Increased oxidative stress and apoptosis in the hypothalamus of diabetic male mice in the insulin receptor substrate-2 knockout model

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ABSTRACT
Insulin receptor substrate-2-deficient (IRS2−/−) mice are considered a good model to study the development of diabetes because IRS proteins mediate the pleiotropic effects of insulin-like growth factor-I (IGF-I) and insulin on metabolism, mitogenesis and cell survival. The hypothalamus might play a key role in the early onset of diabetes, owing to its involvement in the control of glucose homeostasis and energy balance. Because some inflammatory markers are elevated in the hypothalamus of diabetic IRS2−/− mice, our aim was to analyze whether the diabetes associated with the absence of IRS2 results in hypothalamic injury and to analyze the intracellular mechanisms involved. Only diabetic IRS2−/− mice showed increased cell death and activation of caspase-8 and -3 in the hypothalamus. Regulators of apoptosis such as FADD, Bcl-2, Bcl-xL and p53 were also increased, whereas p-IκB and c-FLIP, were decreased. This was accompanied by increased levels of Nox-4 and catalase, enzymes involved in oxidative stress. In summary, the hypothalamus of diabetic IRS2−/− mice showed an increase in oxidative stress and inflammatory markers that finally resulted in cell death via substantial activation of the extrinsic apoptotic pathway. Conversely, non-diabetic IRS2−/− mice did not show cell death in the hypothalamus, possibly owing to an increase in the levels of circulating IGF-I and in the enhanced hypothalamic IGF-IR phosphorylation that would lead to the stimulation of survival pathways. In conclusion, diabetes in IRS2-deficient male mice is associated with increased oxidative stress and apoptosis in the hypothalamus.

KEY WORDS: Diabetes, Cell death, IRS2, Apoptosis, Oxidative stress, Hypothalamus

INTRODUCTION
Insulin receptor substrates (IRSs) mediate the pleiotropic effects of insulin-like growth factor-I (IGF-I) and insulin on metabolism, mitogenesis and cell survival. Upon activation of receptors for insulin or IGF-I, phosphorylation of several IRSs occurs, leading to the activation of major regulatory intracellular pathways involved in proliferation and metabolism (White, 2014). Male IRS2-deficient mice (IRS2−/−) are used as a type 2 diabetes model because they exhibit defects in hepatic insulin signalling, resulting in impaired suppression of glucose production (Withers et al., 1998; Kubota et al., 2000; Previs et al., 2000), and β-cell failure due to disruption of the IGF-I receptor (IGF-IR) mitogenic signalling (Withers et al., 1999) and increased β-cell apoptosis (Lingohr et al., 2003). Furthermore, IRS2-deficient mice recapitulate the fulminate onset of human diabetes because a significant proportion of these mice develop diabetes abruptly at 12-16 weeks of age (Hashimoto, 2011; García-Barrado et al., 2011). Also, IRS2-deficient mice show central leptin resistance resulting in alterations in the control of neuropeptides in the arcuate nucleus (Masaki et al., 2012). Interestingly, the magnitude of glucose deregulation in IRS2-deficient mice can be variable, with certain congenic strains only presenting prediabetic changes (Hashimoto, 2011). This phenotypic divergence might allow an experimental tool to analyze pathogenic factors involved in central insulin signalling pathways leading to two different outcomes: prediabetes or overt diabetes (Cai, 2012). In a previous study (Burgos-Ramos et al., 2012), we found activation of hypothalamic inflammatory pathways that differentially correlate with the absence or presence of diabetes in IRS2-deficient mice, suggesting that the inflammatory process could be related to the onset of disease.

Induction of oxidative stress actively participates in tissue damage caused by hypoglycaemia and diabetes, and results in deterioration of glucose homeostasis (Singh et al., 2004). The mechanisms and pathways involved in this process are complex. If reactive oxygen species (ROS) are not detoxified, cellular components are damaged and stress-sensitive intracellular signalling pathways mediated by nuclear factor-kappa B (NFκB), p38 and Jun N-terminal kinase [JNK; also known as stress-activated kinases (SAPK)] are altered (Newsholme et al., 2007). Although the brain consumes 20% of the oxygen in the body and has a high content of unsaturated fatty acids and catecholamines that are readily oxidized, it has a low content of antioxidants (Rizzo et al., 2010), which makes it a susceptible organ to oxidative damage (Uttara et al., 2009). Oxidation produces lipid peroxides and DNA oxides that produce cell disturbances that lead to inflammation and deterioration of the central nervous system. Multiple mechanisms have been proposed to protect cells from apoptosis, including the activation of insulin signalling mediators through IRS2, such as the phosphoinositide 3-kinase (PI3K)/protein kinase B (Akt) (Franke...
et al., 1997; Valverde et al., 2004) and Ras/mitogen-activated protein kinases (MAPK) pathways (Schubert et al., 2004). Hence, in the present study, we analyzed whether diabetes caused by IRS2 deficiency affects cell death in the hypothalamus, because this neuroendocrine organ is a key target for inflammation and oxidative stress in diabetes (Cai and Liu, 2011), and we analyzed the mechanisms involved.

