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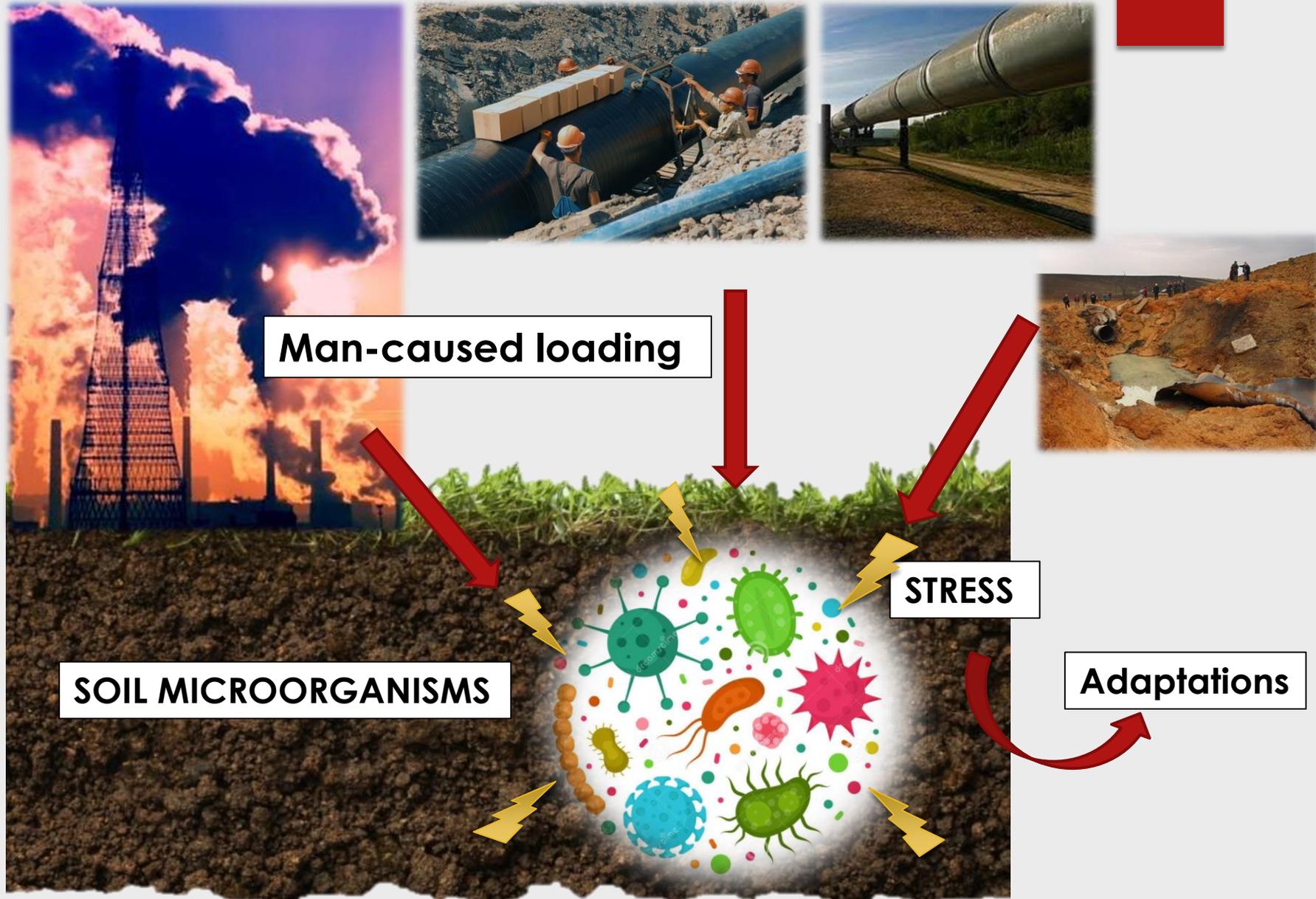
FATTY ACIDS COMPOSITION OF TOTAL LIPIDS OF SULFATE-REDUCING BACTERIA, ISOLATED FROM MAN-CAUSED ECOTOPES

