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Regulation of Cystathionine γ-Lyase Expression by Lipopolysaccharide in Human Umbilical Vein Endothelial Cells: Involvement of NF-κB Signaling

Maoxian Wang, PhD

Department of Biological Sciences, Hanshan Normal University, Chaozhou, P. R. China

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ABSTRACT

Hydrogen sulfide (H_2S) acts as a signaling molecule that modulates vascular tone, protects against oxidative stress, and functions as an oxygen sensor. Cystathionine γ-lyase (CSE) facilitates the production of H_2S, and the CSE/H_2S signaling pathway is implicated in endotoxin-induced inflammation, such as that induced by lipopolysaccharide (LPS). Therefore, it is essential to examine the expression and regulation of CSE in human umbilical vein endothelial cells (HUVECs) following LPS stimulation. LPS treatment for 6 hours significantly increased CSE mRNA and protein levels in HUVECs. A dual-luciferase reporter plasmid pGL4.12-HuCSE710, containing either the wild-type CSE gene promoter or its mutant variant, was co-transfected with the pRL-CMV vector into HEK-293T cells. This study investigated the effects of nuclear factor-κB (NF-κB) transcription factor binding to this promoter on the transcriptional regulation of the CSE gene in HUVECs after LPS treatment. The DNA sequence GGACATTCC within the CSE gene promoter was significantly associated with the transcriptional regulation of CSE in response to LPS treatment. These findings have substantial implications for further research on the regulatory mechanisms of CSE in inflammation and offer promising insights with potential clinical relevance. Therefore, LPS regulates CSE expression in HUVECs primarily through NF-κB activation, with the NF-κB binding site on the CSE promoter being critical for LPS-induced upregulation and subsequent inflammatory response.

Keywords: hydrogen sulphide (H_2S), cystathionine γ-lyase (CSE), lipopolysaccharide (LPS), nuclear factor-κB (NF-κB), transcription factor

Introduction

Hydrogen sulfide (H_2S) functions as a signaling molecule that regulates vascular tone, protects tissues from oxidative stress, and facilitates oxygen sensing.[1] Cystathionine γ-lyase (CSE) is one of the key enzymes responsible for the production of H_2S in mammalian tissues.[2] The CSE/H_2S signaling pathway has been implicated in various inflammatory conditions, including those induced by bacterial endotoxins.[3]

Lipopolysaccharide (LPS), a major component of Gram-negative bacterial cell walls, is a potent inducer of inflammatory responses. Previous studies have demonstrated that LPS enhances the biosynthesis of CSE and H_2S in macrophages primarily through Toll-like receptor-4 (TLR-4)-dependent mechanisms involving both p38 MAPK and NF-κB pathways.[4] Exogenous H_2S has been shown to suppress IκB-α degradation and NF-κB activity,[5] and the CSE/H_2S system protects against LPS-induced inflammation and cell hyperpermeability by blocking NF-κB transactivation.[6] Furthermore, LPS-induced inflammation in murine macrophages is associated with H_2S production, and CSE/H_2S attenuates LPS-induced sepsis by inhibiting oxidative stress.[7,8]

The interaction between H_2S and NF-κB signaling appears to be bidirectional and context-dependent. Endogenous H_2S has been shown to deactivate IKKβ, thereby inhibiting NF-κB pathway activation and regulating inflammation in pulmonary artery endothelial cells. [9] Additionally, H_2S regulates LPS-induced inflammation and apoptosis by activating the PI3K/Akt/NF-κB signaling pathway.[10] Recent studies have further expanded our understanding of the CSE/H_2S pathway in various pathological conditions. For instance, endothelial endogenous CSE/H_2S alleviates endothelial pyroptosis by activating sirtuin-1, thereby preventing LPS-induced acute lung injury.[11] H_2S also attenuates hypertrophy in human ventricular cardiomyocytes by modulating stress-response signaling and suppressing its own methylation.[12] In the context of vascular inflammation, exogenous H_2S mitigates angiotensin II-induced inflammation and cytotoxicity by inhibiting the endothelin-1 (ET-1)/NF-κB signaling pathway in HUVECs.[13]

Studying the relationship between the CSE gene promoter and its expression regulation is vital for elucidating the molecular mechanisms of related diseases and identifying new drug targets.[14] Endothelial injury and barrier dysfunction during sepsis occur via modulation of tumor necrosis factor-α/NF-κB signaling, providing new insights into the mechanisms of endothelial injury in sepsis.[15] H_2S may mitigate trimethylamine N-oxide (TMAO)-induced macrophage inflammation by decreasing p65 NF-κB phosphorylation through upregulation and sulfhydration of sirtuin-1 activity, suggesting that H_2S could be used for treating inflammatory vascular diseases.[16]

