

ERN1 knockdown modifies the impact of glucose and glutamine deprivations on the expression of EDN1 and its receptors in glioma cells

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Objective. The aim of the present investigation was to study the impact of glucose and glutamine deprivations on the expression of genes encoding EDN1 (endothelin-1), its cognate receptors (EDNRA and EDNRB), and ECE1 (endothelin converting enzyme 1) in U87 glioma cells in response to knockdown of ERN1 (endoplasmic reticulum to nucleus signaling 1), a major signaling pathway of endoplasmic reticulum stress, for evaluation of their possible implication in the control of glioma growth through ERN1 and nutrient limitations.

Methods. The expression level of EDN1, its receptors and converting enzyme 1 in control U87 glioma cells and cells with knockdown of ERN1 treated by glucose or glutamine deprivation by quantitative polymerase chain reaction was studied.

Results. We showed that the expression level of *EDN1* and *ECE1* genes was significantly up-regulated in control U87 glioma cells exposure under glucose deprivation condition in comparison with the glioma cells, growing in regular glucose containing medium. We also observed up-regulation of *ECE1* gene expression in U87 glioma cells exposure under glutamine deprivation as well as down-regulation of the expression of EDN1 and EDNRA mRNA, being more significant for EDN1. Furthermore, the knockdown of ERN1 signaling enzyme function significantly modified the response of most studied gene expressions to glucose and glutamine deprivation conditions. Thus, the ERN1 knockdown led to a strong suppression of *EDN1* gene expression under glucose deprivation, but did not change the effect of glutamine deprivation on its expression. At the same time, the knockdown of ERN1 signaling introduced the sensitivity of *EDNRB* gene to both glucose and glutamine deprivations as well as completely removed the impact of glucose deprivation on the expression of *ECE1* gene.

Conclusions. The results of this study demonstrated that the expression of endothelin-1, its receptors, and *ECE1* genes is preferentially sensitive to glucose and glutamine deprivations in gene specific manner and that knockdown of ERN1 significantly modified the expression of *EDN1*, *EDNRB*, and *ECE1* genes in U87 glioma cells. It is possible that the observed changes in the expression of studied genes under nutrient deprivation may contribute to the suppressive effect of ERN1 knockdown on glioma cell proliferation and invasiveness.

Key words: ERN1 knockdown, mRNA expression, EDN1, EDNRA, EDNRB, ECE1, glucose and glutamine deprivations, U87 glioma cells

The unfolded protein response is a highly conserved protein quality control mechanism, activated in response to endoplasmic reticulum stress. The growing tumor requires the endoplasmic reticulum stress for own neovascularization and growth as well as for inhibition of apoptosis under stressful environmental conditions (Drogat et al. 2007; Auf et al. 2010; Doultinos et al. 2017). The endoplasmic reticulum stress signaling represents an integrated signal transduction pathway that transmits information about the protein folding status at the endoplasmic reticulum to the nucleus and cytosol to restore proteostasis (Bravo et al. 2013; Chevet et al. 2015; Lhomond et al. 2018; Marciniak 2019). Malignant tumors use the unfolded protein response and its signaling pathways to augment cancer cells proliferation (Dejeans et al. 2015; Manie et al. 2014; Papaioannou et al. 2018). It is interesting to note that stimulation of ERN1/IRE1 (endoplasmic reticulum to nucleus signaling 1/inositol requiring enzyme 1) division of the endoplasmic reticulum stress response is tightly linked to apoptosis and cell death, and inhibition of its functional activity has been demonstrated to result in substantial anti-proliferative effect in glioma growth (Auf et al. 2010, 2013; Johnson et al. 2011; Minchenko et al. 2014, 2015c; Markouli et al. 2020). Additionally, suppression of ERN1 endoribonuclease has more robust anti-proliferative influence on glioma cells and preferentially different impact on the expression of some ERN1-related pathway genes (Auf et al. 2013; Minchenko et al. 2015c).

Glioblastoma multiforme is the most common and malignant type of primary brain tumor of the central nervous system with poor prognosis and high mortality. The current clinical treatments for glioblastoma consist of tumor resection, radiotherapy, and chemotherapy (Nayak and Reardon 2017; Almanza et al. 2019; Yang et al. 2020). The rapid growth of cancers generates microenvironmental changes in regards to nutrient deprivation, thus inducing the activation of endoplasmic reticulum stress signaling pathways, cell proliferation, and survival (Obacz et al. 2017; Zhao et al. 2017; Obiedat et al. 2019; Liu et al. 2020). Furthermore, a better knowledge of tumor responses to nutrient deprivation is required to elaborate better therapeutical strategies of cell sensibilization, based on the blockade of survival mechanisms (Iurlaro et al. 2017; Riabovol et al. 2019; Teramoto and Katoh 2019; Minchenko et al. 2020a, b; Ratushna 2020). Cell proliferation and apoptosis are strongly dependent on glycolysis and glucose level, because there is the molecular connection between metabolism, cell cycle progression, and the delivery of nutrients essen-

tial for this purpose (Huber et al. 2013; Parzych et al. 2019). Glucose as well as glutamine are important substrates for glycolysis and glutaminolysis, which are important to glioma development and a more aggressive behavior through regulation of the cell cycle at distinct stages (Colombo et al. 2011).

