

Bacterial community analysis in environmental monitoring programs: a useful approach?



Introduction

Detailed investigations at a dumping site

From 2005 to 2010 6 mio m³ of dredged material were dumped 15 kilometres south off Helgoland in the German Bight (North Sea). Dumping activities may cause physical disturbance, including burial of benthic organisms and changes in substrate matter, affecting all benthic communities. The monitoring programs of dumping sites base on international conventions (London convention) for dredged material handling. These recommend the assessment of defined physical, chemical and biological parameters to examine the impact of the disposal. Bacterial communities are disregarded by these recommendations. In an interdisciplinary project with environmental agencies we investigated the bacterial community response to dumping activities. Our study aims to assess the suitability of bacterial communities as a proxy for perturbation events and consequently for the applicability in monitoring programs. We applied 16S ribosomal tag-sequencing and functional gene arrays (GeoChip 4.2) to investigate structure and function of bacterial communities at the dumping site.

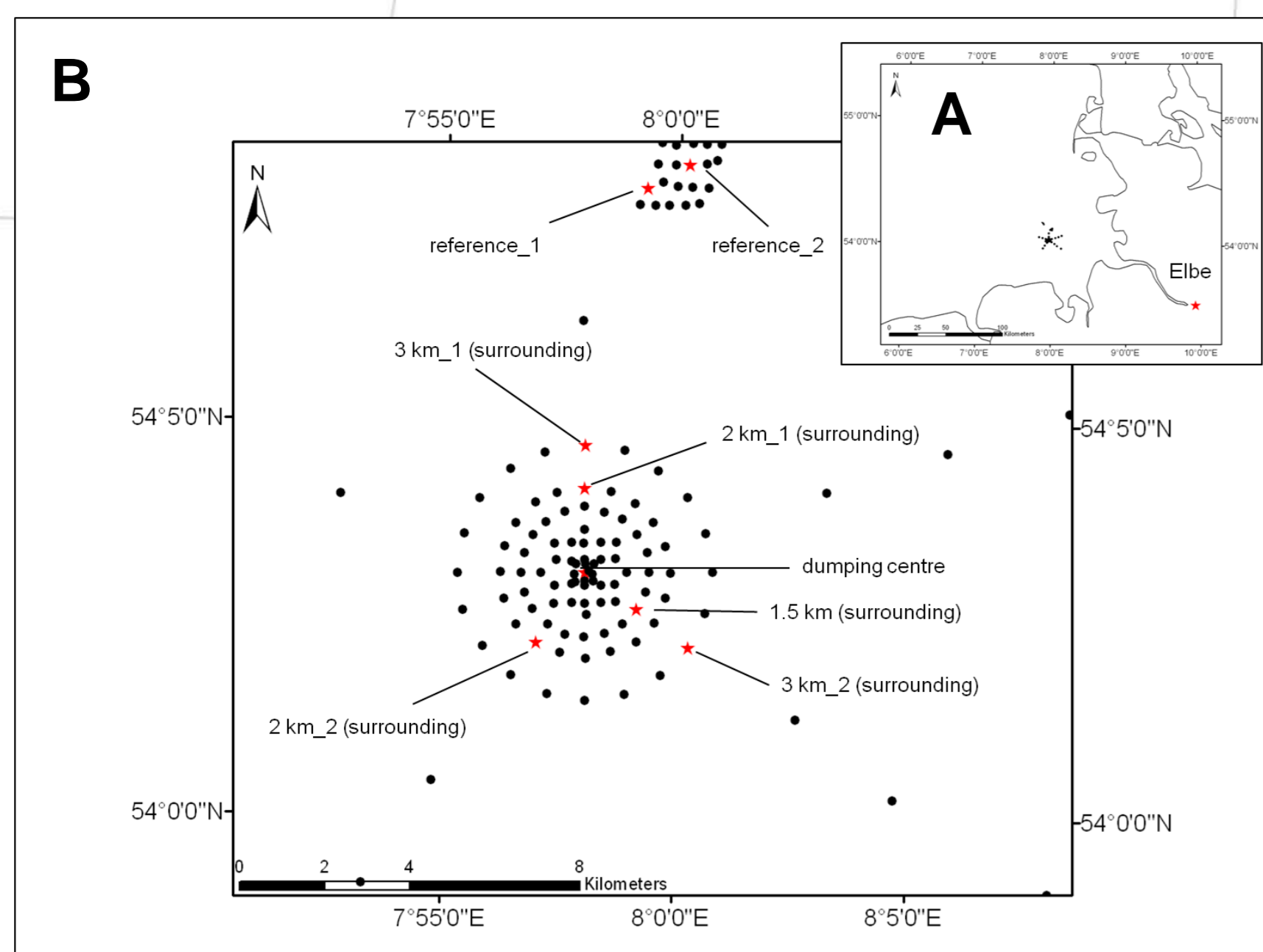


Fig. 1 (A) Dumping site in the German Bight and the dredging zone (Elbe River), (B) Sampling scheme of monitoring at the dumping site. Red stars represent samples subjected to 16S ribosomal tag-sequencing and functional gene array (GeoChip 4.2)

