

INTRODUCTION

Far below the euphotic zone, below 1000 meters, there is much less biological activity than in other ocean layers. Nevertheless, more than the 75% of oceanic water corresponds to the zone known as deep sea which ranges from 1000 to 6000 meters below the surface, meaning this dark and seemingly motionless environment is the biggest habitat in the world.

Knowing the global diversity and its distribution patterns is a key factor in order to anticipate changes in marine ecosystems over environmental changes.

Studies have been traditionally focused on the euphotic zone. However, for the last decade, technology has come along its own limitations and opened the way to the furthest ocean depths. Many new studies are appearing, but most of them are at the local scale. Only a few are starting to focus on a wider perspective which includes whole oceans or even a global scale.

Large projects and data-bases have proven useful for comparing and standardizing different results, such is the case of the open access dataset of the International Census of Marine Microbes (ICoMM) which provides a huge compilation of information about many different research projects regarding ocean diversity.

The objective of this minireview is to analyse the diversity found by other projects and picture it globally in order to have a preliminary view of the global distribution diversity patterns (Table 1). Nevertheless it must be taken into account that diversity patterns present in local scale studies are hardly representative of the diversity pattern of the whole area.

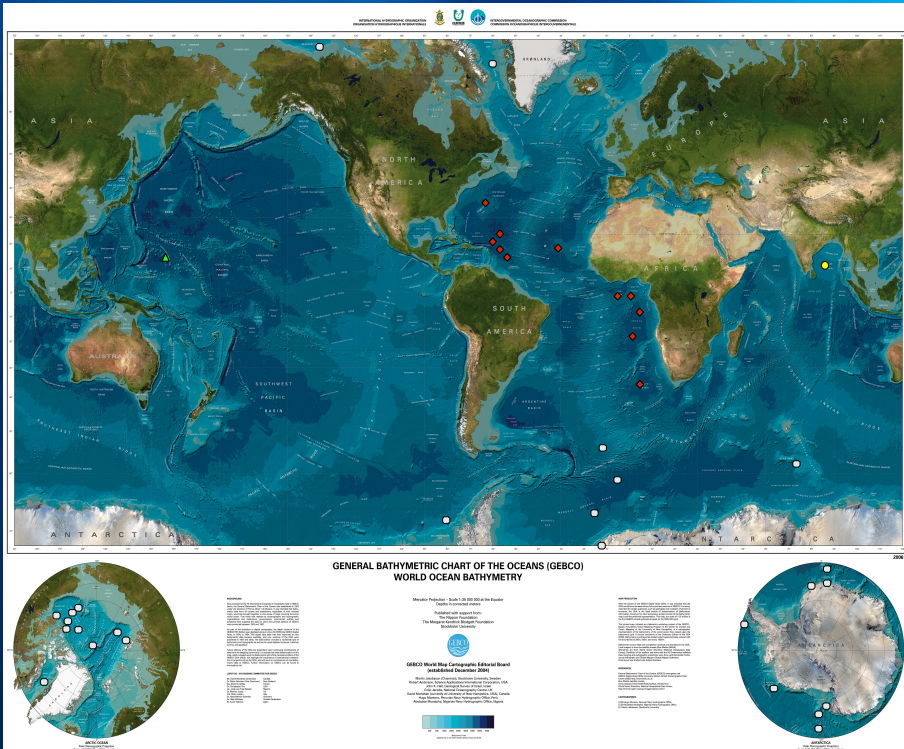


Figure 1. Modified from General Bathymetric Chart of the Oceans (GEBCO) world map. This map shows the bathymetry of the world's ocean floor. Originally taken from GEBCO web page; <http://www.gebcoc.org>

	Pacific Ocean	Polar Oceans	Atlantic Ocean	Indian Ocean
<i>Gammaproteobacteria</i>	Present	Present	Present	Present
<i>Alphaproteobacteria</i>	Present	Present	Present	Present
<i>Acidobacteria</i>	Present	Present	Present	Present
<i>Planctomycetes</i>	Present	Present	Present	Present
<i>Deltaproteobacteria</i>	Present	Present	Present	Present
<i>Chloroflexi</i>	Present	Present	Present	Present
<i>Betaproteobacteria</i>	Present	Present	Present	Present
<i>Actinobacteria</i>	Present	Present	Present	Present
<i>Firmicutes</i>	Present	Present	Present	Present
<i>Verrucomicrobia</i>	Present	Present	Present	Present
Low G+C Gram-positive Bacteria	Present	Present	Present	Present
Other Groups	Present	Present	Present	Present

Table 2. Absence / Presence table of the main phylogenetic groups in the deep ocean sediments of the different sampling zones.