It is interesting to note that endoplasmic reticulum stress and glucose as well as glutamine level are very important and complementary factors for tumor growth and that ERN1 mediated stress signaling can significantly modify the effects of glutamine and glucose deprivations as well as hypoxia on numerous gene expressions (Minchenko et al. 2014, 2016, 2017; 2019; Zhao et al. 2017; Tsymbal et al. 2020). However, the detailed molecular mechanisms of the interaction of hypoxia and glucose deprivation with ERN1 mediated stress signaling pathway are complex yet and warrant further study.

The peptide hormone endothelin-1 (EDN1; ET-1) and its related receptors, such as EDNRA and EDNRB, play an important role not only in the maintenance of vascular tone, but they are also localized to non-vascular structures including epithelial cells, glia and neurons and play multiple, complex roles (Dashwood and Loesch 2009; Khimji and Rockey 2010; Stow et al. 2011). Endothelin-1 and its receptors also have co-mitogenic activity, potentiating the effects of other growth factors such as PDGF and have been linked to variable diseases including diabetes, traumatic shock, and tumorigenesis (Minchenko et al. 1999, 2003; Dashwood and Loesch 2009; Khimji and Rockey 2010; Stow et al. 2011; Palmer et al. 2012; Cook et al. 2015; Dojo Soeandy et al. 2019). There are also data indicating that EDN1 is a neuropeptide, which is implicated in a number of neural circuits where its transmitter affects range from a role in pain and temperature control to its action on the hypothalamo-neurosecretory system (Dashwood and Loesch 2009). Recently, it was shown that mRNA levels encoding EDN1 and its receptors, known to be elevated in amyotrophic lateral sclerosis, were sharply increased by knockdown of C9 (*C9ORF72*) gene, which encodes a protein that functions in control of endothelin and glutamate signaling (Fomin et al. 2018). Differential and tissue-specific production of EDN1 must be tightly regulated in order to preserve these biologically diverse actions.

It is interesting to note that the palmitic acid increases ET-1 expression in endothelial cells through the induction of endoplasmic reticulum stress and the activation of protein kinase C, providing a novel mechanistic insight into the pathogenesis of obesity-associated hypertension and cardiovascular diseases

including atherosclerosis (Zhang et al 2018). The primary mechanism thought the control of EDN1 bioavailability is the rate of transcription from the *EDN1* gene. Studies conducted on a variety of cell types have identified key transcription factors including HIF that govern *EDN1* expression (Aversa et al. 1997; Minchenko and Caro 2000; Stow et al. 2011).

The endothelin receptor type A plays a role in potent and long-lasting vasoconstriction and cell proliferation. Thus, Arabanian et al. (2018) have shown that overexpression of EDNRA led to an increased proliferation and resistance to apoptosis of bone marrow cells *in vitro* and that MEIS1 binds to the EDNRA promoter region, suggesting a regulatory role for MEIS1 in endothelin-1 receptor type A expression and in HOXA9/MEIS1-driven leukemogenesis. Furthermore, the endothelin axis (EDN1 and EDN1 receptor A) is involved in cellular growth, differentiation, cell motility, invasiveness, and tumor progression as well as drug resistance in several cancers. Polymorphisms of these genes increase the risk of papillary thyroid cancer developing (Aydin et al. 2019; Pulido et al. 2020). Recently, it was observed an abnormal expression of endothelin receptor type B (EDNRB) in hepatocellular carcinoma and confirmed its potential clinical significance (Zhang et al. 2019). Thus, endothelin-1 receptor blockade is a new possible therapeutic approach in ovarian cancer and multiple myeloma, because the majority of multiple myeloma cell lines and primary malignant plasma cells express high levels of EDNRA and EDNRB and release EDN1 (Rosano et al. 2017; Russignan et al. 2017).

