Insulin enhances gene expression of Midnolin, a novel genetic risk factor for Parkinson’s disease, via ERK, PI3-kinase and multiple transcription factors in SH-SY5Y cells

Naoki Sagehashi¹, Yutaro Obara¹*, Ohki Maruyama¹, Tadashi Nakagawa², Toru Hosoi², Kuniaki Ishii¹

¹Department of Pharmacology, Yamagata University School of Medicine, Iida-Nishi 2-2-2, Yamagata 990-9585, Japan
²Department of Clinical Pharmacology, Faculty of Pharmaceutical Sciences, Sanyo-Onoda City University, Daigaku-Dori 1-1-1, Sanyo Onoda, 756-0884, Japan.
a) Running title: Insulin regulates gene expression of Midnolin.

b) Correspondence should be addressed to: Yutaro Obara, Ph.D.

Department of Pharmacology, Yamagata University School of Medicine, Iida-Nishi 2-2-2, Yamagata 990-9585, Japan.

Phone: +81-23-628-5233; FAX: +81-23-628-5235; E-mail: obaray@med.id.yamagata-u.ac.jp

c) Text: 30 pages.

Table: 0
Figures: 9
References: 46
Abstract: 247 words
Introduction: 620 words
Discussion: 1310 words
Supplementary figure: 8
Supplementary Tables: 4

d) Abbreviations:

AP-1, activator protein 1; ATF, activating transcription factor; ATRA, all-trans retinoic acid; BDNF, brain-derived neurotrophic factor; ChIP, chromatin immunoprecipitation; CREB, cAMP response element-binding protein; EGF, epidermal growth factor; ERK, extracellular-signal regulated kinase; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GIGYF2, Grb10-interacting GYF protein 2; IGF, insulin-like growth factor; MIDN, midnolin; NGF, nerve growth factor; ODN, oligodeoxynucleotide; PC12, pheochromocytoma; PD, Parkinson’s disease; RT-qPCR, reverse transcription-quantitative polymerase chain reaction; TBST, Tris-buffered saline containing 0.1% tween-20; TFAP2, transcription factor AP-2; TSS, transcription start site.
e) Recommended section: Cellular and Molecular
Abstract

Parkinson’s disease (PD) is the second most common neurodegenerative disease. Although many monogenic variants have been identified that cause familial PD, most cases are sporadic and the mechanisms of sporadic PD onset remain unclear. We previously identified Midnolin (MIDN) as a novel genetic risk factor for PD in Japanese population. MIDN copy number loss was strongly associated with sporadic PD, which was replicated in British population. Furthermore, suppression of MIDN expression in rat PC12 cells inhibits neurite outgrowth and expression of Parkin ubiquitin ligase. However, the detailed molecular mechanisms of MIDN expression are unknown. We, therefore, investigated the molecular mechanism of MIDN expression in human neuroblastoma SH-SY5Y cells. We found that MIDN expression was promoted by insulin via extracellular-signal regulated kinase (ERK)1/2 and PI3-kinase-dependent pathways. In addition, MIDN promoter activity was enhanced by mutations at transcription factor AP-2 consensus sequences and reduced by mutations at cAMP response element-binding protein (CREB) and activator protein 1 (AP-1) consensus sequences. The dominant-negative CREB mutant did not block MIDN promoter activity, but both the pharmacological inhibitor and decoy oligodeoxynucleotide for AP-1 significantly blocked its activity. Additionally, DNA binding of c-FOS and c-JUN to the AP-1 consensus sequence in the MIDN promoter was enhanced by insulin as determined by chromatin immunoprecipitation, which suggested that AP-1 positively regulated MIDN expression. Taken together, this study reveals molecular mechanisms of MIDN gene expression induced by insulin in neuronal cells, and drugs which promote MIDN expression may have potential to be a novel medicine for PD.

Significance Statement:

We demonstrated that insulin promotes MIDN expression via ERK1/2 and PI3-kinase pathways. Furthermore, we identified the important region of the MIDN promoter and showed that transcription factors, including AP-1, positively regulate MIDN expression, whereas TFAP2
negatively regulates basal and insulin-induced *MIDN* expression. We believe that our observations are important and that they contribute to the development of novel drugs to treat Parkinson’s disease.

**Keywords:** Midnolin (MIDN), Parkinson’s disease, extracellular-signal regulated kinase (ERK), PI3-kinase, SH-SY5Y cells, insulin, AP-1, TFAP (AP-2)
Introduction

Parkinson’s disease (PD) is the second most common neurodegenerative disease after Alzheimer’s disease. PD prevalence increases with age and it affects more than 1% of the population over the age of 60 (Lill, 2016). Typical symptoms include resting tremor, bradykinesia, rigidity, and postural instability, and loss of dopaminergic neurons projecting from the substantia nigra in the midbrain to the striatum is pathologically observed. Approximately 10% of PD cases are familial and many monogenic variants and genetic risk factors have been identified, including SNCA, PRKN, LRRK2, and GBA (Lill, 2016; Scott et al., 2017; Billingsley et al., 2018; Smolders and Van Broeckhoven, 2020). The remaining cases are sporadic and it is assumed that diverse genetic, epigenetic and environmental factors interact in a complex manner to affect disease risk and progression; however, the mechanisms of sporadic PD onset remain unclear.

Midbrain nucleolar protein (Midnolin or MIDN) was discovered in embryonic stem cells by a gene trap method in 2000 (Tsukahara et al., 2000). Midn was named after its specific expression pattern in the midbrain of embryonic (E)12.5 mouse embryos and the intracellular localization of MIDN in the nucleus and nucleolus. A ubiquitin-like domain and a nucleolar localizing sequence are adjacent to the amino and carboxy termini, respectively (Tsukahara et al., 2000). Although MIDN is abundant in the midbrain at early developmental stages, in the adult mouse it is also widely observed in other organs, including heart, spleen, lung, liver, skeletal muscles, kidney, and testis (Tsukahara et al., 2000). The physiological roles of MIDN were unclear for a long time, but in 2013 its ubiquitin-like domain was shown to interact with glucokinase (Hofmeister-Brix et al., 2013). MIDN inhibits glucokinase activity in vitro and glucose-induced insulin secretion from MIN6 cells. Meanwhile, exome analysis of Caucasian girls with autism spectrum disorder revealed many potential genetic variants, one of which was in MIDN (Butler et al., 2015), while array-based analyses showed duplications in 19p13.3, a region including MIDN and other genes that is associated with male infertility (Singh et al.,
Molecular epidemiological analyses show *MIDN* to be a novel genetic risk factor for sporadic PD. *MIDN* copy number loss (deletion) was significantly associated with sporadic PD in a Japanese cohort and this association was replicated in a large-scale British cohort (Obara et al., 2017; Obara et al., 2019). In Yamagata prefecture in northeast Japan, *MIDN* loss was observed in 10.5% of patients with sporadic PD whereas *MIDN* loss was not observed at all in healthy people. In Britain, *MIDN* loss was similarly observed in 6.55% of patients with sporadic PD and in 1.64% of a general population. This frequency (6.55%–10.5%) is large compared with those of other causal variants, which are usually very small (< 0.5%). In rat pheochromocytoma (PC12 cells), *MIDN* expression was enhanced by nerve growth factor (NGF). In addition, NGF-induced neurite outgrowth and expression of Parkin ubiquitin ligase were substantially inhibited by suppression of *MIDN* expression using genome-editing or RNA interference approaches (Obara et al., 2017; Obara and Ishii, 2018). Although typical DNA-binding or transcription-activating domains have not been identified in the MIDN protein, MIDN affects the transcription levels of a number of genes, including PD-related genes (Obara and Ishii, 2018), indicating that MIDN functions as a transcription modulator. Thus, we believe that *MIDN* loss is associated with PD although this is controversial (Billingsley et al., 2020; Obara et al., 2020).

*MIDN* expression in response to NGF is accompanied by the activation of extracellular signal-regulated kinase (ERK) 1/2 and ERK5 in PC12 cells (Obara et al., 2017). However, the detailed molecular mechanisms, particularly the *cis*-elements and transcription factors responsible for *MIDN* expression, are unknown. In this study, we therefore investigated the molecular mechanism of *MIDN* expression in human neuroblastoma SH-SY5Y cells.