The effects of H_2S on smooth muscle relaxation, inflammation suppression, and cell protection have been well studied,[17] and the CSE/H_2S signaling pathway is involved in endotoxin-induced inflammation such as that induced by LPS. Syndecan-3 (SDC3) inhibits the LPS-induced inflammatory response of bovine mammary epithelial cells through the NF-κB pathway, in which NF-κB p50 may be an important target of SDC3.[18] Inhibition of fatty acid-binding protein 4 (FABP4) reduces LPS-induced HUVEC damage via inactivation of NF-κB p65 and activation of peroxisome proliferator-activated receptor γ (PPARγ) signaling.[19] A novel 4-trifluoromethylquinoline derivative (TKL002) exerts potent anti-glioblastoma activity via modulation of the CTH/H_2S/NF-κB/EMT signaling axis.[20] The protective effects of alpha-lipoic acid (ALA) depend on the reduction of CSE expression in LPS-stimulated RAW 264.7 macrophages.[21]

Our previous study identified that the DNA sequence GGGACATTCC located within the promoter region of the mouse CSE gene is intricately associated with the transcriptional regulation of the mouse CSE gene following LPS treatment. The NF-κB binding site within the CSE promoter is crucial for LPS-induced expression of CSE in mammalian cells.[22] However, whether a similar regulatory mechanism exists in human endothelial cells remains to be determined. Consequently, it is imperative to examine the expression and regulation of CSE in HUVECs following LPS stimulation.

The present study aimed to: (i) investigate the effect of LPS on CSE expression at both the mRNA and protein levels in HUVECs; (ii) identify and characterize the NF-κB binding site within the human CSE promoter; and (iii) determine whether this binding site is functionally required for LPS-induced transcriptional regulation of

CSE. Elucidating these mechanisms will advance the understanding of vascular inflammation and may identify novel therapeutic targets for inflammatory cardiovascular diseases.

Methods

Construction of A Luciferase Reporter under Cystathionine γ-Lyase Promoter Control

HUVECs were cultured to 80-90% confluence and subsequently collected in a 1.5-mL centrifuge tube. Genomic DNA was extracted from HUVECs using TransGen Biotech protocols. The promoter sequence of the CSE gene was identified in the GenBank database (NC_000001.11), and primers for both the upstream and downstream regions were designed accordingly. The target DNA fragment was 710 bp, spanning from −696 to +16 nucleotides. PCR primers were designed using the online tool Primer-BLAST, and a 710-bp DNA fragment of the CSE gene was amplified by PCR using pGL4.12-HuCSE710 as the template. The forward primer sequence was 5′-CGGGGTACCCATTAGGG GGAGTTTCTCTCTGT-3′, and the reverse primer sequence was 5′-CCGCTCGAGCTGCAGTCTCACGAT CACAGT-3′. The PCR product was subsequently digested with the restriction enzymes *Kpn*I and *Xho*I (Takara Bio, China) and cloned into a promoterless pGL4.12 vector (Promega, USA). The resulting construct was designated pGL4.12-HuCSE710. A reporter vector containing the mutant CSE promoter was constructed using the same procedure, except that an alternative forward primer (5′-CGGGGTACCCATTAGGATCTGTTTCTCTCTGT-3′) was used for PCR amplification.

Bioinformatics Analysis of the Cystathionine γ-lyase Gene Promoter

The cloned sequences of the CSE gene 5′ flanking region were analyzed using the online Neural Network Promoter Prediction tool (http://fruitfly.org:9005/seq_tools/promoter.html) and the FPROM/Human Promoter Prediction tool (http://www.softberry.com/berry.phtml?topic=fprom&group=programs&subgroup=promoter) to identify and evaluate promoters. These findings were integrated with literature reports, CpG island prediction software (http://www.urogen e.org/cgi-bin/methprimer/methprimer.cgi) and JASPAR CORE online software (http://jaspar.genereg.net/) to predict CpG islands and transcription factor binding sites.

Cell Culture and Treatment

The HEK-293T cell line (Cat# GNHu17) was procured from the Cell Bank of the Chinese Academy of Sciences, and HUVECs were obtained from the School of Pharmacy at Fudan University. Transfected cell lines were cultured at a density of $0.5\text{-}1\times10^6$ cells per 35-mm dish. Subsequently, the cells were incubated with LPS at concentrations of 0.1, 0.5, and 2.0 μg/mL for 6 hours at 37°C. Control cells were treated with an equivalent volume of saline.

