ORIGINAL ARTICLE



# Oscillating glucose and constant high glucose induce endoglin expression in endothelial cells: the role of oxidative stress

Lucia La Sala · Gemma Pujadas · Valeria De Nigris · Silvia Canivell · Anna Novials · Stefano Genovese · Antonio Ceriello

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#### Abstract

*Aim* High glucose-induced oxidative stress has been suggested as one of the mediators of endothelial damage in diabetes. The major endothelial protein, endoglin, has been found overexpressed in the vessels during pathological situations, but little is known about its relation to diabetic vascular complications. To clarify the role of endoglin in endothelial injury, we sought to determine the effects of high and oscillating glucose on its expression.

*Materials* Furthermore, the activation of the Krüppel-like factor 6 (KLF-6) and the hypoxia-inducible factor-1 $\alpha$  (HIF-1 $\alpha$ ) as possible regulators of endoglin expression has been evaluated. The possible role of the oxidative stress has been studied evaluating the effects of the antioxidant alphalipoic acid (ALA) and the cellular antioxidant response mediated by NAD(P)H:quinine-oxido-reductase-1 (NQO-1) and heme oxygenase-1 (HO-1).

*Results* Primary HUVECs were cultured for 21 days in normal, high and oscillating glucose (5, 25 and 5/25 mmol/l every 24 h, respectively) with/without ALA. In oscillating

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L. La Sala  $\cdot$  G. Pujadas  $\cdot$  V. De Nigris  $\cdot$  S. Canivell  $\cdot$  A. Novials  $\cdot$  A. Ceriello ( $\boxtimes$ )

Institut d'Investigación Biomédiques August Pi i Sunyer (IDIBAPS) and Centro de Investigación Biomedica en Red de Diabetes y Enfermedades Metabolicas Asociadas (CIBERDEM), Hospital Clinic, C/Rosselló, 149-153, 08036 Barcelona, Spain e-mail: aceriell@clinic.ub.es

#### S. Genovese

Department of Cardiovascular and Metabolic Diseases, IRCCS, Gruppo Multimedica Sesto San Giovanni (MI), Milan, Italy

and high glucose total endoglin, its soluble form (sEng), KLF-6 and HIF-1 $\alpha$  were significantly increased. Simultaneously, the oxidative DNA stress markers 8-OHdG and H2A.X were elevated. Moreover, ENG gene transcriptional rate increased during glucose exposures concomitantly with increased KLF-6 nuclear translocations. ALA significantly reduced all these phenomena. Interestingly, during oscillating and chronic high glucose, NQO-1 and HO-1 did not increase, but ALA induced their overexpression.

*Conclusions* Together, these findings provide novel clue about endoglin in the regulation of high glucose-mediated vascular damage in HUVECs and the role of oxidative stress in this regulation.

Keywords Endoglin  $\cdot$  KLF-6  $\cdot$  HIF-1 $\alpha$   $\cdot$  Diabetic vascular complications  $\cdot$  Oxidative stress  $\cdot$  Oscillating glucose  $\cdot$  High glucose  $\cdot$  Alpha-lipoic acid  $\cdot$  Antioxidant defenses

#### Introduction

There is growing evidence that oxidative stress is involved in the pathogenesis of vascular disease in diabetes [1] and that hyperglycemia induces early endothelial damage through the generation of oxidative stress at mitochondrial level [2–4].

Endoglin (Eng, also known as CD105), a trans-membrane auxiliary receptor (T $\beta$ RIII) that modulates multiple cellular response to members of TGF-beta signaling, is weakly expressed in resting endothelial cells, but is increased during angiogenesis [5, 6]. Numerous studies have reported a high expression of Eng on endothelial cells (ECs) in several vascular pathological situations, including active site of inflamed tissues, atherosclerosis, in response to arterial injury [7, 8] and in wound healing [9]. Besides membranebound Eng, also a soluble form (s-Eng) exists, resulting from the shedding of the membrane-bound receptor [10]. Although the mechanism by which s-Eng is released into the circulation has not been revealed yet, a recent study showed that Eng is proteolytically cleaved near the plasma membrane by matrix metalloproteinases (MMPs), and s-Eng is released into the blood stream [11–13]. Recently, elevated plasma levels of s-Eng have been observed in subjects with vascular diabetic complications [14].