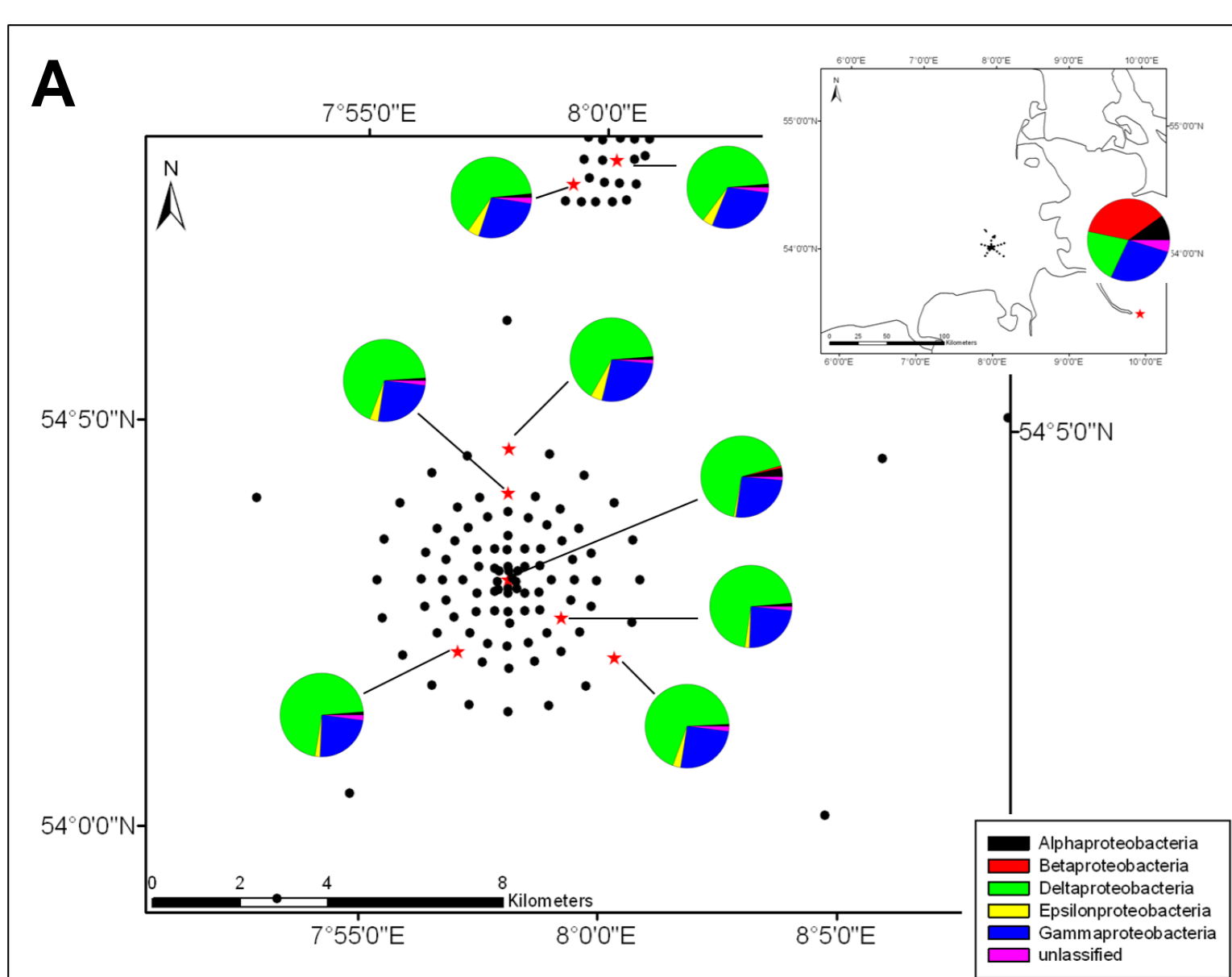
Ribosomal tag-sequencing

Results

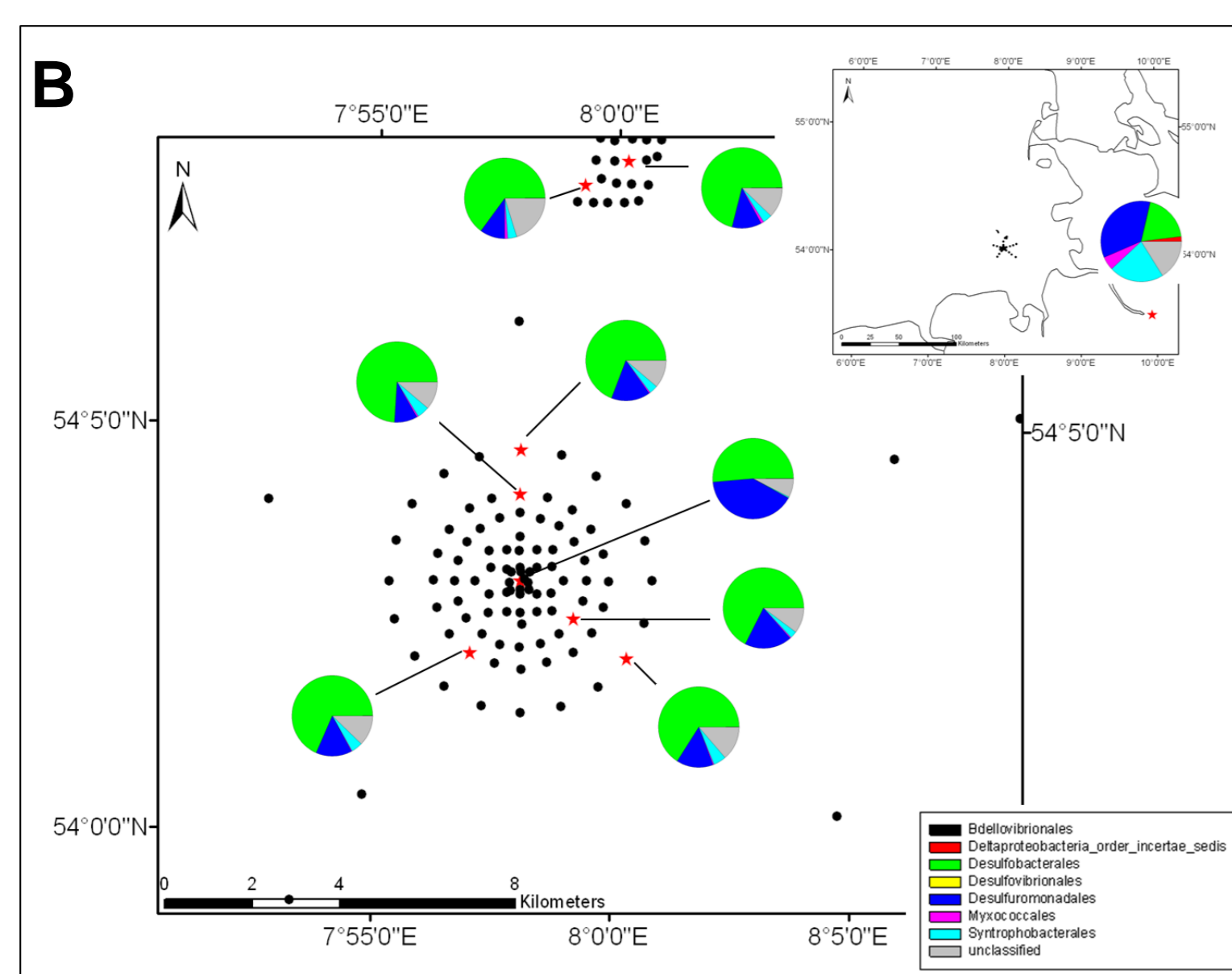
Dumping centre:

- ❖ Low alpha-diversity as revealed by ribosomal tag-sequencing
- ❖ Remarkably high numbers of sequences affiliated to *Desulfuromonadaceae*
- ❖ Significantly lower diversity in functional genes as compared to a reference site