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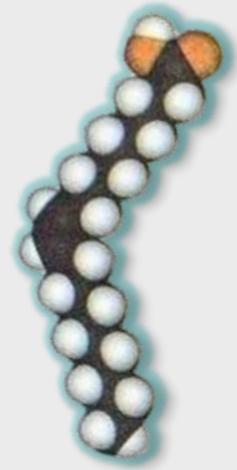
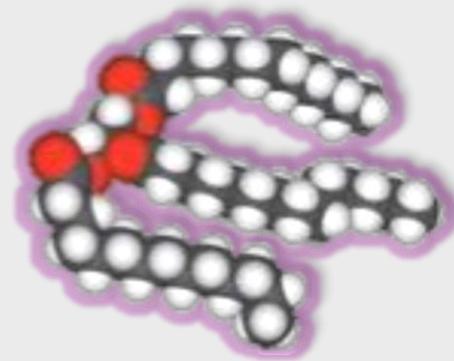
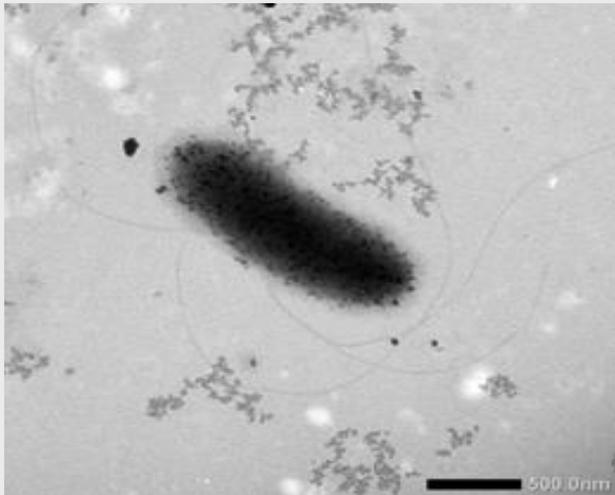
Relevance of the study

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The aim of the study:

- ▶ *to study of fatty acids composition of cellular lipids of sulfate-reducing bacteria (SRB) isolated from different man-caused ecotopes*



Objects:

No	Bacterial strain	Collection	The place of isolation
1	<i>Desulfovibrio</i> sp. 10	UCM B-11503	Corrosion products of steel construction of DniproHES, Zaporizzhya, Ukraine (UCM collection)
2	<i>Desulfovibrio vulgaris</i> UCM B-11502	DSM644	Soil (DSMZ collection, Germany)
3	<i>D. desulfuricans</i> UCM B-11501	DSM642	Mixture of resin and sand near the gas-pipeline in Great Britain (DSMZ collection, Germany)
4	<i>Desulfovibrio</i> sp. TC2	UCM B-11504	Corrosion products and slime from city heat systems (Kyiv, Ukraine)
5	<i>Desulfotomaculum</i> sp. TC3	UCM B-11505	
7	<i>Desulfomicrobium</i> sp. TC4	UCM B-11506	
8	<i>Desulfovibrio</i> sp. K1	*	Soil near surface of main gas-pipeline «Souz» (IvanoFrankivsk region, Ukraine)
9	<i>Desulfovibrio</i> sp. K2	*	
10	<i>Desulfotomaculum</i> sp. K1/3	*	

Notes: * Bacterial strains store at the collection of the Department of General and Soil Microbiology

Methods:

- ▶ **Microbiological** (bacterial cultivation on liquid Postgate B media during 10-11 days)
- ▶ **Biochemical** (probe preparing of methyl esters of cellular fatty acids)
- ▶ **Physical** GS-MS (Agilent 6890N/5973 inert)
- ▶ **Statistical**