In ECs, the response to vascular injury is mediated by Kröppel-like factor-6 (KLF-6), a transcription factor that has recently been related to diabetic complication [15]. KLF-6 is considered an injury-response factor that transactivates several target genes by direct binding to their promoters, as Eng gene among others [16]. A role for KLF-6 in transcriptional activation of Eng is suggested by its rapid induction in response to endothelial denudation during vascular injury [17]. However, KLF-6 mRNA results upregulated by oxidative stress [18] and in high glucose conditions [19, 20]. Oxidative stress activates the hypoxiainducible factor  $1\alpha$  (HIF- $1\alpha$ ), which is stabilized in cytoplasm by the inhibition of prolyl hydroxylases (PHDs), through the oxidation of the ferrous ion, essential for its catalytic mechanism [21]. HIF-1 $\alpha$  binds to the hypoxiaresponsive elements (HREs) of target genes and upregulates their transcriptions [7], among them, Eng gene [7]. Interestingly, it has already been reported that HIF-1 $\alpha$  is overexpressed in high glucose [22]. In previous studies, we have reported that both oscillating glucose and constant high glucose are dangerous for ECs and that oxidative stress is one of the mediators of the damage [4]. With these premises, we have explored the regulation of Eng expression, the functional activation of KLF-6 and HIF-1 $\alpha$  and the possible role of oxidative stress, in HUVECs, cultured in high glucose, both constant and oscillating. In order to evaluate the possible role of oxidative stress, the effect of alpha-lipoic acid (ALA) and the intracellular antioxidant response, NAD(P)H:quinine-oxido-reductase-1 (NQO-1) and heme oxygenase-1 (HO-1), has been studied. Furthermore, two markers of oxidative stress, 8-hydroxydeoxyguanosine (8-OHdG) and histone 2A variant (H2A.X), which have been proven to be increased in oxidative stress-associated disease [23] and in genotoxic events [24], have been evaluated.

## Materials and methods

#### Materials and cells cultures

The primary pooled HUVECs were purchased from Lonza (Lonza Bioresearch LBS, Basel, Switzerland) and maintained for 3 weeks in endothelial basal medium (EBM-2), supplemented with 2 % heat-inactivated fetal bovine serum, hydrocortisone (0.04 %), basal fibroblastic growth factor (bFGF, 0.4 %), epidermal growth factor (rhEGF, 0.1 %), heparin (0.1 %) and gentamicin/amphotericin (GA-1000, 0.1 %) (all from Lonza) in a humified incubator with 5 % carbon dioxide added.

Experimental design and glucose exposures

HUVECs were seeded in 6-well plates (Corning, NY, USA) at a density of  $1 \times 10^5$  cells/wells. Cells were exposed to three different glucose concentrations: (1) normal glucose (NG, 5 mmol/l), (2) oscillating glucose (OG, 5/25 mmol/l), (3) high glucose (HG, 25 mmol/l). In oscillating glucose condition, glucose concentration in the medium was changed alternatively every day (from 5 to 25 mmol/l) for 21 days [4]. Protein and mRNA were collected from oscillating conditions, while the cells were in NG medium. Experimental control was performed incubating the cells in any condition with mannitol at the same concentration of glucose. Cells were treated with/without alpha-lipoic acid (ALA, DL-6,8-thioctic acid, Sigma-Aldrich, St. Louis, MO, USA, 62.5 µmol/l) for the whole treatment [25]. α-Lipoic acid is an organosulfur compound derived from octanoic acid containing two sulfur atoms (at C6 and C8) connected by a disulfide bond and is thus considered to be a very good antioxidant [26].

Determination of 8-OHdG and sEng

8-OHdG in the HUVECs was determined using Bioxytech 8-OHdG-EIA Kit (OXIS Health Products, Portland, OR, USA). s-Eng in the culture supernatants was measured using specific ELISA Kits (R&D systems UK), following the manufacturer's recommendation. Assays were repeated three times, and each sample was run in triplicate.

