

## MICROBIOLOGY AND VIROLOGY

### EXPRESSION OF THE *soxRS* REGULON IN BACTERIAL CELLS EXPOSED TO VARIOUS STRESS FACTORS

Akhova A.V.<sup>1,2</sup>,  
Tkachenko A.G.<sup>1,2</sup>

<sup>1</sup> Institute of Ecology and Genetics  
of Microorganisms, Ural Branch  
of the Russian Academy of Sciences –  
Branch of the Perm Federal Research Center  
UB RAS (Goleva str. 13, Perm 614081,  
Russian Federation)

<sup>2</sup> Perm State University (Bukireva str. 15,  
Perm 614068, Russian Federation)

Corresponding author:  
**Anna V. Akhova,**  
e-mail: akhovan@mail.ru

#### ABSTRACT

**Background.** Some stress responses contribute to the formation of bacterial antibiotic resistance, including the *soxRS* oxidative defense regulon. Elevation of reactive oxygen species production and oxidative stress was detected in bacterial cells exposed to various environmental stresses. It can be supposed that a stress-mediated increase in the level of reactive oxygen species will activate the expression of the *soxRS* regulon genes, which may provide pre-adaptation to antibiotics.

**The aim.** To study changes in the expression of *soxRS* regulon genes in *Escherichia coli* cells exposed to NaCl, acetic acid, and heating.

**Materials and methods.** Gene expression was measured in cells bearing reporter gene fusions (*soxS::lacZ*, *nfo::lacZ*). An overnight broth culture was diluted in fresh LB broth to OD<sub>600</sub> = 0.1 and cultivated at 37 °C without stirring until OD<sub>600</sub> = 0.3, then the stressors were applied.

**Results.** Exposure to NaCl and acetic acid activated the expression of *soxRS* regulon genes, while heating caused a decrease in gene expression. An increase in the expression level was observed in cells subjected to stresses of low intensity (which did not cause a decrease in the number of colony-forming units (CFU) by the 4<sup>th</sup> hour of exposure compared to the beginning of the stress exposure) and medium intensity (which caused a 10-fold decrease in the number of CFU), whereas high-intensity stresses (which caused a decrease in the number of CFU by more than 10 times), regardless of their nature, were accompanied by a decrease in the expression of the *soxRS* regulon genes.

**Conclusion.** Under the conditions studied, only the osmotic stress caused by the addition of NaCl was accompanied by a significant activation of the *soxRS* regulon genes. Sublethal exposure to NaCl, causing an increase in the expression of *soxRS* regulon genes by 2–2.5 times, may provide pre-adaptation of bacteria to the factors that this regulon is aimed at counteracting, including antibacterial drugs.

**Key words:** osmotic shock, acid stress, heat shock, oxidative stress, antibiotics, *soxS*

Received: 17.10.2022  
Accepted: 17.02.2023  
Published: 05.05.2023

**For citation:** Akhova A.V., Tkachenko A.G. Expression of the *soxRS* regulon in bacterial cells exposed to various stress factors. *Acta biomedica scientifica*. 2023; 8(2): 117-123. doi: 10.29413/ABS.2023-8.2.11

## ЭКСПРЕССИЯ ГЕНОВ *soxRS*-РЕГУЛОНА В КЛЕТКАХ БАКТЕРИЙ, ПОДВЕРГНУТЫХ ДЕЙСТВИЮ РАЗЛИЧНЫХ СТРЕСС-ФАКТОРОВ

Ахова А.В.<sup>1,2</sup>,  
Ткаченко А.Г.<sup>1,2</sup>

<sup>1</sup> Институт экологии и генетики микроорганизмов Уральского отделения Российской академии наук – филиал ФГБУН Пермского федерального исследовательского центра УрО РАН (614081, г. Пермь, ул. Голева, 13, Россия)

<sup>2</sup> ФГАОУ ВО «Пермский государственный национальный исследовательский университет» (614068, г. Пермь, ул. Букирева, 15, Россия)

Автор, ответственный за переписку:  
**Ахова Анна Викторовна,**  
e-mail: akhovan@mail.ru

### РЕЗЮМЕ

**Актуальность.** В формирование устойчивости бактерий к антибиотикам вносят вклад различные адаптивные механизмы, в том числе гены защитного ответа на окислительный стресс, объединённые в *soxRS*-регулон. В стрессовых условиях в клетках бактерий происходит повышение продукции активных форм кислорода и развитие окислительного стресса. Можно предположить, что повышенный уровень активных форм кислорода будет активировать экспрессию генов *soxRS*-регулона, что может обеспечить преадаптацию бактерий к воздействию антибиотиков.

