FATTY ACID COMPOSITION OF SULFATE-REDUCING BACTERIA ISOLATED FROM TECHNOCgenic ECOTOPES

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The growth of technogenic (man-caused) load on the environment leads to the disturbance of natural ecotopes and is a stress factor for the widespread sulfate-reducing bacteria (SRB). Changes of SRB fatty acid composition are considered to be not only one of the mechanisms of adaptation and protection from negative stress but also one of the chemotaxonomic features that can be used as the indicator of bacteria genus and its presence in natural ecotopes. The aim of the work was to determine the fatty acid composition of sulfate-reducing bacteria strains isolated from different technogenic ecotopes. The spectrum of 17 fatty acids was determined by gas chromatography-mass spectrometry. The predominance of saturated C14:0, C15:0, C16:0 and C18:0 and the presence of unsaturated C16:1 and C18:1 fatty acids in SRB lipids were demonstrated. Correlation analysis showed that SRB isolated from the same technogenic locations were characterized by substantial similarity of fatty acid profiles despite belonging to different genera. Thus, fatty acid compositions of SRB strains Desulfovibrio sp. K1 and K2 isolated from soils near gas main-pipeline had correlation index $r = 0.94$ and that Desulfovibrio sp. TC2, Desulfotomaculum sp. TC3 and Desulfomicrobium sp. TC4 isolated from city heat system ecotope had correlation index $r = 0.97-0.99$. The obtained data on increased saturation degree of SRB fatty acids and decreased membrane fluidity indexes could be used for assessing the degree of SRB adaptation to the influence of man-caused loading as a stress factor.

Keywords: fatty acid profiles, sulfate-reducing bacteria, ecotopes, correlation analysis.
and varied by saturated straight chain acids with different amount of carbon atoms. Significant number of studied Desulfovibrio strains had high content of isoC17:1 acid (up to 44.0%), but some representatives of Desulfovibrio genus had small amount of this marker fatty acid (only 0-9.5%). In other SRB strains were dominated anteiso-pentadecenoic acid anteisoC15:1 (30.0-54.0%), at the same time in Desulfovibrio strains this acid was in minor amounts [5]. The comparative study of fatty acid content of the corrosive-relevant SRB isolated from various man-caused ecotopes in the zones of exploitation of underground industrial facilities had not conducted.

Recently, there is data lack about the effect of technogenesis on the fatty acid profiles of total bacterial lipids, but there is a lack of data about fatty acid analysis of SRB which exposed and isolated from different man-caused conditions, so the aim of the study was the determination of fatty acid composition of cell lipids of SRB, isolated from various man-caused ecotopes.

**Materials and Methods**

The objects of study were collection SRB strains, isolated from man-caused ecotopes: main gas-pipeline, city heat systems and reinforced concrete buildings. Desulfovibrio desulfuricans DSM642 (UCM B-11501), Desulfovibrio vulgaris DSM644 (UCM B-11502), obtained from the Deutch Collection (DSMZ). Bacterial strains Desulfovibrio sp. 10 (UCM B-11503), Desulfovibrio sp. TC2 (UCM B-11504), Desulfotomaculum sp. TC3 (UCM B-11505), Desulfomicrobium sp. TC4 (UCM B-11506) stores in the Ukrainian Collection of Microorganisms and Desulfovibrio sp. K1, Desulfovibrio sp. K2, Desulfotomaculum sp. K1/3 obtained from the collection of the Department of General and Soil Microbiology (Table 1).

Bacterial cultivation was performed in the liquid Postgate B medium, during 10 days at 28 °C. Initial amount of SRB cells was 10⁵ cells/ml. The determination of bacterium amount were performed by the method of serial dilutions on liquid Postgate B media with subsequent calculation (in cell per ml) with using of the MacCrady tables [7]. After cultivation to obtain bacterial biomass cultural liquid (45-50 ml) was centrifuged at 8000 rpm, 20 min on centrifuge with rotor 5415R (Eppendorf).

