SHELF WATERS OFF GALICIA (NW IBERIAN PENINSULA): PATTERNS AND DRIVERS SHAPING THE DIVERSITY

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Ecological and biogeochemical processes in the ocean are dependent on a diverse assemblage of microbes, including members of Bacteria (Glöckner et al. 2012). These bacterial assemblages occurs in vast numbers and represent a huge genetic diversity, fulfilling a wide of ecological roles in the marine system such as carbon biogeochemical cycle and energy transfer into higher trophic levels. We combined flow cytometry, CARD-FISH and 16S rRNA gene tag pyrosequencing to investigate the short-term variability of the bacterial communities in samples collected along a transect in the shelf off NW Iberian Peninsula over one week.

Location of stations 1c, 2, 3c, and 4, sampled during the oceanographic cruise HERCULES III in the shelf waters off the coast of A Coruña. The numbers between brackets indicate the depth of each station.
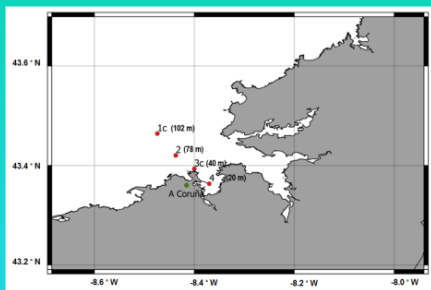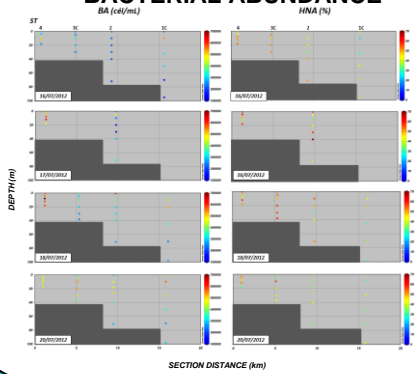

HYDROGRAPHIC CHARACTERIZATION
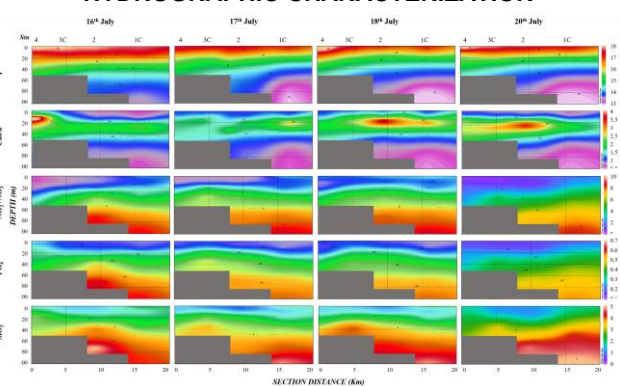
Evolution of physical, chemical and biological variables sampled during the oceanographic cruise HERCULES III in the shelf waters off the coast of A Coruña. T: temperature; Chl-a: Chlorophyll-a concentration, $NO_2 + NO_3$: nitrate + nitrite; PO_4: phosphate; SO_3: silicate.

BACTERIAL ABUNDANCE

Distribution of bacterial abundance (cells ml^{-1}) and the percentage of high nucleid acid (%, HNA) content (%) in the shelf waters off the coast of A Coruña. The figure was produced with the ODV (Ocean Data View) software.
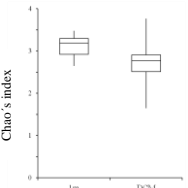
CARD-FISH

Percentage of relative abundance (mean ± standard deviation) of the main groups of bacteria in the different sampling points in the shelf waters off the coast of A Coruña.