The endothelin-converting enzyme-1 (ECE1) is also involved in proteolytic processing of endothelin precursor to biologically active peptide. Active EDN1 has a short half-life, so its biological effects are completely dependent on its enzymatic activation by ECE1. There are data indicating that expression of *ECE1* gene is elevated in several tumors and cancer cell lines and that this protein has relation to cancer cell proliferation and invasiveness (Niechi et al. 2015; Tapia and Niechi 2019). Furthermore, Miners and Love (2017) have shown that endothelin-converting enzymes degrade alpha-synuclein and are reduced in dementia with Lewy bodies. Thus, it participates in the metabolism of α -synuclein that could contribute to the development and progression of dementia. It is interesting to note that miR-199a-5p, which negatively regulated ECE1, and silencing the *ECE1* gene are protected the rat spinal cord injury after ischemia-reperfusion (Bao et al. 2018). The *ECE1* gene is

hypoxia responsible. Its promoter and intron regions contain the HIF binding sites (Khamaisi et al. 2015). It has also been shown that endothelin-1 production is controlled by TIMAP-protein phosphatase 1-complex via ECE1 dephosphorylation (Boratko et al. 2016).

The aim of this study was to examine the impact of glucose and glutamine deprivations on the expression of genes encoded EDN1, its receptors, and converting enzyme 1 in U87 glioma cells in response to knockdown of ERN1 activity for evaluation of their possible significance in the control of glioma growth through endoplasmic reticulum stress signaling mediated by IRE1 and nutrient limitation.

Materials and methods

Cell lines and culture conditions. The glioma cell line U87 was obtained from ATCC (USA) and grown in high glucose (4.5 g/l) Dulbecco's modified Eagle's minimum essential medium (Gibco, Invitrogen, Carlsbad, CA, USA) supplemented with glutamine (2 mM), 10% fetal bovine serum (Equitech-Bio, Inc., USA), penicillin (100 units/ml; Gibco) and streptomycin (0.1 mg/ml; Gibco) at 37°C in incubator with 5% CO₂. In this work, we used two sublines of these cells, which were described previously (Auf et al. 2010, 2013). One subline was obtained by selection of stable transfected clones with overexpression of empty vector pcDNA3.1, which was used for creation of dnERN1. This untreated subline of glioma cells (control glioma cells) was used as control 1 in the study of the effect of glucose and glutamine deprivations on the expression level of genes encoding EDN1, its receptors (EDNRA, EDNRB), and endothelin converting enzyme ECE1. Second subline was obtained by selection of stable transfected clones with overexpression of ERN1 dominant/negative construct (dnERN1), having suppression of both the protein kinase and endoribonuclease activities of this signaling protein (Auf et al. 2010). All used sublines of glioma cells in this study are grown in the presence of geneticin (G418), while these cells carrying empty vector pcDNA3.1 or dnERN1 construct. Glucose and glutamine deprivation conditions were created by changing the complete DMEM medium into culture plates on DMEM medium without glucose or glutamine and plates were exposed to this condition for 16 h.

RNA isolation. Total RNA was extracted from glioma cells using the Trizol reagent according to manufacturer's protocol (Invitrogen, Carlsbad, CA, USA). The RNA pellets were washed with 75%

ethanol and dissolved in nuclease-free water. For additional purification RNA samples were re-precipitated with 95% ethanol and re-dissolved again in nuclease-free water. RNA concentration and spectral characteristics were measured using NanoDrop One Spectrophotometer (Thermo Scientific).

Reverse transcription and quantitative PCR analysis. The impact of glucose and glutamine deprivations on the expression level of endothelin-1 and its receptors (EDNRA and EDNRB) and ECE1 mRNAs as well as ACTB as housekeeping gene were measured in control U87 glioma cells and cells with a deficiency of ERN1, introduced by dnER1, by quantitative polymerase chain reaction using SYBRGreen Mix (ABgene, Thermo Fisher Scientific, Epsom, Surrey, UK) and “QuantStudio 5 Real-Time PCR System” (Applied Biosystems, USA). Thermo Scientific Verso cDNA Synthesis Kit (Germany) was used for reverse transcription as described previously (Minchenko *et al.* 2019). Polymerase chain reaction was performed in triplicate. The expression of beta-actin mRNA was used as control of analyzed RNA quantity. The pair of primers specific for each studied gene was received from Sigma-Aldrich (St. Louis, MO, U.S.A.) and used for quantitative polymerase chain reaction as described previously by Minchenko *et al.* (2019).

Quantitative PCR analysis was performed using a special computer program “Differential expression calculator” and statistical analysis using Excel program and OriginPro 7.5 software as described previously (Bochkov *et al.* 2006; Rudnytska *et al.* 2021). Comparison of two means was performed by the use of two-tailed Student’s t-test. The value $p < 0.05$ was considered significant in all cases. The values of *EDN1*, *EDNRA*, *EDNRB*, and *ECE1* gene expressions were normalized to the expression of beta-actin mRNA and represented as percent of control (100%). All values are expressed as mean \pm SEM from triplicate measurements performed in 4 independent experiments. The amplified DNA fragments were also analyzed on a 2% agarose gel and that visualized by SYBR* Safe DNA Gel Stain (Life Technologies, Carlsbad, CA, USA).