**Analysis of cellular fatty acid composition.**

The bacterial cells were washed twice from the cultural liquid residues with phosphate buffer (6 mM K₂HPO₄, 2 mM KH₂PO₄, pH 7.6). SRB biomass purification from ferric sulphides was carried out by 5% sodium citrate solution. Lipid components were removed from bacterial biomass with 5 ml of 1.0% H₂SO₄ solution in methanol [7]. Methyl esters of cellular fatty acids were separated on GC/MS Agilent 6890N/5973 inert in gradient temperature mode from 150 to 250 °C [9]. Column HP-5MS, size 30 m×0.25 mm×0.25 µm, temperature program mode – (4 °C/min), carrier gas – helium, flow rate – 1.2 ml/min. The evaporator temperature 250 °C; flow distribution was 1:100. Fatty acids were identified using the PC database and the standard mixture of the fatty acid methyl esters. The quantitative ratios of individual fatty acids were expressed as a percentage (%) to total sum of fatty acids.

The unsaturation index was determined using formula [10]:

\[
UI = A + (2 \cdot B) + (3 \cdot C)/100,
\]

where \(UI\) – is the index of unsaturation; \(A\) – the content of monounsaturated fatty acids, %; \(B\) – content biunsaturated fatty acids, %; \(C\) – content triunsaturated fatty acids, %.

The index of membrane viscosity was determined using formula [3]:

\[
I_{VM} = A + (B_{trans}/B_{cis}) + C,
\]

where \(I_{VM}\) – index of membrane viscosity; \(A\) – saturated fatty acids, %; \(B\) – content of trans-unsaturated fatty acids, %; \(C\) – content of cis-unsaturated fatty acids, %; \(C\) – content of fatty acids with cyclopropane ring, %.

The average carbon chain length of fatty acids was determined with formula [11]:

\[
L = \frac{\sum_{ni} (FA \cdot C)}{100},
\]

where \(L\) – the average carbon chain length; \(FA\) – the content of fatty acid in cells, %; \(C\) – the number of carbon atoms in the direct chain of fatty acid.

Correlation analysis was performed using Pearson’s method to determine interval correlations. Pearson pair correlation coefficient was calculated using formula:

\[
r_{xy} = \frac{\sum_{i=1}^{n} (x_i - \bar{x}) \cdot (y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2 \cdot (y_i - \bar{y})^2}}
\]

Full correlation was indicated as \(r = 1\), partial \(0 < r < \pm 1\); no correlation \(r = 0\) [12]. Statistical analysis of results was calculated using the arithmetic mean (\(M \pm m, P < 0.05\)) with MS Excel 2010 program software and Statistica ver. 10 (StatSoft Inc, USA, http://www.statsoft.com/).
### Table 1. The studied SRB cultures

| № | Bacterial strain       | Collection   | The place of isolation                                                                 | Reference |
|---|------------------------|--------------|----------------------------------------------------------------------------------------|-----------|
| 1 | Desulfovibrio vulgaris | DSM644       | Soil (DSMZ collection, Germany)                                                        | –         |
| 2 | Desulfovibrio desulfuricans | DSM642 | Mixture of resin and sand near the gas-pipeline in Great Britain (DSMZ collection, Germany) | –         |
| 3 | Desulfovibrio sp. 10   | UCM B-11503  | Corrosion products of steel construction of DniproHES, Zaporizzhya, Ukraine (UCM collection) | [6]       |
| 4 | Desulfovibrio sp. K1   | *            | Soil near surface of main gas-pipeline “Souz” (IvanoFrankivsk region, Ukraine)         | [7]       |
| 5 | Desulfovibrio sp. K2   | *            |                                                                                       |           |
| 6 | Desulfotomaculum sp. K1/3 | *          |                                                                                       |           |
| 7 | Desulfovibrio sp. TC2  | UCM B-11504  | Corrosion products and slime from city heat systems (Kyiv, Ukraine)                    | [8]       |
| 8 | Desulfotomaculum sp. TC3 | UCM B-11505 |                                                                                       |           |
| 9 | Desulfomicrobium sp. TC4 | UCM B-11506 |                                                                                       |           |

Notes: * Bacterial strains store at the collection of the Department of General and Soil Microbiology Danylo Zabolotny Institute of Microbiology and Virology NAS of Ukraine.

### Results and Discussion

It is known that in response to physical and chemical environmental changes the protective mechanisms and metabolic adaptive reactions in bacterial cells may occur [13]. One of the mechanisms of bacterial adaptation to negative environmental factors is change the fatty acid composition of the lipid bacterial membranes and the unsaturation degree of cellular fatty acids [11, 14, 15]. Since collection SRB were isolated from various ecotopes i.e. main gas-pipeline, city heat systems and iron-concrete structure, and therefore previously were under different stress man-caused load, so comparative analysis of fatty acid composition of studied bacterial cell lipids was carried out.