Luciferase Assay

HEK-293T cells were cultured to 70-80% confluence prior to transfection. Subsequently, 5 μg of either pGL4.12-HuCSE710 or pGL4.12-HuCSE710m, along with 0.028 μg of the pRL-CMV control vector, were introduced into the cells in a 3.5-cm dish using Xfect transfection reagent (Takara Bio USA, Inc.). Firefly and *Renilla* luciferase activities were measured using a TransDetect Double-Luciferase Reporter Assay Kit (TransGen Biotech, Beijing, China) in conjunction with a Multimode Microplate Reader (Berthold Technologies GmbH & Co. KG).

RNA Isolation and Quantitative Real-time PCR

Total RNA was isolated using TransZol Up reagent (TransGen Biotech, Beijing, China), and the extracted RNA was dissolved in RNase-free water. First-strand cDNA was synthesized by incubation at 42°C for 30 minutes using anchored oligo$(dT)_{18}$ primers. The reaction mixture contained 2 μg of RNA, 1 μL of anchored oligo$(dT)_{18}$ primers, 10 μL of 2× TS reaction mix, TransScript™ RT/RI Enzyme mix (TransGen Biotech, Beijing, China), and RNase-free water in a total volume of 20 μL. Quantitative real-time PCR was performed in a final volume of 25 μL containing 11 μL of cDNA diluted with double-distilled H_2O (1:20), 0.5 μL of 0.2 μM primer, 0.5 μL of Passive Reference Dye II, and 12.5 μL of 2× TransStart™ Green qPCR SuperMix (TransGen Biotech, Beijing, China). All reactions were conducted in quadruplicate on a LightCycler 96 system (Roche Molecular Systems, Inc.) under the following conditions: 95°C for 10 minutes, followed by 45 cycles of 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 10 seconds. The primer pair Q-CSE forward/Q-CSE reverse (Table 2) was designed to determine the relative expression of CSE in the samples. Genomic DNA and primer contamination controls included either non- RT or

template-free PCR. The PCR efficiency was between 95% and 100% for all primer sets. After verifying that the *ACTB* and *CSE* mRNA primers had similar amplification efficiencies, relative mRNA quantities were normalized to those of the housekeeping gene *ACTB*.

Western Blot

For protein extraction, 0.5×10^6 HUVECs were incubated with 120 µL of mild RIPA buffer (TransGen Biotech, China). The lysate was cleared at 12,000×g and 4°C for 15 minutes, and the supernatant was denatured at 95-100°C for 10 minutes. Proteins were separated using 10% SDS-PAGE to detect CSE and ACTB (Sangon Biotech, Shanghai). The proteins were transferred onto polyvinylidene fluoride (PVDF) membranes (0.45 µm). The membranes were incubated overnight at 4°C with anti-CSE antibodies (1:1,000) and anti-ACTB antibodies (1:2,000). The membranes were then incubated at 4°C with horseradish peroxidase (HRP)-conjugated goat anti-mouse antibodies (1:5,000) (Sangon Biotech Co., Ltd., Shanghai, China). The results were scanned and quantified using FluorChem HD2 sensitive chemiluminescent imaging software (ProteinSimple, USA).

Statistical Analysis

The results are shown as the mean ± SEM of at least three independent experiments. Differences were analyzed using one-way or two-way ANOVA with Tukey's test. Statistical significance was set at $P < 0.05$.