Results

The possible role of endoplasmic reticulum stress signaling mediated by ERN1 signaling protein in the control of endothelin-1, its receptors, and endothelin converting enzyme 1 gene expressions in U87 glioma cells was studied. As shown in Figure 1, the expression of *EDN1* mRNA in control U87 glioma cells (transfected by empty vector), treated by glucose

deprivation, is significantly up-regulated (+57%) in comparison with non-treated cells. At the same time, inhibition of ERN1 signaling completely modifies the effect of glucose deprivation on the expression of endothelin-1 gene expression (Figure 1). Thus, the exposure of these cells under glucose deprivation leads to a strong down-regulation (–68%) of *EDN1* mRNA expression. We next investigated the effect of ERN1 knockdown on the expression of gene encoding endothelin receptor type A in glioma cells treated by glucose deprivation. As shown in Figure 2, the expression level of *EDNRA* mRNA is not significantly changed in both control and ERN1 knockdown U87 glioma cells in comparison with cells, growing with glucose. Furthermore, similar results in the expression of *EDNRB* gene we received in control glioma cells (Figure 3). However, inhibition of ERN1 functional activity by dnER1 introduces sensitivity of *EDNRB* gene expression to glucose-limited condition and leads to small but statistically significant up-regulation (+12%) of this gene expression as compared to appropriate control (dnER1) glioma cells (Figure 3).

We also studied the expression of gene encoding endothelin converting enzyme 1, which play an

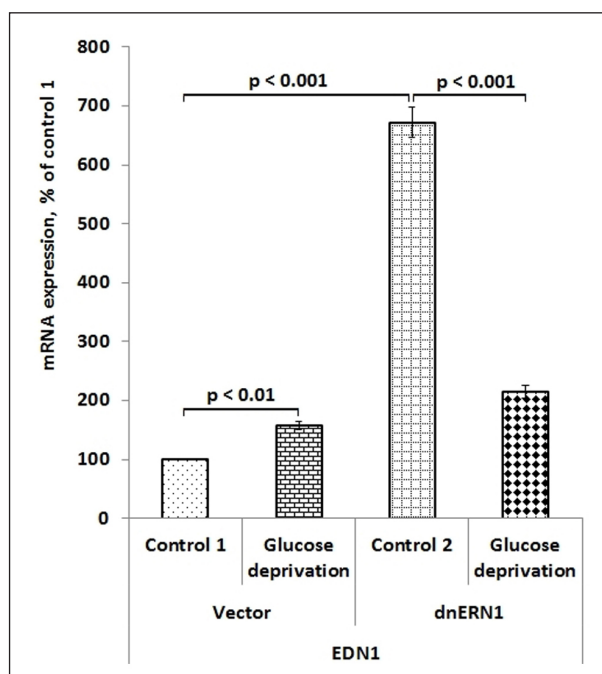


Figure 1. Impact of glucose deprivation on the expression level of endothelin 1 (*EDN1*) gene expression in control U87 glioma cells (Vector) and cells with a blockade of the ERN1 (dnER1) measured by qPCR. Values of *EDN1* mRNA expression were normalized to the level of beta-actin mRNA and represented as percent of control 1 (100 %); $n = 4$.

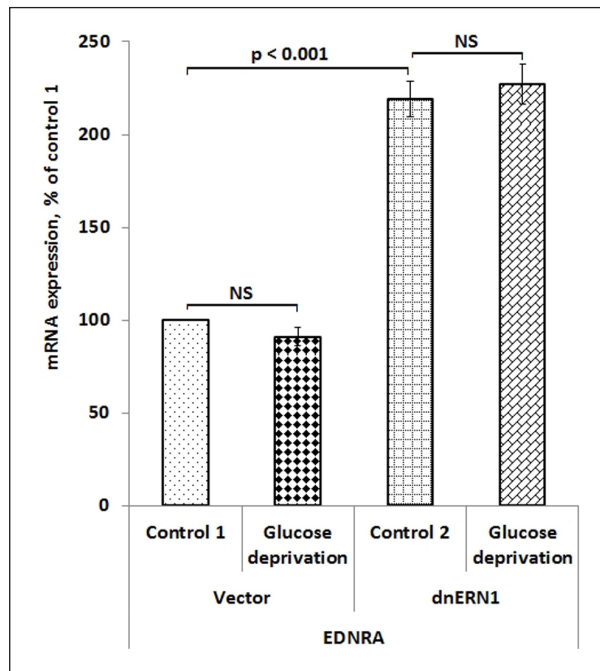


Figure 2. Impact of glucose deprivation on the expression level of endothelin receptor type A (*EDNRA*) gene expression level in control U87 glioma cells (Vector) and cells with a blockade of the ERN1 (dnERN1) measured by qPCR. Values of *EDNRA* mRNA expression were normalized to the level of beta-actin mRNA and represented as percent of control 1 (100%); n=4.