#### Western immunoblots

Cells were harvested, and whole cell lysates were prepared using RIPA buffer (150 mM NaCl, 10 mM Tris, pH 7.2, 0.1 % SDS, 1.0 % Triton X-100, 5 mM EDTA, pH 8.0) containing protease and phosphatase inhibitor cocktail. Protein content of the lysates was determined using the Bradford reagent (Sigma-Aldrich, St. Louis, MO, USA). Samples were subjected to 8–16 % Tris–glycine gradient (SDS-PAGE) gels in reducing conditions and blotted onto polyvinylidene fluoride (PVDF) membrane. After blocking with 5 % non-fat dry milk (NFDM) in 20 mM Tris–HCI (pH 7.5), 135 mM NaCl and 0.1 % Tween-20, blots were incubated with monoclonal antibodies against endoglin (D50G1), HIF-1 $\alpha$ , phospho-histone 2AX; obtained from Cell Signaling (Beverly, MA, USA); washed with 20 mM Tris–HCl (pH 7.5), 135 mM NaCl and 0.1 % Tween-20; and incubated with a horseradish peroxidase-conjugated secondary antibody. Proteins were detected using ECL system (Pierce Chemical Co Rockford, IL, USA) according to the manufacturer's instructions and revealed in CCD camera (ImageQuantLAS4000, GE Healthcare, UK). Antibodies against NQO-1 and HO-1 were obtained from BioVision (San Francisco, CA, USA) while against KLF-6 were obtained from Santa Cruz Biotechnology (R-173; Santa Cruz Biotechnology, CA, USA). The  $\beta$ -actin and  $\alpha$ tubulin (Sigma-Aldrich, St. Louis, MO, USA) and lamin-1B (Cell Signaling, Beverly, MA, USA) were used as loaded controls. Protein content quantification was performed using computer-assisted densitometry (www.ima gej.nih.gov, ImageJ, NIH).

## Subcellular protein extracts

Cytoplasmic and nuclear fraction extracts were prepared using Subcellular Protein Fractionation Kit for Cultured Cells (Pierce Chemical Co Rockford, IL, USA) as manufacturer described. Thus, HUVEC  $(1 \times 10^6)$  cells were fractionated; equal amounts of extracts  $(10 \ \mu g)$  were separated in 4–20 % Tris–glycine gradient gels (Lonza Bioresearch LBS, Basel, Switzerland) and then run on SDS-PAGE in reducing conditions.

### Real-time quantitative-PCR (q-PCR) analysis

Total RNA from HUVECs was extracted using RNA purification kit (Norgen Biotek, Thorold, ON, Canada). RNA was stored at -80 °C if not used immediately. RNA purity was assessed by spectrophotometric analysis (Nanodrop, Wilmington, DE, USA). One micrograms of total RNA was reverse-transcribed using the SuperScript III reverse transcriptase and random hexamers (Invitrogen, Life Technologies, Grand Island, NY, USA). Real-time q-PCR was performed using ABI 7900 HT thermo-cycler (Applied Biosystems, Zurich, Switzerland), in reaction buffer using TaqMan PCR Master Mix. Pre-optimized primers and probes gene expression assay were purchased from Applied Biosystems (ENG: Hs00923996\_m1; HMOX1: Hs01110250\_m1; NQO-1: Hs00168547\_m1; KLF-6: Hs00810569\_m1; HIF-1α: Hs00153153\_m1; H2AFX: Hs00266783\_s1). All q-PCR were normalized to 18 s ribosomal RNA expression provided as a pre-optimized control probe. Data were obtained as Ct values.

#### Statistical analysis

Results are expressed as mean  $\pm$  SEM. Statistical analysis was performed using GraphPrism6.0<sup>®</sup> (www.graphpad. com). Differences between groups were evaluated using

the one way ANOVA, followed by Tukey's post hoc test or when appropriate, by Holm-Sidak's multiple comparison test. Statistical significance was assumed at p < 0.05. For kinetic study, the interactions among the parts were evaluated using two-way ANOVA, followed by Bonferroni's post hoc test. At least three different experiments were performed in triplicate to ensure reproducibility.

## Results

Endoglin, HIF-1 $\alpha$  and KLF-6 expression levels increased in oscillating and high glucose in HUVECs

To test whether high glucose (constant and oscillating) was able to activate Eng expression via HIF-1 $\alpha$  and KFL-6 regulations, we have detected mRNA and protein expression levels. The results show increased Eng mRNA expression in OG (p < 0.001) and in HG conditions (p < 0.05; Fig. 1a). The effects were significantly lowest during ALA treatments (OG vs OG + ALA, p < 0.001; HG vs HG + ALA, p < 0.001; Fig. 1a).