The data obtained from fatty acid profiles analysis of total SRB lipids revealed spectrum from 17 fatty acids with total carbon chain length from 10 to 18 (Table 2).

In total SRB cell lipids fatty acids composition were 14 saturated and 3 unsaturated fatty acids. Next saturated fatty acids were detected in all strains (% of total acids): tetradecanoic C14:0 (2.08-8.69), hexadecanoic C16:0 (12.9-44.60%) and octadecanoic C18:0 (1.20-4.72%). Pentadecanoic acid C15:0 was prevealed in Desulfovibrio sp. K1 (30.35%) and hexadecanoic nad octadecanoic acids in Desulfotomaculum sp. K1/3 (44.66% and 4.72, respectively). Both strains were isolated from the same ecotope i.e. main gas-pipeline in Carpathians.

Unsaturated fatty acid hexadecenoic C16:1 (3.04-30.90%) was found in the lipid composition of all studied SRB strains. Trans-octadecenoic transC18:1 (2.73-6.77%) also were in all strains excluding Desulfovibrio sp. 10, and cis-octadecenoic C18:1 was in small amounts in D. desulfuricans DSM642 and Desulfovibrio sp. TC2 and Desulfovibrio sp. K2 (1.08-1.93%) and Desulfotomaculum sp. K1/3 (2.30%).

According to the fatty acid composition of lipids among bacteria of Desulfovibrio genus two strains were significantly differed such as D. desulfuricans DSM642, isolated from a mixture of resin and sand around the gas-pipeline (United Kingdom) and Desulfovibrio sp. 10, isolated from reinforced concrete corrosion products (DniproHES, Ukraine). In the fatty acid composition of D. desulfuricans DSM642 total lipids only 5 saturated and 3 unsaturated fatty acids as cis- and trans-octadecenoic C18:1 (1.93 and 2.73%, respectively) and in significant amount hexadecenoic acid 16:1 (30.90%) were revealed. In Desulfovibrio sp. 10 8 saturated and only
### Table 2. The total lipids fatty acid compositions of SRB, % from total content of fatty acids

| Fatty acid         | Chain lengths | Desulfovibrio sp. 10 | D. desulfuricans DSM642 | D. vulgaris DSM444 | Desulfovibrio sp. TC2 | Desulfotomaculum sp. TC3 | Desulfotomaculum sp. TC4 | Desulfovibrio sp. K1 | Desulfotomaculum sp. K1/3 | Desulfovibrio sp. K2 |
|--------------------|---------------|----------------------|-------------------------|-------------------|----------------------|------------------------|------------------------|------------------|-------------------------|---------------------|
| Decanoic 10:0      |               | 1.73                 | 0                       | 0                 | 0                    | 0                      | 0                      | 0                | 0                       | 0                   |
| Undecanoic 11:0    |               | 0                    | 0                       | 0                 | 3.64                 | 0                      | 0                      | 0                | 0                       | 0                   |
| Tridecanoic 13:0   |               | 0                    | 0                       | 0                 | 1.34                 | 1.57                   | 2.03                   | 2.07             | 2.03                   | 1.94                |
| Tetradecanoic 14:0 |               | 6.55                 | 2.08                    | 6.53              | 7.90                 | 7.99                   | 8.3                    | 6.42             | 8.69                    | 5.22                |
| 3-hydroxytetradecanoic OH14:0 | 0 | 0                    | 6.99                    | 0                 | 0                    | 0                      | 0                      | 0                | 0                       | 0                   |
| Pentadecanoic 15:0 |               | 26.87                | 0                       | 16.52             | 23.73                | 27.01                  | 27.83                  | 30.35            | 0                       | 19.91               |
| iso-pentadecanoic iso15:0 |           | 2.89                 | 13.7                    | 4.2               | 0                    | 0.95                   | 1.09                   | 3.12             | 1.91                    |                     |
| anteiso-pentadecanoic aiso15:0 |       | 20.73                | 0                       | 3.39              | 4.77                 | 8.09                   | 6.70                   | 8.88             | 12.05                   | 11.54               |
| Hexadecanoic 16:0  |               | 3.04                 | 30.90                   | 12.87             | 9.52                 | 8.36                   | 7.42                   | 7.68             | 14.54                   | 7.35                |
| Heptadecanoic 17:0 |               | 12.64                | 0                       | 7.31              | 3.91                 | 3.53                   | 5.98                   | 3.75             | 4.16                    |                     |
| iso-heptadecanoic iso17:0 |     | 117.0                | 0                       | 10.55             | 2.26                 | 0                      | 0                      | 0                | 0                       | 0                   |
| cis,9,10 heptadecanoic cis9,10 17:0 | | 0 | 0 | 0 | 21.25 | 21.38 | 20.42 | 20.18 | 0 | 23.72 |
| Octadecanoic 18:0  |               | 3.18                 | 3.62                    | 4.44              | 1.71                 | 1.89                   | 1.20                   | 1.17             | 4.72                    | 2.22                |
| Hydroxyoctadecanoic 3OH18:0 |         | 0                    | 0                       | 0                 | 0                    | 1.87                   | 1.24                   | 0                | 0                       | 0                   |
| Cis-octadecenoic cis18:1 |           | 0                    | 1.93                    | 0                 | 1.08                 | 0                      | 0                      | 0                | 2.30                    | 1.32                |
| Trans-octadecenoic trans18:1 |        | 0                    | 2.73                    | 4.40              | 6.77                 | 5.00                   | 3.98                   | 5.43             | 3.38                    | 6.29                |