Class distribution *Proteobacteria*



Order distribution *Deltaproteobacteria*



Family distribution *Desulfuromonadales* and *Desulfobacterales*

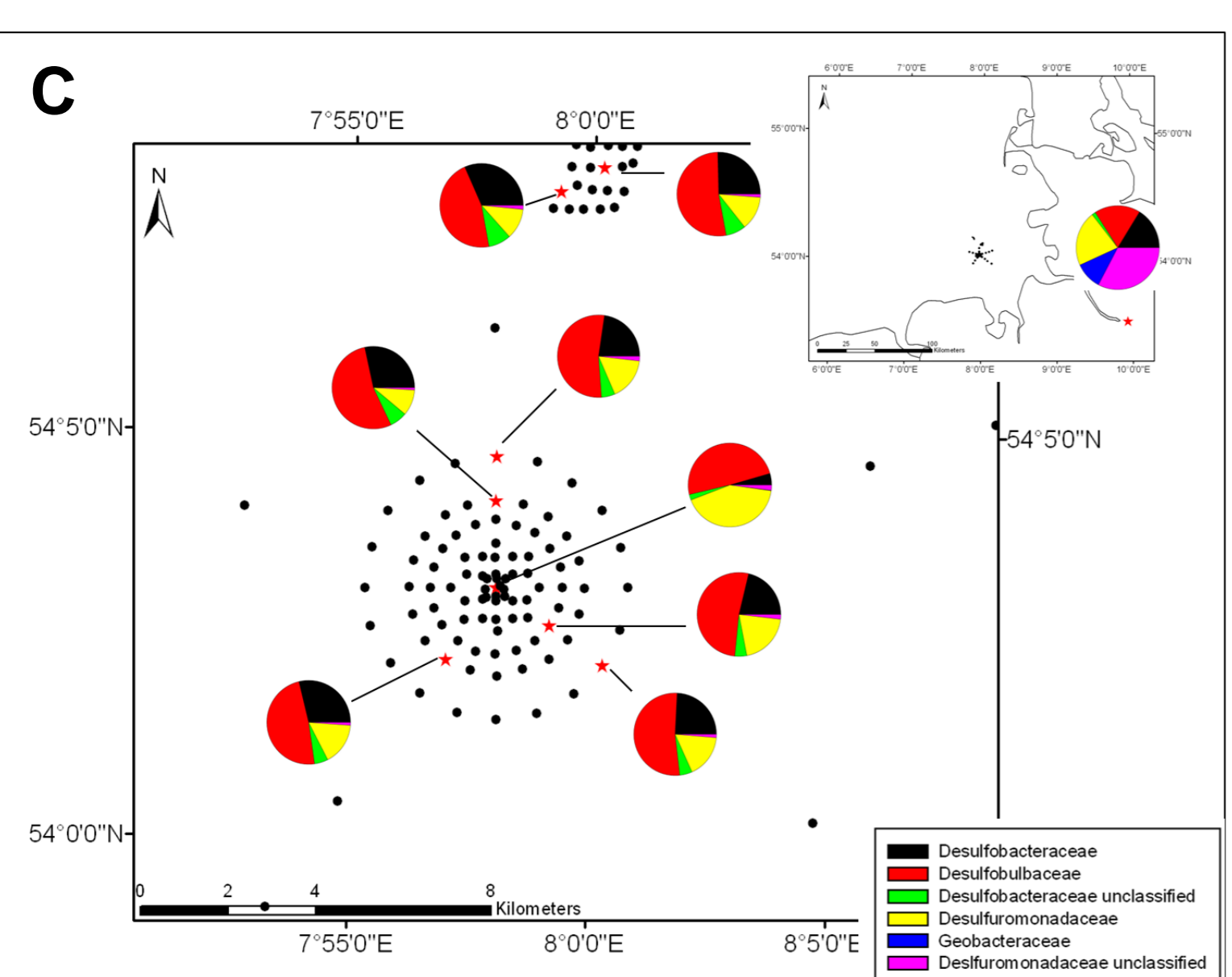


Fig. 2 Pie charts showing the percentage of sequences (0.97) affiliated to (A) *Proteobacteria*, (B) *Deltaproteobacteria* and (C) the orders *Desulfuromonadales* and *Desulfobacterales* derived from tag-sequencing.