Results

Amplification of the Cystathionine γ-lyase Gene 5' Promoter Region

Genomic DNA was extracted from HUVECs, and PCR products were detected by 1.0% agarose gel electrophoresis as a single target band of 710 bp. After double digestion of the pGL4.12-HuCSE710 recombinant plasmid with *Kpn*I and *Xho*I, the products were separated by 1.0% agarose gel electrophoresis, revealing two bands (0.71 kb and 4.4 kb) corresponding to the CSE gene promoter fragment and pGL4.12 vector, respectively. Sequencing and comparison confirmed that the 5' flanking sequence of CSE was 100% homologous to the sequence reported in the GenBank database. CpG island predictions were performed using an online forecasting tool (http://www.urogene.org/cgi-bin/methprimer/methprimer.cgi). Two CpG islands were identified in the amplified CSE gene promoter HuCSE710 (Figure 1), in which the total content of C and G was >50.0%. [23] The CSE gene promoter was analyzed using the online prediction tool JASPAR CORE (http://jaspar.genereg.net/) with keywords CORE, ChIP-seq, and *Homo sapiens* to identify transcription factor-binding sites with relative profile score thresholds >90%. Among the binding sites, one was predicted for AR, one for BATF:JUN, one for C/EBP, three for E2F1, one for EBF1, eight for FOX, one for GATA, one for KLF5, one for MYB, one for NFYB, one for NR1H4, one for NRF1, one for SOX10, two for SP1, one for SP2, three for STAT3, three for TFAP, one for TFDP1, and three for THAP1. Moreover, the relative profile score threshold for NFKB1 transcription factors was >85%, with HuCSE710 fragments showing an NFKB1 binding site score of 10.1692, whereas HuCSE710m fragments showed no NFKB1 binding sites. The results of the bioinformatics analysis of the CSE gene promoter are shown in Table 1.

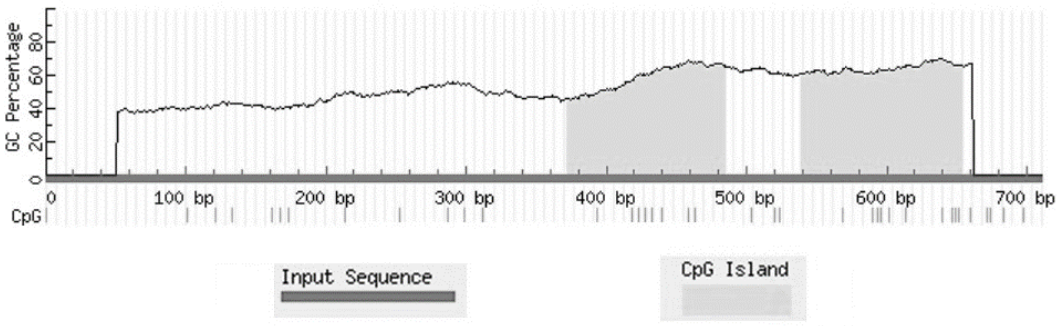


Figure 1. CpG island prediction for HuCSE710. Using criteria of island size > 100 bp, GC percentage > 50.0%, and observed/expected ratio > 0.6, two CpG islands were identified in HuCSE710: island 1 (113 bp, positions 372–484) and island 2 (116 bp, positions 539–654).

Table 1. Results of bioinformatics analysis of the CSE gene promoter.

Software	Starting site/bp	Termination site/bp	Score
Neural Network Promoter Prediction	622	672	0.93
FROM/Human promoter prediction	632	-	7.994

Table 2. Primers used for quantitative RT-PCR assays.

Gene	GenBank Accession number	Forward Primer/Reversed Primer	Exon	Amplicon size
CSE	NM_001902.5	5'- GGCTCTACCTGCGTGCTTTA -3'	1	118 bp
		5'- CGCGAAAGAAGAAGAGAGGA -3'	1	
ACTB	NM_001101.3	5'- CTCTTCCAGCCTTCCTTCCT -3'	2	109 bp
		5'- TGTTGGCGTACAGGTCTTTG -3'	2	

Determination of Cystathionine γ-lyase Promoter Activity

To investigate the involvement of NF-κB in the regulation of CSE expression, we performed a reporter assay incorporating both the wild-type and mutant variants of the NF-κB binding site adjacent to the CSE gene (Figure 2). This assay was conducted in transiently transfected HEK-293T cells. Following treatment with LPS, the transfected HEK-293T cells (seeded at 1×10^6 cells per 35-mm dish) were assessed for firefly and *Renilla* luciferase activities 48 hours after DNA transfection using a dual-luciferase reporter assay kit (TransGen Biotech, Beijing, China) according to the manufacturer's protocol. The results are presented in Figure 3. The relative activity of the pGL4.12-HuCSE710 vector was 36.66-fold higher than that of pGL4.12, whereas the relative activity of the pGL4.12-HuCSE710m vector was 14.73-fold higher than that of pGL4.12. The subcloned plasmids exhibited high activity and were suitable for subsequent experiments.

Figure 2. The wild-type and mutant promoters of the CSE gene were inserted into the pGL4.12 vector.