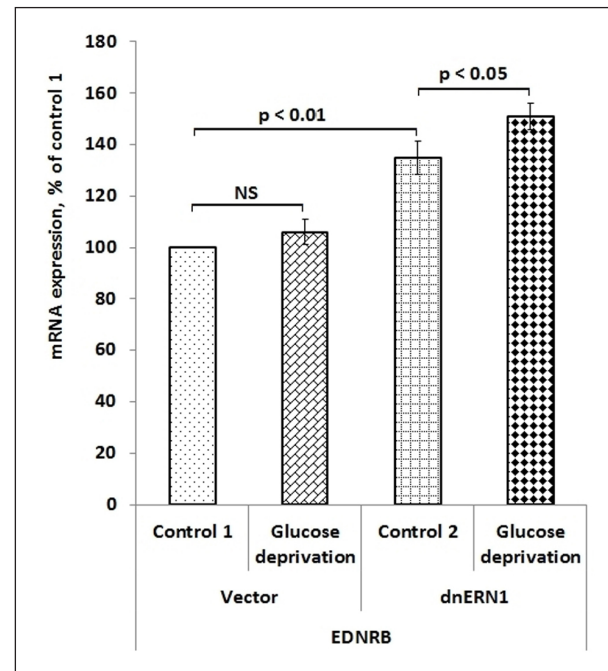


Figure 3. Impact of glucose deprivation on the expression level of endothelin receptor type B (*EDNRB*) gene expression level in control U87 glioma cells (Vector) and cells with a blockade of the ERN1 (dnERN1) measured by qPCR. Values of *EDNRB* mRNA expression were normalized to beta-actin mRNA level and represent as percent for control 1 (100%); n=4.

important role in the regulation of endothelin-1 activity and showed its strong sensitivity to glucose deprivation (Figure 4). Thus, the expression level of *ECE1* gene is significantly up-regulated (+133%) in glioma cells without both ERN1 protein kinase and endoribonuclease activities in comparison with cells, transfected by empty vector. At the same time, knockdown of ERN1 signaling protein completely eliminated the sensitivity of *ECE1* gene expression to glucose-limited condition (Figure 4).

We next investigated the impact of glutamine deprivation on the expression of genes encoding endothelin-1 and related proteins in U87 glioma cells in relation to inhibition of ERN1 signaling protein function. It was shown that in control glioma cells (transfected by empty vector) the expression level of *EDN1* gene is strongly down-regulated (-63%) under glutamine-limited condition in comparison with cells growing in regular DMEM medium (Figure 5). Furthermore, inhibition of ERN1 signaling enzyme function does not significantly change the sensitivity of endothelin-1 gene expression to glutamine deprivation condition as compared to corresponding

control cells (dnERN1) (-64%; Figure 5). At the same time, the impact of glutamine deprivation on the expression of gene encoding endothelin receptor type A and B genes in control glioma cells was different (Figures 6 and 7). Thus, the exposure of control glioma cells under glutamine-limited condition leads to down-regulation of *EDNRA* gene expression (-20%) but *EDNRB* gene expression was resistant to this experimental condition. It is interesting to note that inhibition of ERN1 signaling enzyme function modifies effect of glutamine deprivation on endothelin receptor type B gene expression and leads to up-regulation of the expression of this endothelin receptor gene (+38%) in comparison to appropriate control cells (Figure 7). As shown in Figure 8, the exposure of control glioma cells under glutamine-limited condition leads to significant up-regulation of endothelin converting enzyme 1 gene expression (+37%) in comparison with control cells growing with glutamine-containing medium. At the same time, the inhibition of ERN1 functional activity decreases the sensitivity of *ECE1* gene expression to glutamine deprivation. Therefore, the expression level of *ECE1*