Correlation analysis was performed using Pearson's method

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

Full correlation $r=1$

Partial correlation $0 < r < \pm 1$

No correlation $r=0$



The fatty acids profiles of SRB

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Fatty acid	Chain lengths	<i>Desulfovibrio</i> sp. 10	<i>D. desulfuricans</i> DSM642	<i>D. vulgaris</i> DSM644	<i>Desulfovibrio</i> sp. TC2	<i>Desulfotomaculum</i> m sp. TC3	<i>Desulfomicrobium</i> sp. TC4	<i>Desulfovibrio</i> sp. K1	<i>Desulfotomaculum</i> m sp. K1/3	<i>Desulfovibrio</i> 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	0	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
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	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	22.31	34.46	31.03	14.33	13.25	13.89	12.91	44.66	14.37
Hexadecenoic	16:1	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	0	4.16
iso-heptadecanoic	i17:0	0	10.55	2.26	0	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

*The quantitative ratios of individual fatty acids were expressed as percentage (%) to total sum of fatty acids

Indexes of membrane fluidity

Unsaturation index

$$UI = A + (2 \cdot B) + (3 \cdot C) / 100$$

A – the content of monounsaturated fatty acids, %;

B – content biunsaturated fatty acids, %;

C – content triunsaturated fatty acids, %.

Index of membrane viscosity

$$I_{VM} = A + (B_{trans} / B_{cis}) + C$$

A – saturated fatty acids, %;

B_{trans} – content of trans-unsaturated fatty acids, %;

B_{cis} – content of cis-unsaturated fatty acids, %;

C – content of FA with cyclopropane ring, %.