**Цель.** Исследовать изменение экспрессии генов, входящих в *soxRS*-регулон, в клетках *Escherichia coli*, подвергнутых действию NaCl, повышенных температур и уксусной кислоты.

**Материалы и методы.** Уровень экспрессии генов определяли с использованием штаммов *E. coli*, несущих репортерные генные слияния промотора исследуемого гена (*soxS*, *pfo*) со структурной частью гена *lacZ*, в условиях периодического культивирования в бульоне LB без перемешивания.

**Результаты.** Активацию экспрессии генов *soxRS*-регулона вызывало воздействие NaCl и уксусной кислоты, а тепловой шок сопровождался снижением генной экспрессии. Увеличение уровня экспрессии наблюдалось в клетках, подвергнутых стрессам низкой (не вызывавшим снижения количества колониеобразующих единиц в культуре к четвёртому часу воздействия по сравнению с началом стрессового воздействия) и средней интенсивности (вызывавшим снижение количества колониеобразующих единиц на порядок), а стрессовые воздействия высокой интенсивности (вызывавшие снижение количества колониеобразующих единиц более чем на порядок) вне зависимости от их физико-химической природы сопровождалось снижением экспрессии генов *soxRS*-регулона.

**Заключение.** В исследованных условиях только осмотический стресс, вызванный внесением NaCl, сопровождался значимой активацией генов, входящих в *soxRS*-регулон. Сублетальное воздействие NaCl, вызывая повышение экспрессии генов *soxRS*-регулона в 2–2,5 раза, может обеспечивать преадаптацию бактерий к факторам, на противодействие которым направлен данный регулон, в том числе к антибактериальным препаратам.

**Ключевые слова:** осмотический шок, кислотный стресс, нагревание, окислительный стресс, антибиотики, *soxS*

Статья поступила: 17.10.2022

Статья принята: 17.02.2023

Статья опубликована: 05.05.2023

**Для цитирования:** Ахова А.В., Ткаченко А.Г. Экспрессия генов *soxRS*-регулона в клетках бактерий, подвергнутых действию различных стресс-факторов. *Acta biomedica scientifica*. 2023; 8(2): 117-123. doi: 10.29413/ABS.2023-8.2.11

The formation of resistant forms of microorganisms is the reason for the reduced effectiveness of antibiotic therapy. The mechanisms underpinning drug resistance include target alteration or protection, modification and inactivation of the antimicrobial compound, rearrangement of metabolic pathways, or restriction of antibiotic accumulation in the microbial cell (by reducing the transport of the drug into the cell and increasing its active release from the cell) [1–3].

Various mechanisms of defense responses to natural stress factors may be involved in the adaptation of bacteria to antibiotic drugs [4, 5]. In particular, in response to antibiotic exposure, the expression of *soxRS* regulon genes that protect bacteria from oxidative stress is activated. The increased baseline level of expression of this regulon in some cases results in clinically relevant antibiotic resistance in bacteria [6–9].

*SoxRS* regulon is a two-stage control system. The SoxR protein enters the active form and triggers the expression of the *soxS* gene; the newly synthesised SoxS protein then activates the expression of other genes within this regulon. The SoxR protein is activated by one-electron oxidation of its [2Fe-2S] clusters or their nitrosylation by reactive nitrogen species [10–13]. The *soxRS* regulon includes genes encoding superoxide dismutase that neutralizes superoxide anions (*sodA*), endonuclease involved in DNA repair (*nfo*), isoforms of enzymes resistant to oxidative damage (*fumC*, *acnA*), iron transport regulator (*fur*), proteins limiting the accumulation of hydrophilic xenobiotics in the cell (*tolC*, *micF*, *acrAB*), proteins presumably involved in the maintenance of the reduced form of iron-sulfur sites of enzymes (*fldAB*, *fpr*), and other proteins with unknown functions [14].