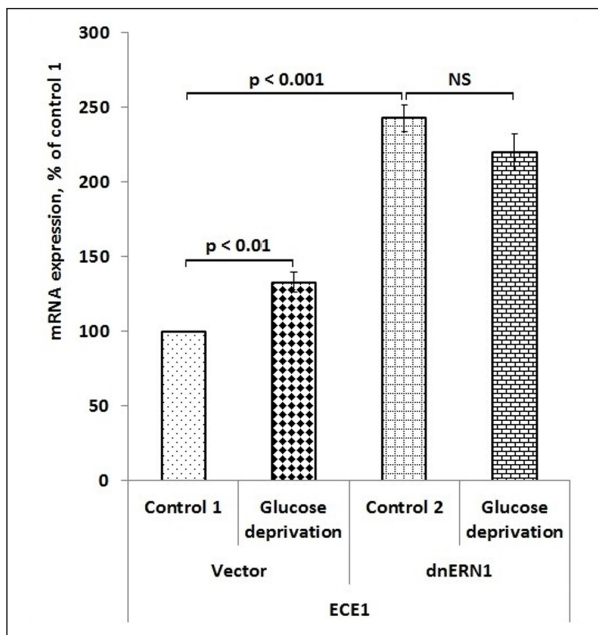


Figure 4. Impact of glucose deprivation on the expression level of endothelin converting enzyme 1 (*ECE1*) gene expression level in control U87 glioma cells (Vector) and cells with a blockade of the ERN1 (dnERN1) measured by qPCR. Values of *ECE1* mRNA expression were normalized to beta-actin mRNA level and represented as percent for control 1 (100%); n=4.

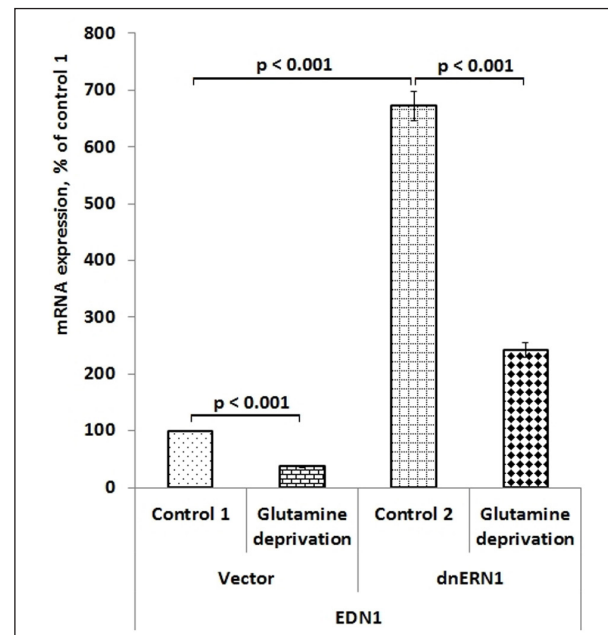


Figure 5. Impact of glutamine deprivation on the expression level of EDN1 mRNA in control U87 glioma cells (Vector) and ERN1 knockdown glioma cells (dnERN1) measured by qPCR. Values of EDN1 mRNA expression were normalized to beta-actin mRNA level and represented as percent for control 1 (100%); n=4.

gene in ERN1 knockdown glioma cells growing under glutamine deprivation condition is also increased but to a much lesser extent (+18%; Figure 8).

Thus, the glucose and glutamine deprivation affects the expression of most studied genes but in different ways and preferentially in ERN1 dependent manner.

Discussion

In this work, we studied the impact of glucose and glutamine deprivation on the expression of genes encoding endothelin-1, its receptors (EDNRA and EDNRB) and endothelin converting enzyme 1, which have relation to functional activity of EDN1, in relation to inhibition of ERN1, the major signaling pathway of the unfolded protein response, in U87 glioma cells with ERN1 knockdown, introduced by dnERN1. Results of these experiments are summarized in Figure 9. These data are important for evaluation of possible significance of these genes in the control of glioma growth through endoplasmic reticulum stress signaling mediated by ERN1, because this stress signaling pathway is involved in numerous metabolic pathways and inhibition of ERN1 signaling enzyme activity in glioma cells had