Stn	Depth	% DAPI	% EUBACTERIA					
				PROTEOBACTERIA				BACTEROIDETES
				Alphaproteobacteria		Gammaproteobacteria		
		EUBACTERIA	SAR-11	Roseobacter	Gamma	SAR-86	
4	1m	72,4 ± 1,6	29,5 ± 3,1	18,0 ± 2,4	23,1 ± 3,4	14,0 ± 2,0	34,9 ± 3,5
	DCM	74,8 ± 3,2	31,1 ± 4,5	14,2 ± 4,4	21,2 ± 4,6	13,8 ± 3,0	29,2 ± 3,9
3C	1m	72,9 ± 1,6	29,7 ± 3,1	13,4 ± 2,4	22,4 ± 3,4	9,4 ± 2,0	27,9 ± 3,5
	DCM	69,0 ± 3,2	21,9 ± 4,5	12,3 ± 4,4	23,8 ± 4,6	9,1 ± 3,0	27,4 ± 3,9
2	1m	69,6 ± 1,6	31,8 ± 3,1	15,4 ± 2,4	29,7 ± 3,4	13,1 ± 2,0	34,8 ± 3,5
	DCM	67,5 ± 3,2	31,3 ± 4,5	22,4 ± 4,4	29,9 ± 4,6	14,9 ± 3,0	35,9 ± 3,9
1C	1m	73,0 ± 1,6	24,6 ± 3,1	18,6 ± 2,4	26,1 ± 3,4	11,3 ± 2,0	30,2 ± 3,5
	DCM	69,4 ± 3,2	26,3 ± 4,5	16,0 ± 4,4	19,2 ± 4,6	9,5 ± 3,0	28,5 ± 3,9

16s GENE TAG 454 PYROSEQUENCING
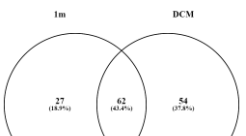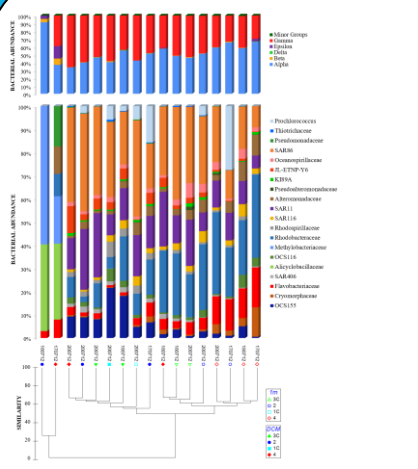
Venn diagram of shared 16S rRNA gene based OTUs between the two groups of samples: surface and depth chlorophyll maximum (DCM).

Comparison of bacterial diversity, derived from the Bray-Curtis similarity coefficients calculated from the square root transformed relative abundance of each OTU, between the different sampling points in the shelf waters off the coast of A Coruña.

Bacterial richness estimates (Chao 1) by type of samples: surface and depth chlorophyll maximum (DCM).

ENVIROMENTAL PARAMETERS/PHYLA AND BACTERIAL OTUs
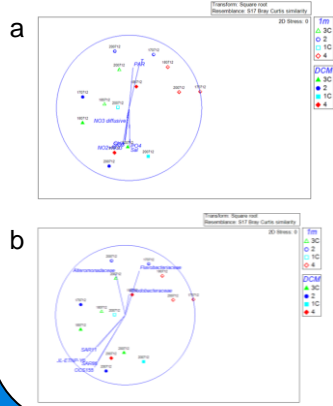
nMDS analysis showing the correlation between (a) different environmental variables and (b) specific taxonomic phyla and the relative abundance of bacterial OTUs in the different samples. Sampling points that are close together are more similar in their bacterial composition than those that are far apart.

CONCLUSIONS:

● Bacterial abundance and community composition was stable over the temporal scale of days. Higher abundance and relative activity (expressed as a percentage of high-nucleic acid content cells) was found in surface waters at stations closer to the coast.

● CARD-FISH analysis displayed that SAR11, SAR86 and Roseobacter were the most abundant bacterial taxa at all samples.

● Using pyrosequencing, we found a higher diversity and number of operational taxonomic units (OTUs) in the deep chlorophyll maximum (DCM) compared to surface waters. Surface communities were mainly dominated by Flavobacteriaceae and Alteromonadaceae, whereas samples collected at the DCM were affiliated to Acidomicrobiales, SAR406 and Oceanopirillales

● Bacterial communities inhabiting in surface waters were associated with higher temperature and light conditions, whereas deep samples exhibited a significant positive relationship with salinity, inorganic nutrients and chlorophyll a.