It is known that exposure to antibacterial drugs and natural stress factors of different nature causes increased production of free radicals and development of oxidative stress in bacterial cells. While the role of reactive oxygen species and their contribution to the death of cells exposed to various stress factors remains a debatable issue, the accumulation of free radicals caused by stress factors not directly related to their production has been confirmed by numerous publications [15–20]. Many of these stressors, e. g. high osmolarity of the medium, heating, exposure to ethanol and short-chain fatty acids, are used as antimicrobial treatments or preservatives. If these stressors cause induction of *soxRS* regulon, their sublethal effects may contribute to the pre-adaptation of bacteria to antibiotic exposure.

In this study, the expression of the *soxRS* regulon genes was studied in *Escherichia coli* cells exposed to sodium chloride, elevated temperatures and acetic acid (CH<sub>3</sub>COOH) using the gene fusion method.

## MATERIALS AND METHODS

**Objects of the study and cultivation conditions.** *Escherichia coli* strains carrying transcriptional gene fusions were used as study objects. *E. coli* EH40 strain (GC4468, but *soxS::lacZ*) was kindly provided by B. Demple [21], *E. coli*

N9213 strain (GC4468, but *nfo::lacZ Δmar rob::kan*) was kindly provided by R.G. Martin [22].

Bacteria maintained on LB slant agar were transferred to 5 ml of LB broth and cultured without agitation at 37 °C for 5–6 h. The grown cells were transferred into 50 ml of LB broth and cultured at 37 °C for 14–16 h. The bacterial culture was then diluted in fresh nutrient medium to an optical density measured at a wavelength of 600 nm (OD<sub>600</sub>) of 0.1 and cultured under the conditions described above. Once the bacterial culture reached OD<sub>600</sub> = 0.3, it was exposed to stressors. Sodium chloride and acetic acid were added to the bacterial culture and the culture was placed on a water bath with appropriate temperature to reproduce heat shock.

**The gene expression level** was determined using reporter gene fusions of the promoter of the studied gene and the structural part of the *lacZ* gene encoding β-galactosidase. It is assumed that the amount (activity) of the reporter protein is directly proportional to the expression level of the studied gene. β-galactosidase activity was measured in cells pretreated with a mixture of sodium dodecyl sulfate and chloroform using *o*-nitrophenyl-β-D-galactopyranoside as a substrate. β-galactosidase activity was determined and calculated (in Miller units) according to the standard protocol proposed by J. Miller [23].

**Bacterial culture density** was estimated by measuring its OD<sub>600</sub> using a UV1280 spectrophotometer (Shimadzu, Japan) and a cuvette with 10 mm optical path.

**The number of colony-forming units (CFUs)** was determined by plating on the surface of LB agar in Petri dishes. The number of colonies formed was counted after incubation at 37 °C for 16–18 h.

**Statistical data processing** was performed using Statistica 6.0 software package (StatSoft Inc., USA). Data are presented as mean and standard error of the mean calculated from at least three independent experiments. The statistical significance of the differences between the mean values of the compared groups was determined using unpaired t-test at  $p \leq 0.050$ .

## RESULTS AND DISCUSSION

Osmotic stress was caused by addition of sodium chloride, acid shock was induced by addition of acetic acid, and heat stress was induced by heating from 37 to 42–55 °C. The effect of these stresses of different intensities on the expression of the *soxS* gene, which encodes a transcriptional regulator responsible for the activation of genes of the regulon, and its target gene *nfo*, which encodes a DNA repair enzyme, was studied. The intensity of stress was assessed by the change in the number of colony-forming units by the fourth hour of stress exposure relative to the moment of the onset of stress exposure (Table 1). Several levels of stress strength were distinguished: subinhibitory exposure (the number of CFUs in the stressed culture increased during the cultivation time); mild stress (inhibitory exposure, the number of CFUs in the culture remained at the same level as at the time

of stressor application); moderate stress (the number of CFUs decreased by about one order of magnitude) and severe stress (the number of CFU decreased by more than one order of magnitude).