One unsaturated fatty acid hexadecenoic C16:1 in small amount (3.04%) was revealed. Other SRB belonged to Desulfovibrio genus had minor differences in the fatty acid composition of cellular lipids.

According to the literature data, the lipids of anaerobic bacteria contain large amounts of iso- and anteiso branched fatty acids. The high content of these fatty acids found in SRB of Desulfovibrio genus. It had reported that in D. africanus lipids the content of branched fatty acids was 30% as well as in D. gigas and D. desulfuricans strains was 57% and 61%, respectively [15, 16]. In our studied SRB iso- and anteisoacids were appeared in small amounts. Only, in Desulfovibrio sp. 10 anteiso-pentadecanoic acid C15:0 was dominant in amount 20.73%.

Bacteria Desulfotomaculum sp. TC3 and Desulfotomaculum sp. K1/3, isolated from various man-caused ecotopes, significantly differed in fatty acid profiles, although for phenotypic and phylogenetic characteristics were belonged to the same genus [8]. During determining of chemotaxonomic characteristics of bacteria of Desulfotomaculum genus performed by T.N. Nazina [17] it had shown that in the fatty acids spectra major fatty acids such as C15:0 and C17:0, as well in fatty acid profiles of Desulfotomaculum strains were significant amount of C16:0 and C16:1 acids. In our work it were determined such isoacids as isoC15:0 (14.90-29.60%), isoC17:0 (14.20-25.0%), hexadecenoic C16:0 (24.10-26.60%) and octadecanoic C18:0 (16.7-22.4%). However, in the studied fatty acids profiles of Desulfotomaculum genus iso-heptadecanoic acid isoC17:0 was absent and iso-pentadecanoic acid isoC15:0 was detected only in Desulfotomaculum sp. K1/3 in small amounts (3.12%). The result of comparing the fatty acid profiles of both strains was revealed that Des-
\textit{Desulfotomaculum} sp K1/3 contained more unsaturated fatty acids as well as hexadecenoic and cis-, trans-octadecenoic acids (only 20.23%) and only 5 saturated fatty acids (69.88%). \textit{Desulfotomaculum} sp. TC3, in contrast, had 9 saturated (86.58%) and only 2 unsaturated fatty acids (13.36%). We noted that these SRB strains were isolated from various ecotopes with different conditions. In particular, \textit{Desulfotomaculum} sp. TC3 was isolated from the heating systems site, which was operated for temperature of 60 °C. There is evidence that due to influence of high temperatures in bacterial cell the content of saturated fatty acids had increasing. In particular, the increasing of the saturation degree of lipids due to high temperatures influence was found in the SRB cells of \textit{Desulfovibrio indonesiensis} [18].