RESULTS

Cell death and apoptotic pathways in the hypothalamus of non-diabetic and diabetic IRS2−/− mice

Cell death in the hypothalamus was quantified by ELISA. Only diabetic IRS2−/− mice showed increased cell death [non-diabetic (ND): 121%; diabetic (D): 211% of wild-type (WT) values, Fig. 1A]. To determine the signalling pathways involved in the observed cell death, activation of caspases was analyzed. Activation of caspase-3, measured by bead array, was detected in diabetic IRS2−/− mice (144% of WT values), but not in non-diabetic IRS2−/− mice (99% of WT values, Fig. 1B). Caspase-8 (initiator caspase of the extrinsic apoptotic pathway) and caspase-9 (initiator caspase of the intrinsic pathway) were measured by western blotting. Levels of fragmented caspase-8 increased in diabetic IRS2−/− mice (ND: 103%; D: 212% of WT values, Fig. 1C); however, levels of fragmented caspase-9 did not change in either group (Fig. 1D).

Taking into account these data, levels of TNF-related apoptosis-inducing ligand (TRAIL) and Fas-associated death domain (FADD), two proteins involved in the extrinsic pathway of apoptosis, were assayed by western blotting. Levels of FADD were increased in diabetic IRS2−/− mice (ND: 83%; D: 192% of WT values; Fig. 2A). By contrast, levels of TRAIL were not different in diabetic and non-diabetic IRS2−/− mice (ND: 104% and D: 105% of WT values, Fig. 2B).

Next, we studied the levels of the apoptosis inhibitory proteins X-linked inhibitor of apoptosis (XIAP) and FADD-like IL-1β-converting enzyme-inhibitory protein large (FLIP). Levels of XIAP...
were not statistically different among groups (ND: 70%; D: 84% of WT values, Fig. 2C), whereas diabetic IRS2\(^{-/-}\) mice showed decreased FLIPL levels compared to the controls (ND: 96%; D: 80% of WT values, Fig. 2D).

Activation of NFkB was assayed by studying the levels of phosphorylated IxB. In diabetic IRS2\(^{-/-}\) mice, decreased levels of phosphorylated IxB were found (ND: 90%; D: 47% of WT value; Fig. 2E). In contrast, the mRNA levels of Nfkbia mRNA,
which encodes IκBα, were increased in the hypothalamus of diabetic IRS2−/− mice (ND: 117%; D 154% of WT value).

Moreover, levels of p53 increased in IRS2−/− mice, with this increase being statistically significant only in diabetic mice (ND: 142%; D: 193% of WT mice; Fig. 2F).

Levels of the anti-apoptotic proteins Bcl-2 and Bcl-xL, and pro-apoptotic proteins BAD, BID and BIM, were analyzed by western blotting. Bcl-2 and Bcl-xL were increased in diabetic IRS2−/− mice (185% and 141% of WT values, respectively) but did not change in non-diabetic IRS2−/− mice (114% and 122% of WT values,

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**Fig. 3. Regulation of Bcl-2 family proteins in the hypothalamus of non-diabetic and diabetic IRS2−/− mice.** Immunoblots probed with antibodies against Bcl-2 (A), Bcl-xL (B), BAD (C), BID (D) and BIM (E) in the hypothalamus of wild-type (WT), non-diabetic IRS2-deficient (ND IRS2−/−) and diabetic IRS2-deficient (D IRS2−/−) mice. (F) Representative immunoblots for Bcl-2, Bcl-xL, BAD, BID, BIM and GAPDH. Data are presented as means±s.e.m. Statistical significance by ANOVA: *P<0.05 vs WT mice; n=6/group.
respectively; Fig. 3A,B). Levels of pro-apoptotic proteins did not change in any IRS2−/− group regardless of diabetes: BAD (ND: 101%; D: 99% of WT values), truncated BID (t-BID)/BID (ND: 96%; D: 101% of WT values) and BIM (ND: 96%; D: 112% of WT values; Fig. 3C,D and E, respectively).