**TABLE 1**  
**THE NUMBER OF COLONY-FORMING UNITS IN *E. COLI***  
**CULTURE AFTER FOUR-HOUR EXPOSURE TO STRESSORS**

Conditions	IgCFU/ml
Control, unstressed	8.3 ± 0.4*
30 mg/ml of NaCl	8.1 ± 0.3*
50 mg/ml of NaCl	7.6 ± 0.1
70 mg/ml of NaCl	6.9 ± 0.6
100 mg/ml of NaCl	6.1 ± 0.4*
200 mg/ml of NaCl	2.8 ± 1.9*
0.125 mg/ml of CH <sub>3</sub> COOH	8.4 ± 0.5*
0.25 mg/ml of CH <sub>3</sub> COOH	7.5 ± 0.4
0.5 mg/ml of CH <sub>3</sub> COOH	7.3 ± 0.1
2 mg/ml of CH <sub>3</sub> COOH	5.7 ± 1.2*
42 °C	8.2 ± 0.3*
45 °C	8.1 ± 0.2*
55 °C	0

**Note.** The number of CFU/ml at the time of stressor application was  $7.4 \pm 0.3$ ; \* – statistically significant difference from that at the time of stressor application ( $N \geq 3$ ; T-test;  $p \leq 0.050$ ).

Subinhibitory exposure had no effect on the expression level of the *soxRS* regulon genes (data not shown). In response to exposure of 50–100 mg/ml sodium chloride (mild and moderate stress), the level of *soxS* gene expression increased in *E. coli* cells in a dose-response manner; more intense osmotic stress did not induce changes in gene expression (Fig. 1b).

Under mild osmotic stress, the change in expression occurred in two stages: the gene expression level decreased after an increase in the initial stage of sodium chloride exposure and then began to increase again after the third hour of cultivation. An increase in *soxS* gene expression after ad-

dition of acetic acid to the concentrations that did not reduce the number of CFUs in the culture (0.25–0.5 mg/ml) was observed in the first 15 min from the onset of exposure; more intense acid stress was accompanied by a decrease in gene expression (Fig. 1g). The expression of *soxS* was lower in cells subjected to heating compared to cells grown under optimal conditions (37 °C) regardless of the severity of heat stress (Fig. 1e).

Changes in *nfo* gene expression under stress factors were similar to changes in *soxS* gene expression: mild and moderate osmotic shock caused an increase in gene expression, acid shock, which did not decrease the number of CFUs, slightly increased gene expression (Fig. 2), and more severe acid stress and heat exposure led to a decrease in gene expression (data not shown).