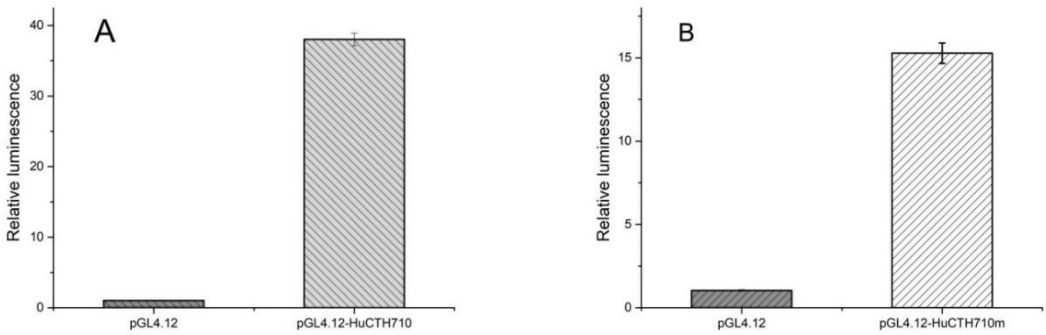


Figure 3. Determination of CSE promoter activity. (A) Activity of pGL4.12-HuCSE710 in HEK-293T cells; (B) activity of pGL4.12-HuCSE710m. The relative activity of the pGL4.12-HuCSE710 vector was 36.7-fold higher than that of pGL4.12, while the activity of the pGL4.12-HuCSE710m vector was 13.5-fold higher than that of pGL4.12.

Effect of Lipopolysaccharide on Cystathionine γ-lyase mRNA Expression

To examine the influence of LPS on CSE gene transcription in HUVECs, we evaluated CSE mRNA expression levels. As shown in Figure 4, exposure to LPS at concentrations of 0.1, 0.5, and 2.0 μg/mL for 6 hours increased CSE mRNA levels in HUVECs, with particularly notable increases at 0.1 and 0.5 μg/mL LPS. However, the higher concentration (2.0 μg/mL) showed reduced effects, which may be attributable to the toxic or inhibitory effects of LPS on HUVECs.

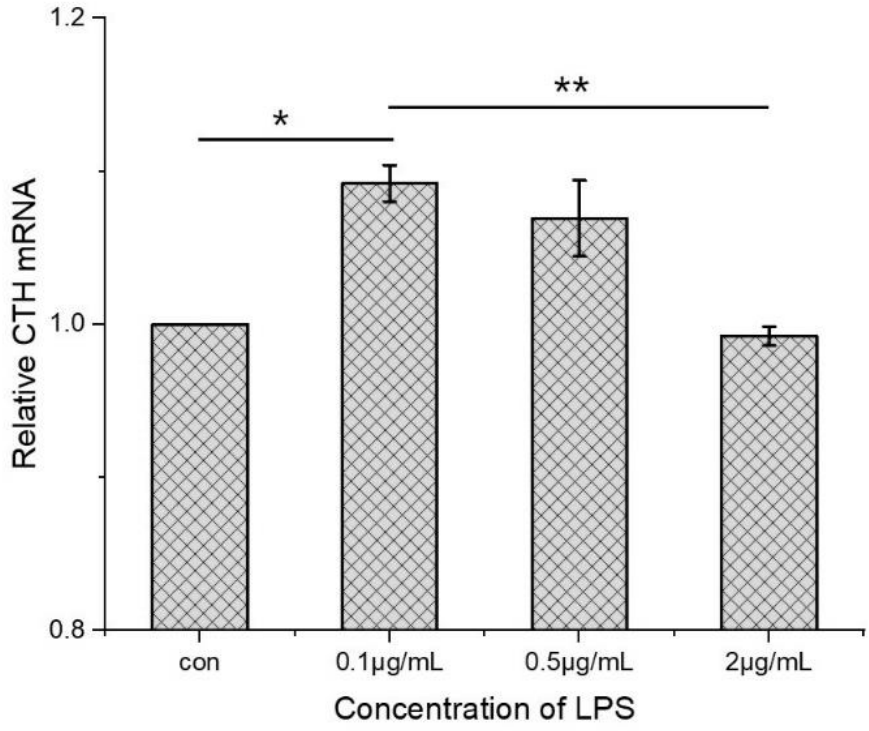


Figure 4. Effect of LPS on CSE mRNA expression. After treatment with LPS (0.1, 0.5, or 2.0 μg/mL) for 6 h, CSE mRNA levels in HUVECs increased, particularly at 0.1 and 0.5 μg/mL. A higher concentration of LPS (2.0 μg/mL) had a smaller

Effects of Lipopolysaccharide on Cystathionine γ-lyase Protein Expression

We examined the effects of LPS on CSE protein expression in HUVECs. As shown in Figure 5, after LPS treatment (0.1, 0.5, and 2.0 μg/mL) for 6 hours, the CSE protein level was obviously increased by 0.1 and 0.5 μg/mL LPS. Compared with those lower concentrations, LPS treatment at 2.0 μg/mL for 6 hours decreased the CSE protein level.