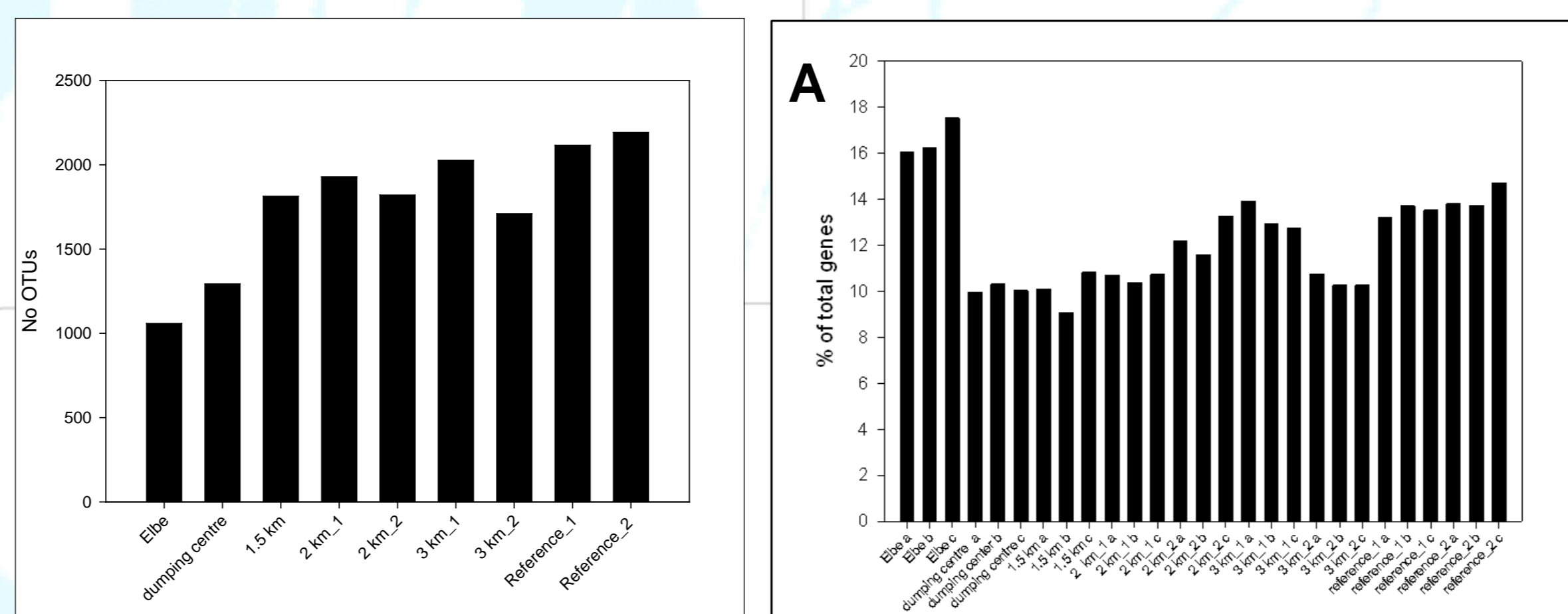


Fig. 3 Number of OTUs (0.97) derived from tag-sequencing

	SQ	FG	MQ	F	p
constant	2.652	1	2.652	48908.440	0.000
Sample	0.012	8	0.002	28.064	0.000
Error	0.001	18	0.000		

	Elbe	dumping centre	1.5 km	2 km_1	2 km_2	3 km_1	3 km_2	Reference_1	Reference_2
Elbe		0.000	0.000	0.000	0.000	0.012	0.000	0.311	0.240
dumping centre	0.000		0.999	1.000	0.947	0.002	1.000	0.000	0.000
1.5 km	0.000	0.999		0.999	0.684	0.001	0.951	0.000	0.000
2 km_1	0.000	1.000	0.999		0.952	0.002	1.000	0.000	0.000
2 km_2	0.000	0.947	0.684	0.952		0.022	0.999	0.001	0.001
3 km_1	0.012	0.002	0.001	0.002	0.022		0.006	0.714	0.805
3 km_2	0.000	1.000	0.951	1.000	0.999	0.006		0.000	0.000
Reference_1	0.311	0.000	0.000	0.000	0.001	0.714	0.000		1.000
Reference_2	0.240	0.000	0.000	0.000	0.001	0.805	0.000	1.000	