To study the inflammatory state of the hypothalamus, we measured the levels of several cytokines involved in the inflammatory process. As shown in Table 1, TNF-α, IL-6 and IL-1β were increased in the hypothalamus of diabetic IRS2−/− mice, whereas IL-10 was decreased although the latter did not reach statistical significance. By contrast, non-diabetic IRS2−/− mice showed reduced levels of IL-6.

### Oxidative stress in the hypothalamus of non-diabetic and diabetic IRS2−/− mice

To study the role of oxidative stress, different enzymes were assessed. NADPH oxidase 4 (Nox-4) mRNA levels were increased in diabetic IRS2−/− mice (ND: 93%; D: 157% of WT values, Fig. 4A). Catalase protein levels, measured by western blotting, were also increased in diabetic IRS2−/− mice (ND: 113%; D: 140% of WT values; Fig. 4B).

Levels of glutathione reductase and malondialdehyde (MDA), determined by western blotting, did not change in diabetic or non-diabetic mice (glutathione reductase ND: 101%, D: 109% of WT values; MDA: ND: 102%, D: 103% of WT values; Fig. 4C).

### Table 1. Levels of several cytokines involved in the inflammatory process

<table>
<thead>
<tr>
<th>Cytokine</th>
<th>WT</th>
<th>ND IRS2−/−</th>
<th>D IRS2−/−</th>
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<tbody>
<tr>
<td>TNF-α</td>
<td>1.7±0.2</td>
<td>1.1±0.4</td>
<td>3.2±0.1**</td>
</tr>
<tr>
<td>IL-6</td>
<td>6.4±0.3</td>
<td>0.8±0.1**</td>
<td>8.4±0.3**</td>
</tr>
<tr>
<td>IL-1β</td>
<td>25.6±1.7</td>
<td>16.8±4</td>
<td>30±4#</td>
</tr>
<tr>
<td>IL-10</td>
<td>17±2.6</td>
<td>22±5</td>
<td>11.4±2.4</td>
</tr>
</tbody>
</table>

Cytokine concentrations (pg/mg of protein) in the hypothalamus of WT, ND IRS2−/− and D IRS2−/− mice. **P<0.01 vs WT mice; # P<0.05 and ## P<0.01 vs ND IRS2−/−; n=6/group.

Fig. 4. Analysis of oxidative stress markers in the hypothalamus of non-diabetic and diabetic IRS2−/− mice. Relative mRNA levels of Nox-4 (A), and immunoblots probed with antibodies against catalase (B), glutathione reductase (C) and malondialdehyde (MDA) (D) in the hypothalamus of wild-type (WT), non-diabetic IRS2-deficient (ND IRS2−/−) and diabetic IRS2-deficient (D IRS2−/−) mice. Data are presented as means±s.e.m. Statistical significance by ANOVA: *P<0.05 vs WT mice; # P<0.05 vs ND IRS2−/−. n=6/group.
Identification of cell types susceptible to apoptosis in the hypothalamus of IRS2−/− mice

We measured glial fibrillary acidic protein (GFAP) as a marker of astrocytes and neuronal β-III tubulin (Tuj-1), as a marker of neurons, by western blotting. Only diabetic IRS2−/− mice presented decreased levels of GFAP (ND: 90%; D: 26% vs WT mice). Levels of Tuj-1 were similar in all groups (ND: 84%; D: 101% vs WT mice; Fig. 5A and B, respectively).

