



Bacteria and archaea biodiversity in sediments of Venice lagoon and their impact on sediment anoxia

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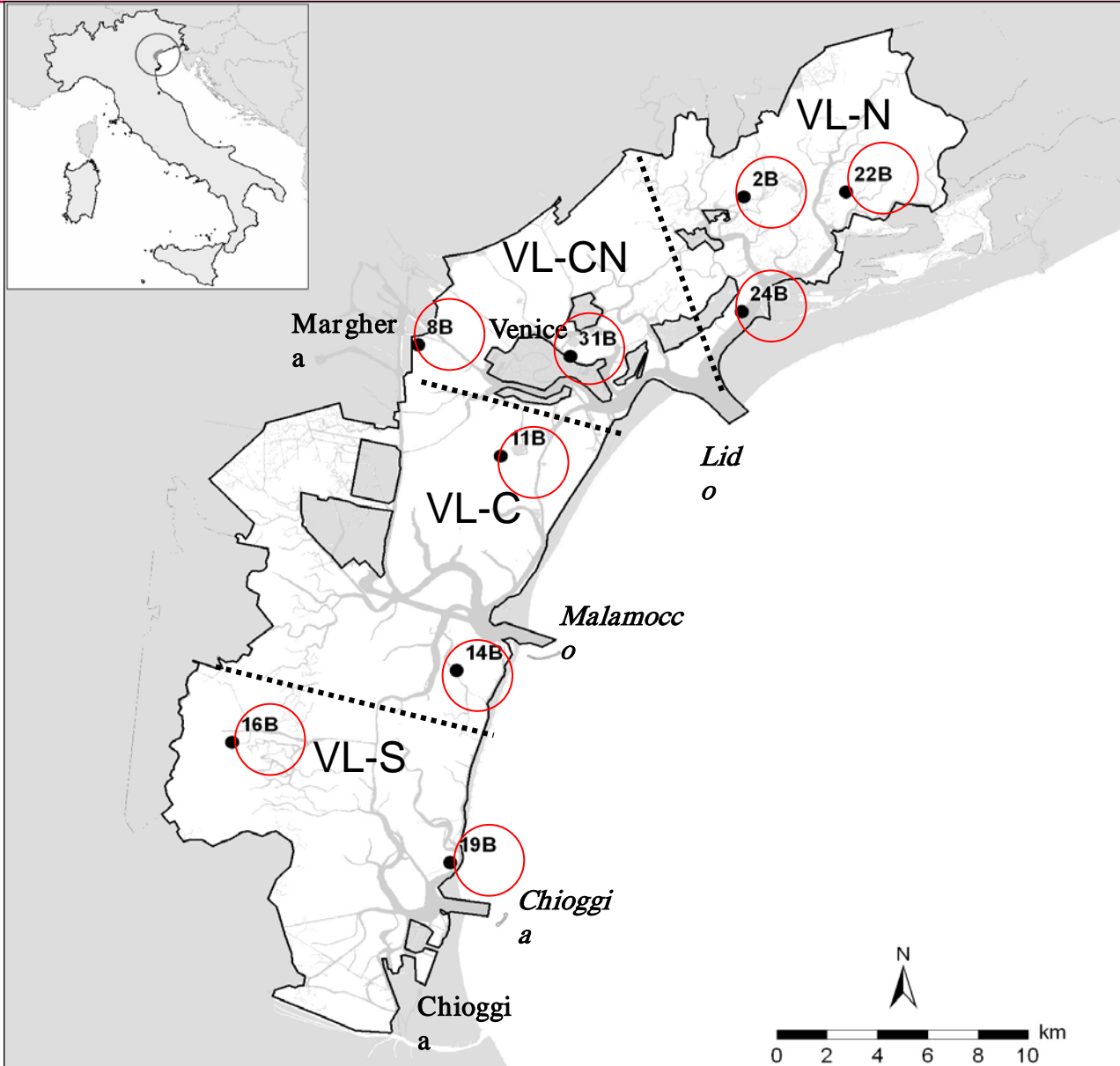
Patrizia Bidinotto , Laura Montobbio CVN-VE

SEDNET 2011 Venezia, 6-9 Aprile



Study of Microbial Biodiversity in sediments at Venice Lagoon

1. Study of population structure by ARISA in sediments of 9 stations
2. Principal Component analyses (PCA) to focus on few sediments
3. Genomic libraries in 3 Stations



