



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



Fine scale investigations at a dumping site

Introduction

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 the whole 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. Benthic bacterial communities are disregarded by these recommendations. In an interdisciplinary project with environmental agencies we investigated benthic bacterial community in response to dumping activity. Our study aims to assess the suitability of bacterial community analysis as a proxy for environmental perturbation and consequently the applicability for mandatory monitoring programs.

We applied ribosomal community analyses (ARISA fingerprints, 16S ribosomal tag-sequencing) and functional gene arrays (GeoChip 4.2) to investigate structure and function of benthic bacterial communities at the dumping site.

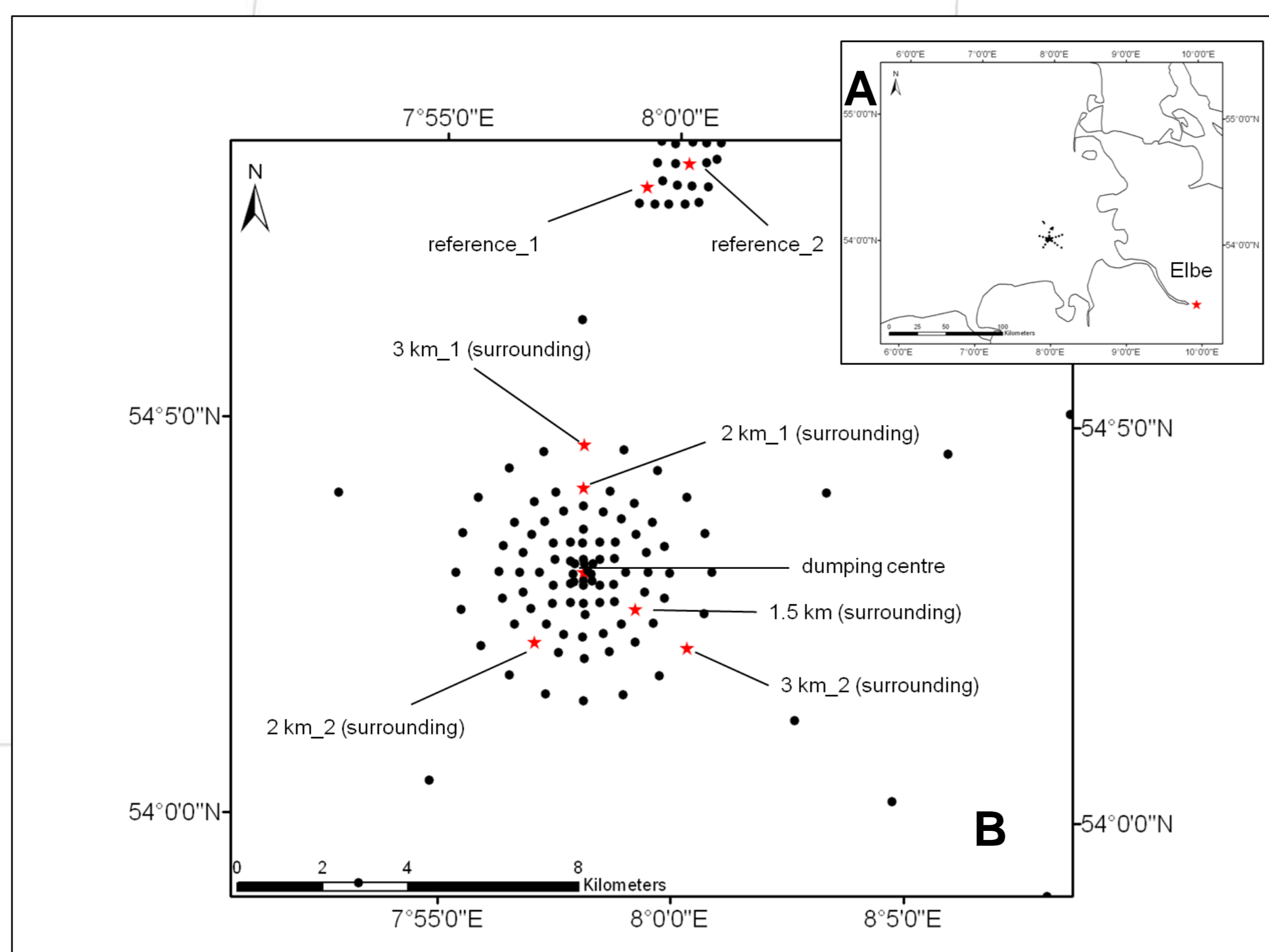


Fig. 1 The dumping site in the German Bight and the dredging zone in the Elbe River (A) Sampling scheme of monitoring at the dumping site (B) Red stars represent samples subjected to 16S ribosomal tag-sequencing and functional gene array (GeoChip 4.2)