Fig. 5. Analysis of the cell type susceptible to apoptotic cell death in the hypothalamus of IRS2−/− mice. Immunoblots probed with antibodies against GFAP (A) and Tuj-1 (B) in the hypothalamus of wild-type (WT), non-diabetic IRS2-deficient (ND IRS2−/−) and diabetic IRS2-deficient (D IRS2−/−) mice. The average of three independent assays performed in duplicate is shown. Statistical significance by ANOVA: *P<0.05 vs WT mice. n=6/group. (C) Colocalization of TUNEL and GFAP in the hypothalamus of WT, ND IRS2−/− and D IRS2−/− mice. Arrows indicate astrocytes with apoptotic nuclei. (D) Colocalization of cleaved caspase-8 and GFAP, and of cleaved caspase-8 and NeuN, in the hypothalamus of WT, ND IRS2−/− and D IRS2−/− mice. Arrows indicate colocalization of GFAP and cleaved caspase-8. Scale bar: 50 µm; inset, 100 µm.
Diabetes causes cellular dysfunction through various mechanisms and this can result in tissue injury. Hyperglycaemia associated with diabetes causes cellular oxidative stress in the hypothalamus of diabetic IRS2−/− mice, which is essential to bridge members of the TNF receptor (TNFR) superfamily to procaspase-8 to assemble the death-inducing signalling complex (DISC) during apoptosis (Micheau and Tschopp, 2003). In turn, caspase-8 can then activate caspase-3, which is considered an important mediator of diabetic complications (Inoguchi et al., 2007). In order to study the role of oxidative stress and the relationship with inflammatory processes described in diabetes, we analyzed the levels of key enzymes involved in oxidative stress in the hypothalamus of IRS2−/− mice and found that protein levels of catalase were increased in diabetic IRS2−/− mice. This effect could be attributed to higher levels of H2O2, reflected by increased Nox-4 mRNA levels, because H2O2 is the major form of ROS generated by this NADPH oxidase (Lambeth, 2007; Serrander et al., 2007).

Oxidative stress induced by hyperglycaemia serves as a key trigger of inflammatory gene expression (Gumieniczek et al., 2005). Pro-inflammatory cytokines play an important role in the pathology of diabetes (Bodles and Barger, 2004). TNF-α has been suggested to participate in the development of diabetes by impairing insulin actions (Lechleitner et al., 2000; Tuttle et al., 2004). TNF-α also stimulates the production of ROS that directly signal cells to undergo apoptosis (Kim et al., 2010). In this regard, we found increased levels of cell death in the hypothalamus of diabetic IRS2−/− mice, compared with non-diabetic IRS2−/− and WT mice, that could be due to increased levels of pro-inflammatory cytokines such as TNF-α, IL-6 and IL-1β. TNF-α could activate caspase-8, involving the adaptor protein FADD (MORT1); this activation is essential to bridge members of the TNF receptor (TNFR) superfamily to procaspase-8 to assemble the death-inducing signalling complex (DISC) during apoptosis (Micheau and Tschopp, 2003). In turn, caspase-8 can then activate caspase-3, although a direct pathway for caspase-8-elicited apoptosis has also been described (Benchoua et al., 2002). The intrinsic and extrinsic pathways are not completely independent. In fact, in some cells, activation of caspase-8 results in the activation of the mitochondrial pathway through the cleavage of the BH3-only proteins BIM, BID and p53 up-regulated modulator of apoptosis (PUMA); this is essential for the activation of the BAX- and BAK-dependent cell death program (Ren et al., 2010; Favaloro et al., 2012). However, our results showed that BIM and BID were not cleaved in the hypothalamus of IRS2−/− mice, therefore excluding the involvement of the intrinsic pathway in apoptosis. These results were also supported by the lack of activation of caspase-9.