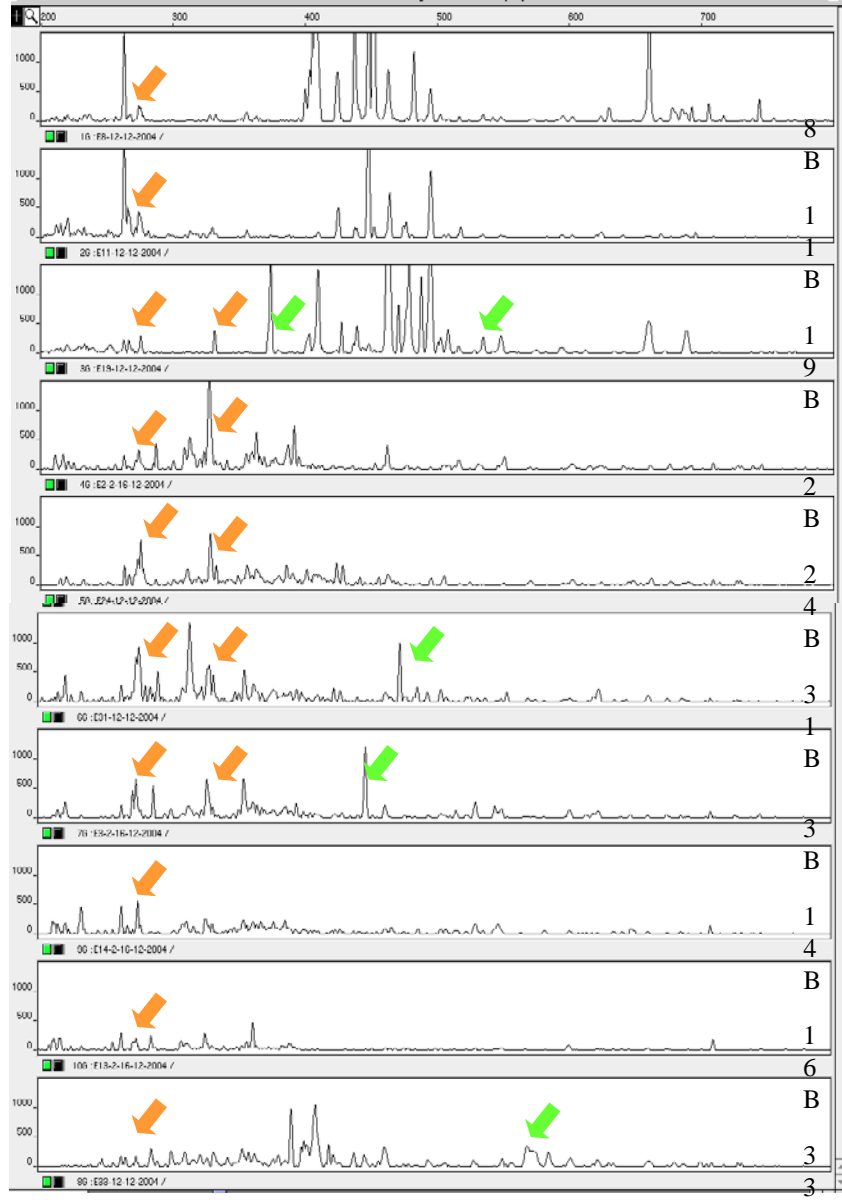
4-sub-basins

Sub-division
based on
Hazard Quotient
278 stations
25 years

Apitz et al. Environ. Assess.