During the impact of heavy metal ions the increased saturation degree of lipids in bacterial cells was also observed. For example, due to influence of Cadmium, Nickel, Zinc and Cooper ions in cells of \textit{K. pneumoniae} and \textit{Enterobacter intermedius} the degree of lipid saturation had increased [19]. It was shown that the content of unsaturated fatty acids decreases in SRB cells due to the toxic effect of the stress factor i.e., increasing of ferric citrate content. From the other hand, the content of fatty acids with a branched carbon chain had increased to maintain the required level of cytoplasmic membrane fluidity [20]. There are assumptions that increasing of the content of saturated fatty acids with simultaneous decreasing the content of unsaturated fatty acids protects lipids from damages in the double bond sites [19].

Changes in the degree of saturation of fatty acids play an important role in the level membrane fluidity. Cytoplasmic membrane fluidity is the most important parameter determining cell survival under stressful conditions [15].

It is known that one of the mechanisms of bacterial adaptation to stress factors is to maintain an appropriate level of cytoplasmic membrane fluidity. This parameter had estimated by such indicators as the unsaturation degree of cell lipids, the bacterial membrane viscosity and the length of the fatty acid carbon chain [3, 21].

As compared with SRB of \textit{Desulfovibrio} genus the indexes of cytoplasmic membrane fluidity confirmed that both strains \textit{Desulfovibrio} sp. 10 and \textit{D. desulfuricans} DSM642 significantly were differ from others, despite their belonging to the same genus. The unsaturation index for \textit{Desulfovibrio} sp. 10 strain was the lowest among all the studied bacteria (0.03), because in fatty acid composition of this strain was only one unsaturated acid C16:1 (hexadecenoic). Instead in \textit{D. desulfuricans} DSM642 the unsaturation index was 0.35, the lowest viscosity membrane index (65.84) and the carbon chain length (9.28). The other bacteria of \textit{Desulfovibrio} genus had similar indexes such as unsaturation degree (0.11-0.17) and index of membrane viscosity (107.06-113.50) (Table 3). We can suggest that difference in fatty acids profiles of studied strains of \textit{Desulfovibrio} genus would be explained by their belongings to different species. The features of the cytoplasmic membrane fluidity of studied bacteria of \textit{Desulfotomaculum} genus were also significantly differed. \textit{Desulfoto-
maculum sp. K1/3 had unsaturation degree (0.26), index of membrane viscosity (77.55) and the lowest average length of the carbon chain from all the studied strains (8.79). In contrast, the fluidity of the cytoplasmic membrane Desulfotomaculum sp. TC3 was differed in almost 2 times: the index of unsaturation (0.13), the membrane viscosity index (108.0) and twice longer carbon chain (15.20). Similar to the strain Desulfotomaculum sp. TC3 indicators of the degree of unsaturation, membrane viscosity index and carbon chain length were determined in Desulfomicrobium sp. TC4.

According literature data it is known that increasing the content of fatty acids with short chain leads to increasing the fluidity of the cytoplasmic membrane [21]. Other mechanisms of membrane fluidity regulation are also described, in particular, shortening or lengthening of the fatty acid chain, changes in the content of fatty acids with branched carboxylic chain or fatty acids that contain cyclopropane ring, and isomerization of the double bond of fatty acids with cis/trans configuration [11].

To compare the fatty acid profiles of SRB isolated from various ecotopes and belonging to different taxonomic positions a correlation analysis with calculating of Pearson’s indexes was carried out (Table 4). Correlation analysis of the fatty acids profiles of collection SRB strains conducted by M. B. Vanstein was shown that the values of the indexes r were under different conditions of cultivation of the same SRB strain (r = 0.99); for different strains of the same species (r = 0.98) and for close species of the same genus r values were 0.94-0.96. The using of correlation indexes for comparison of SRB strains allows us evaluates not only qualitative coincidences for the presence of the same compounds, but quantitative using their concentration [5].

According to obtained from correlation analysis data of fatty acid profiles of Desulfovibrio sp. K1 and Desulfovibrio sp. K2 isolated near the main gas-pipeline zone were similar with a correlation indexes r = 0.94. The fatty acid profile of Desulfotomaculum sp. K1/3 strain was differed from mentioned above strains significantly (the correlation indexes were r = 0.27-0.37, respectively), but this strain was similar to collection strains D. desulfuricans DSM642, D. vulgaris DSM644 with indexes 0.79 and 0.81, respectively. As well as Desulfotomaculum sp. K1/3 mentioned above collection strains were also isolated from the samples collected near the main gas-pipeline. So we could suggest that similarity of the fatty acid profiles depends not only from taxonomic position, but also from ecotope of strain isolation.