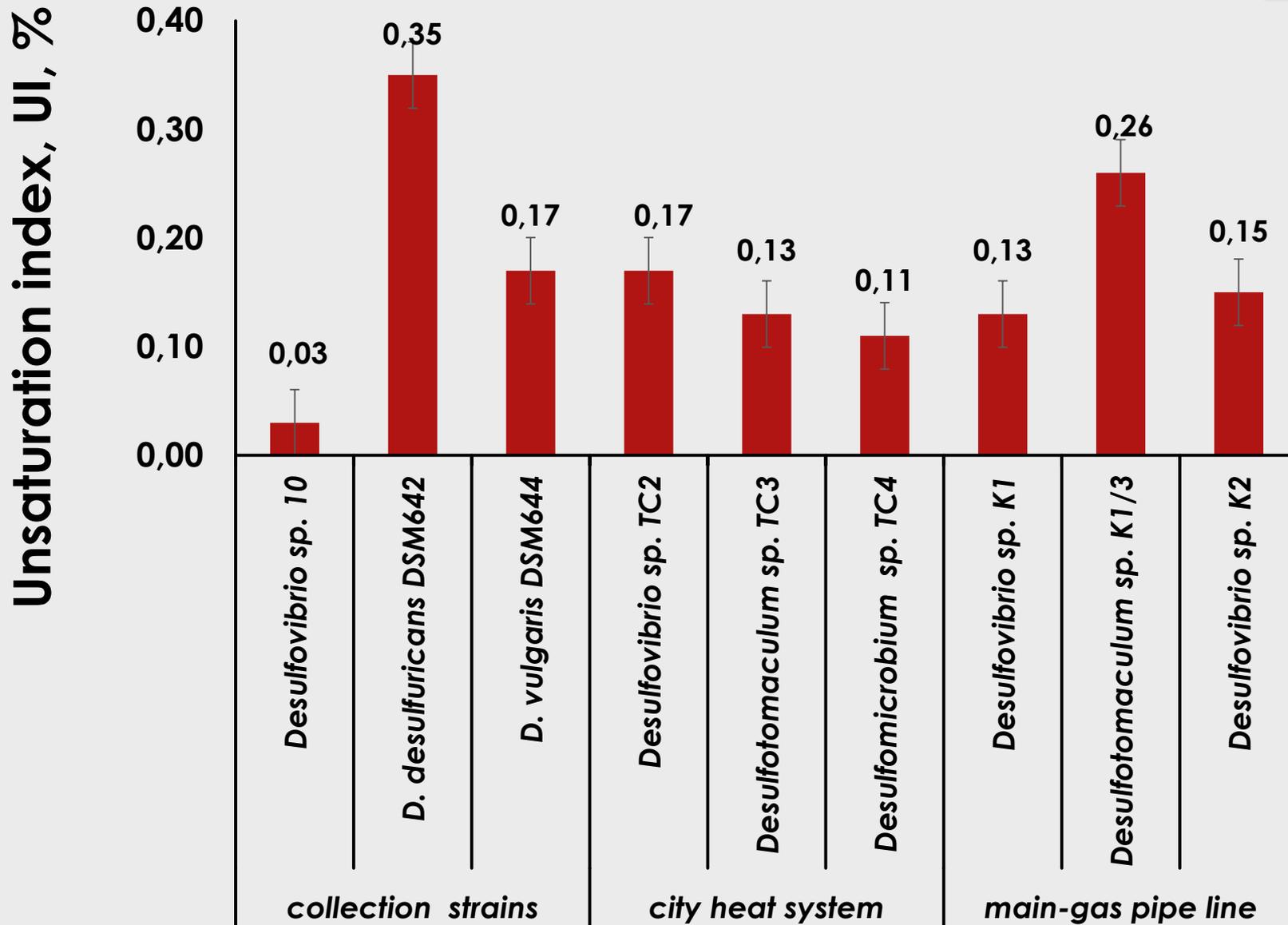
Average length of Carbon chain

$$L = \Sigma(FA \cdot C) / 100$$