Other relevant proteins involved in apoptosis that have been found to be upregulated in the hypothalamus of diabetic IRS2−/− mice are the transcription factor p53 and NFκB. p53, a key factor in apoptosis (Reinhardt and Schumacher, 2012), is activated in response to oxidative stress and DNA damage induced by H2O2 (Han et al., 2008). Furthermore, the activation of caspase-8 has been implicated in p53-mediated apoptosis (Haupt et al., 2003). Hyperglycaemia has also been shown to activate p53, resulting in cell death (Eid et al., 2010). In addition, TNF-α, which was elevated in the serum and hypothalamus of diabetic IRS2−/− mice together...
with IL-6 and IL-1β, could activate both caspase-8 and p53 in the hypothalamus of diabetic IRS2−/− mice, and this activation could explain the elevated cell death. On the other hand, NFκB has been associated with the extrinsic cell-death pathway because it can be activated by pro-apoptotic signals, including death receptors (Dickens et al., 2012). However, NFκB has a dual role and can also participate in cell survival (Morgan and Liu, 2011; Singh et al., 2015) through the activation of inhibitors of apoptosis (IAPs) and other survival proteins such as Bcl-2 and Bcl-xL (Dolcet et al., 2005). Although there are a few exceptions, NFκB contributes to cell death (Perkins and Gilmore, 2006) in most cases. In this regard, various recent reports have shown that overexpression of NFκB impairs survival, proliferation and differentiation of hypothalamic neural stem cells, with an increase in apoptosis by induction of pro-apoptotic members of Bcl-2 family and caspases and upregulation of anti-apoptotic genes (Li et al., 2012). Therefore, the increased levels of NFκB might be associated with activation of the extrinsic cell-death pathway and contribute to the cell death found in the hypothalamus of diabetic IRS2−/− mice, although further studies directed to inhibit inflammatory mediators are necessary to complete this issue. Moreover, the increase in pro-inflammatory cytokines in the hypothalamus could lead to a decay of Nfkbia mRNA levels, which encodes IkBα. The resulting loss of IkBα could trigger the activation of hypothalamic NFκB, which in turn might be responsible for the inflammatory changes (Yan et al., 2014). However, we found increased Nfkbia mRNA levels in diabetic IRS2−/− mice, with overexpression of p65-NFκB that could increase the transcription of Nfkbia mRNA in an auto-regulatory loop, ensuring that NFκB is retained in the cytoplasm until cells are specifically induced to translocate it to the nucleus (Scott et al., 1993). Our results suggest that the IkBα feedback could be dependent on NFκB but other processes dependent on the molecular characteristics of the protein itself are probably involved; for example, import, export and modulation of half-life (Fagerlund et al., 2016).

One of the main signalling pathways that intersects with NFκB with regards to ROS and cell death is the crosstalk that occurs between NFκB and JNK (Morgan et al., 2008). As previously reported (Burgos-Ramos et al., 2012), levels of JNK are higher in the hypothalamus of diabetic IRS2−/− mice and phosphorylated IκBα is downregulated. Furthermore, NFκB and p53 transcriptionally regulate the c-FLIP gene. A decrease in c-FLIP1 was observed in the hypothalamus of diabetic IRS2−/− mice. The anti-apoptotic protein c-FLIP contains a death effector domain (DED) and suppresses caspase-8 activation, preventing apoptotic processes (Safa, 2012). Whereas NFκB suppresses c-FLIP transcription (Safa et al., 2008; Bagnoli et al., 2010), p53 might induce c-FLIP gene transcription and c-FLIP degradation (Safa and Pollok, 2011). c-FLIP1 possesses dual functions: at high levels it can inhibit the activation of caspase-8 induced by Fas, but at low levels it enhances caspase-8 activation (Safa et al., 2008; Bagnoli et al., 2010) as observed in the hypothalamus of diabetic IRS2−/− mice. On the other hand, H2O2, which is the most diffusible ROS, decreases c-FLIP expression in a dose-dependent manner (Nitobe et al., 2003). Based on this, downregulation of c-FLIP could be one possible mechanism by which the hypothalamus of diabetic IRS2−/− mice is prone to apoptosis.

To determine which population of cells is dying in the hypothalamus of diabetic IRS2−/− mice, we measured GFAP and TuJ-1 as markers of astrocytes and neurons, respectively. We found that only diabetic IRS2−/− mice showed decreased levels of GFAP. On the other hand, levels of TuJ-1 were similar in all groups. TUNEL assays in combination with immunofluorescence for GFAP confirmed that astrocytes were dying by apoptosis in the hypothalamus of diabetic IRS2−/− mice. Likewise, activated caspase-8 was also colocalized mainly with GFAP in the hypothalamus of diabetic IRS2−/− mice. Previous studies in rats have demonstrated that caspase-8 is present in the brain, particularly in neurons and astrocytes, and plays a key role in the apoptotic cell death response after injury (Villapol et al., 2007). Of note, because cell death is a continuous process, cells can be found in different stages. Astrocytes with active caspase-8 are probably at an early process of apoptosis.