HIF-1a mRNA (Fig. 1b) was upregulated in OG and HG conditions (OG, p < 0.01; HG, p < 0.05) compared to normal glucose (NG). ALA reduced the HIF-1a mRNA expression levels (OG vs OG + ALA, p < 0.01; HG vs HG + ALA, p < 0.01; Fig. 1b). The results of the densitometry (Fig. 1d) showed that OG and HG increased the Eng protein level compared to NG, an effect counterbalanced by ALA in both OG and HG (p < 0.001). The protein expression of HIF-1 $\alpha$  was increased in high and oscillating conditions compared to NG (OG, p < 0.001; HG, p < 0.01; Fig. 1e). ALA reduced the HIF-1 $\alpha$  protein expression in both the conditions (OG vs OG + ALA, p < 0.001, HG vs HG + ALA, p < 0.001; Fig. 1e). During glucose, the KLF6 expression increased in OG (p < 0.001) and HG (p < 0.01) compared to NG (Fig. 1c) and ALA counterbalanced these effects (HG vs H+, p < 0.01; OG vs OG + ALA, p < 0.001. Fig. 1c). The Western blot assay demonstrated that KLF-6 was induced coherently in high and oscillating glucose (HG, p < 0.01; OG, p < 0.001; Fig. 1f) and that with ALA its expression returned to basal condition (OG vs OG + ALA, p < 0.05; HG vs HG + ALA, p < 0.01. Fig. 1f).

# Oxidative stress markers

In order to estimate the damage mediated by oxidative stress, we measured 8-OHdG contents and H2AX levels in HUVECs. Our results show increased 8-OHdG in both OG (p < 0.001) and HG (p < 0.01) compared to NG (Fig. 2a). ALA supplementation restored 8-OHdG generation to the basal levels in both HG (HG vs HG + ALA (p < 0.001)



**Fig. 1** High and oscillating glucose induce endoglin, HIF-1 $\alpha$  and KLF-6 expression in HUVECs. Upregulation of endoglin, HIF-1 $\alpha$  and KLF-6 expression revealed by mRNA q-PCR real time (**a**, **b** and **c**, respectively), densitometry analyses and one representative Western blot (**b**, **d** and **f**, respectively), during oscillating (OG), stable high

(HG) and normal glucose (NG), with or without ALA. Data are expressed as mean (±SEM, n = 6-9).  $p^{\dagger} < 0.05$ ,  $p^{\dagger} < 0.01$ ,  $p^{\dagger} < 0.01$ ,  $p^{\dagger} < 0.01$  vs control. Symbols over the *bars* refer to differences between the conditions shown under the *bars*,  $p^{\dagger} < 0.05$ ,  $p^{\ast} < 0.01$ ,  $p^{\ast} < 0.01$ 

and OG (OG vs OG + ALA, p < 0.001, Fig. 2a). H2AX mRNA was upregulated in OG (p < 0.001) and in HG (p < 0.05) compared to NG. In ALA-treated cells, the results show a significant reduction of the transcriptional activity (p < 0.001) respect to NG. Moreover, HG promoted increased double-strand breaks (DSBs) in the cells that could be demonstrated by  $\gamma$ -H2AX formation. Exposition to OG (p < 0.01) and HG (p < 0.05) resulted in a rapid phosphorylation of H2A.X at Ser139 level, which was suppressed with ALA (OG vs OG + ALA, p < 0.05; HG vs HG + ALA, p < 0.05; Fig. 2c).