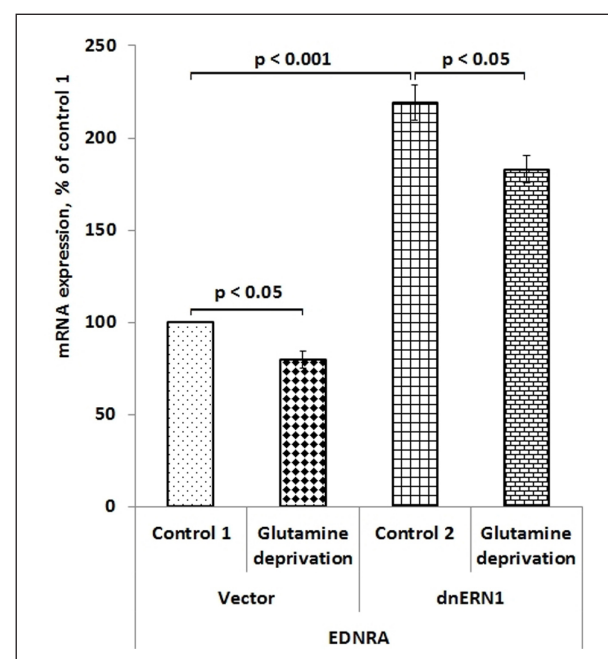


Figure 6. Impact of glutamine deprivation on the expression level of EDNRA mRNA in control U87 glioma cells (Vector) and ERN1 knockdown glioma cells (dnERN1) measured by qPCR. Values of this mRNA expression were normalized to beta-actin mRNA level and represented as percent for control 1 (100%); n=4.

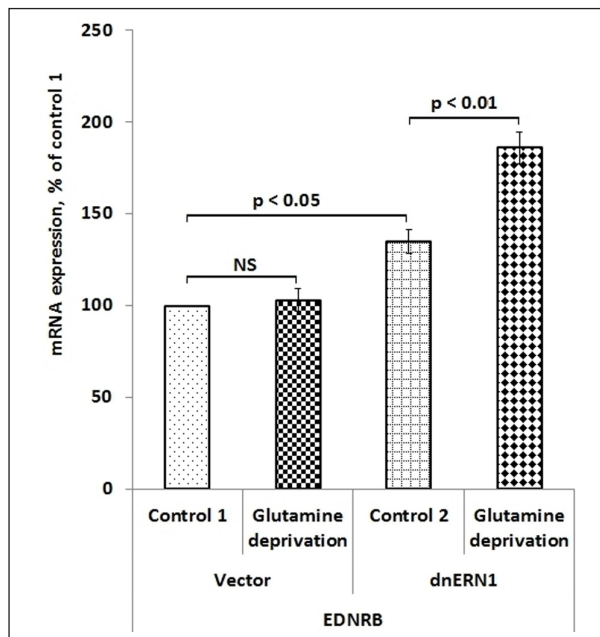


Figure 7. Impact of glutamine deprivation on the expression level of EDNRB mRNA in control U87 glioma cells (Vector) and ERN1 knockdown glioma cells (dnERN1) measured by qPCR. Values of EDNRB mRNA expression were normalized to beta-actin mRNA level and represented as percent for control 1 (100%); n=4.

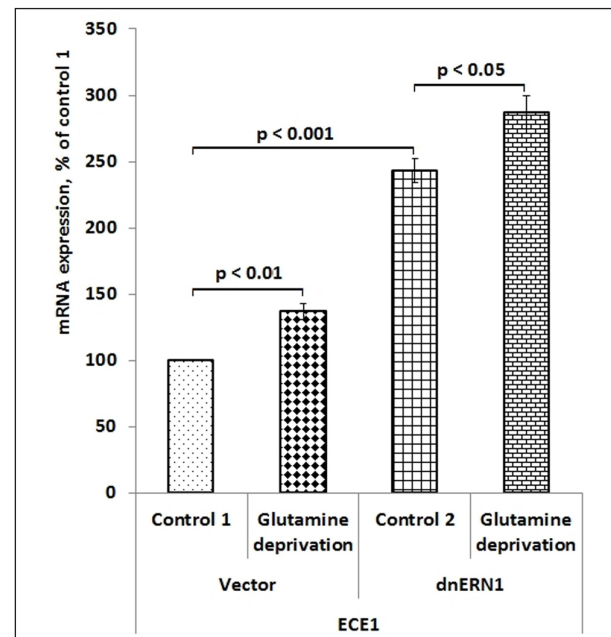


Figure 8. Impact of glutamine deprivation on the expression level of ECE1 mRNA in control U87 glioma cells (Vector) and ERN1 knockdown glioma cells (dnERN1) measured by qPCR. Values of this mRNA expression were normalized to beta-actin mRNA level and represented as percent for control 1 (100%); n=4.