**Materials and Methods**

**Materials**
Recombinant human insulin, all-trans retinoic acid and wortmannin were purchased from Wako Pure Chemicals (Osaka, Japan). Brain-derived neurotrophic factor (BDNF) was purchased from Sigma-Aldrich (St. Louis, MO). Luciferin was purchased from AAT Bioquest (Sunnyvale, CA). SR11302 was purchased from Cayman Chemical (Ann Arbor, MI). U0126, primary antibodies against phospho-Akt (S473) (#9271), phospho-ERK1/2 (T202/Y204) (#9101), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (#3683), transcription factor AP-2β (TFAP2B) (#2509), phospho-cAMP response element-binding protein (CREB) (S133) (#9198), CREB (#9197) and c-FOS (#2250), and horseradish peroxidase-conjugated secondary antibody against rabbit IgG (#7074), were purchased from Cell Signaling Technology (Beverly, MA). Anti-ERK2 antibody (#sc-154) was purchased from Santa Cruz Biotechnology (Santa Cruz, CA). A synthetic double-stranded decoy oligodeoxynucleotide (ODN) was obtained from Fasmac (Atsugi, Japan). The decoy ODN was generated by annealing equimolar amounts of single-stranded sense and antisense phosphorothioate-modified ODNs that contained an AP-1-binding sequence (Moriyama et al., 2008). A scrambled double-stranded ODN was also generated and used as a control for the AP-1 decoy ODN. The phosphorothioate ODN used in this study was as follows: scrambled ODN (5′-TGT CTC TCT GAT GTC-3′ and 5′-GAC ATG AGA GAG ACA-3′) and decoy ODN for AP-1 (5′-TGT CTG ACT CAT GTC-3′ and 5′-GAC ATG AGT CAG ACA-3′) (AP-1 consensus sequences are underlined).

**Cell culture**

Human neuroblastoma cells (SH-SY5Y cells) were kindly provided by Dr. Takeo Kato (Yamagata University, Japan) and grown in Dulbecco’s modified Eagle’s medium supplemented with 10% foetal bovine serum, penicillin (50 units/ml) and streptomycin (50 μg/ml) in a 5% CO₂ incubator at 37°C. Differentiation of the cells was induced by adding all-trans retinoic acid (10 μM) and incubating for 5 days as described above. For measurement of gene expression and protein phosphorylation levels, cells were incubated in serum-free
medium before insulin and other drug stimulation.

**DNA constructs**

The human *MIDN* promoter (-600 bp~+125 bp) was amplified from genomic DNA of SH-SY5Y cells using a primer set (5′-CCC GCT AGC GCA TCC CCT CAC CAC ACT CCC-3′ and 5′-CCC CTC GAG CCC CCT CCA CAC TCA CCG-3′) and PrimeStar MAX (Takara, Tokyo, Japan), and inserted between the NheI and XhoI sites of the pGL3-basic luciferase vector (Promega, Madison, WI). Deletion or variations were created by *in vitro* mutagenesis reactions using PrimeStar MAX. DNA plasmids encoding *TFAP2B* or its dominant-negative mutant (R225C) were kindly provided by Dr. Satoshi Maegawa (Shiga University of Medical Science, Japan) (Fuke et al., 2010). A plasmid encoding β-actin promoter-driven β-galactosidase was a kind gift from Dr. Philip Stork (Vollum Institute, Oregon Health Sciences University, OR). Plasmids that encoded *CREB* or its dominant-negative mutant (S133A) were a kind gift from Dr. Takeo Saneyoshi (Kyoto University, Japan).

**Western blotting**

Cells were lysed in Laemmli buffer and proteins were separated on 11% polyacrylamide gels by electrophoresis. Then, the proteins were transferred to polyvinylidene difluoride membranes (GE healthcare, Buckinghamshire, UK) using a semi-dry method. After blocking membranes with 5% skimmed milk, they were incubated with primary antibodies (1:1000 dilution). The membranes were washed three times and incubated with secondary antibody (1:5000 dilution). After rinsing the membranes, they were developed using an enhanced chemiluminescence kit (PerkinElmer, Waltham, MA or GE healthcare), and visualized with a ChemiDoc XRS imaging system (BioRad, Hercules, CA). The relative band intensities were analysed using Image-J densitometry software (National Institute of Health, Bethesda, MD). The sample number for Western blotting was three for all cases. Quantitative data are shown in supplementary figures.
Luciferase assay

SH-SY5Y cells were seeded into 24-well plates at 1 x 10^5 cells/well. Plasmids encoding the MIDN promoter linked to the firefly luciferase and β-actin-driven β-galactosidase genes, were co-transfected into cells using Lipofectamine 2000 (Invitrogen, Grand Island, NY). After culture for 2 days, the cells were incubated in the presence or absence of insulin (1 μM) overnight. The cells were lysed and luciferase activity was measured using a GloMax20/20 luminometer (Promega) as described previously (Honda et al., 2015). As an internal control, β-actin promoter-driven β-galactosidase activity was measured to normalize for transfection efficiency as described previously (Honda et al., 2015).

Reverse transcription-quantitative polymerase chain reaction (RT-qPCR)

Total RNA from SH-SY5Y cells was extracted using TriPure isolation reagent (Roche, Indianapolis, IN) according to the manufacturer’s protocol. The RNA was then reverse transcribed using an RT-PCR kit (Toyobo, Osaka, Japan), and real-time PCR was performed using FastStart Essential DNA Green Master for real-time PCR and a LightCycler Nano thermal cycler (Roche), as described previously (Kashino et al., 2018). The PCR primers used were as follows: MIDN (5′-GAG CAG ATG GAC TGC TCC CC-3′ and 5′-ACA AAG CTC TCG ATG ACG GC-3′), c-FOS (5′-CAG ACT ACG AGG CGT CAT CC-3′ and 5′-AGT TGG TCT GTC TGC TCC GCT TG-3′), and GAPDH (5′-ACC ACA GTC CAT GCC ATC AC-3′ and 5′-TCC ACC ACC CTG TTG CTG TA-3′). PCR products were quantified and normalized to the GAPDH control before presentation as a fold change.

Chromatin immunoprecipitation (ChIP) analysis

ChIP assays were performed as described previously (Nakagawa et al., 2020) with some modifications. Briefly, ten million SH-SY5Y cells were fixed and centrifuged. The cell pellets
were suspended in nuclear extraction buffer, and centrifuged again. The resulting pellets were suspended in Buf NUC solution, mixed with CaCl₂, and digested with micrococcal nuclease (New England Biolabs, M0247S). After the addition of 2 x sonication buffer to stop the reaction, the sample was centrifuged, and the supernatants were incubated with 6 μg antibodies [IgG control (MBL, PM035), anti-c-JUN (Cell Signaling Technology, 9165) or anti-c-FOS (Cell Signaling Technology, 2250) antibody] conjugated to magnetic beads (Thermo Fisher, DB10004). Bead-bound proteins were washed with buffer A, buffer B, buffer C, TE buffer, and the samples were then eluted by RNase A, proteinase K, and NaCl. After incubation with proteinase K again, DNA was purified with AMPure XP beads, eluted with TE buffer, and subjected to real-time PCR analysis with the use of Fast SYBR™ Green Master Mix (Thermo Fisher, 4385612). The primers for amplification of the MIDN promoter were 5’-TGG CTC GGG GCA TTC AAG-3’ and 5’-TTT ATC CGC GCC GCC TTC-3’ and those of MIDN intron 1 were 5’-CGG CTT TTC CCG GAC GAA-3’ and 5’-ACG GGT CTG GTA CCC CTC-3’.

Statistics

Data are expressed as the mean ± S.E.M, and the statistical significance of the differences was analysed using Student’s T-test (Fig. 8E) or one-way ANOVA with post hoc Tukey’s test (Figs. 2C, 3A, 4A, 4B, 8A, 8C, 8D, S4, S5, S7 and S8) or Dunnett’s test (Figs. 1A, 1B, 2A, 5B, 5C, 6A, 7B, S1, S2, S3, and S6) for multiple comparisons. StatView software (ver5.0) (SAS institute Inc., Tokyo, Japan) was used for statistical analysis.

Results

**Insulin enhances MIDN gene expression in SH-SY5Y cells.** Human neuroblastoma SH-SY5Y cells were incubated with insulin (1 μM) or BDNF (30 or 50 ng/ml) for 2 h, and MIDN expression levels were examined by RT-qPCR (Fig. 1A). MIDN expression was significantly enhanced by insulin, but not by BDNF. Next, we subcloned the human MIDN promoter region
either side of the transcription start site (TSS) (-650→+125 bp) into pGL3, which encodes a promoter-less firefly luciferase. In SH-SY5Y cells transfected with this DNA construct, the luciferase gene is efficiently expressed when the MIDN promoter is activated by a stimulant. We measured the human MIDN promoter activity in response to insulin (1 nM to 1 μM) and found it to be significantly increased in a concentration-dependent manner (Fig. 1B). To examine the signalling pathways activated by insulin, phosphorylation levels of ERK1/2 and Akt were examined as indices of activation of ERK1/2 and PI3-kinase, respectively. Insulin promoted phosphorylation of both ERK1/2 and Akt, but BDNF failed to cause the phosphorylation of Akt or ERK1/2 (Figs. 1C and 1D and Supplementary Figs. S1 and S2). SH-SY5Y cells express the BDNF TrkB receptor and acquire sensitivity to BDNF during neuronal differentiation by retinoic acid (Sakane and Shidoji, 2011; Shiohira et al., 2012); therefore, the cells were incubated with retinoic acid (10 μM) for 5 days and were then stimulated with BDNF (50 ng/ml) or insulin (1 μM) for 1 or 2 h. BDNF, in addition to insulin, significantly enhanced MIDN expression in these differentiated cells (Fig. 2A). BDNF (30 or 50 ng/ml) treatment for 5 min also caused phosphorylation of both ERK1/2 and Akt (Fig. 2B and Supplementary Fig. S3), confirming that the TrkB receptor tyrosine kinase was activated by BDNF in the differentiated cells. When MIDN expression was compared between undifferentiated and differentiated cells under the same conditions, MIDN expression in differentiated cells was significantly higher than that in undifferentiated cells, although insulin increased MIDN expression levels to a similar extent regardless of differentiation states (Fig. 2C). Phosphorylation of ERK1/2 and Akt was related to MIDN expression levels (Fig. 2D and Supplementary Fig. S4). However, because the effect of insulin was more potent than that of BDNF and obvious in both undifferentiated and differentiated cells, we focused on insulin signalling that led to MIDN expression in undifferentiated cells. SH-SY5Y cells were pre-incubated in the presence or absence of a MEK inhibitor, U0126 (30 μM), or a PI3-kinase inhibitor, wortmannin (500 nM), for 30 min, then stimulated with insulin (1 μM) for 2 h.
RT-qPCR analysis showed that insulin increased *MIDN* expression, which was largely blocked by U0126 or wortmannin and was completely suppressed by the combination of U0126 and wortmannin (Fig. 3A). Inhibition of PI3-kinase and ERK1/2 by these inhibitors was confirmed by Western blotting (Fig. 3B and Supplementary Fig. S5). These data indicate that insulin promotes *MIDN* expression accompanied by the activation of ERK1/2 and PI3-kinase in SH-SY5Y cells.

