects of pro-inflammatory cytokines on the Dmt1 gene expression in insulin-producing RINm5F cells. RINm5F cells were incubated for 24 h with IL1β (600 U/ml) alone (grey bars) or a cytokine mixture (IL1β 60 U/ml, TNFα 185 U/ml, IFNγ 14 U/ml, black bars). After incubation, total RNA was isolated and the Dmt1 isoform expression and total Dmt1 expression was analyzed by qRT-PCR with specific primers. The expression levels were normalized to the housekeeping gene β-actin and the expression level of each Dmt1 isoform or the total Dmt1 expression under control conditions was set as 100%. Data are mean ± S.E.M. from five to six individual experiments.

*P < 0.05, **P < 0.01, ***P < 0.005 compared with the control incubation.
These changes resulted also in a significantly increased total \textit{Dmt1} expression, by 2.5-fold after 24 h and 3.3-fold after 48 h of cytokine treatment (Fig. 3).

\textbf{Effects of different pro-inflammatory cytokines on \textit{Dmt1} gene expression in insulin-producing INS-1E cells}

To investigate the role of the different pro-inflammatory cytokines in the induction of the \textit{Dmt1} expression, INS-1E cells were incubated with the different cytokines alone or in two different combinations, namely IFN\textgamma together with TNF\textalpha and IL1\beta together with TNF\textalpha and IFN\textgamma. The expression pattern of all investigated \textit{Dmt1} isoforms and the total \textit{Dmt1} expression in response to the employed cytokines were similar, although the expression levels were different (Fig. 4).

IL1\beta alone or the complete cytokine mixture, containing IL1\beta, TNF\alpha, and IFN\textgamma, caused the highest induction up to 12.5-fold for the \textit{Dmt1} 1A isoform and 5.5-fold for the +IRE isoform. In contrast, exposure of INS-1E cells to TNF\alpha or IFN\textgamma alone did not change the expression of any \textit{Dmt1} isoform or the total \textit{Dmt1} expression significantly. The mixture of both cytokines (TNF\alpha and IFN\textgamma) also did not significantly increase the \textit{Dmt1} expression. Thus, total \textit{Dmt1} expression was only (approximately 2.5-fold) induced by IL1\beta and the complete cytokine mixture \((P<0.05)\), whereas all other cytokines had no significant effects on the overall \textit{Dmt1} expression (Fig. 4). This indicates that the IL1\beta- and the cytokine mixture-induced increase in the \textit{Dmt1} expression is most probably NF-\kappaB mediated.

\textbf{Effects of pro-inflammatory cytokines on the \textit{Dmt1} protein expression in insulin-producing INS-1E cells}

To show that the cytokine-induced increase in \textit{Dmt1} gene expression results also in detectable changes in the \textit{Dmt1} protein level, the \textit{Dmt1} protein expression was analyzed by western blot analyses.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure4.png}
\caption{Effects of different pro-inflammatory cytokines on \textit{Dmt1} gene expression in insulin-producing INS-1E cells. INS-1E cells were incubated for 24 h under control conditions (white bars), with IL1\beta (600 U/ml), IFN\textgamma (140 U/ml), or TNF\alpha (1850 U/ml) alone (light grey bars), with IFN\textgamma (14 U/ml) together with TNF\alpha (185 U/ml, dark grey bars) or with the cytokine mixture (IL1\beta 60 U/ml, TNF\alpha 185 U/ml, IFN\textgamma 14 U/ml, black bars). After incubation total RNA was isolated and the \textit{Dmt1} isoform expression and total \textit{Dmt1} expression were analyzed by qRT-PCR with specific primers. The expression levels were normalized to the housekeeping gene \beta-actin and the expression level of each \textit{Dmt1} isoform or the total \textit{Dmt1} expression under control conditions was set as 100%. Data are mean ± S.E.M. from three individual experiments. \(*P<0.05, \,**P<0.01\) compared with the control incubation.}
\end{figure}
A 48-h incubation with 600 U/ml IL1β induced Dmt1 protein expression only slightly by 15%. However, INS-1E cells exposed to the cytokine mixture showed a 33% higher Dmt1 protein expression than untreated cells ($P<0.05$, Fig. 5). After 24 h of incubation with cytokines, quantification of Dmt1 protein expression revealed no significant changes (data not shown).

**Effects of pro-inflammatory cytokines on Ft gene expression in insulin-producing RINm5F cells**

In addition to the iron import through Dmt1, iron chelation by Ft is another important element of intracellular iron homeostasis and the prevention of iron-catalyzed production of hydroxyl radicals. Thus, the effects of pro-inflammatory cytokines on the Ft gene expression were quantified by qRT-PCR after 8 and 24 h incubation.

Incubation of RINm5F cells with 600 U/ml IL1β had no influence on the expression of Ft-H, Ft-L, and Mtft after 8 or 24 h incubation. But the cytokine mixture caused a slight significant increase (30%) in the expression of Ft-H after 8 h and a twofold increase after 24 h (Fig. 6A). For the Ft-L subunit after 24 h incubation only, a slight significant induction (25%) was observed with the cytokine mixture (Fig. 6B), whereas for the expression of Mtft no changes after incubation with IL1β alone or the cytokine mixture were seen (Fig. 6C).