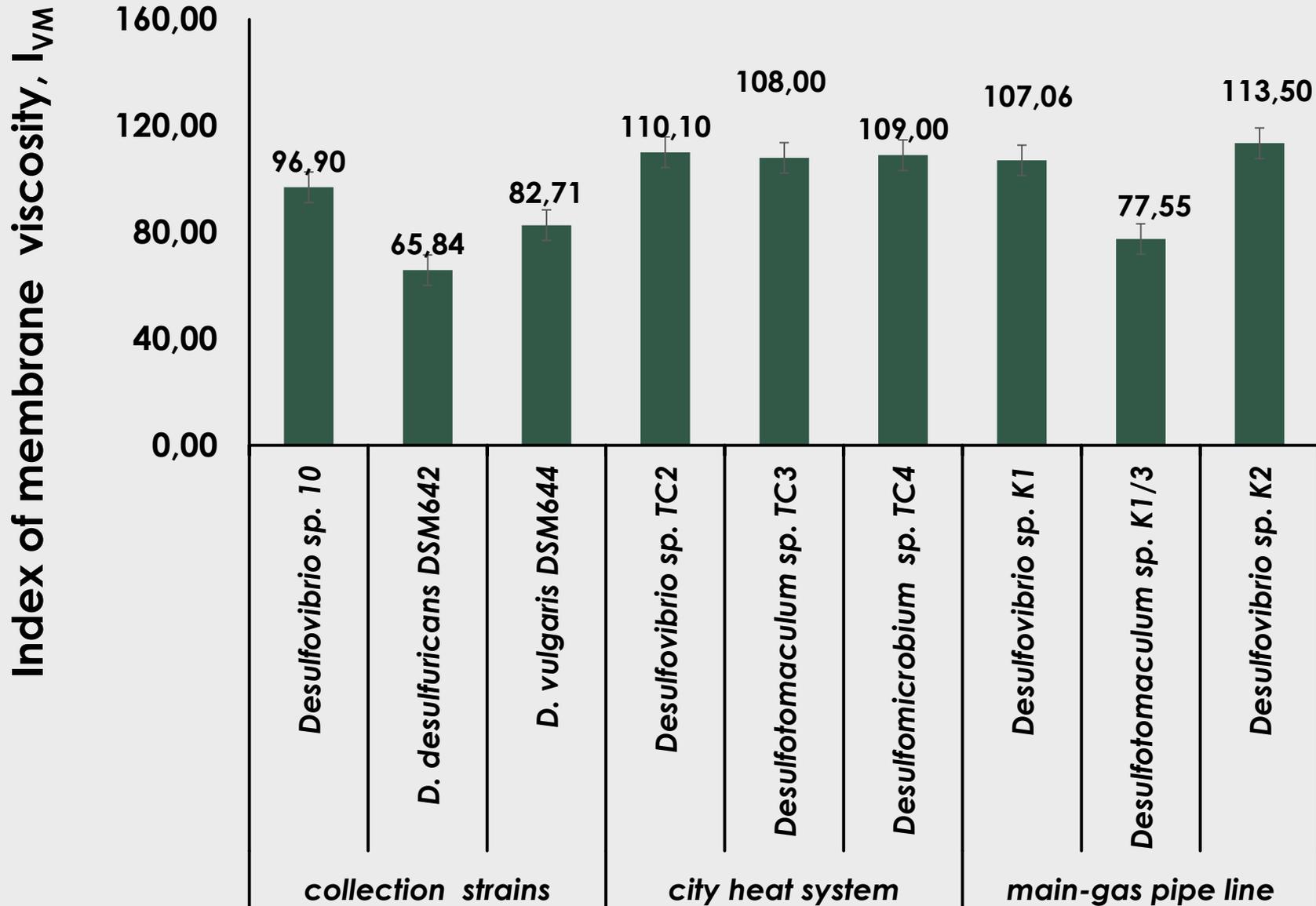
FA – the content of fatty acids in cells, %;