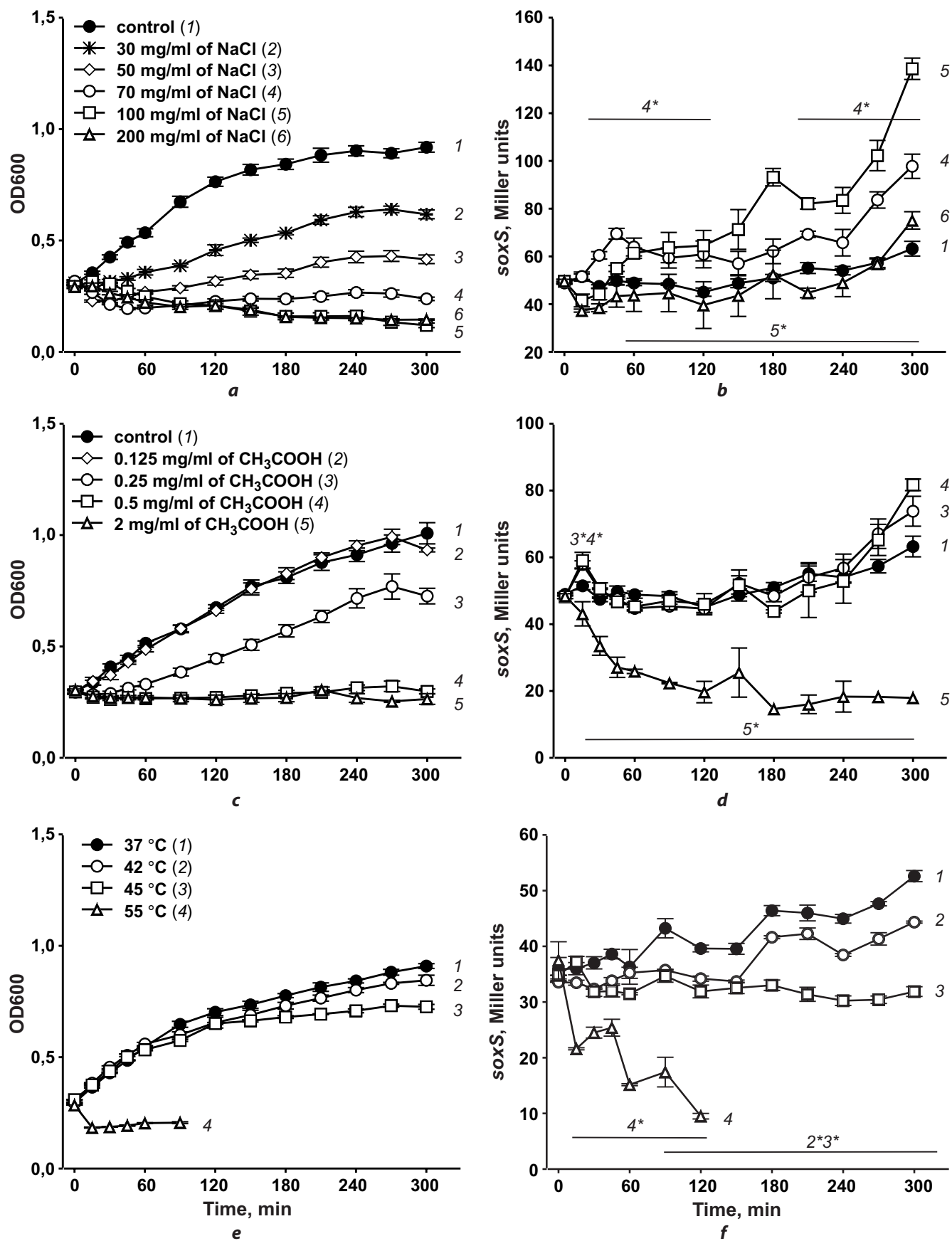
Therefore, under the conditions studied, activation of *soxRS* regulon gene expression was induced by exposure to sodium chloride and, to a lesser extent, acetic acid, while heat shock was accompanied by a decrease in gene expression. An increase in the expression level was observed in cells subjected to mild and moderate stresses, while severe stresses, which caused the death of a significant number of bacterial culture cells regardless of their physicochemical nature, were accompanied by a decrease in *soxRS* regulon gene expression. A decrease in gene fusion expression does not appear to be a specific response, but rather a consequence of a general metabolic suppression and inhibition of protein synthesis, including the reporter  $\beta$ -galactosidase.

The data obtained are consistent with the results of transcriptome analysis, which demonstrated an increase in the expression of the *soxRS* regulon genes (*soxS*, *fumC*, *fpr*, *acnA*) in *E. coli* cells when exposed to 0.3 M (17.5 mg/ml) sodium chloride [24]. Activation of *soxS* gene expression was also observed in *E. coli* cells subjected to osmotic shock induced by exposure to 0.4 and 0.9 M sucrose [25].

An increase in *sodA* mRNA synthesis in *Bacillus cereus* cells grown in media with pH = 5.4–4.5 and an increase in superoxide dismutase activity in *Staphylococcus aureus* cells grown in medium with pH = 4.0 and pH = 2.0, compared to cultivation in medium with neutral pH, have been previously shown [26, 27], suggesting activation of the *soxRS* regulon under conditions of acid stress. In this study, we demonstrated a slight increase in *soxRS* regulon gene expression during the initial stages of development of acid stress induced by acetic acid exposure.

Our results showed a decrease in the level of gene expression in cells grown at temperatures higher than optimal (37 °C). Earlier studies showed an increased level of *soxS* gene expression in cells grown at 43 °C compared to cells grown at 30 °C, which is regarded as an activation of expression in response to heat [24]. On the other hand, decreasing the cultivation temperature relative to the optimal level could cause a decrease in gene expression, which could also explain the observed differences in *soxS* expression level.