Effects of Lipopolysaccharide on Wild-type or Mutant Cystathionine γ-lyase Promoters

The effect of LPS on the CSE promoter was studied using transient transfection. LPS treatment increased CSE expression in HEK-293T cells. Bioinformatics analysis

using an algorithm for searching transcription factor binding sites[24] identified a potential NF-κB binding site in the promoter of the CSE gene with the DNA sequence 5′-GGACATTCC-3′. To investigate the regulatory role of NF-κB on the CSE gene, we performed a reporter assay using luciferase under the control of either a wild-type CSE gene promoter region (containing the NF-κB binding site) or a mutant promoter region (lacking this site), as depicted in Figure 6. As illustrated in Figure 6A, following treatment with LPS at 0.1, 0.5, and 2.0 μg/mL for 6 hours, the activity of the wild-type CSE promoter in transfected HEK-293T cells increased relative to the control group, with a pronounced response at 0.5 μg/mL LPS. Conversely, as shown in Figure 6B, the activity of the mutant CSE promoter was reduced compared with the control group, particularly in response to 0.1 μg/mL LPS. The observed increase in wild-type CSE promoter activity after LPS treatment, in contrast to the decrease in mutant CSE promoter activity, suggests that mutations in the NF-κB binding site affect the transcriptional regulation of the CSE gene by LPS.

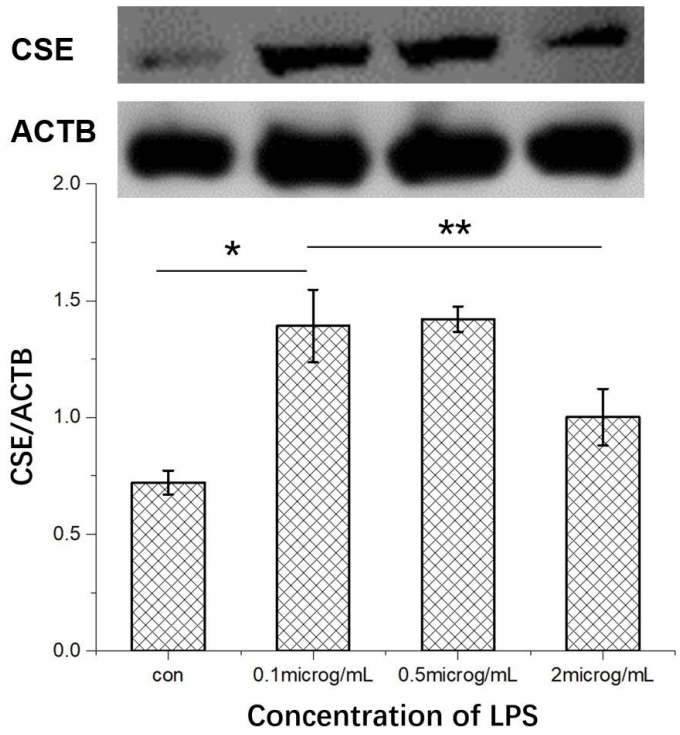
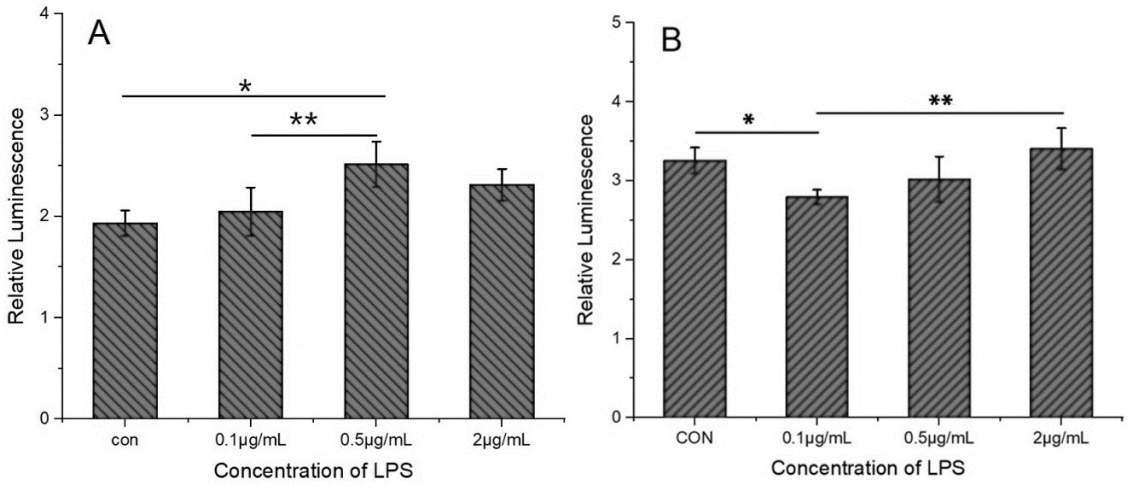