Insulin-like peptides are neuroprotective and might be involved in the pathophysiology of a number of neurological diseases, representing possible therapeutic objectives for these disorders (Benaroch, 2012; Werner and LeRoith, 2014). In particular, IGF-I exerts anti-apoptotic/pro-survival actions in a variety of systems, including the brain (Guan et al., 2015). Furthermore, IGF-I is a potent neuroprotective agent and also protects against oxidative stress induced by the lipid-peroxidizing agent H2O2 (Heck et al., 1999). The activation of the insulin receptor or IGF-IR transduces their biological effects by tyrosine phosphorylation of IRSs and Src homology 2 domain containing (Shc), and this, in turn, initiates a signalling cascade through the PI3K/Akt and Ras/MAPK kinase pathways (Siddle, 2011). Additionally, IGF-I mediates the neuroprotection exerted by some substances by augmenting the levels of anti-apoptotic proteins such as Bcl-2 and decreasing the levels of the pro-apoptotic protein BAX and the activation of caspases (Jiang et al., 2015). Non-diabetic IRS2−/− mice did not manifest an increase in cell death in the hypothalamus, which could possibly be due to the increased levels of circulating IGF-I and the enhanced phosphorylation of the IGF-IR that would lead to the activation of survival pathways through ERK and Akt as previously reported (Burgos-Ramos et al., 2011), although further studies would be necessary to clearly demonstrate this issue.

In summary, our findings suggest that the diabetic condition in IRS2−/− mice entails an increase in oxidative stress and inflammation in the hypothalamus that finally could result in cell death via activation of the extrinsic apoptotic pathway. By contrast, non-diabetic IRS2−/− mice did not show increased hypothalamic cell death, possibly owing to the rise in circulating IGF-I levels and IGF-IR phosphorylation, which would lead to stimulation of survival pathways (summarized in Fig. 7). Hence, the exposure to an inflammatory and oxidative milieu results in a diabetic-induced hypothalamic injury in this model.

**MATERIALS AND METHODS**

**Materials**

Electrophoresis reagents were from Bio-Rad Laboratories (Hercules, CA) and the rest of the chemicals and reagents were purchased from Sigma or Merck (Barcelona, Spain) unless otherwise indicated.

**Animals**

All procedures were carried out in accordance with the local ethics committee and complied with Royal Decree 53/2013 pertaining to the protection of experimental animals and with the European Communities Council Directive (2010/63/EU).

Wild-type (WT) and IRS2−/− mice, maintained on a similar mixed genetic background (C57BL/6J×129sv), were purchased from the Jackson Laboratory (Bar Harbor, ME). Adult (11- to 12-week-old) male mice were housed individually and maintained in a ventilated room at a constant temperature (22°C) and humidity (50%) with free access to standard chow and water on a 12-h light/dark cycle. In this study, we grouped mice in: WT mice as controls, diabetic IRS2−/− (D IRS2−/−) with non-fasting glucose
levels over 500 mg/dl (determined by the glucose oxidase method by using the Precision G glucose meter; Abbott Laboratories, North Chicago, IL), and age-matched non-diabetic IRS2+/− mice (ND IRS2+/−) with glucose levels under 200 mg/dl (n=6 in each group). At 6-7 days after the debut of diabetes, animals were sacrificed by decapitation at 10:00 a.m. under non-fasting conditions. Mice from the control and ND IRS2+/− groups were sacrificed at the same time as the D IRS2−/− mice. Trunk blood was collected in cooled tubes and centrifuged at 3000 g for 10 min at 4°C. The serum was stored at −80°C until processed.

**Protein extraction and quantification**
The hypothalami were homogenized on ice in 250 µl of lysis buffer (pH 7.6) containing EDTA (10 mM), HEPES 50 (mM), sodium pyrophosphate (50 mM), NaF (0.1 M), Na3VO4 (10 mM), 1% Triton X-100, phenylmethylsulfonyl fluoride (2 mM), leupeptin (10 µg/ml) and aprotinin (10 µg/ml). The lysates were incubated overnight at −80°C and then clarified by centrifugation at 12,000 g at 4°C. The pellets were washed in 75% ethanol (1 ml), centrifuged at 7500 rpm for 2 h at 25°C, washed and posterior incubations performed for 1 h.