**Transcription factors, including TFAP2 and AP-1, regulate human MIDN promoter activity in SH-SY5Y cells.** To examine the insulin signalling pathway involved in increased *MIDN* expression in more detail, we measured *MIDN* promoter activity using reporter plasmids encoding various length of the *MIDN* promoter (-600, -450, -300, -150, -100 and -50 bp to +125 bp). We found a region that negatively regulates promoter activity between -150 bp and -100 bp and a region that positively regulates its activity between -100 and -50 bp (Fig. 4A). This was also observed after insulin stimulation (Fig. 4B), suggesting that multiple transcription factors are involved in *MIDN* expression.

*In silico* analysis of the JASPAR2020 database (Fornes et al., 2020), identified TFAP2 consensus sequences between -121 bp and -99 bp upstream of the TSS (5'-AGC CGT CAA GGC GCC CCA GGG CC-3'). The highest TFAP2 family member binding affinity scores were 12.9646 for TFAP2A, 12.2031 for TFAP2B and 12.6803 for TFAP2C, indicating that the sequence in this region of the *MIDN* promoter is highly similar to the consensus sequence for all TFAP2 isoforms (Table S1). We also discovered the consensus sequence for activator protein 1 (AP-1) and for the CREB/Activating transcription factor (ATF) family in the promoter region between -71 bp and -57 bp (5'-GTC TGC GTC ACC GCC-3') (Table S2–S4). The highest scores for binding affinity with these transcription factors were 10.5189 for FOSL1/JUN, 10.9754 for ATF1 and 11.1485 for CREB1. Furthermore, there is a region between these sites putatively recognized by various other transcription factors including KLF, SP, and EGR family
members. To identify the specific cis-elements involved in MIDN expression, the putative binding sequences for these transcription factors were mutated as indicated in Fig. 5A. Both basal and insulin (1 µM)-stimulated MIDN promoter activity was significantly enhanced by mutations at TFAP2 consensus sites (Mut 1 and 2) and also by mutations 3 and 4 (Fig. 5B). In contrast, basal and insulin (1 µM)-stimulated MIDN promoter activity was significantly reduced by the mutation at the CREB/ATF family and AP-1 family consensus sites (Mut 5) (Fig. 5C).

Because TFAP2 was suggested to be involved in regulation of MIDN expression, wild-type TFAP2B and its dominant-negative mutant (R225C) were overexpressed in SH-SY5Y cells and MIDN promoter activity (-150→+125) was measured. This dominant-negative mutant lacks DNA-binding ability (Fuke et al., 2010). Although overexpression of TFAP2 did not reduce the promoter activity, its dominant-negative mutant promoted promoter activity (Fig. 6A), indicating that TFAP2B negatively regulates MIDN expression. Overexpression of TFAP2B and TFAP2B R225C was confirmed by Western blotting (Fig. 6B and Supplementary Fig. S6).

To investigate the activity and involvement of CREB in MIDN expression, phosphorylation levels of CREB and ATF1 were also examined by Western blotting as an index of activation. This phoso-specific CREB antibody used also recognizes phospho-ATF1 (S63), but only phosphorylation of CREB was enhanced by insulin (1 µM); there was no conclusive phosphorylated ATF1 band (Fig. 7A). Densitometric analysis showed that U0126 (30 µM) blocked this CREB phosphorylation by 50.0% (n=3, p<0.05), while wortmannin (500 nM) only reduced it by 17.3% (n=3, p>0.05), indicating that insulin activates CREB, which was accompanied mainly by ERK1/2 signalling (Supplementary Fig. S7). Additionally, a dominant-negative mutant of CREB S133A, which lacked its phosphorylation sites at Ser133, was overexpressed in cells stimulated with insulin (1 µM). However, the MIDN promoter was not inhibited by the CREB S133A mutant (Fig. 7B).

Next, to investigate the activity and involvement of AP-1 in MIDN expression, mRNA and protein expression levels of c-FOS were measured by RT-qPCR and Western blotting,
respectively, as an index of AP-1 transcriptional activity. Insulin (1 µM) significantly enhanced c-FOS mRNA expression, which was significantly reversed by U0126 (30 µM), but not wortmannin (500 nM), which suggested that the ERK1/2 pathway was involved in c-FOS induction (Fig. 8A). c-FOS protein was also induced by insulin treatment (1 µM) for 2 h, which was completely inhibited by U0126 (30 µM) and partially, but significantly, inhibited by wortmannin (500 nM) (Fig. 8B and Supplementary Fig. S8). To examine the involvement of AP-1 in MIDN expression, the decoy ODN (2 µg/well) for AP-1 was cotransfected with reporter genes into cells that were stimulated with insulin (1 µM). As a result, the decoy ODN for AP-1 completely inhibited the insulin (1 µM)-induced MIDN promoter activation (Fig. 8C). To confirm the roles of AP-1, we used a pharmacological inhibitor, SR11302, which is a synthetic retinoid derivative that inhibits AP-1 activity without activating retinoid response elements (Li et al., 1997). SR11302 (30 µM) significantly inhibited the MIDN promoter activation induced by insulin (Fig. 8D). Finally, a ChIP assay was performed using c-FOS and c-JUN antibodies to confirm that AP-1 bound to its consensus sequence (-71 to -57 bp) in the MIDN promoter and identify the AP-1 isoforms involved in this case (Fig. 8E). As expected, insulin (1 µM) significantly promoted DNA binding of both c-FOS and c-JUN to its predicted corresponding sequence, but not to intron 1 (+840 to +969 bp) as a negative control sequence. Taken together, these results suggest that AP-1 rather than CREB is involved in insulin-induced MIDN expression, although CREB is also activated by insulin in an ERK1/2-dependent manner.

Discussion

In this study, we found that insulin promoted MIDN expression in human neuroblastoma cells via ERK1/2 and PI3-kinase-dependent pathways. In addition, the MIDN promoter was regulated in multiple ways by various transcription factors. AP-1 enhance whereas TFAP2 suppresses MIDN expression. These signalling pathways are depicted in Fig. 9.
Although insulin generally modulates peripheral glucose metabolism, it is efficiently transported into the brain through its specific mechanism to cross the blood brain barrier (Ghasemi et al., 2013; Gray and Barrett, 2018). Insulin transcripts have been detected in GABAergic neurogliaform cells in the cortex, which act in cortical microcircuits (Molnar et al., 2014), and in the rat hippocampus (Nemoto et al., 2014). Furthermore, insulin-like growth factor (IGF) 1/2, which interacts with insulin receptors, is biosynthesized in glial cells. Insulin receptor is abundantly expressed in the central nervous system, especially in post-synaptic neurons (Wada et al., 2005), which suggests that central insulin regulates behaviour and cognitive functions other than glucose homeostasis (Zhao and Alkon, 2001). Moreover, dysfunction in insulin signalling is associated with neurodegenerative diseases (Moroo et al., 1994; Craft and Watson, 2004; Trejo et al., 2004). Remarkably, Grb10-interacting GYF protein 2 (GIGYF2) interacts with insulin and IGF receptors through Grb10, and mutations in the GIGYF2 gene within the Park11 locus have been associated with PD (Lautier et al., 2008; Blauwendraat et al., 2020). Gigyf2 knockout mice exhibit motor dysfunction and α-synuclein-positive plaques, which implies that abnormal insulin signalling is associated with PD (Giovannone et al., 2009).