ARISA fingerprints

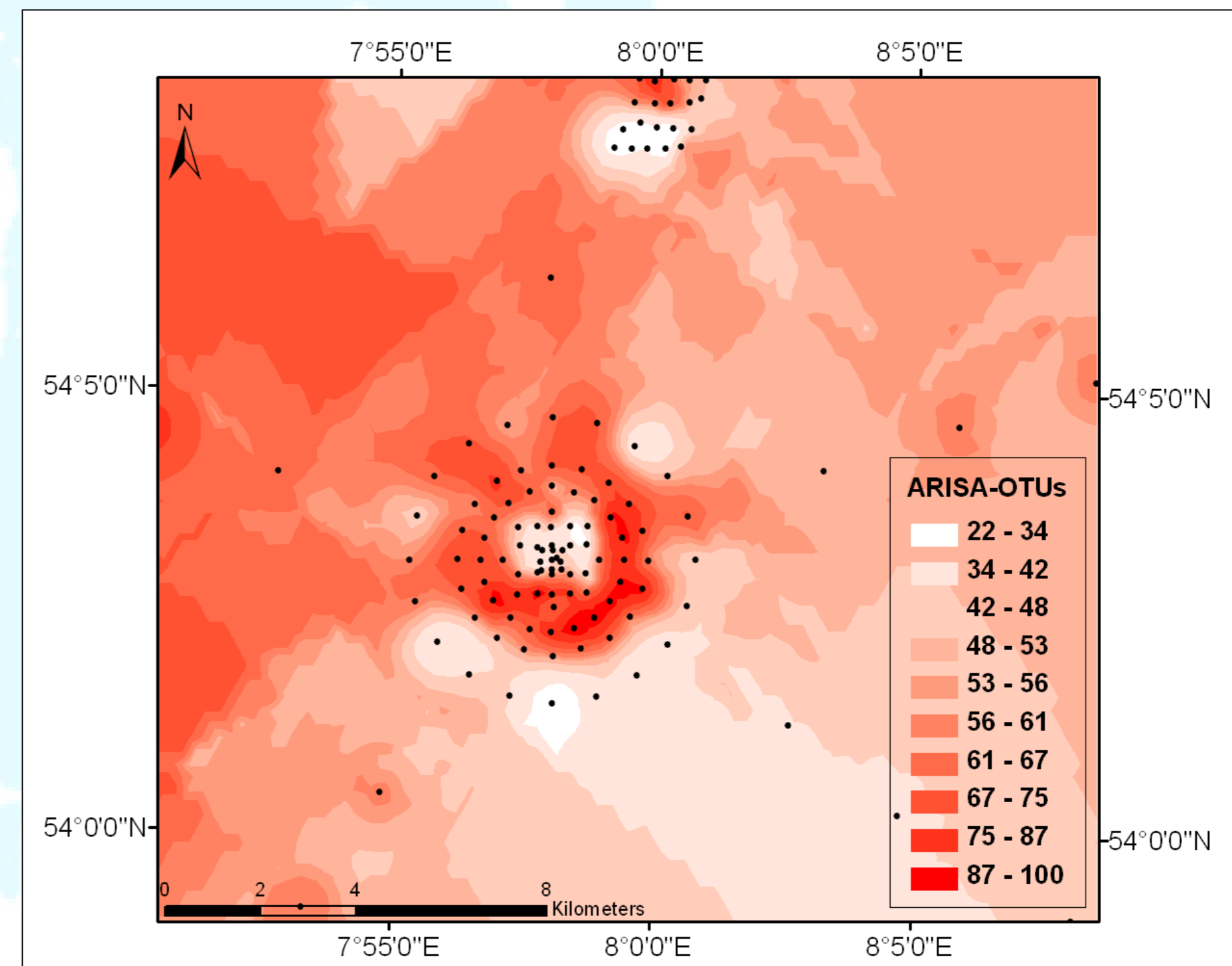


Fig. 2 Spatial distribution of the sum of ARISA-OTUs as calculated by ordinary kriging. Dots represent the 125 sampling stations.