**Western blot**
A total of 40 µg of protein was loaded in all wells and resolved using an 8-12% SDS-PAGE and then transferred onto polyvinyl difluoride (PVDF) membranes (Bio-Rad). Filters were blocked with Tris-buffered saline containing 0.1% Tween 20 (TTBS) with 5% (w/v) bovine serum albumin (BSA) or non-fat milk during 2 h at 25°C and incubated overnight at 4°C with the primary antibody at a dilution of 1:1000 in blocking buffer. Primary antibodies included: phosphorylated IκBα from Cell Signaling Technology (Danvers, MA); BAD and glutathione reductase from Santa Cruz Biotechnology Inc. (Santa Cruz, CA); anti-FADD (M033-3; Clone 1F7) and caspase-9 from MBL International (Woburn, MA); caspase-8 from Neomarkers (Fremont, CA); TRAIL, Bcl-2, BID and β-III tubulin (Tuj-1) from R&D Systems (Minneapolis, MN); XIAP and Bcl-xl from BD Transduction Laboratories (Franklin Lakes, NJ); FLIP, catalase and GFAP from Sigma-Aldrich (St Louis, MO), BIM from BD Pharmingen (Mississauga, ON, Canada), and malondialdehyde from Cell Biolabs (San Diego, CA). The membranes were washed three times with TTBS and incubated with the corresponding secondary antibody conjugated with peroxidase (Thermo Fisher Scientific Inc., Waltham, MA) at a dilution of 1:2000 in non-fat milk during 90 min at 25°C. The proteins were detected by chemiluminescence using an immune-star western chemiluminiscent kit (Bio-Rad) and quantified by densitometry using a Kodak Gel Logic 1500 Image Analysis system and Molecular Imaging Software version 4.0 (Rochester, NY). All blots were re-blotted with anti-glyceraldehyde-3-phosphate dehydrogenase (GAPDH, AnaSpec, San Jose, CA) to normalize for gel-loading variability.

**Bead array assay**
The content of TNF-α, IL-6, IL-1β, IL-10 and phosphorylated and total p53 and IGF-IR were measured by using a bead array assay (Merck Millipore, Darmstadt, Germany) as previously described (Khan et al., 2004). Briefly, beads conjugated to antibody and lysates (50 µl each) were incubated for 18 h at 25°C, washed and incubated with biotin-conjugated antibody (25 µl) for 30 min. Then the beads were incubated with 50 µl streptavidin conjugated to phycoerythrin (PE) (streptavidin-PE, diluted 1:100) for 30 min. Fluorescence was analyzed using a Bio-Plex suspension array system 200 (Bio-Rad Laboratories). Raw data [mean fluorescence intensity (MFI)] were analyzed using the Bio-Plex Manager software 4.1 (Bio-Rad Laboratories). For caspase-3 determination, 100 µg of protein and beads were incubated at 700 rpm for 2 h at 25°C, washed and posterior incubations performed for 1 h.

**RNA purification**
Total RNA was extracted following the instructions of TriReagent (Invitrogen, Carlsbad, CA). Briefly, each hypothalamus was homogenized in 1 ml of TriReagent and incubated for 5 min at room temperature (RT) to dissociate nucleoprotein complexes. Chloroform (0.2 ml) was added and samples were vortexed, incubated for 15 min at RT and then centrifuged at 12,000 g for 15 min at 4°C. The aqueous phase was transferred to new tubes and isopropanol (0.5 ml) was added to precipitate RNA. Samples were incubated for 10 min at RT and then centrifuged at 12,000 g for 10 min at 4°C. Pellets were washed in 75% ethanol (1 ml), centrifuged at 7500 g for 5 min at 4°C, and dissolved in RNase-free water. Absorbance at 260 nm was measured to determine concentrations.

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**Fig. 7. Graphical summary.** Diagram representing the mechanism proposed for activation of cell death in astrocytes of diabetic IRS2−/− (D IRS2−/−) mice in the hypothalamus (A) or inhibition of cell death in the hypothalamic astrocytes of non-diabetic IRS2−/− (ND IRS2−/−) mice in the hypothalamus (B).
Reverse transcription (RT) and real-time RT-PCR
The reverse transcription reaction was performed on 2 μg of total RNA using the high-capacity cDNA kit (Applied Biosystems, Foster City, CA). Real-time RT-PCR was performed in an ABI Prism 7000 Sequence Detection System (Applied Biosystems). Nfkbia mRNA levels were measured using the TaqMan gene expression assay (Mm00477798_m1; Applied Biosystems). The PCR mixture contained 300 nM of each primer. Relative gene expression comparisons were carried out using an invariant endogenous control (GAPDH). Nox4 mRNA levels were measured with SYBR Green (Roche, Mannheim, Germany), with primers purchased from Sigma. The forward and reverse sequences were the following: 5’-AGCTCTATTCGCCACAG-3’ and 5’-CGGAGTTCCATACATTGAGG-3’. The PCR mixture contained 300 nM of each primer. Relative gene expression comparisons were carried out using an invariant endogenous control (GAPDH: 4352339E). According to the manufacturer’s guidelines, the ΔΔCT method was used for relative quantification.