Although the relationship between PD and diabetes mellitus has been controversial, the shared biological mechanisms and positive clinical and epidemiological association between type2 diabetes and PD are currently an interesting hypothesis (Sánchez-Gómez et al., 2020; 2021). Whereas certain oral anti-diabetic drugs, which include pioglitazone and metformin, have not had a significant benefit in clinical trials, daily intranasal administration of insulin improved motor impairment and had a positive effect on cognitive functions (Novak et al., 2019). Furthermore, exenatide, an agonist of the glucagon-like peptide-1 receptor, exerted a positive effect on practically defined off-medication motor scores in a clinical trial for PD patients, although the effect of exenatide on pathophysiology and long-lasting symptomatic improvement remains unclear (Athauda et al., 2017; 2019). The relevance of PD to diabetes and
the effectiveness of anti-diabetic drugs on PD should be clarified in both in vitro and in vivo/clinical studies.

We previously showed that MIDN expression was enhanced by NGF, but not by epidermal growth factor (EGF) or basic fibroblast growth factor in PC12 cells (Obara et al., 2017). In addition, the NGF-induced MIDN expression was both ERK1/2 and ERK5-dependent. In this study, insulin enhanced MIDN expression in SH-SY5Y cells accompanied by activation of ERK1/2 and PI3-kinase (Figs. 1 and 3). MIDN expression was also enhanced by BDNF in cells differentiated by retinoic acid and in which TrkB receptor was induced (Sakane and Shidoji, 2011; Shiohira et al., 2012) (Fig. 2). The majority of neurotrophic factors and growth factors activate both ERKs and PI3-kinase in a similar manner through their specific receptor tyrosine kinases. However, there are differences in the intracellular signalling that depend on the growth factors and cell type. For example, NGF causes sustained ERK1/2 activation via the small G-proteins, Ras and Rap1, whereas this activation is only transient and Ras-dependent in case of EGF in PC12 cells (York et al., 1998; Obara et al., 2004). This difference affects cell fate; NGF induces neuronal differentiation and EGF promotes proliferation. The reason why only certain neurotrophic factors or growth factors affect MIDN expression remains unknown, but it is suggested that NGF or insulin-specific signalling pathways in addition to those involving ERKs and PI3-kinase may be responsible for MIDN expression. Because growth/neurotrophic factors, including insulin, BDNF and glial cell-derived neurotrophic factor, have neurotrophic effects and clinical potential for the treatment of PD (Allen et al., 2013; Shaughness et al., 2020), it is important to examine whether they induce MIDN expression, particularly in vivo.

By MIDN promoter analysis, we found that TFAP2 negatively regulated MIDN expression. Deleting or mutating the TFAP2 consensus sequence between -121 bp and -99 bp upstream of the TSS (5’-AGC CGT CAA GGC GCC CCA GGG CC-3’) increased promoter activity (Figs. 4 and 5, Table S1). In addition, the promoter activity was promoted by overexpression of a dominant-negative TFAP2B mutant that lacks DNA binding activity (Fig. 6A). However,
overexpression of wild-type TFAP2B did not cause a significant reduction of promoter activity. SH-SY5Y cells express TFAP2B (Fig. 6B), which may be sufficient for negative regulation of the *MIDN* promoter. Generally, TFAP2 forms homo- or hetero-dimers with other TFAP2 family members, and functions as both an activator and repressor of gene transcription. TFAP2B mediates retinoic acid-induced noradrenergic neuronal differentiation in neuroblastoma, including SH-SY5Y cells (Ikram et al., 2016). In our study, TFAP2 suppressed *MIDN* gene expression in SH-SY5Y cells, but the physiological significance of this remains unknown. It is necessary to clarify the molecular mechanism by which insulin regulates TFAP2 activity and how TFAP2 inhibits *MIDN* expression. We discovered that the promoter region between -71 bp and -57 bp (5′-GTC TGC GTC ACC GCC-3′), which contains consensus binding sequences for AP-1 and the CREB/ATF family (Table S2-S4), was required for *MIDN* expression. Furthermore, this sequence is conserved among mammals, which suggests universal roles in *MIDN* expression. We found that AP-1 activity, rather than CREB, was involved in *MIDN* expression as demonstrated by attenuation of *MIDN* promoter activity by both a pharmacological inhibitor (SR11302) and decoy ODN for AP-1, whereas the dominant-negative CREB S133A mutant did not decrease its promoter activity (Figs. 7 and 8). Additionally, insulin promoted DNA binding of both c-FOS and c-JUN isoforms to the predicted AP-1 consensus binding sequence (Fig. 8E), which suggested that both AP-1 isoforms are required for *MIDN* expression. AP-1 activity is regulated at multiple levels. For example, expression of AP-1 components is controlled by mRNA synthesis and stability as ERKs strongly stimulate AP-1 activity via *de novo* synthesis of c-FOS and c-JUN. Additionally, the DNA-binding ability and transactivating capacity of AP-1 are controlled by post-translational modifications, which include phosphorylation and ubiquitination as JUN N-terminal kinase phosphorylates c-JUN. In our study, insulin actually promoted c-FOS expression at mRNA and protein levels in an ERK1/2-dependent manner (Figs. 8A and 8B) and ERK1/2 was involved in *MIDN* expression induced by insulin (Fig. 3), indicating that the ERK1/2/AP-1 pathways are essential for *MIDN*
expression. Because c-FOS protein levels were partially, but significantly, reduced by a PI3-kinase inhibitor (Fig. 8B and Supplementary Fig S8), AP-1 activity was also regulated by the PI3-kinase pathway via a post-translational modification. Because inhibition of PI3-kinase and ERK1/2 suppressed MIDN expression to similar extents (Fig. 3), the PI3-kinase pathway is also required for MIDN expression although the down-stream signalling pathway is unclear. Both ERK1/2 and PI3-kinase are essential for neuronal differentiation and survival, and targeting these pathways has been proposed as a reasonable approach to suppress various neurodegenerative disorders (Markus et al., 2002; Obara et al., 2004; Rai et al., 2019). MIDN induced through ERK signalling is responsible for neurite outgrowth in PC12 cells (Obara et al., 2017); therefore, MIDN is assumed to be a key regulator in the maintenance of appropriate neuronal functions, and MIDN dysfunction can be a risk factor for the onset and progression of neurodegenerative disorders such as PD. Therefore, drugs that promote the MIDN expression may have potential to be a novel medicine for PD, which may be useful for not only patients who have MIDN copy number loss, but also for those who have the normal copy number.

In summary, we demonstrated that insulin promotes MIDN expression via ERK1/2 and PI3-kinase pathways. Furthermore, we identified the important region of the MIDN promoter and showed that transcription factors, including AP-1, positively regulate MIDN expression, whereas TFAP2 negatively regulates basal and insulin-induced MIDN expression. Identification of MIDN-binding partners and the clarification of MIDN roles in vivo are key future studies.

Acknowledgments

We thank Dr. Satoshi Maegawa (Shiga University of Medical Science, Japan) and Dr. Takeo Saneyoshi (Kyoto University, Japan) for providing the plasmids encoding TFAP2B and CREB mutant, respectively. We thank Ryoko Murakami, Yuki Miyano and Dr. Hidenori Sato (Yamagata University School of Medicine, Japan) for GC-rich DNA sequencing. We thank the JASPAR2020 database (http://jaspar.genereg.net) group members who provided the
transcription factor binding profiles. We thank Jeremy Allen, PhD, from Edanz Group (https://jp.edanz.com/ac) for editing a draft of this manuscript.

Author Contributions

Participated in research design: Obara, Hosoi, Ishii

Performed experiments: Sagehashi, Maruyama, Nakagawa

Performed data analysis: Sagehashi, Nakagawa

Wrote or contributed to the writing of the manuscript: Obara, Nakagawa, Ishii
References


Zhao WQ and Alkon DL (2001) Role of insulin and insulin receptor in learning and memory.
Molecular and cellular endocrinology 177:125-134.

Footnotes

This work was supported in part by Grants-in-Aid from the Japan Society for the Promotion of Science (18K06681 to Y.O), Takeda Science Foundation (Y.O), and Setsuro Fujii Memorial, the Osaka Foundation for Promotion of Fundamental Medical Research (Y.O). The funding sponsors had no role in the design of the study, in the collection, analyses or interpretation of the data, nor in the writing of the manuscript and in the decision to publish the results.

Conflict of interest

The authors declare that they have no conflicts of interest with the contents of this article.

Material availability

There is a restriction to share the DNA plasmids (TFAP2 WT and mutants). Please contact Dr. Satoshi Maegawa (Shiga University of Medical Science, Japan) for permission to obtain the DNA plasmids.
Figure legends

Figure 1: Insulin promotes *MIDN* expression in SH-SY5Y cells. (A) SH-SY5Y cells were stimulated with insulin (1 μM) or BDNF (30 or 50 ng/ml) for 2 h, then expression levels of *MIDN* were examined by RT-qPCR. Insulin significantly promoted *MIDN* expression (n=3–9, *p*<0.05). (B) SH-SY5Y cells were transfected with *MIDN* promoter (-600--+125 bp) linked to luciferase in a promoter-less plasmid (pGL3). After stimulation with insulin (1 nM to 1 μM), *MIDN* promoter activity was examined by measuring luciferase activity. Insulin significantly promoted *MIDN* promoter activity (n=3, *p*<0.05). (C) SH-SY5Y cells were stimulated with insulin (1 μM) for 5, 15, and 30 min, then phosphorylation of Akt and ERK1/2 was examined by Western blotting. (D) SH-SY5Y cells were stimulated with insulin (1 μM) or BDNF (30 or 50 ng/ml) for 5 min, then phosphorylation of Akt and ERK1/2 was examined by Western blotting.