Manag. 2007

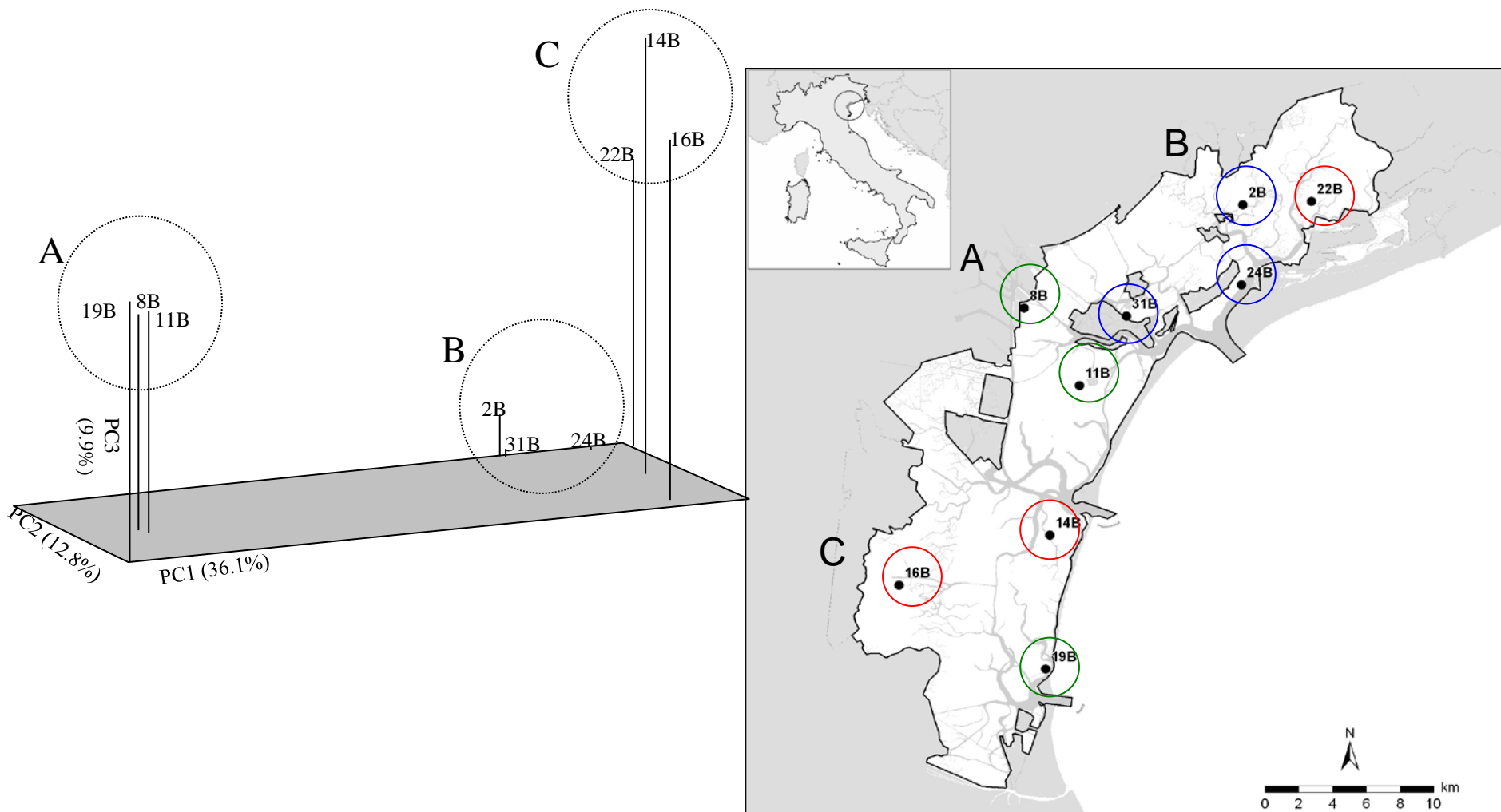
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electropherograms