Thus, only osmotic stress induced by sodium chloride application, out of the three stress conditions investigated (exposure to acetic acid, sodium chloride, or heating), was accompanied by a significant activation of *soxRS*-regu-



**FIG. 1.** Changes in the optical density (OD600) of *E. coli* culture and *soxS* gene expression in *E. coli* EH40 cells in response to osmotic (a, b), acid (c, d), and heat stress (e, f): \* – statistically significant difference from the unstressed culture (control (1)) ( $N \geq 3$ , T-test;  $p \leq 0.050$ )



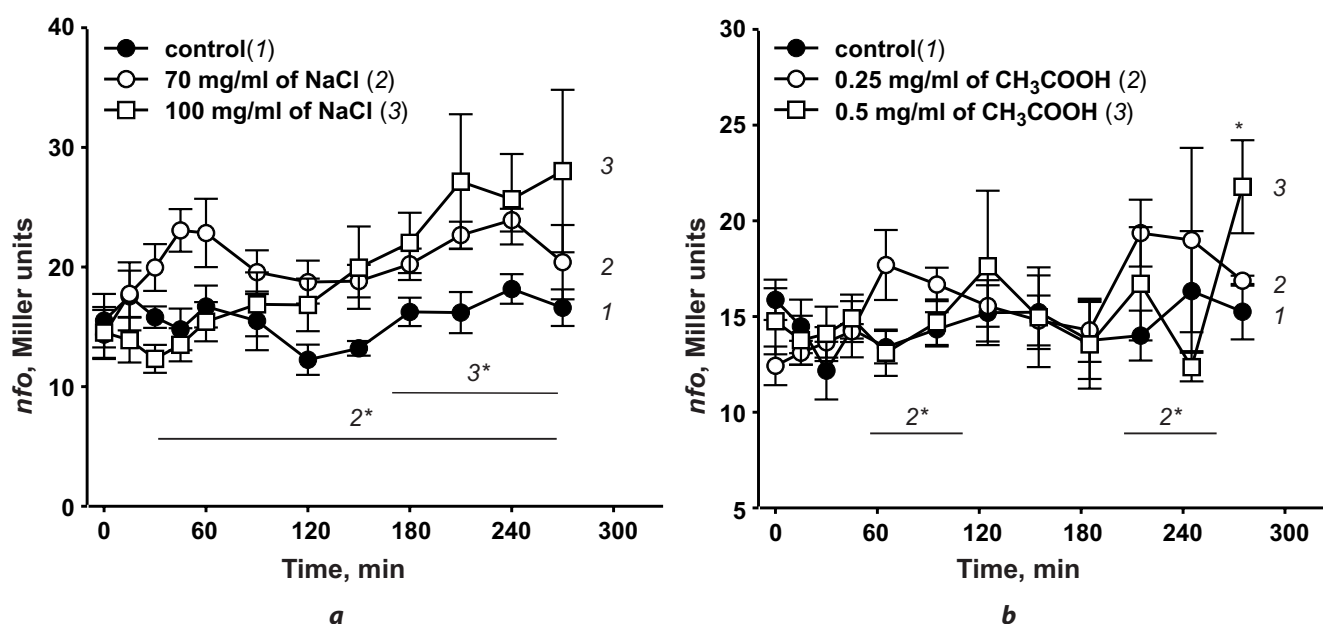


FIG. 2.

Changes in *nfo* gene expression in *E. coli* N9213 cells in response to osmotic (a) and acid (b) stress: \* – statistically significant difference from the unstressed culture (control (1)) ( $N \geq 3$ ; T-test;  $p \leq 0.050$ )

lon genes of antioxidant defence. Sublethal exposure to sodium chloride, causing a 2–2.5-fold increase in the expression of *soxRS* regulon genes, may provide pre-adaptation of bacteria to the factors that this regulon is aimed at counteracting, including antibacterial drugs.

### Financing

This study was financially supported by the Ministry of Science and Higher Education of the Russian Federation (AAAA-A19-119112290009-1).

### Conflict of interest

The authors of this article declare the absence of a conflict of interest.

The studies were conducted without the use of animals and without using humans as test subjects.

### Acknowledgements.

The authors express their sincere gratitude to Prof. B. Demple and Prof. R.G. Martin for providing the bacterial strains.