Figure 2: BDNF and insulin promote *MIDN* expression in differentiated SH-SY5Y cells. (A) SH-SY5Y cells differentiated by all-trans retinoic acid (10 μM) for 5 days were stimulated with insulin (1 μM) or BDNF (50 ng/ml) for 1 or 2 h, then expression levels of *MIDN* were examined by RT-qPCR. Insulin and BDNF significantly promoted *MIDN* expression (n=3, *p*<0.05). (B) Differentiated SH-SY5Y cells were stimulated with insulin (1 μM) or BDNF (30 or 50 ng/ml) for 5 min, then phosphorylation of Akt and ERK1/2 was examined by Western blotting. (C) SH-SY5Y cells were incubated in the presence or absence of all-trans retinoic acid (ATRA) (10 μM) for 5 days and then stimulated with insulin (1 μM) for 2 h. Then, expression levels of *MIDN* were examined by RT-qPCR. *MIDN* expression in differentiated cells was significantly higher than that in undifferentiated cells (n=3, *p*<0.05). (D) Undifferentiated and differentiated SH-SY5Y cells were stimulated with insulin (1 μM) for 5 min and then phosphorylation of Akt and ERK1/2 was examined by Western blotting.
Figure 3: Insulin promotes MIDN expression via PI3-kinase and ERK1/2 in SH-SY5Y cells.  
(A) SH-SY5Y cells were pre-incubated with or without U0126 (U, 30 μM) or wortmannin (Wort, 500 nM) for 30 min, then stimulated with insulin (1 μM) for 2 h. Expression levels of MIDN were examined by RT-qPCR. Insulin significantly promoted MIDN expression (*p<0.05), which was significantly blocked by U0126 and wortmannin (n=3-6, #p<0.05). (B) SH-SY5Y cells were pre-incubated with or without U0126 (U, 30 μM) or wortmannin (Wort, 500 nM) for 30 min, then stimulated with insulin (1 μM) for 2 h. Phosphorylation of Akt and ERK1/2 was examined by Western blotting.

Figure 4: Insulin regulates MIDN promoter activity between -150 and -50 bp upstream of the transcription start site. (A) SH-SY5Y cells were transfected with different length MIDN promoters (-600, -450, -300, -150, -100 or -50 to +125 bp) linked to luciferase in a promoter-less plasmid (pGL3) and MIDN promoter activity was examined by measuring luciferase activity. MIDN promoter activity of the -100→+125 bp fragment was significantly enhanced compared with that of the -150→+125 bp fragment (n=6, *p<0.05). The activity of the -50→+125 bp fragment was significantly reduced compared with that of the -100→+125 bp fragment (n=6, #p<0.05). (B) SH-SY5Y cells were transfected with different length MIDN promoters (-150, -100 or -50 to +125 bp) linked to luciferase in a promoter-less plasmid (pGL3) and stimulated with insulin (1 μM). MIDN promoter activity was examined by measuring luciferase activity. MIDN promoter activity of the -100→+125 bp fragment was significantly enhanced compared with that of the -150→+125 bp fragment (n=3, *p<0.05) and the activity of the -50→+125 bp fragment was significantly reduced compared with that of the -100→+125 bp fragment (n=3, #p<0.05) in both the presence and absence of insulin.

Figure 5: cis-elements for TFAP2, AP-1 and CREB/ATF are involved in basal and
**insulin-induced MIDN expression. (A)** Depiction of mutated sites in the MIDN promoter between -150 and -50 bp. Putative binding sequences for various transcription factors were mutated as indicated (Mut 1–5). (B) SH-SY5Y cells were transfected with wild-type or mutated (Mut 1–4) MIDN promoter (-150~+125 bp) linked to luciferase in a promoter-less plasmid (pGL3), and stimulated with insulin (1 μM). MIDN promoter activity was examined by measuring luciferase activity. The mutated MIDN promoter activity was significantly enhanced compared with the wild-type promoter activity in both the presence and absence of insulin (n=3, *: #p<0.05). (C) SH-SY5Y cells were transfected with wild-type or mutated (Mut 5) MIDN promoter (-100 or -50 ~+125 bp) linked to luciferase in a promoter-less plasmid (pGL3), and stimulated with insulin (1 μM). MIDN promoter activity was examined by measuring luciferase activity. The activity of MIDN promoter (Mut 5 and -50~+125 bp) was significantly reduced compared with the wild-type promoter activity (-100~+125 bp) in both the presence and absence of insulin (n=6, *:*#p<0.05).

**Figure 6: A dominant-negative TFAP2B mutant enhanced MIDN promoter activity in SH-SY5Y cells.** (A) SH-SY5Y cells were co-transfected with wild-type MIDN promoter (-150~+125 bp) linked to luciferase in a promoter-less plasmid (pGL3) and empty vector (pcDNA3.1), wild-type TFAP2B (WT) or a dominant-negative TFAP2B mutant (R225C). MIDN promoter activity was examined by measuring luciferase activity. MIDN promoter activity was significantly enhanced by overexpression of TFAP2B R225C (n=6, *p<0.05). (B) SH-SY5Y cells were co-transfected with reporter plasmids and TFAP2B WT or its dominant-negative mutant as described above, and overexpression of TFAP2B and TFAP2B-R225C was examined by Western blotting.

**Figure 7: CREB is not involved in MIDN promoter activation by insulin in SH-SY5Y cells.** (A) SH-SY5Y cells were preincubated in the presence or absence of U0126 (U, 30 μM) or
wortmannin (Wort, 500 nM) for 30 min and then stimulated with insulin (1 μM) for 2 h. Phosphorylation of CREB was examined by Western blotting. (B) SH-SY5Y cells were cotransfected with wildtype MIDN promoter (-100–+125 bp) linked to luciferase in a promoter-less plasmid (pGL3) and empty vector (pcDNA3.1), wildtype CREB (WT) or a dominant-negative CREB mutant (S133A) and then stimulated with insulin (1 μM). MIDN promoter activity was examined by measuring luciferase activity. MIDN promoter activity was significantly enhanced by overexpression of CREB WT and the S133A mutant (n=3, *p<0.05).

Figure 8: Insulin promotes c-FOS expression and AP-1 is involved in MIDN promoter activation by insulin in SH-SY5Y cells. (A) SH-SY5Y cells were pre-incubated in the presence or absence of U0126 (U, 30 μM) or wortmannin (Wort, 500 nM) for 30 min, then stimulated with insulin (1 μM) for 2 h. Gene expression levels of c-FOS were examined by RT-qPCR. Insulin significantly promoted c-FOS expression (n=3-6, *p<0.05), which was significantly blocked by U0126 (n=3–6, #p<0.05). (B) SH-SY5Y cells were pre-incubated in the presence or absence of U0126 (U, 30 μM) or wortmannin (Wort, 500 nM) for 30 min, then stimulated with insulin (1 μM) for 2 h. c-FOS and GAPDH levels were examined by Western blotting. (C) SH-SY5Y cells were cotransfected with wildtype MIDN promoter (-100–+125 bp) linked to luciferase in a promoter-less plasmid (pGL3) and scrambled or decoy ODNs (2 μg) and then stimulated with insulin (1 μM). MIDN promoter activity was examined by measuring luciferase activity. Insulin significantly promoted MIDN promoter activity (n=6, *p<0.05), which was significantly blocked by the decoy ODN (n=6, #p<0.05). (D) SH-SY5Y cells were transfected with the wildtype MIDN promoter (-100–+125 bp) linked to luciferase in a promoter-less plasmid (pGL3). The cells were preincubated with or without SR11302 (10–30 μM) and then stimulated with insulin (1 μM). MIDN promoter activity was examined by measuring luciferase activity. Insulin significantly promoted MIDN promoter activity (n=4-8,
*p<0.05), which was significantly blocked by SR11302 (n=4–8, "p<0.05). (E) SH-SY5Y cells were stimulated with insulin (1 μM) for 2 h. Then, ChIP assays were performed using control IgG, c-JUN, and c-FOS antibodies. The MIDN promoter region (-185 to +7 bp), which included the predicted AP-1 consensus sequence (-71 to -57 bp), and intron 1 (+840 to +969 bp) was amplified by qPCR. Insulin significantly promoted DNA binding of both c-JUN and c-FOS to the MIDN promoter region (n=3, *p<0.05).

**Figure 9: A putative insulin signalling pathway for promoting MIDN expression.** Insulin upregulates MIDN expression accompanied by the activation of ERK1/2 and PI3-kinase pathways. It is assumed that AP-1 rather than CREB promotes MIDN expression downstream of ERK1/2 and PI3-kinase pathways, whereas TFAP2 suppresses MIDN expression.
Fig. 1
**Fig. 2**

(A) Graph showing MIDN/GAPDH mRNA (fold) levels with treatment conditions: (-), Insulin, BDNF, Insulin, BDNF at 1 h and 2 h.