RESULTS

***Gammaproteobacteria* is the most dominant in all but the Indian Ocean.** Other groups such as *Alphaproteobacteria* and *Acidobacteria* were highly represented in all Oceans (Table 2). *Betaproteobacteria* were present in all sampling zones too but usually in lower proportions.

Indian Ocean showed the most diverse community (Table 1). Reasons of this are still unclear, one hypothesis is that it is a rather isolated Ocean engulfed between continental blocks. Nevertheless, it is still in contact with other water flows through the West Australia Current (Fig. 2) which would allow for long distance migrations from other environments.

Results from the Pacific Ocean are not representative (they are from a Cobalt-rich zone) This ocean is the largest in the world and it would be of great interest to have information from many other sampling zones within the area so more representative data could be shown.

Some phylotypes can be found almost everywhere, which suggests that some microorganisms can disperse through huge distances, and therefore are cosmopolitan. However, this is usually only considered through studies which do not identify up to species level, so it would be more correct to speak about **cosmopolitan phyla** or classes rather than species.

Importance of experimental design

16S rRNA libraries allow for a good coverage but the technique presents some issues which must be taken into account. Second Generation Sequencing techniques generate a lot of information. However a new bottleneck has appeared as the volume of new data is way bigger than the current analytical capacity. Hence new quantitative statistical tools are needed if we are willing to overcome this bottle-neck.

Moreover, a standardized sampling method and data treatment should be established. The existence of many different approaches hampers data comparison and possible future reviews.

The importance of culture approaches must not be forgotten. Such methods are the only way to isolate a determined strain for further studying and characterization. Culture methods are a key factor, not only with practical interests in mind but also for a proper taxonomic classification and validation.