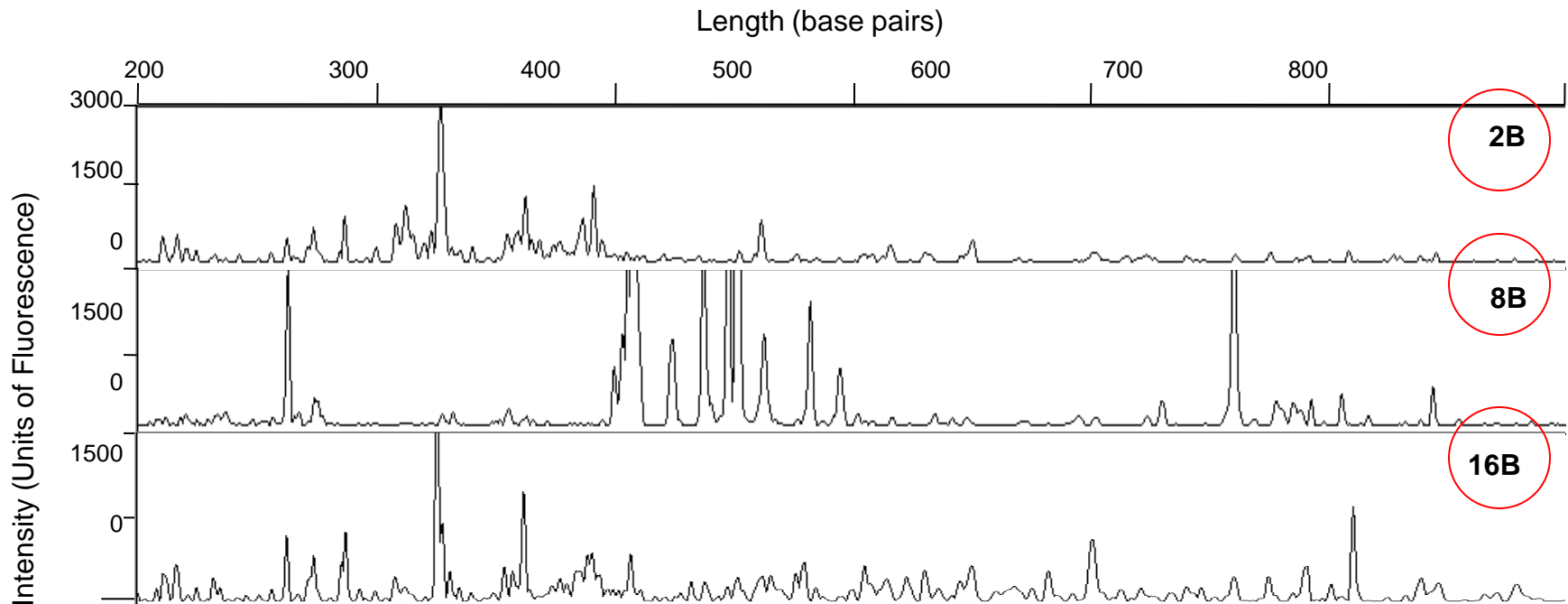


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PC analysis based on presence or absence of ARISA peaks



Intergenic 16S-23S distribution



Electropherograms



GENOMIC LIBRARIES

Only for samples 2B, 8B and 16B



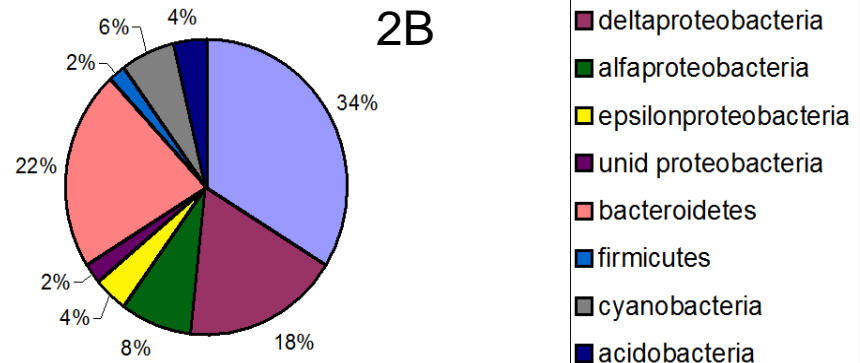
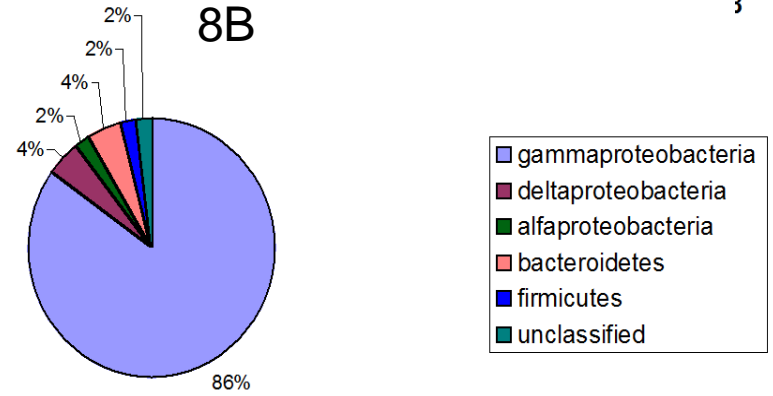
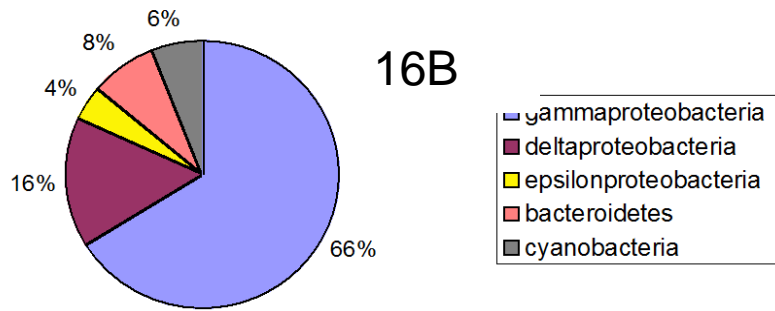
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PHYLUM	STATIONS			CLASS	STATIONS			ORDER and/or FAMILY and/or GENUS	STATIONS		
	2B	8B	16B		2B	8B	16B		2B	8B	16B
ARCHAEA											
<i>Euryarchaeota</i>	76	56	92								
<i>Crenarchaeota</i>	24	44	8	<i>Crenarchaeota</i> unknown							
				<i>Thermoprotei</i>	6		8				