(B) Immunoblot analysis showing p-Akt (S473), p-ERK1/2 (T202/Y204), ERK2, and GAPDH proteins with treatment conditions: (-), Insulin, 30 ng/ml, 50 ng/ml BDNF.

(C) Graph showing MIDN/GAPDH mRNA (fold) levels with treatment conditions: (-), ATRA, (-), ATRA with Insulin treatment.

(D) Immunoblot analysis showing p-Akt (S473), p-ERK1/2 (T202/Y204), ERK2, and GAPDH proteins with treatment conditions: (-), ATRA, (-), ATRA.

* indicates statistical significance.
Fig. 3

(A) MIDN/GAPDH mRNA (fold)

(B) Insulin

(-) (-) +U +Wort +U +Wort

p-Akt (S473)
p-ERK1/2 (T202/Y204)
ERK2
GAPDH
Fig. 4

(A) Exon 1

-600 bp
-450 bp
-300 bp
-150 bp
-100 bp
-50 bp

(B) Exon 1

-150 bp
-100 bp
-50 bp

MIDN promoter activity (fold)

Luc

(-)

Insulin

* #

0 1 2 3 4 5

0 1 2 3 4 5 6

This article has not been copyedited and formatted. The final version may differ from this version.

JPET Fast Forward. Published on March 3, 2022 as DOI: 10.1124/jpet.121.001076

Downloaded for JX. stir. on March 20, 2022 jpet.aspetjournals.org Downloaded from
Fig. 6
Insulin

(A) Insulin

(B) MIDN promoter activity (fold)

- (-) (-) +U +Wort +U +Wort

p-CREB (Ser133)

CREB

pGL3 pcDNA 3.1

CREB WT

CREB S133A

Fig. 7
Fig. 8
Insulin

ERK1/2  PI3K/Akt

TFAP2  CREB  AP-1  X

Silencing MIDN expression  Enhancing MIDN expression

MIDN gene

Fig. 9
Insulin enhances gene expression of *Midnolin*, a novel genetic risk factor for Parkinson’s disease, via ERK, PI3-kinase and multiple transcription factors in SH-SY5Y cells

Naoki Sagehashi¹, Yutaro Obara¹*, Ohki Maruyama¹, Tadashi Nakagawa², Toru Hosoi², Kuniaki Ishii¹

¹Department of Pharmacology, Yamagata University School of Medicine, Iida-Nishi 2-2-2, Yamagata 990-9585, Japan

²Department of Clinical Pharmacology, Faculty of Pharmaceutical Sciences, Sanyo-Onoda City University, Daigaku-Dori 1-1-1, Sanyo Onoda, 756-0884, Japan.

*Corresponding author: Yutaro Obara, Ph.D.

Department of Pharmacology, Yamagata University School of Medicine, Iida-Nishi 2-2-2, Yamagata 990-9585, Japan.

Phone: +81-23-628-5233; FAX: +81-23-628-5235; E-mail: obaray@med.id.yamagata-u.ac.jp
Supplementary Figure S1: SH-SY5Y cells were stimulated with insulin (1 µM) for 5, 15, and 30 min. Phosphorylation of Akt and ERK1/2 was examined by Western blotting and relative band intensities were analysed. Phosphorylation of Akt and ERK1/2 was significantly promoted by insulin (n=3, *p<0.05).
**Supplementary Figure S2:** SH-SY5Y cells were stimulated with insulin (1 µM) or BDNF (30 or 50 ng/ml) for 5 min. Phosphorylation of Akt and ERK1/2 was examined by Western blotting and relative band intensities were analysed. Phosphorylation of Akt and ERK1/2 was significantly promoted by insulin, not BDNF (n=3, *p*<0.05).
Supplementary Figure S3: SH-SY5Y cells were incubated in the presence of all-trans retinoic acid (10 µM) for 5 days, and stimulated with insulin (1 µM) or BDNF (30 or 50 ng/ml) for 5 min. Phosphorylation of Akt and ERK1/2 was examined by Western blotting and relative band intensities were analysed. Phosphorylation of Akt and ERK1/2 was significantly promoted by BDNF (30 or 50 ng/ml) (n=3, p<0.05).
Supplementary Figure S4: SH-SY5Y cells were incubated in the presence or absence of all-trans retinoic acid (ATRA) (10 µM) for 5 days, and stimulated with insulin (1 µM) for 5 min. Phosphorylation of Akt and ERK1/2 was examined by Western blotting and relative band intensities were analysed. Phosphorylation of ERK1/2 by insulin was significantly promoted by ATRA (n=3, *p<0.05).
Supplementary Figure S5: SH-SY5Y cells were pre-incubated with or without U0126 (U, 30 µM) or wortmannin (Wort, 500 nM) for 30 min, then stimulated with insulin (1 µM) for 2 h. Phosphorylation of Akt and ERK1/2 was examined by Western blotting and relative band intensities were analysed. Phosphorylation of Akt was promoted by insulin (n=3, *p<0.05), which was significantly blocked by wortmannin and combination of wortmannin and U0126 (n=3, #p<0.05). Phosphorylation of ERK1/2 was promoted by insulin (n=3, *p<0.05), which was significantly blocked by U0126, wortmannin and combination of wortmannin and U0126 (n=3, #p<0.05).
Supplementary Figure S6: SH-SY5Y cells were co-transfected with wild-type *MIDN* promoter (-150→+125 bp) linked to *luciferase* in a promoter-less plasmid (pGL3) and empty vector (pcDNA3.1), wild-type TFAP2B (WT) or a dominant-negative TFAP2B mutant (R225C). Overexpression of TFAP2B and TFAP2B-R225C was examined by Western blotting and relative band intensities were analysed. TFAP2B expression levels were significantly increased by transfection with TFAP2 WT or R225C mutants (n=3, *p*<0.05).
Supplementary Figure S7: SH-SY5Y cells were preincubated in the presence or absence of U0126 (U, 30 µM) or wortmannin (Wort, 500 nM) for 30 min and then stimulated with insulin (1 µM) for 2 h. Phosphorylation of CREB at Ser133 was examined by Western blotting and relative band intensities were analysed. Insulin significantly promoted CREB phosphorylation (n=3, *p<0.05), which was inhibited by U0126 and the combination of U0126 and wortmannin (n=3, #p<0.05).
Supplementary Figure S8: SH-SY5Y cells were preincubated in the presence or absence of U0126 (U, 30 µM) or wortmannin (Wort, 500 nM) for 30 min and then stimulated with insulin (1 µM) for 2 h. c-FOS expression was examined by Western blotting and relative band intensities were analysed. Insulin significantly promoted c-FOS protein expression (n=3, *p<0.05), which was inhibited by U0126, wortmannin, and combination of U0126 and wortmannin (n=3, †p<0.05).
Supplementary Table S1: *In silico* JASPAR database analysis. TFAP2 family members that putatively bind to the MIDN promoter region (-121 bp to -99 bp: 5′-AGC CGT CAA GGC GCC CCA GGG CC-3′) are shown with scores and predicted sequences. Relative profile score threshold was 80%.