Immunoenzymometric assay (IEA) for determination of IGF-I in serum
The quantitative determination of serum IGF-I was performed with the OCTEIA immunoenzymometric assay from IDS, Immunodiagnostics Systems Limited (Boldon, Tyne and Wear, UK). The method was performed according to the manufacturer’s instructions. Briefly, serum samples were incubated with a reagent to inactivate binding proteins (10 min) and then diluted for assay. Samples were added to antibody-coated wells for 2 h, at RT on a shaking platform. The wells were washed and horseradish peroxidase was added (30 min, RT); after washing, a solution of tetra-methyl-benzidine was added to develop colour (30 min, RT). The reaction was stopped and the absorbance read (450 nm; reference 650 nm) in a microtiter plate reader (Tecan Infinite M200, Grödig, Austria), with colour intensity being directly proportional to the amount of rat IGF-I present in the sample. This assay has a sensitivity limit of 63 ng/ml. The intra- and inter-assay coefficients of variation were 4.3% and 6.3%, respectively.

Cell death detection ELISA
This assay was carried out according to the manufacturer’s instructions (Roche). Briefly, tissue was homogenized in incubation buffer and microtiter plates were coated with anti-histone antibody. The samples were added (in duplicate) and incubated (90 min, RT). The wells were then washed and incubated with anti-DNA-peroxidase (90 min, RT). After washing, substrate solution was added until the colour developed adequately (approximately 15 min). The samples were measured at 405 nm on an automatic microplate analyzer (Tecan Infinite M200, Grödig, Austria). Background measurements at 490 nm were made and this value subtracted from the mean value of each sample.

TUNEL plus immunohistochemistry
Cell death detection by TUNEL assay was performed following the manufacturer’s instructions (Roche). Briefly, after fixation in 4% paraformaldehyde in 0.1 M phosphate buffer (pH 7.4), cryostat brain sections (20 μM) were washed three times in phosphate buffer and incubated for 30 min with 0.1% sodium citrate, 0.1% Triton X-100 solution to increase tissue permeability. Slides were again washed, and incubated with TUNEL solution for 90 min at 37°C in a humid chamber in the dark. After washing, the slides were incubated with an anti-GFAP antibody (1:2000), in TBS containing 5% BSA and 1% Triton X-100 and left for 48 h at 4°C. The slides were incubated with Alexa Fluor anti-fluorescin-488 and -633-conjugated goat anti-mouse IgG (1:2000; Molecular Probes, Eugene, OR) in blocking buffer, both at a dilution of 1:1000. Finally, after washing, the slides were mounted in Clear Mount (Electronic Microscopy Sciences, Hatfield, PA). Immunofluorescence was visualized directly by using a DM IRB confocal microscope (Leica, Wetzlar, Germany).

Immunofluorescence
Double-immunofluorescence for GFAP and active caspase-8 (Novus Biologicals Europe, Cambridge, UK) or NeuN (Merck Millipore) and active caspase-8 were carried out on sections (30 μm) obtained on a vibratome. Sections were blocked in phosphate buffer 0.1 M pH 7.4 containing 3% BSA, 1% Triton X-100 for 24 h at 4°C. Afterwards, sections were incubated with anti-GFAP (1:500) or anti-NeuN (1:500) and anti-active caspase-8 (1:500) diluted in blocking buffer for 48 h at 4°C. Sections were then washed with phosphate buffer (PB) with 0.1% Triton X-100 and incubated for 90 min at RT with anti-rabbit IgG-biotin (1:1000; Thermo Scientific) diluted in blocking buffer, washed and incubated with streptavidin Alexa Fluor 488 (1:1000, Molecular Probes) and Alexa Fluor 633 anti-mouse IgG (1:1000) for 90 min at RT. After washing, sections were cover-slipped with Clear Mount. Immunofluorescence was visualized directly by using a DM IRB confocal microscope.

Statistical analysis
All results are presented as mean±s.e.m. Statistical analysis of all data was carried out by one-way ANOVA followed by a Bonferroni’s test. The values were considered significantly different when the P-value was less than 0.05. Statistical analyses were performed using Prisma software 4.0 (Prisma, GraphPad, San Diego, CA).

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Competing interests
The authors declare no competing or financial interests.

Author contributions

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