Results

Dumping centre:

- ❖ Low alpha-diversity as revealed by *automated ribosomal intergenic spacer analysis* (ARISA) and ribosomal tag-sequencing
- ❖ Highest number of sequences affiliated to *Desulfuromonadaceae*
- ❖ Significantly lower diversity in functional genes as compared to a reference site, exemplarily shown for functional genes involved in organic remediation

Ribosomal tag-sequencing

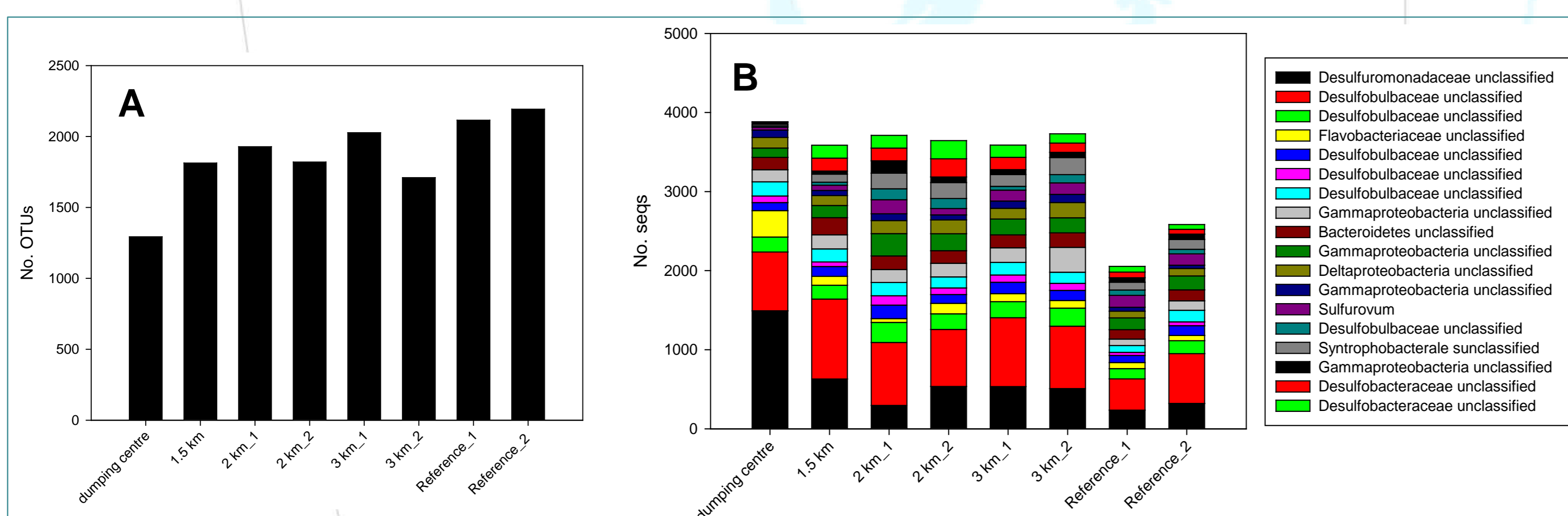


Fig. 3 OTUs (0.97) derived from tag sequencing: Number of OTUs (A) and top 18 OTUs (contributing > 10% to the whole community) at the sampling sites.