Archea (• 10%):

Euryrarcheota and Craenoarcheota (*Thermoprotei*)
–Unknown functionalities in this habitat.

Different Phyla distribution





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Phylum	2B	8B	16B	Class	2B	8B	16B	Genus	2B	8B	16B
BACTERIA											
Unknown Bacteria	2		9								
<i>Bacteroidetes</i>	20	3	8	unknown <i>Bacteroidetes</i>	5	1	3				
				<i>Flavobacteria</i>	12	2	3	<i>Flavobacteriaceae</i> unknown	5		1
								<i>Flavobacteriaceae, Maribacter</i>	2	1	
								<i>Flavobacteriaceae, Robiginitalea</i>	4		
								<i>Flavobacteriaceae, Ulvibacter</i>			1
				<i>Sphingobacteria</i>	3		5	<i>Sphingobacterales</i> unknown			1
								<i>Sphingobacterales, Flexibacteraceae</i>			2





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Taxa	2B	8B	16B	Class	2B	8B	16B	Genus	2B	8B	16B
<i>Chloroflexi</i>		1									
<i>Cyanobacteria</i>	7	1	4	<i>Cyanobacteria</i>	7	1	4	<i>Cyanobacteria</i> unknown	7	1	3
								<i>Plochlorales, Prochlorococcus</i>			1
<i>Deferribacteres</i>		2	1	<i>Deferribacteres</i>		2	1	<i>Deferribacterales</i>		2	1
<i>Firmicutes</i>	1			<i>Clostridia</i>	1			<i>Clostridiales</i>	1		
<i>Planctomycetes</i>			1	<i>Planctomycetacia</i>			1	<i>Planctomycetales, Planctomycetaceae</i>			1
<i>Proteobacteria</i>	72	91	77	<i>Proteobacteria</i> unknown	1	1					
				<i>Alfaproteobacteria</i>	12	3	4	<i>Alfaproteobacteria</i> unknown	2	1	1
								<i>Rhodobacterales, Rhodobacteraceae</i>	10	1	3
								<i>Rhodospirillales</i>		1	
								<i>Rhizobiales</i>			1
				<i>Betaproteobacteria</i>			1	<i>Burkolderiaceae, Schlegelella</i>			1



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Class	2B	8B	16B	Genus
<i>Deltaproteobacteria</i>	18	3	17	<i>Deltaproteobacteria</i> unknown
				<i>Desulfobacteraceae</i> unknown
				<i>Desulfobacteraceae</i> , <i>Desulfobacula</i>
				<i>Desulfobacteraceae</i> , <i>Desulfofaba</i>
				<i>Desulfobacteraceae</i> , <i>Desulfonema</i>
				<i>Desulfobulbaceae</i>
				<i>Desulfuromonadaceae</i> unknown
				<i>Desulfuromonadaceae</i> , <i>Pelobacter</i>
<i>Epsilonproteobacteria</i>				<i>Bdellovibrionales</i>
	4		3	<i>Campylobacterales</i> unknown
				<i>Helicobacteraceae</i> , <i>Sulfurimonas</i>