## REFERENCES

1. Blair JM, Webber MA, Baylay AJ, Ogbolu DO, Piddock LJ. Molecular mechanisms of antibiotic resistance. *Nat Rev Microbiol.* 2015; 13(1): 42-51. doi: 10.1038/nrmicro3380
2. Darby EM, Trampari E, Siasat P, Gaya MS, Alav I, Webber MA, et al. Molecular mechanisms of antibiotic resistance revisited. *Nat Rev Microbiol.* 2022 Nov 21. doi: 10.1038/s41579-022-00820-y
3. Windham S, Kollef MH. How to use new antibiotics in the therapy of serious multidrug resistant Gram-negative infections? *Curr Opin Infect Dis.* 2022; 35(6): 561-567. doi: 10.1097/QCO.0000000000000858

4. Poole K. Bacterial stress responses as determinants of antimicrobial resistance. *J Antimicrob Chemother.* 2012; 67(9): 2069-2089. doi: 10.1093/jac/dks196
5. Chetri S, Das BJ, Bhowmik D, Chanda DD, Chakravarty A, Bhattacharjee A. Transcriptional response of *mar*, *sox* and *rob* regulon against concentration gradient carbapenem stress within *Escherichia coli* isolated from hospital acquired infection. *BMC Res Notes.* 2020; 13(1): 168. doi: 10.1186/s13104-020-04999-2
6. Koutsolioutsou A, Peña-Llopis S, Demple B. Constitutive *soxR* mutations contribute to multiple-antibiotic resistance in clinical *Escherichia coli* isolates. *Antimicrob Agents Chemother.* 2005; 49(7): 2746-2752. doi: 10.1128/AAC.49.7.2746-2752.2005
7. Tkachenko AG, Akhova AV, Shumkov MS, Nesterova LY. Polyamines reduce oxidative stress in *Escherichia coli* cells exposed to bactericidal antibiotics. *Res Microbiol.* 2012; 163(2): 83-91. doi: 10.1016/j.resmic.2011.10.009
8. Fàbrega A, Martin RG, Rosner JL, Tavio MM, Vila J. Constitutive SoxS expression in a fluoroquinolone-resistant strain with a truncated SoxR protein and identification of a new member of the *marA-soxS-rob* regulon, *mdtG*. *Antimicrob Agents Chemother.* 2010; 54(3): 1218-1225. doi: 10.1128/AAC.00944-09
9. Aly SA, Boothe DM, Suh S-J. A novel alanine to serine substitution mutation in SoxS induces overexpression of efflux pumps and contributes to multidrug resistance in clinical *Escherichia coli* isolates. *J Antimicrob Chemother.* 2015; 70(8): 2228-2233. doi: 10.1093/jac/dkv105
10. Hidalgo E, Bollinger JM Jr, Bradley TM, Walsh CT, Demple B. Binuclear [2Fe-2S] clusters in the *Escherichia coli* SoxR protein and role of the metal centers in transcription. *J Biol Chem.* 1995; 270(36): 20908-20914. doi: 10.1074/jbc.270.36.20908
11. Nunoshiba T, Hidalgo E, Amábile Cuevas CF, Demple B. Two-stage control of an oxidative stress regulon: the *Escherichia coli* SoxR protein triggers redox-inducible expression of the *soxS* regulatory gene. *J Bacteriol.* 1992; 174(19): 6054-6060. doi: 10.1128/jb.174.19.6054-6060.1992