Sampling Zone	Diversity Table		Observations	References
	Main Group and abundance	Phylogenetic Groups		
Pacific Ocean	<i>Gammaproteobacteria</i> 23%	Order <i>Stenotrophomonas</i>	Three bacterial 16S gene clones libraries were constructed from sediment layers 0-3 cm, 3-8 cm and 8-16 cm. Sampling made in a Cobalt-Rich crust in July 2007. 417 bacterial clones were sequenced.	Liao L. et al. 2011 Xu M. et al. 2005
		Order <i>Ecotiarhodospiraceae</i>		
		Order <i>Alteromonadales</i>		
	<i>Alphaproteobacteria</i> 18%	Order <i>Legionellales</i>		
		Order <i>Korarchaeales</i>		
		Order <i>Rhodospirillales</i>		
	<i>Deltaproteobacteria</i> 17,5%	Family <i>Rhodobacteraceae</i>		
		Genus <i>Ochrobactrum</i>		
	<i>Acidobacteria</i> 7,7%	Genus <i>Hyphomicrobium</i>		
		Genus <i>Filomicrobium</i>		
	<i>Planctomycetes</i> 7,2%	Order <i>Myxococcales</i>		
		Genus <i>Nitrospina</i>		
	<i>Chloroflexi</i> 6,2%	Uncultured clones related to ones recovered from the ocean waters of Hawaii and the Sargasso Sea		
		<i>Firmicutes</i> <4%		
	<i>Verrucomicrobia</i> <4%	NA		
<i>Actinobacteria</i> <4%		Genus <i>Rhodococcus</i> Genus <i>Coxsackia</i>		
<i>Betaproteobacteria</i> <4%	Genus <i>Nitrospina</i>			
	Unidentified isolates			
Other Groups <4%	Phylum <i>Bacteroidetes</i>			
	Phylum <i>Gemmatimonadetes</i>			
	Phylum <i>Deferribacteres</i>			
	Phylum <i>Fibrobacteres</i>			
	Phylum <i>Spirarchaeotes</i>			
	Candidate division OD1			
Polar Ocean	<i>Gammaproteobacteria</i> NA	NA	Comparative study between Arctic and Antarctic regions. There were differences between northern and southern oceans in <i>Betaproteobacteria</i> , <i>Actinobacteria</i> and <i>Acidobacteria</i> , which were more common in the Arctic (3-4% each) than in Antarctic Ocean (less than 2% each).	Ghiglione J. F. et al. 2012
	<i>Alphaproteobacteria</i> NA	NA		
	<i>Flavobacteria</i> NA	NA		
	<i>Betaproteobacteria</i> NA	NA		
	<i>Actinobacteria</i> NA	NA		
Atlantic Ocean	<i>Acidobacteria</i> NA	NA	Data based on both cultured isolations and 16S rRNA libraries. Cultured samples were taken from North-west Atlantic Ocean while the libraries were made from sediments of the South Atlantic Ocean from three different basins (The Cape, Angola and Guinea basins).	Fang J. et al. 2010 Fang J., Kato C. 2010 Schauer R. et al. 2010
	<i>Gammaproteobacteria</i> 41%	Genus <i>Shewanella</i> Genus <i>Photobacterium</i> Genus <i>Colwellia</i> Genus <i>Moritella</i> Genus <i>Psychromonas</i>		
Indian Ocean	<i>Deltaproteobacteria</i> 12,5%	NA	Data based on a 16S rRNA library which gave a total of 84 sequences and 60 different OTUs.	Houbou W. et al. 2011
	<i>Alphaproteobacteria</i> 7%	NA		
	<i>Planctomycetes</i> 7%	NA		
	<i>Bacteroidetes</i> 7%	NA		
	<i>Acidobacteria</i> 5%	NA		
	<i>Chloroflexi</i> 5%	NA		
	<i>Betaproteobacteria</i> 2%	NA		
	Unclassified 40%	NA		
	<i>Alphaproteobacteria</i> 20%	NA		
	<i>Acidobacteria</i> 13%	NA		
<i>Gammaproteobacteria</i> 10%	NA			
Indian Ocean	<i>Deltaproteobacteria</i> 10%	NA		
	<i>Actinobacteria</i> <10%	NA		
	<i>Planctomycetes</i> <10%	NA		
	<i>Chloroflexi</i> <10%	NA		
	<i>Betaproteobacteria</i> <10%	NA		
	<i>Nitrospira</i> <10%	NA		
	Low G+C Gram-positive Bacteria <10%	NA		
		NA		

Table 1. Diversity Table representing the different results from the selected studies performed all over the different oceans.

Environmental pressure

In 1934, Baas Becking stated **"Everything is everywhere but, the environment selects"**. It is unquestionable that abiotic environmental filtering has a deep impact over community structure and distribution. However, both cosmopolitanism and provincialism put in question this hypothesis. Some bacteria (such as *Gammaproteobacteria*) can effectively be found anywhere, no matter the environment, whilst others are only found in a discrete zone but not in similar environments (such as the differences between polar communities).

However, this facts could be the result of differences among studies in the spatial scale used and the taxonomic resolution.

It is still unclear the impact each environmental condition has on bacterial communities. Some authors suggest that macrocosmos studies should be performed.



Figure 2. Global Ocean Current Patterns Map. This map shows the main currents of the oceans. Originally taken from SEOS web page; <http://www.seos-project.eu/home.html>

Future remarks

Defining bacterial marine diversity and its geographic distribution is difficult but of great importance. Sea sediments are rich in uncultured microbial resources waiting to be discovered and exploited. Not only for its industrial potential but also because of **many remarkable ecological questions still unresolved.**

Future research should take advantage of the newest sequencing methods and mathematical tools so estimation and description of diversity becomes a rational and planned activity.

Microbes have at least as much, if not more, impact on our environment and society as geology has. **The knowledge that diversity studies can provide will surely shed light over current knowledge blanks and help understand a massive world that right now, remains mostly unexplored and yet to be discovered.**

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