<table>
<thead>
<tr>
<th>Matrix ID</th>
<th>Name</th>
<th>Score</th>
<th>Relative score</th>
<th>Start</th>
<th>End</th>
<th>Strand</th>
<th>Predicted sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>MA0810.1</td>
<td>TFAP2A(var.2)</td>
<td>12.9646</td>
<td>0.954179721</td>
<td>12</td>
<td>23</td>
<td>+</td>
<td>CGCCCCAGGGCC</td>
</tr>
<tr>
<td>MA0524.1</td>
<td>TFAP2C</td>
<td>12.6803</td>
<td>0.92347673</td>
<td>9</td>
<td>23</td>
<td>+</td>
<td>AGGGGCCCCAGGGCC</td>
</tr>
<tr>
<td>MA0524.2</td>
<td>TFAP2C</td>
<td>12.291</td>
<td>0.933909139</td>
<td>12</td>
<td>23</td>
<td>+</td>
<td>CGCCCGAGGGCC</td>
</tr>
<tr>
<td>MA0814.2</td>
<td>TFAP2C(var.2)</td>
<td>12.2551</td>
<td>0.897942187</td>
<td>10</td>
<td>23</td>
<td>-</td>
<td>GGGGCGGGGGGGCC</td>
</tr>
<tr>
<td>MA0811.1</td>
<td>TFAP2B</td>
<td>12.0311</td>
<td>0.933887188</td>
<td>12</td>
<td>23</td>
<td>+</td>
<td>GCCCGCGGGGGCC</td>
</tr>
<tr>
<td>MA0003.2</td>
<td>TFAP2A</td>
<td>12.035</td>
<td>0.880604059</td>
<td>9</td>
<td>23</td>
<td>+</td>
<td>AGGGGCCCCAGGGCC</td>
</tr>
<tr>
<td>MA0811.1</td>
<td>TFAP2B</td>
<td>11.628</td>
<td>0.919278026</td>
<td>12</td>
<td>23</td>
<td>-</td>
<td>GGGGCTGGGGGGG</td>
</tr>
<tr>
<td>MA1569.1</td>
<td>TFAP2E</td>
<td>11.666</td>
<td>0.952010793</td>
<td>12</td>
<td>22</td>
<td>+</td>
<td>GCGCCAGGGGGCC</td>
</tr>
<tr>
<td>MA1569.1</td>
<td>TFAP2E</td>
<td>11.0593</td>
<td>0.949249415</td>
<td>12</td>
<td>22</td>
<td>-</td>
<td>GGGCTGGGGGGCC</td>
</tr>
<tr>
<td>MA0524.2</td>
<td>TFAP2C</td>
<td>10.8386</td>
<td>0.910307731</td>
<td>12</td>
<td>23</td>
<td>-</td>
<td>GGGCCTGGGGGGG</td>
</tr>
<tr>
<td>MA0810.1</td>
<td>TFAP2A(var.2)</td>
<td>10.8509</td>
<td>0.920674597</td>
<td>12</td>
<td>23</td>
<td>-</td>
<td>GGGCGTGGGGGGG</td>
</tr>
<tr>
<td>MA0003.3</td>
<td>TFAP2A</td>
<td>10.5649</td>
<td>0.920878931</td>
<td>12</td>
<td>22</td>
<td>+</td>
<td>GGGCCAGGGGGCC</td>
</tr>
<tr>
<td>MA0003.4</td>
<td>TFAP2A</td>
<td>10.2957</td>
<td>0.859193157</td>
<td>10</td>
<td>23</td>
<td>+</td>
<td>GGGGCCAGGGGGCC</td>
</tr>
<tr>
<td>MA0003.1</td>
<td>TFAP2A</td>
<td>10.0665</td>
<td>0.989385105</td>
<td>14</td>
<td>22</td>
<td>-</td>
<td>GCCCTGGGGCC</td>
</tr>
<tr>
<td>MA0003.1</td>
<td>TFAP2A</td>
<td>10.0297</td>
<td>0.98818336</td>
<td>13</td>
<td>21</td>
<td>+</td>
<td>GCCCCAGGGG</td>
</tr>
<tr>
<td>MA0813.1</td>
<td>TFAP2B(var.3)</td>
<td>9.36804</td>
<td>0.859461323</td>
<td>1</td>
<td>13</td>
<td>+</td>
<td>AGCGGTCAAGGGCG</td>
</tr>
<tr>
<td>MA0872.1</td>
<td>TFAP2A(var.3)</td>
<td>9.90176</td>
<td>0.849320252</td>
<td>1</td>
<td>13</td>
<td>+</td>
<td>AGCGGTCAAGGGCG</td>
</tr>
<tr>
<td>MA0812.1</td>
<td>TFAP2B(var.2)</td>
<td>8.89191</td>
<td>0.886348154</td>
<td>12</td>
<td>22</td>
<td>+</td>
<td>GGGCCAGGGCC</td>
</tr>
<tr>
<td>MA0813.1</td>
<td>TFAP2B(var.3)</td>
<td>8.8645</td>
<td>0.851962608</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>GGGCTTGAGGGCGT</td>
</tr>
<tr>
<td>MA0815.1</td>
<td>TFAP2C(var.3)</td>
<td>8.82907</td>
<td>0.855807495</td>
<td>1</td>
<td>13</td>
<td>+</td>
<td>AGCGGTCAAGGGCG</td>
</tr>
<tr>
<td>MA0815.1</td>
<td>TFAP2C(var.3)</td>
<td>8.58279</td>
<td>0.855394067</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>GGGCCTTGAGGGCT</td>
</tr>
<tr>
<td>MA0814.1</td>
<td>TFAP2C(var.3)</td>
<td>8.21686</td>
<td>0.8796537</td>
<td>12</td>
<td>22</td>
<td>+</td>
<td>GGGCCAGGGGC</td>
</tr>
<tr>
<td>MA0872.1</td>
<td>TFAP2A(var.3)</td>
<td>7.82864</td>
<td>0.830381906</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>GGGCCTTGAGGGCT</td>
</tr>
<tr>
<td>MA0814.1</td>
<td>TFAP2C(var.2)</td>
<td>7.46944</td>
<td>0.867666673</td>
<td>12</td>
<td>22</td>
<td>-</td>
<td>GCCCCTGGGGCC</td>
</tr>
<tr>
<td>MA0003.3</td>
<td>TFAP2A</td>
<td>6.95694</td>
<td>0.864161308</td>
<td>12</td>
<td>22</td>
<td>-</td>
<td>GCCCCTGGGGCC</td>
</tr>
<tr>
<td>MA0812.1</td>
<td>TFAP2B(var.2)</td>
<td>6.88858</td>
<td>0.854612353</td>
<td>12</td>
<td>22</td>
<td>-</td>
<td>GCCCCTGGGGCC</td>
</tr>
<tr>
<td>MA1569.1</td>
<td>TFAP2E</td>
<td>6.5672</td>
<td>0.889256628</td>
<td>13</td>
<td>23</td>
<td>+</td>
<td>GGGCGGCGGGGCC</td>
</tr>
<tr>
<td>MA1569.1</td>
<td>TFAP2E</td>
<td>6.41803</td>
<td>0.887274736</td>
<td>13</td>
<td>23</td>
<td>-</td>
<td>GGGCGGCGGGGCC</td>
</tr>
<tr>
<td>MA0003.1</td>
<td>TFAP2A</td>
<td>5.87727</td>
<td>0.852680514</td>
<td>4</td>
<td>12</td>
<td>-</td>
<td>GCCTTGAGCG</td>
</tr>
<tr>
<td>MA0003.1</td>
<td>TFAP2A</td>
<td>5.51403</td>
<td>0.840827035</td>
<td>2</td>
<td>10</td>
<td>+</td>
<td>GCCGTCAAG</td>
</tr>
<tr>
<td>MA0003.3</td>
<td>TFAP2A</td>
<td>3.96691</td>
<td>0.817158131</td>
<td>13</td>
<td>23</td>
<td>+</td>
<td>GCCCGAGGGGCC</td>
</tr>
</tbody>
</table>
Supplementary Table S2: In silico JASPAR database analysis. FOS family members that putatively bind to the MIDN promoter region (-71 bp to -57 bp: 5′-GTC TGC GTC ACC GCC-3′) are shown with scores and predicted sequences. Relative profile score threshold was 80%.

<table>
<thead>
<tr>
<th>Matrix ID</th>
<th>Name</th>
<th>Score</th>
<th>Relative score</th>
<th>Start</th>
<th>End</th>
<th>Strand</th>
<th>Predicted sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>MA1128.1</td>
<td>FOSL1::JUN</td>
<td>10.5189</td>
<td>0.888102383</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>CGTGACGCAGAC</td>
</tr>
<tr>
<td>MA1141.1</td>
<td>FOS::JUND</td>
<td>10.1338</td>
<td>0.876127251</td>
<td>1</td>
<td>13</td>
<td>+</td>
<td>GTCTGCTACCC</td>
</tr>
<tr>
<td>MA1130.1</td>
<td>FOSL2::JUN</td>
<td>10.0364</td>
<td>0.87397998</td>
<td>1</td>
<td>12</td>
<td>+</td>
<td>GTCTGCTACCC</td>
</tr>
<tr>
<td>MA0605.1</td>
<td>AM3</td>
<td>10.0341</td>
<td>0.917590904</td>
<td>5</td>
<td>12</td>
<td>-</td>
<td>GTGACGC</td>
</tr>
<tr>
<td>MA0099.3</td>
<td>FOS::JUN</td>
<td>9.85091</td>
<td>0.888647329</td>
<td>3</td>
<td>12</td>
<td>+</td>
<td>CTGGTACCC</td>
</tr>
<tr>
<td>MA1137.1</td>
<td>FOSL1::JUNB</td>
<td>9.82596</td>
<td>0.872382981</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>CGTGACGCAGAC</td>
</tr>
<tr>
<td>MA1144.1</td>
<td>FOSL2::JUND</td>
<td>8.85723</td>
<td>0.870163853</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACGCAG</td>
</tr>
<tr>
<td>MA1142.1</td>
<td>FOSL1::JUNB</td>
<td>8.71236</td>
<td>0.881633579</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACGCAG</td>
</tr>
<tr>
<td>MA1135.1</td>
<td>FOSB::JUNB</td>
<td>8.42115</td>
<td>0.865478321</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACGCAG</td>
</tr>
<tr>
<td>MA1134.1</td>
<td>FOS::JUNB</td>
<td>7.81613</td>
<td>0.844404127</td>
<td>2</td>
<td>13</td>
<td>+</td>
<td>TCTGGTACCC</td>
</tr>
<tr>
<td>MA0099.2</td>
<td>FOS::JUN</td>
<td>7.79437</td>
<td>0.899254664</td>
<td>4</td>
<td>10</td>
<td>-</td>
<td>TGACGCA</td>
</tr>
<tr>
<td>MA1138.1</td>
<td>FOSL2::JUNB</td>
<td>7.68241</td>
<td>0.851448171</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACGCAG</td>
</tr>
<tr>
<td>MA1143.1</td>
<td>FOSL1::JUND(var.2)</td>
<td>7.49865</td>
<td>0.830699773</td>
<td>2</td>
<td>11</td>
<td>-</td>
<td>GTGACGCAG</td>
</tr>
<tr>
<td>MA0477.1</td>
<td>FOSL1</td>
<td>7.21865</td>
<td>0.868823434</td>
<td>2</td>
<td>12</td>
<td>-</td>
<td>GTGACGCAGA</td>
</tr>
<tr>
<td>MA0099.1</td>
<td>JUN::FOS</td>
<td>7.20198</td>
<td>0.84893485</td>
<td>4</td>
<td>11</td>
<td>-</td>
<td>GTGACGCA</td>
</tr>
<tr>
<td>MA0478.1</td>
<td>FOSL2</td>
<td>6.825</td>
<td>0.867514027</td>
<td>3</td>
<td>13</td>
<td>-</td>
<td>CGTGACGCAG</td>
</tr>
<tr>
<td>MA0099.1</td>
<td>JUN::FOS</td>
<td>6.48991</td>
<td>0.82535644</td>
<td>3</td>
<td>10</td>
<td>+</td>
<td>CTGGTAC</td>
</tr>
<tr>
<td>MA0477.2</td>
<td>FOSL1</td>
<td>5.92422</td>
<td>0.81566667</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>CGTGACGCAGAC</td>
</tr>
<tr>
<td>MA0099.2</td>
<td>FOS::JUN</td>
<td>5.52117</td>
<td>0.812273091</td>
<td>4</td>
<td>10</td>
<td>+</td>
<td>TGCGTCA</td>
</tr>
<tr>
<td>MA0476.1</td>
<td>FOS</td>
<td>3.91938</td>
<td>0.841211694</td>
<td>2</td>
<td>12</td>
<td>+</td>
<td>TCTGGTACCC</td>
</tr>
<tr>
<td>MA0476.1</td>
<td>FOS</td>
<td>2.12657</td>
<td>0.805163909</td>
<td>2</td>
<td>12</td>
<td>-</td>
<td>GTGACGCAGA</td>
</tr>
</tbody>
</table>
**Supplementary Table S3: In silico JASPAR database analysis.** JUN family members that putatively bind to the MIDN promoter region (−71 bp to −57 bp: 5′−GTC TGC GTC ACC GCC−3′) are shown with scores and predicted sequences. Relative profile score threshold was 80%.