GeoChip 4.2 approach

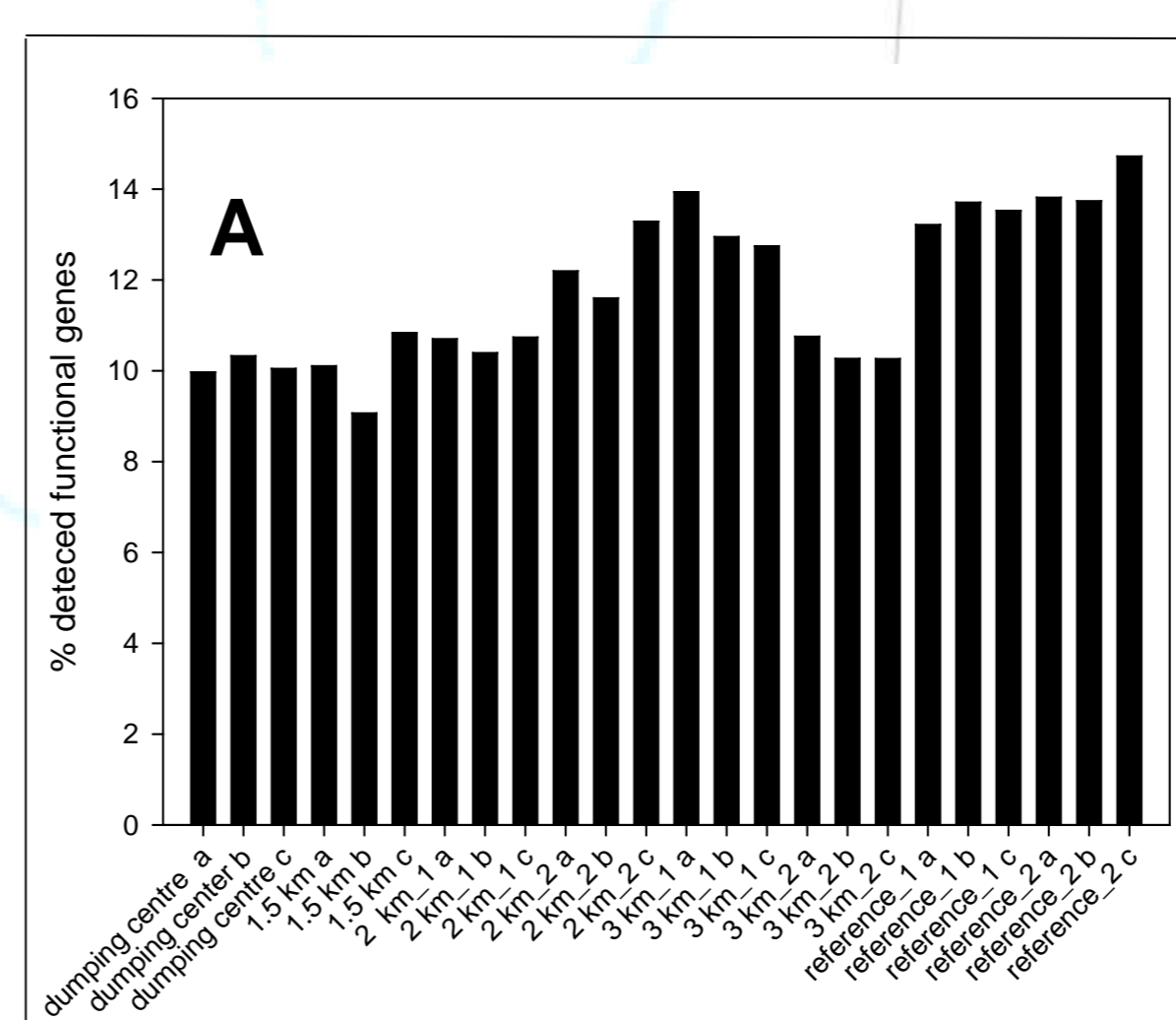


Fig. 4 (A) Bar chart showing the percentage of detected functional genes for the subsamples (B) Differences were tested applying the analysis of variance and *post hoc* Tukey tests for pair wise comparison ($p < 0.05$)

	dumping centre	1.5 km	2 km	2 km 2	3 km 1	3 km 2	Reference 1	Reference 2
dumping centre	1.000	0.933	0.002	0.000	0.994	0.000	0.000	0.000
1.5 km	0.933	1.000	0.001	0.000	0.963	0.000	0.000	0.000
2 km	0.002	0.001	1.000	0.001	0.000	0.000	0.000	0.000
2 km 2	0.000	0.000	0.001	1.000	0.000	0.000	0.000	0.000
3 km 1	0.994	0.963	0.000	0.000	1.000	0.000	0.000	0.000
3 km 2	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000
Reference 1	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.904
Reference 2	0.000	0.000	0.000	0.000	0.000	0.000	0.904	1.000

Conclusion

- Perturbation caused by dumping activities affects structure and function of bacterial communities favoring a less diverse but possibly more specialised bacterial community
- bacterial community analyses represent a promising tool for the assessment of environmental perturbation
- We recommend the inclusion of bacterial community analyses in mandatory monitoring programs