Figure 5. Effects of LPS on CSE protein expression. After treatment with LPS (0.1, 0.5, or 2.0 μg/mL) for 6 h, CSE protein levels in HUVECs increased, particularly at 0.1 and 0.5 μg/mL. The level after 2.0 μg/mL LPS treatment was compared with those after 0.1 and 0.5 μg/mL treatment. (*P < 0.01, **P < 0.05) effect than lower concentrations. (*P < 0.01, **P < 0.01)



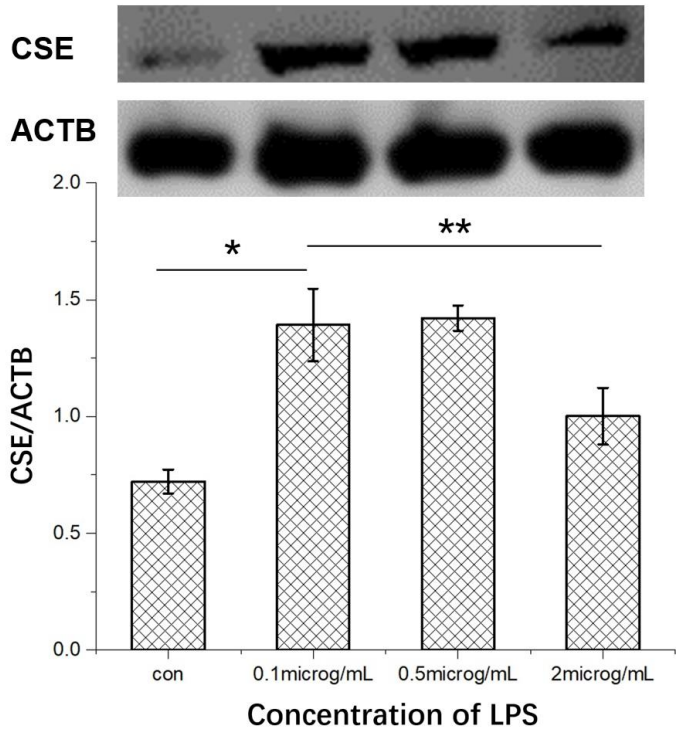


Figure 6. Effects of LPS on wild-type and mutant CSE gene promoter activity. HEK-293T cells were transfected with promoter constructs and then treated with different concentrations of LPS for 6 h. (A) Wild-type CSE promoter; (B) mutant CSE promoter. (*P < 0.01, **P < 0.05)

Discussion

This study demonstrates that LPS regulates CSE expression in HUVECs in a concentration-dependent manner primarily via NF-κB signaling. The GGACATTCC sequence in the CSE promoter is a critical NF-κB binding site essential for LPS-induced transcriptional activation. To our knowledge, this is the first evidence that CSE modulates LPS-induced inflammatory responses in human cells, including both pro-inflammatory and co-inflammatory effects.

Our findings extend prior mammalian studies: [22] the NF-κB binding site on the CSE promoter is critical for LPS-induced CSE expression in mouse macrophages and HEK-293 cells, and its disruption abrogates promoter activity. The present study corroborates this in human HUVECs and shows that CSE transcriptional regulation is mediated via this site in HEK-293T cells. Moreover, LPS significantly affects post-transcriptional regulation, suggesting additional mechanisms beyond promoter binding. A notable finding is the biphasic, concentration-dependent effect of LPS on CSE expression: 0.1 and 0.5 μg/mL LPS for 6 h increased CSE mRNA and protein levels, whereas 2.0 μg/mL reduced them. This may reflect dual CSE/H_2S roles—downregulation in early inflammation to limit vasodilation, and upregulation later to promote resolution. This interpretation is supported by the concentration-dependent dual bioactivity of H_2S, [25] and the interaction between the CSE/H_2S pathway and NF-κB signaling is bidirectional and context-dependent. Numerous studies have established that the CSE/H_2S signaling pathway is involved in endotoxin-induced inflammation.[26-28] For instance, H_2S has been shown to promote prostate cancer progression through the IL-1β/NF-κB signaling pathway and acts as an inflammatory mediator via the NF-κB/ERK pathway in macrophages.[29,30] Conversely, H_2S exerts a protective effect on pulmonary arterial hypertension (PAH) by inhibiting the activation of the NF-κB signaling pathway and the subsequent endothelial-to-mesenchymal transition (EndMT) in pulmonary arteries.[31] H_2S also regulates LPS-induced inflammation and apoptosis by activating the PI3K/Akt/NF-κB signaling pathway.[32]