Intracellular antioxidant (NQO-1 and HO-1) response in high and oscillating glucose: the effect of ALA

Both NQO-1 and HO-1 were dysregulated at the transcriptional and protein level during exposure to OG and HG, leading to a lack of activation of cellular defense systems (Fig. 3a–d). ALA strongly induced mRNA levels of both NQO-1 (OG vs OG + ALA p < 0.001, HG vs HG + ALA p < 0.001, NG vs NG + ALA p < 0.001, respectively) and HO-1 (OG vs OG + ALA p < 0.001, HG vs HG + ALA p < 0.001, NG vs NG + ALA p < 0.001, HG vs HG + ALA p < 0.001, NG vs NG + ALA p < 0.001, respectively), even in NG (Fig. 3a–b). Consistently, ALA strongly induced the protein levels of both NQO-1 (OG vs OG + ALA p < 0.001, HG vs HG + ALA p < 0.001, NG vs NG + ALA p < 0.001, respectively) and HO-1 (OG vs OG + ALA p < 0.001, HG vs HG + ALA p < 0.001, NG vs NG + ALA p = NS, respectively; Fig. 3c–d).

High and oscillating glucose induce the activation of the transcription factor KLF-6 and HIF-1 $\alpha$  in HUVECs

Functional activity of KLF-6 was demonstrated by Western blot analyses of cytoplasmic and nuclear fractions in both oscillating and high glucose conditions. Our results revealed that KLF-6 localized predominantly to the nuclear compartment in OG (*fig. s1A*; p < 0.001 vs OG<sub>cyt</sub>; p < 0.05 vs NG<sub>nuc</sub>) and HG (p < 0.001 vs HG<sub>cyt</sub>; p < 0.05 vs NG<sub>nuc</sub>). Moreover, the translocation in HG is higher than in OG (p < 0.05 HG<sub>nuc</sub> vs OG<sub>nuc</sub>).

To evaluate the potential role of KLF-6 or HIF-1 $\alpha$  as activators of Eng transcription after glucose exposure, kinetic analyses were performed at different time points. mRNA expression after high glucose stimulation (25 mmol/l) was measured in real time. The expressions

Fig. 2 Effects of high and oscillating glucose, with or without ALA, on the markers of oxidative stress in HUVECs. a 8-OHdG content (ng/ml) in HUVEC at 21 days of experiments, during oscillating (OG), stable high (HG) and normal glucose (NG), with or without ALA. b mRNA expression levels of H2A.X (histone 2A.X) in HUVEC at 21 days of experiments, during oscillating (OG), stable high (HG) and normal glucose (NG), with or without ALA. c Western blot of  $\gamma$ -H2AX, a marker of oxidative stress-induced doublestrand breaks, in HUVEC at 21 days of experiments, during oscillating (OG), stable high (HG) and normal glucose (NG), with or without ALA. Data are expressed as mean (±SEM, n = 6). p < 0.05, p < 0.01,  $^{\ddagger \ddagger \ddagger} p < 0.001$  vs control. Symbols over the bars refer to differences between the conditions shown under the *bars*, \**p* < 0.05, \*\**p* < 0.01, \*\*\*p < 0.001





HG

for Eng, KLF6 and HIF-1 $\alpha$  are shown with a graphic summarizing the dynamic expressions during glucose exposure (*fig. s1C*). KLF-6 mRNA was rapidly induced within the third hour of injury. After the early induction of KLF-6, Eng mRNA expression increased approximately twofold at 6–12 h and decreased thereafter. The kinetics of Eng mRNA revealed a time delay of Eng respect to KLF-6 and HIF-1 $\alpha$ . Two-way ANOVA reveals significant interactions between ENG and KLF-6 (3 h, p < 0.01; 12 h, p < 0.01; and 72 h, p < 0.05) and ENG and HIF-1 $\alpha$  (12 h, p < 0.05 and 48 h, p < 0.001). KLF-6 induction in timedependent manner is significantly consistent with the possibility that leads to the upregulation of Eng.

Effects of high and oscillating glucose on release of sEng in HUVEC

In order to assess the release of sEng into the media, we additionally performed ELISA quantification in the supernatants of HUVECs treated with/without ALA during 21 days of culture. The data revealed significant increased amounts in OG (p < 0.05 vs control) and HG (p < 0.001 vs control) (*fig. s*1B), whereas they were found reduced in ALA treatment (OG vs OG + ALA, p < 0.05; HG vs HG + ALA, p < 0.05).