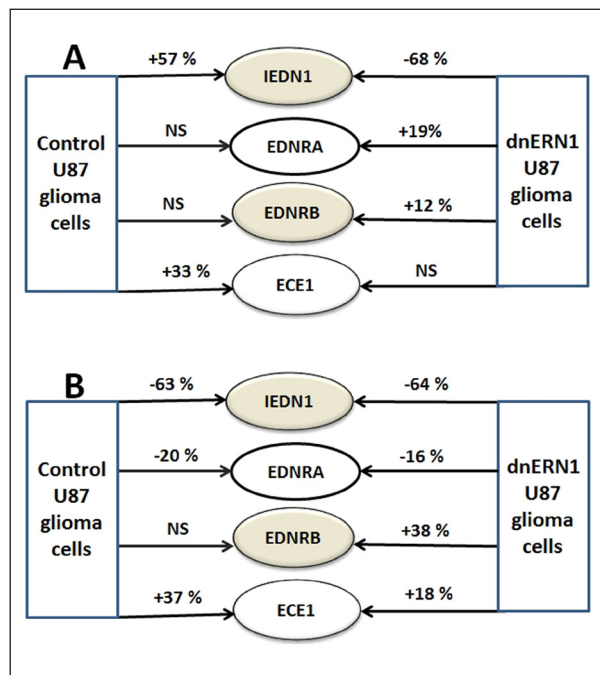


Figure 9. Schematic demonstration of glucose (A) and glutamine deprivations (B) on EDN1, EDNRA, EDNRB, and ECE1 genes expression profile in control and ERN1 knockdown glioma cells; NS – no significant changes.

clear anti-tumor effects (Auf et al. 2010, 2013; Bravo et al. 2013; Manie et al. 2014; Minchenko et al. 2013, 2015a, b; Logue et al. 2018).

Recently, we showed that the expression of EDN1, its receptors, and ECE1 genes is responsible to endoplasmic reticulum stress signaling mediated by ERN1. However, molecular mechanisms of changes in these genes' expression are different (Minchenko et al. 2019). Thus, the expression of EDNRA and ECE1 genes is regulated by ERN1 endoribonuclease, but EDN1 and EDNRB genes – preferentially by ERN1 protein kinase through mechanisms described by Auf et al. (2013) and Minchenko et al. (2015c). Endoplasmic reticulum stress dependent regulation of EDN1 and related proteins agree well with its involving in cancer biology as well as in many other important processes (Teoh et al. 2014; Cook et al. 2015; Niechi et al. 2015; Tapia and Niechi 2019; Minchenko and Caro 2000; Minchenko et al. 2003). At the same time, the prominent pathophysiological aspects of the endothelin system in glioma cells as well as in astrocytes are not clear yet.

We also showed that glucose deprivation enhanced the expression of EDN1 and ECE1 genes and that knockdown of ERN1 signaling enzyme function

significantly modified the response of these genes to glucose-limited condition (Figure 9A). It is possible that the ERN1 signaling is very important for induction of these genes' expression under glucose deprivation and in this connection the knockdown of ERN1 removes sensitivity of *ECE1* gene to glucose-limited condition and leads to a strong suppression of *EDN1* gene expression at this experimental state. At the same time, the expressions of both endothelin receptors are resistant to glucose-limited condition. These data clearly demonstrate that glucose-dependent regulation of endothelin system is preferentially realized through *EDN1* and *ECE1* gene expressions. It is possible that glucose limitation affects different signaling pathways of endoplasmic reticulum stress and thus changes the ERN1 signaling, because there are data that glucose deprivation alters the proapoptotic PERK-CHOP/GADD153 pathway as well as ATF4-mediated apoptosis (Huber et al. 2013; Iurlaro et al. 2017). Furthermore, there are data that glucose deprivation condition can augment the sensitivity of cancer cells to anti-cancer drugs, particularly arctigenin, which inhibits the growth of numerous cancer cells and induces tumor cell death under glucose-limited condition, possibly by blocking the unfolded protein response (He et al. 2018). Results of our study clarify possible mechanisms of glucose deprivation on the proliferation of ERN1 knockdown glioma cells through specific changes in the expression of genes encoding endothelin-1 and related proteins.

At the same time, we observed a strong suppressive impact of glutamine deprivation on the expres-

sion of *EDN1* gene and significantly lesser – on *EDNRA* gene expressions both in control and ERN1 knockdown glioma cells (Figure 9B). It is possible that this effect of glutamine-limited condition on *EDN1* and *EDNRA* gene expressions reflects the sensitivity of these genes to glutamine supply. Thus, these results validate tight interaction of endoplasmic reticulum stress signaling with the delivery of essential nutrients such as glutamine and glucose, which are important substrates for glycolysis and glutaminolysis, as well as glioma growth (Colombo et al. 2011; Huber et al. 2013). However, precise molecular mechanisms are not clear yet and warrant further investigations.

This study provides unique insights into the molecular mechanisms regulating the expression of genes encoding endothelin-1, its receptors, and endothelin converting enzyme 1 in glioma cells under glucose and glutamine deprivations in response to inhibition of ERN1 activity, attesting to the fact that endoplasmic reticulum stress is a necessary component of malignant tumor growth. In this regards, endoplasmic reticulum stress signaling pathways are important targets in combined strategies for glioblastoma therapy (Johnson et al. 2011; Festuccia et al. 2020; Liu et al. 2020; Markouli et al. 2020).

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