Despite the fact that Desulfovibrio sp. TC2, Desulfotomaculum sp. TC3 and Desulfomicrobium sp. TC4 strains, isolated from same man-caused location, i.e. city heat systems were belonged to different genera they revealed high similarity (r = 0.97-0.99). Desulfotomaculum sp. TC3 and Desulfomicrobium sp. TC4 strains almost did not differ in fatty acid composition and membrane fluidity, their similarity were r = 0.99. Thus, sulfate-re-

| Table 4. Data of correlation analysis of SRB fatty acids profiles |
|---------------------------------------------------------------|
|| Bacterial culture          | Collection strains | Strains from man-caused ecotopes |
||                             |                   | city heat systems | main gas-pipeline |
||                            |                   | TC2   | TC3   | TC4   | K1   | K1/3 | K2   |
|| Desulfovibrio sp. 10       | 1.00              | 0.28  | 0.74  | 0.61  | 0.67 | 0.70 | 0.71 | 0.54 | 0.64 |
|| D. desulfuricans DSM642    | -                 | 1.00  | 0.74  | **0.27** | **0.20** | **0.20** | **0.18** | 0.79 | 0.24 |
|| D. vulgaris DSM644         | -                 | -     | 1.00  | 0.59  | 0.56 | 0.59 | 0.56 | 0.81 | 0.53 |
|| Desulfovibrio sp. TC2      | -                 | -     | -     | 1.00  | 0.98 | 0.97 | 0.96 | **0.34** | 0.95 |
|| Desulfotomaculum sp. TC3   | -                 | -     | -     | -     | 1.00 | 0.99 | 0.99 | **0.30** | 0.96 |
|| Desulfomicrobium sp. TC4   | -                 | -     | -     | -     | -    | 1.00 | 0.99 | **0.29** | 0.94 |
|| Desulfovibrio sp. K1       | -                 | -     | -     | -     | -    | -    | 1.00 | **0.27** | 0.94 |
|| Desulfotomaculum sp. K1/3  | -                 | -     | -     | -     | -    | -    | -    | 1.00 | **0.37** |
|| Desulfovibrio sp. K2       | -                 | -     | -     | -     | -    | -    | -    | -    | 1.00 |

Note: significant correlations are marked as regular black (r > 0.4, P < 0.05), non-significant (r ≤ 0.4) as bold black.
duceing bacteria had isolated from same man-caused locations despite their belonging to different genera determined by phenotypic and phylogenetic features were characterized with high degree of similarity in fatty acid profiles.

It was studied the fatty acid composition of total lipids of SRB, isolated from man-caused ecotopes. It was shown that SRB were characterized with high saturation degree of fatty acids, which indicates on the rigidity of the cell wall. Changing the saturation degree of cellular lipids is an important mechanism for maintaining the required level of fluidity of the cytoplasmic membrane and, accordingly, the adaptation of microorganisms to unfavourable environmental factors. The differences in fatty acid composition of SRB were due to decreasing the cytoplasmic membrane fluidity. The decreasing of cytoplasmic membrane fluidity is a protective adaptation reaction of bacteria to unfavourable conditions of existence. The fatty acid composition of total lipids and cytoplasmic membrane fluidity indexes can be serving as an important feature for assessing the degree of SRB adaptation to the influence of man.

The fatty acid composition of total lipids and cytoplasmic membrane fluidity indexes can be serving as an important feature for assessing the degree of SRB and, accordingly, the adaptation of microorganisms to unfavourable environmental factors. The differences in fatty acid composition of SRB were due to decreasing the cytoplasmic membrane fluidity. The decreasing of cytoplasmic membrane fluidity is a protective adaptation reaction of bacteria to unfavourable conditions of existence. The fatty acid composition of total lipids and cytoplasmic membrane fluidity indexes can be serving as an important feature for assessing the degree of SRB adaptation to the influence of man-caused loading.

Further studies of fatty acids profiles of corrosive-relevant SRB isolated from different ecotopes can be ecologically useful for detection of cites with high level of corrosion danger.

Conflicts of interest. Authors have completed the Unified Conflicts of Interest form at http://ukrbiochemjournal.org/wp-content/uploads/2018/12/coi_disclosure.pdf and declare no conflict of interest.

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Ключові слова: профілі жирних кислот, сульфатвідновлювальні бактерії, екотопи, кореляційний аналіз.

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