**Discussion**

Development of type 1 diabetes mellitus is associated with a progressive cellular dysfunction and damage, leading ultimately to β-cell death (Eizirik & Mandrup-Poulsen 2001, Novotny et al. 2012). As shown in previous studies, many steps in this process are mediated by ROS including also interactions with nitric oxide (Gurgul-Convey et al. 2011). Through its extremely low half-life and its high reactivity, the hydroxyl radical is a key element in the β-cell destruction process. A high concentration of intracellular free iron behaves as a catalyst in the Haber–Weiss reaction during the generation of hydroxyl radicals and can therefore contribute to cellular damage (Kehrer 2000, Halliwell & Gutteridge 2007). The influence of β-cell toxic cytokines on the expression balance of iron-importing and intracellular chelating proteins was therefore in the focus of the present study.

Insulin-producing cell lines and primary rat islets exhibited a highly selective expression of *Dmt1* 1B mRNA and a slight preference for the 3'CIRE variant. After transient hypoxia, only the weakly expressed 1A isoform was induced, whereas the 1B isoform was not and the expression of both 3'-variants, +IRE and −IRE respectively, was only slightly increased. These findings are in agreement with those reported for PC12 cells (Lis et al. 2005) and highlight the role of regulatory sequences in the 5' regulatory region of the *Dmt1* gene as binding sites for HIF-1α (Lee et al. 1998). However, due to the near absence of the expression of the 1A isoform, no significant changes in total Dmt1 expression were detected, showing the limited adaption possibilities of insulin-producing cells to hypoxic conditions in contrast to other cell types (Carlsson & Palm 2002).

Pro-inflammatory cytokines, however, were able to induce overall Dmt1 expression, as well as the expression of every single isoform significantly. Furthermore, after
48 h also an increase in protein expression was obvious, whereas after 24 h a significant increase had not yet been observed. Although the delay in protein translation was unusually long, these findings are consistent with the observed kinetics of cytokine-induced cell toxicity in earlier experiments (Gurgul-Convey et al. 2011) and indicate that changes in Dmt1 mRNA expression are followed by changes in protein expression. Though the absolute gene expression level of the 1A isoform was very low under control conditions, the massive induction after 24 and 48 h cytokine treatment could contribute to the changes in overall Dmt1 gene and protein expression and might serve also as an additional marker for cytokine-mediated changes in gene expression in insulin-secreting cells.

Further incubations with single cytokines or with selective combinations revealed the importance of IL-1β for the increase in the Dmt1 expression, mediated most probably by the NF-κB signaling pathway. With these results, we could confirm the data of Hansen et al. (2012), reporting that an enhanced NF-κB transcriptional activity through increased Pdx1 activity potentiated cytokine-induced toxicity through upregulation of Dmt1 expression. Also in other inflammatory diseases, such as rheumatoid arthritis, an accelerated cellular iron uptake has been observed (Telfer & Brock 2004).

A high iron transport capacity through an increased Dmt1 expression does not necessarily result in enhanced oxidative stress, because an effective chelation by Ft should maintain a balanced iron homeostasis and inhibit an increase of the LIP (Harrison & Arosio 1996). However, the expression of the cytosolic Ft H- and L-subunits was only moderately induced after a 24 h incubation with the cytokine mixture, whereas the expression of the mitochondrially located Ft remained unchanged after incubation with cytokines. For the macrophage-derived U937 cell line it has been reported that TNFα and IFNγ induced the κ mRNA expression, whereas IL1β showed no effect (Fahmy & Young 1993). In addition to TNFα interleukin 1α induced also the expression of Ft, which is in mesenchymal cells also selective for the H-isoform (Torti et al. 1988). These reports indicate that the regulation of the Ft expression by pro-inflammatory cytokines is not unique to insulin-secreting cells, but common to many different cell types. However, in β-cells increased Dmt1 expression was associated with a higher cell death rate under pro-inflammatory conditions and suppression of Dmt1 expression by siRNA or chelation of iron under these conditions resulted in significant protection against β-cell toxic cytokines (Hansen et al. 2012), showing the

Figure 6
Effects of pro-inflammatory cytokines on Ft gene expression in insulin-producing RINm5F cells. RINm5F cells were incubated for 24 h under control conditions (white bars) or for 8 and 24 h with IL1β (600 U/ml) alone (grey bars) and with the cytokine mixture (IL1β 60 U/ml, TNFα 185 U/ml, IFNγ 14 U/ml, black bars). After incubation total RNA was isolated and Ft expression was analyzed by qRT-PCR with specific primers. The expression levels were normalized to the housekeeping gene β-actin and the expression level of each Ft subunit under control conditions was set as 100%. Data are mean ± S.E.M. from six individual experiments. *P<0.05, **P<0.01 compared with the control incubation; ***P<0.05, ****P<0.01 compared with IL1β incubation.
relevance of augmented iron import and the increasing Fe\(^{2+}\)-driven radical formation for the pathogenesis of type 1 diabetes mellitus.

The extremely low H\(_2\)O\(_2\) inactivation capacity of insulin-secreting cells (for review, see Lenzen (2008)) goes along with a pronounced increase in Dmt1 expression and even though to a somewhat lesser extent also of iron chelation by Ft in the cytosol, which may, to a certain extent, at least neutralize increased cytokine-mediated iron uptake capacity. However, such a compensation dampening ROS toxicity through increased iron binding is not possible in the mitochondria apparently, since Mtft expression did not increase under the influence of cytokines. This observation may help to explain why pro-inflammatory cytokine toxicity to the mitochondria in insulin-secreting cells has been found to be particularly prominent (Gurgul et al. 2004, Mehmeti et al. 2011a). Future studies will have to show whether iron uptake and chelation may qualify as protective targets for pharmacotherapy in the prevention of \(\beta\)-cell destruction in type 1 diabetes mellitus.

Supplementary data
This is linked to the online version of the paper at http://dx.doi.org/10.1530/JME-13-0261.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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