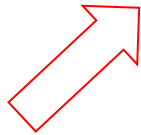
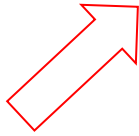
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Class	2B	8B	16B	Genus	2B	8B	16B
<i>Gammaproteobacteria</i>	36	84	52	<i>Gammaproteobacteria</i> unknown	12	28	24
				<i>Alteromonadaceae</i> unknown		1	6
				<i>Alteromonadaceae</i> , <i>Thalassomonas</i>		2	
				<i>Alteromonadaceae</i> , <i>Shewanella</i>		2	
				<i>Chromatiales</i> unknown	21	13	5
				<i>Chromatiales</i> , <i>Ectothiorhodospiraceae</i>			17
				<i>Oceanospirillales</i> unknown	3	4	
				<i>Oceanospirillaceae</i> , <i>Thalassolitus</i>		2	
				<i>Thiotrichales</i> , <i>Piscirickettsiaceae</i>		4	
				<i>Vibrionaceae</i> , <i>Photobacterium</i>		28	



Table 4
Rarefaction analysis and diversity indexes for bacterial and archaeal 16S rRNA clone libraries.

Libraries			2B	8B	16B	
Bacteria	General features	n° clones	99	99	100	
		n° taxa	49	42	54	
		singletons	28	34	43	
		coverage (%)	72	66	57	
	Rarefaction	described taxa (%)	50.2	43.2	47.6	
		st dev	3.2	3	3	
	Diversity indices	dominance	0.036	0.136	0.052	
		Shannon–Weaver	3.629	2.841	3.522	
		Menhinick	4.925	4.221	5.4	
		Margalef	10.45	8.92	11.51	
		equitability	0.932	0.76	0.883	
	Archaea	General features	n° clones	17	16	12
			n° taxa	6	6	4
singletons			4	3	1	
coverage (%)			76	81	92	
Rarefaction		described taxa (%)	54.2	57.7	47.0	
		st dev	1.3	1.3	1.0	
Diversity indices		dominance	0.315	0.218	0.391	
		Shannon–Weaver	1.305	1.555	1.136	
		Menhinick	0.354	0.34	0.372	
		Margalef	0.755	0.744	0.706	
		equitability	0.811	0.966	0.706	





CONCLUSIONS

S-LIBSHUFF analysis demonstrate that the sediments of “group 8B” are statistically different than the rest of sediments at Venice Lagoon

Sediments adjacent to Marghera Venice, and Chioggia (8B group) are distinguished by *Vibrionaceae*, *Alteromonadaceae* and *Oceanospirillaceae* and low biodiversity.

Bacteroidetes (cellulose-degraders) are spread out(20%) especially in stations of “2B group. These sediments show high cellulase activity ($800 \text{ mg O}_2 \text{ Kg}^{-1} \cdot \text{h}^{-1}$)

Microbial stratification to maintain “satisfactory ecological status”

Cyanobacteria & Diatoms

Aerobic b.

Sulfur-sulphides oxidizing b.

Facultative aerobic b.

Anoxic phototrophs (chromatiales)

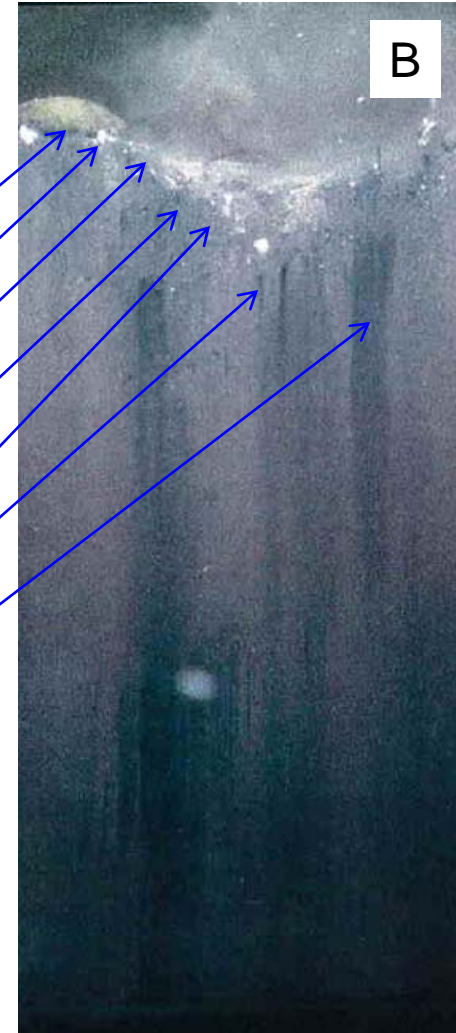
Sulfur-reducing b.