## Discussion

In the present study, we demonstrated that both oscillating glucose and high glucose induce Eng overexpression in ECs and that oxidative stress may be the potential mediator of this effect. Eng modulates the signaling of multiple members of the transforming growth factor- $\beta$  (TGF- $\beta$ ) superfamily. Several published studies have reported that Eng negatively regulates TGF- $\beta$ -mediated signaling in quiescent endothelium [27] and is involved in endothelial proliferation in response to an injury [10] and in the inflammation [28]. Recently, increased plasma levels of s-Eng have been associated with diabetic complications in

Fig. 3 Alpha-lipoic acid (ALA) induces expression of NOO-1 and HO-1 in high and oscillating glucose. NQO-1 (a, c) and HO-1 (b, d) expression in HUVEC at 21 days of experiments, during oscillating (OG), stable high (HG) and normal glucose (NG), with or without ALA. Data are expressed as mean (±SEM, n = 6). p < 0.05, p < 0.01,  $^{\ddagger\ddagger}p < 0.001$  vs control. Symbols over the bars refer to differences between the conditions shown under the bars. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001



diabetes [12, 29]. In this study, for the first time, we report that high glucose, both constant and oscillating, upregulates Eng expression and sEng release in ECs, suggesting a possible direct link between hyperglycemia and increased sEng in diabetes. Multiple mechanisms have been proposed to explain the release of sEng. Eng is an inducible gene, induced via the activation of KLF-6 and HIF-1  $\alpha$  in response to various factors [7, 16, 30-32]. We confirm that HIF-1 $\alpha$  is overexpressed in HG [22], and for the first time, that is increased in OG. KLF-6 is a transcription factor having a crucial role in mediating the transcriptional activation of Eng upon vascular injury in vivo [16, 33]. Our study shows a possible role for KLF-6 in the transcriptional activation of Eng in high glucose, as suggested by its rapid induction within the third hour of glucose exposure. The study of the mRNA kinetics reveals a delay of Eng increase respect to KLF-6 and HIF-1 $\alpha$  of about three-six hours. This effect probably is due to specific stimulus to high glucose. Moreover, the data demonstrate that the transcriptional level of Eng is accompanied by an increase in the translocation into the nucleus of KLF-6 after glucose stimuli.

The increase in 8-OHdG confirms the free radicals production in high glucose in ECs [4, 34, 35]. Consistently,

we also found an increase in the  $\gamma$ -H2AX, a marker of oxidative stress-induced double-strand breaks [36], and in the histone 2AX, which is a critical DNA sensor that undergoes to phosphorylation on serine 139 upon genotoxic stress [36].

ALA has been shown to be effective in the treatment of several conditions in which oxidative injury is thought to be important, as diabetes [37] and, specifically, in the protection of various cell types exposed to HG and OG [25, 38]. The evidence, in our study, that ALA counterbalances the effects of HG and OG clearly suggests a role of oxidative stress in the described phenomena. These data are consistent with the evidence that reactive oxygen species lead to increased levels of s-Eng via the generation of oxysterols [12] and that previous studies have shown a link between endoglin deficiency and glucose metabolism by which endoglin modulates insulin levels [39].

The dysregulation of antioxidant response and the accumulation of ROS and oxidative damage are a causal factor in the development of several diseases [40]. It is worthy of interest that in both HG and OG, the mRNA and the intracellular protein levels of the antioxidant defenses NQO-1 and HO-1 are not changed respect to control. This is consistent with the report showing that HO-1 is

downregulated in an animal model of diabetes [41]. The lack of an efficient defense against the oxidative stress generated by both HG and OG may explain the observed results. Cudmore et al. [42] demonstrated the capability of HO-1 to inhibit s-Eng release from endothelium in mice. It can be hypothesized that, in our study, ALA induces an efficient intracellular increase in both NQO-1 and HO-1, which in turn, protecting endothelial cells, counteracts the induction of Eng and the release of its soluble form.

In conclusion, our data suggest that, during hyperglycemia, oxidative stress is the possible mediator of the ECs damage, leading to the activation of KLF-6 and HIF-1 $\alpha$ , which in turn could trans-activate Eng expression. However, the precise role of Eng in vascular complications of diabetes still remains to be elucidated.

**Conflict of interest** Lucia La Sala, Gemma Pujadas, Valeria De Nigris, Silvia Canivell, Anna Novials, Stefano Genovese, Antonio Ceriello declare that they have no conflict of interest.

**Human and animal rights statement** This article does not contain any studies with human or animal subjects performed by any of the authors.

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