12. Wu J, Weiss B. Two-stage induction of the *soxRS* (superoxide response) regulon of *Escherichia coli*. *J Bacteriol.* 1992; 174(12): 3915-3920. doi: 10.1128/jb.174.12.3915-3920.1992
13. Ding H, Dimple B. Direct nitric oxide signal transduction via nitrosylation of iron-sulfur centers in the SoxR transcription activator. *Proc Natl Acad Sci U S A.* 2000; 97(10): 5146-5150. doi: 10.1073/pnas.97.10.5146
14. Imlay JA. The molecular mechanisms and physiological consequences of oxidative stress: Lessons from a model bacterium. *Nat Rev Microbiol.* 2013; 11(7): 443-454. doi: 10.1038/nrmicro3032
15. Mols M, Abee T. Primary and secondary oxidative stress in *Bacillus*. *Environ Microbiol.* 2011; 13(6): 1387-1394. doi: 10.1111/j.1462-2920.2011.02433.x
16. Liu Y, Imlay JA. Cell death from antibiotics without the involvement of reactive oxygen species. *Science.* 2013; 339(6124): 1210-1213. doi: 10.1126/science.1232751
17. Dwyer DJ, Belenky PA, Yang JH, MacDonald IC, Martell JD, Takahashi N, et al. Antibiotics induce redox-related physiological alterations as part of their lethality. *Proc Natl Acad Sci U S A.* 2014; 111(20): E2100-E21009. doi: 10.1073/pnas.1401876111
18. Akhova AV, Sekatskaya PA, Tkachenko AG. Formation of associated oxidative stress in cells of *Escherichia coli* exposed to different environmental stressors. *Appl Biochem Microbiol.* 2019; 55(6): 582-587. doi: 10.1134/S0003683819060036
19. Imlay JA. Where in the world do bacteria experience oxidative stress? *Environ Microbiol.* 2019; 21(2): 521-530. doi: 10.1111/1462-2920.14445
20. Drlica K, Zhao X. Bacterial death from treatment with fluoroquinolones and other lethal stressors. *Expert Rev Anti Infect Ther.* 2021; 19(5): 601-618. doi: 10.1080/14787210.2021.1840353
21. Hidalgo E, Dimple B. Spacing of promoter elements regulates the basal expression of the *soxS* gene and converts SoxR from a transcriptional activator into a repressor. *EMBO J.* 1997; 16(5): 1056-1065. doi: 10.1093/emboj/16.5.1056
22. Martin RG, Gillette WK, Rosner JL. Promoter discrimination by the related transcriptional activators MarA and SoxS: Differential regulation by differential binding. *Mol Microbiol.* 2000; 35(3): 623-634. doi: 10.1046/j.1365-2958.2000.01732.x
23. Miller HJ. *Experiments in molecular genetics*. Cold Spring Harbor: Cold Spring Harbor Laboratory; 1972.
24. Gunasekera TS, Csonka LN, Paliy O. Genome-wide transcriptional responses of *Escherichia coli* K-12 to continuous osmotic and heat stresses. *J Bacteriol.* 2008; 190(10): 3712-3720. doi: 10.1128/JB.01990-07
25. Smirnova GV, Muzyka NG, Oktyabrsky ON. The role of anti-oxidant enzymes in response of *Escherichia coli* to osmotic upshift. *FEMS Microbiol Lett.* 2000; 186(2): 209-213. doi: 10.1111/j.1574-6968.2000.tb09106.x
26. Clements MO, Watson SP, Foster SJ. Characterization of the major superoxide dismutase of *Staphylococcus aureus* and its role in starvation survival, stress resistance, and pathogenicity. *J Bacteriol.* 1999; 181(13): 3898-3903. doi: 10.1128/JB.181.13.3898-3903.1999
27. Mols M, van Kranenburg R, van Melis CC, Moezelaar R, Abee T. Analysis of acid-stressed *Bacillus cereus* reveals a major oxidative response and inactivation-associated radical formation. *Environ Microbiol.* 2010; 12(4): 873-885. doi: 10.1111/j.1462-2920.2009.02132.x

#### Information about the authors

**Anna V. Akhova** – Cand. Sc (Biol), Researcher Officer at the Laboratory of Microbial Adaptation, Institute of Ecology and Genetics of Microorganisms, Ural Branch of the Russian Academy of Sciences – Branch of the Perm Federal Research Center UB RAS; Senior Research Officer at the Laboratory of Organic Synthesis, Perm State University, e-mail: akhovan@mail.ru, <https://orcid.org/0000-0002-3477-750X>

**Alexander G. Tkachenko** – Dr. Sc (Med), Head of the Laboratory of Microbial Adaptation, Institute of Ecology and Genetics of Microorganisms, Ural Branch of the Russian Academy of Sciences – Branch of the Perm Federal Research Center UB RAS, Professor at the Department of Microbiology and Immunology, Perm State University, e-mail: agtkachenko@ieg.ru, <https://orcid.org/0000-0002-8631-8583>