Sulfates-reducing b.

A

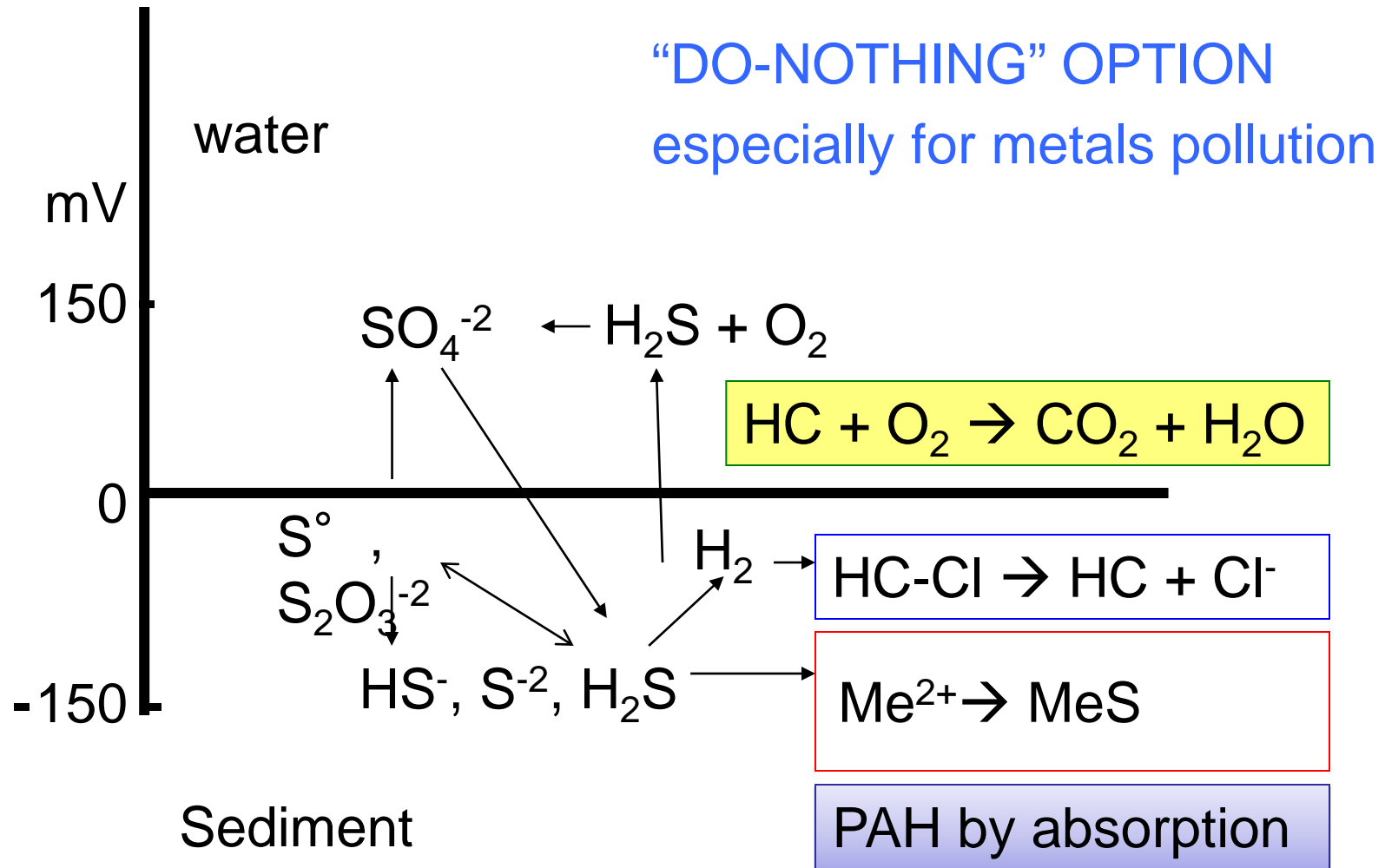


B



3 cm

A rich Sulfur cycle and natural attenuation of pollution





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Thank you for your attention

S. Borin et al. (2009) Res. Microbiol, vol 160:307-314