The anti-inflammatory effects of H_2S are partly mediated by inhibiting NF-κB transactivation. Bourque et al.[33] reported that the CSE/H_2S system protects against LPS-induced inflammation and hyperpermeability by blocking NF-κB transactivation in endothelial cells; LPS decreased CSE expression and H_2S production, and CSE deficiency sensitized mice to vascular inflammation. More

recently, Zhu et al.[11] found that endothelial CSE/H_2S alleviates LPS-induced acute lung injury by activating SIRT1 through protein sulfhydration, thereby inhibiting endothelial pyroptosis. This provides a novel mechanistic link between CSE/H_2S and inflammatory cell death, underscoring the protective role of this axis. Given the central role of vascular inflammation in cardiovascular diseases, identifying the NF-κB binding site on the CSE promoter has significant therapeutic implications. The CSE/H_2S pathway is a promising target for atherosclerosis and hypertension due to its cardioprotective effects.[34,35] Recent advances include positive allosteric modulators of CSE (CSE-PAMs) that augment endogenous H_2S production, reducing inflammation and pathological calcification,[36] as well as H_2S protection against LPS-induced inflammation via the NF-κB/NLRP3 pathway[37] and anti-inflammatory effects in Kawasaki disease via the TLR4/MyD88/NF-κB pathway.[38]

Several limitations of this study should be acknowledged: experiments were limited to HUVECs, requiring validation in other endothelial cells and in vivo models; the concentration-dependent effects of LPS suggest the need for time-course studies; other transcription factors or co-regulatory elements may also contribute to CSE regulation under inflammatory conditions despite the identification of the NF-κB binding site; and post-transcriptional regulation (e.g., mRNA stability or translational efficiency) warrants further investigation. Future research should explore the therapeutic potential of targeting the CSE/NF-κB axis in animal models of vascular inflammatory diseases, such as LPS-induced endotoxemia, atherosclerosis-prone ApoE$^{-/-}$ mice,[40] and angiotensin II-induced hypertension models.[41] The development of selective modulators of CSE expression or activity, including CSE-PAMs, represents a promising strategy for harnessing the anti-inflammatory effects of endogenous H_2S while avoiding the potential adverse effects associated with systemic H_2S donors.[36] Additionally, investigating the crosstalk between the CSE/H_2S pathway and other gasotransmitters, such as NO and CO, in the regulation of vascular inflammation may reveal novel therapeutic opportunities[42,43]

Conclusions

This study validates that the NF-κB binding site (GGACATTCC) within the *CSE* promoter is essential for LPS-induced transcriptional regulation of CSE in HUVECs, providing direct evidence that the NF-κB pathway mediates CSE expression in human endothelial cells. Furthermore, LPS regulates CSE expression in a concentration-dependent manner, with lower concentrations (0.1-0.5 μg/mL) upregulating and a higher concentration (2.0 μg/mL) downregulating CSE levels. These findings establish a molecular mechanism by which the CSE/H_2S signaling pathway participates in vascular inflammation and reveal a critical regulatory node—the NF-κB binding site—that may serve as a potential therapeutic target. By advancing our understanding of how LPS fine-tunes CSE expression through NF-κB, this study lays the groundwork for developing novel strategies to treat inflammatory cardiovascular diseases, including atherosclerosis and hypertension.

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Correspondence:

Maoxian Wang, PhD, Department of Biological Sciences, Hanshan Normal University, Xiangqiao District, Chaozhou 521041, Guangdong, China. Email: wangmx@hstc.edu.cn; wmaoxcn@outlook.com

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

Maoxian Wang made most of the contributions to this study, writing, reviewing and approving the final version of the manuscript.

Ethics approval and consent to participate

Not applicable.

Conflict of interest statement

The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Additional files

Not applicable.

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