C – the number of carbon atoms in the direct chain of fatty acid.

Unsaturation index, % UI

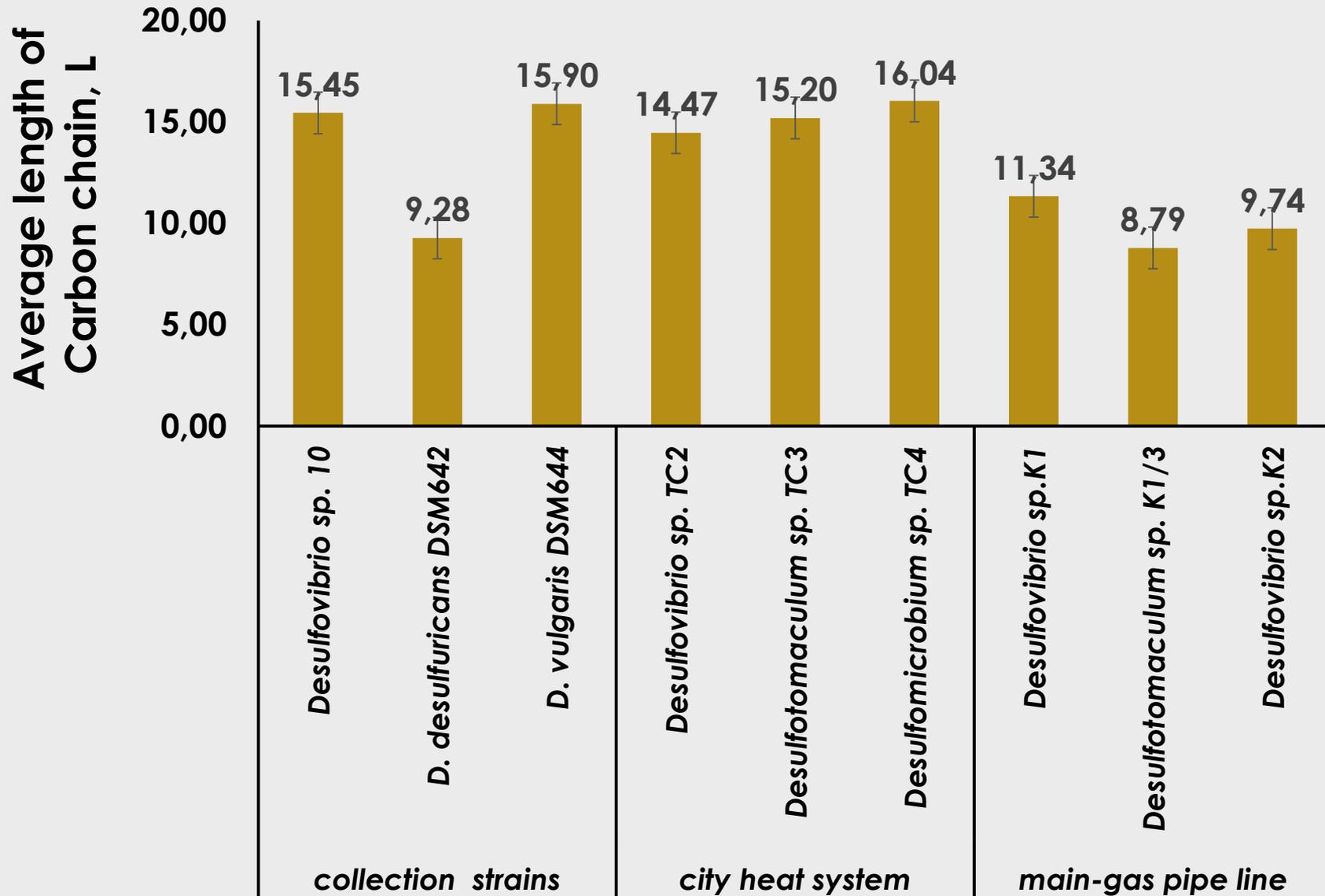


Index of membrane viscosity



Average length of Carbon chain

10



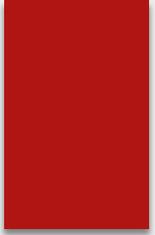
Correlation analysis of SRB fatty acids profiles

Bacterial culture	Collection strains			Strains from man-caused ecotopes					
				city heat systems			main gas-pipeline		
	10	642	644	TC2	TC3	TC4	K1	K1/3	K2
<i>Desulfovibrio</i> sp. 10	1.00*	0.28**	0.74	0.61	0.67	0.70	0.71	0.54	0.64
<i>D. desulfuricans</i> DSM642	-	1.00	0.74	0.27	0.20	0.20	0.18	0.79	0.24
<i>D. vulgaris</i> DSM644	-	-	1.00	0.59	0.56	0.59	0.56	0.81	0.53
<i>Desulfovibrio</i> sp. TC2	-	-	-	1.00	0.98	0.97	0.96	0.34	0.95
<i>Desulfotomaculum</i> sp. TC3	-	-	-	-	1.00	0.99	0.99	0.30	0.96
<i>Desulfomicrobium</i> sp. TC4	-	-	-	-	-	1.00	0.99	0.29	0.94
<i>Desulfovibrio</i> sp. K1	-	-	-	-	-	-	1.00	0.27	0.94
<i>Desulfotomaculum</i> sp.K1/3	-	-	-	-	-	-	-	1.00	0.37
<i>Desulfovibrio</i> sp. K2	-	-	-	-	-	-	-	-	1.00

Note: * significant correlations are marked with **bold** ($r > 0.4$, $p < 0.05$), ** non-significant ($r \leq 0.4$).

Conclusions:

1. Sulfate-reducing bacteria, isolated from man-caused ecotopes were characterized with high saturation degree of fatty acids.
2. Strains from same ecotope, ie city heat system were closely related to fatty acid profiles of SRB and indexes of the cytoplasmic membrane fluidity. It was established that most similar were appeared bacterial strains, isolated from same man-caused ecotope (up to $r=0,99$).
3. The changes in the saturation degree of cellular lipids is an important mechanism for maintaining the required level of fluidity of the cytoplasmic membrane and the adaptation of microorganisms to unfavorable environmental factors. Obtained results indicate about adaptation of the SRB to man-caused loading.



Thank you
for attention