<table>
<thead>
<tr>
<th>Matrix ID</th>
<th>Name</th>
<th>Score</th>
<th>Relative score</th>
<th>Start</th>
<th>End</th>
<th>Strand</th>
<th>Predicted sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>MA1128.1</td>
<td>FOS:L1::JUN</td>
<td>10.5189</td>
<td>0.888102383</td>
<td>1</td>
<td>13</td>
<td>-</td>
<td>CGTGACGCAGAC</td>
</tr>
<tr>
<td>MA1141.1</td>
<td>FOS::JUND</td>
<td>10.1338</td>
<td>0.876127251</td>
<td>1</td>
<td>13</td>
<td>+</td>
<td>GTCTCGGTCAACC</td>
</tr>
<tr>
<td>MA1130.1</td>
<td>FOS:L2::JUN</td>
<td>10.0364</td>
<td>0.887397998</td>
<td>1</td>
<td>12</td>
<td>+</td>
<td>GTCTCGGTCAACC</td>
</tr>
<tr>
<td>MA0099.3</td>
<td>FOS::JUN</td>
<td>9.85091</td>
<td>0.888647329</td>
<td>3</td>
<td>12</td>
<td>+</td>
<td>GTCTCGGTCAACC</td>
</tr>
<tr>
<td>MA1137.1</td>
<td>FOS:L1::JUNB</td>
<td>9.82596</td>
<td>0.872389281</td>
<td>3</td>
<td>13</td>
<td>-</td>
<td>CGTGACGCAGAC</td>
</tr>
<tr>
<td>MA1132.1</td>
<td>JUN::JUNB</td>
<td>9.58854</td>
<td>0.883150386</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGC</td>
</tr>
<tr>
<td>MA1144.1</td>
<td>FOS:L2::JUND</td>
<td>8.85723</td>
<td>0.870163853</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGC</td>
</tr>
<tr>
<td>MA1142.1</td>
<td>FOS:L1::JUND</td>
<td>8.71236</td>
<td>0.881633579</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGC</td>
</tr>
<tr>
<td>MA1135.1</td>
<td>FOSB::JUNB</td>
<td>8.42115</td>
<td>0.865478321</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGC</td>
</tr>
<tr>
<td>MA1134.1</td>
<td>FOS::JUNB</td>
<td>7.81613</td>
<td>0.844404127</td>
<td>2</td>
<td>13</td>
<td>+</td>
<td>TCTCGGTCAACC</td>
</tr>
<tr>
<td>MA0099.2</td>
<td>FOS::JUN</td>
<td>7.79437</td>
<td>0.895254664</td>
<td>4</td>
<td>10</td>
<td>-</td>
<td>TGACGCA</td>
</tr>
<tr>
<td>MA1138.1</td>
<td>FOS:L2::JUNB</td>
<td>7.68241</td>
<td>0.851448171</td>
<td>3</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGC</td>
</tr>
<tr>
<td>MA1143.1</td>
<td>FOSL1::JUND(var2)</td>
<td>7.49865</td>
<td>0.830699773</td>
<td>2</td>
<td>11</td>
<td>-</td>
<td>GTGACACAGA</td>
</tr>
<tr>
<td>MA0099.1</td>
<td>JUN::FOS</td>
<td>7.20198</td>
<td>0.84893485</td>
<td>4</td>
<td>11</td>
<td>-</td>
<td>TGACGCA</td>
</tr>
<tr>
<td>MA0462.2</td>
<td>BATF::JUN</td>
<td>6.76692</td>
<td>0.820083579</td>
<td>2</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGA</td>
</tr>
<tr>
<td>MA0099.1</td>
<td>JUN::FOS</td>
<td>6.48991</td>
<td>0.82535644</td>
<td>3</td>
<td>10</td>
<td>+</td>
<td>CTGGTCCA</td>
</tr>
<tr>
<td>MA0490.1</td>
<td>JUNB</td>
<td>6.10452</td>
<td>0.868813616</td>
<td>3</td>
<td>13</td>
<td>-</td>
<td>CGTGACACAGC</td>
</tr>
<tr>
<td>MA0089.1</td>
<td>MAFG::NFE2L1</td>
<td>5.91912</td>
<td>0.874700179</td>
<td>7</td>
<td>12</td>
<td>-</td>
<td>GTGAC</td>
</tr>
<tr>
<td>MA0099.2</td>
<td>FOS::JUN</td>
<td>5.52137</td>
<td>0.812279091</td>
<td>4</td>
<td>10</td>
<td>+</td>
<td>TGGTCCA</td>
</tr>
<tr>
<td>MA0491.1</td>
<td>JUND</td>
<td>2.17727</td>
<td>0.836314736</td>
<td>2</td>
<td>12</td>
<td>-</td>
<td>GTGACACAGA</td>
</tr>
<tr>
<td>MA0491.1</td>
<td>JUND</td>
<td>1.84511</td>
<td>0.832621369</td>
<td>2</td>
<td>12</td>
<td>+</td>
<td>TCTGGTCAACC</td>
</tr>
</tbody>
</table>
**Supplementary Table S4:** In silico JASPAR database analysis. CREB/ATF family members that putatively bind to the *MIDN* promoter region (-71 bp to -57 bp: 5′-GTC TGC GTC ACC GCC-3′) are shown with scores and predicted sequences. Relative profile score threshold was 80%.

<table>
<thead>
<tr>
<th>Matrix ID</th>
<th>Name</th>
<th>Score</th>
<th>Relative score</th>
<th>Start</th>
<th>End</th>
<th>Strand</th>
<th>Predicted sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>MA0018.1</td>
<td>CREB1</td>
<td>11.1485</td>
<td>0.925408212</td>
<td>4</td>
<td>15</td>
<td>-</td>
<td>GCCGCTGACGCA</td>
</tr>
<tr>
<td>MA0604.1</td>
<td>Ah1</td>
<td>10.9754</td>
<td>0.955555593</td>
<td>4</td>
<td>11</td>
<td>-</td>
<td>GTGACGCA</td>
</tr>
<tr>
<td>MA1474.1</td>
<td>CREB3L4</td>
<td>6.80677</td>
<td>0.802448842</td>
<td>1</td>
<td>12</td>
<td>+</td>
<td>GTCTCGTCAACC</td>
</tr>
<tr>
<td>MA0018.2</td>
<td>CREB1</td>
<td>6.62373</td>
<td>0.818912614</td>
<td>3</td>
<td>10</td>
<td>-</td>
<td>TGACGCA</td>
</tr>
</tbody>
</table>