GeoChip 4.2 approach

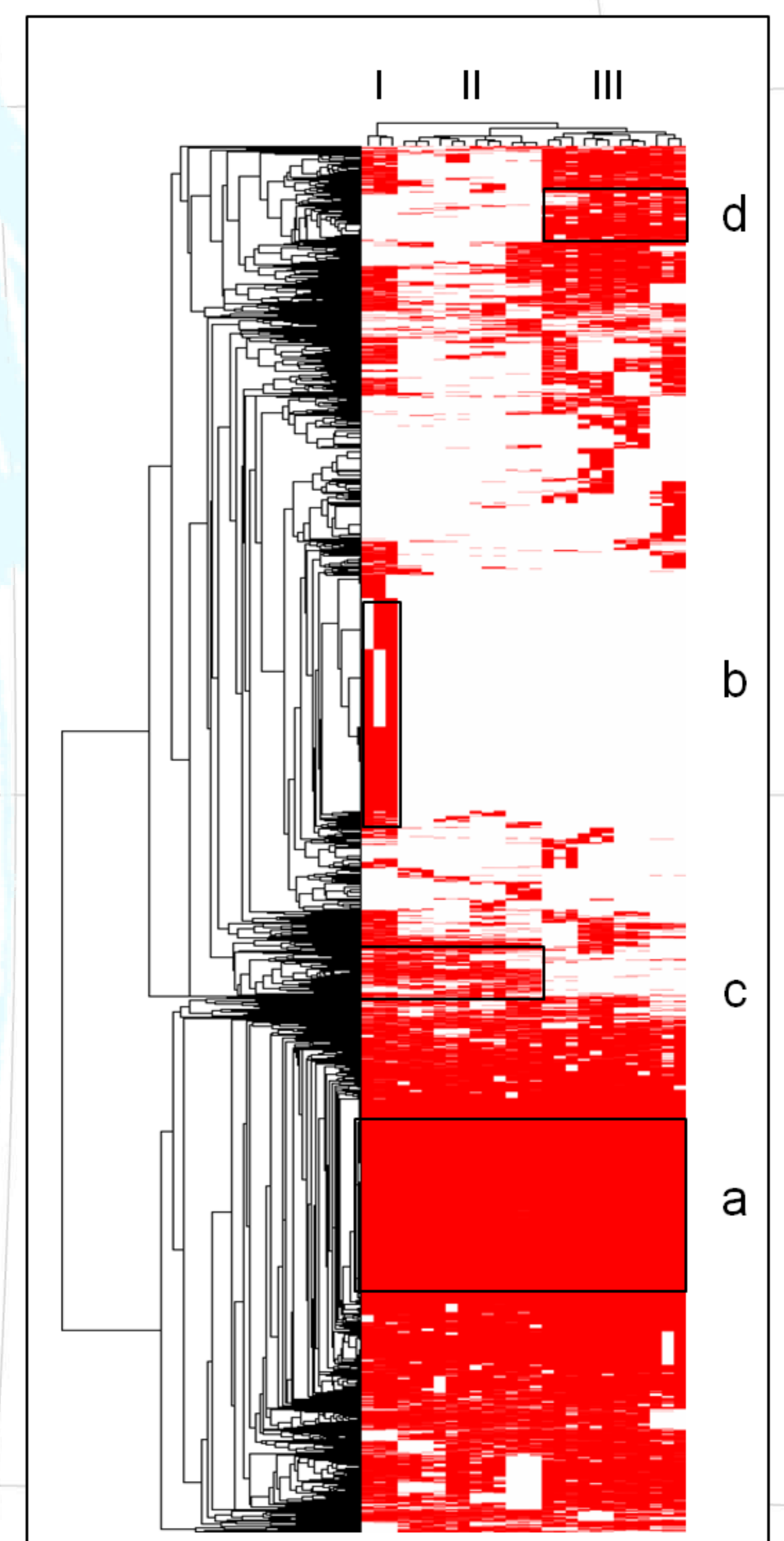


Fig. 4 Hierarchical cluster analysis of functional genes. I) Elbe II) dumping centre and 1.5 km, 2 km_1, 3 km_2 III) reference and 2 km_2, 3 km_1. Probes which showed positive signals a) in all samples b) in the Elbe, c) in the dumping centre and d) in the reference

Fig. 5 (A) Bar chart showing the percentage of detected functional genes (B) Differences were tested applying the analysis of variance and post hoc Tukey tests ($p < 0.05$)

Conclusion

- ❖ Dumping activities affect structure and function of bacterial communities favoring a less diverse but possibly more specialised community
- ❖ Bacterial community analyses represent a promising tool for the assessment of perturbation
- ❖ We recommend the inclusion of bacterial community analyses in monitoring programs