

"The known unknowns..."

Preliminary results of a gap analysis of biogeographic data

Results from EU MIDAS project

Workshop overview

Why is taxonomy important?

What level of taxonomic resolution is needed?

What level of taxonomic resources are available and needed?

Why do we need to have any sort of intercalibration between areas?

Isn't it enough to be sure of the species in each area?

What role will new technologies and approaches make?

Can't we just use genetics and leave the morphology?

How do we use internet resources to ensure information exchange?

MIDAS Objective

Biogeography and connectivity – how species are distributed within and between claim areas

Objective

Assess the distribution patterns of species in key taxonomic groups (meio-, macro and megafaunal organisms) using both molecular and morphological species concepts and appropriate monitoring technologies.

Activity

Gap analyses of existing data to determine what future sampling is required and to provide support for ecological modelling.

CCFZ: Biogeographic patterns

Why do we need to study biogeographic patterns? Why are such patterns important?

What is the environmental risk that species will become extinct due to mining?

Would extinction matter?

CCFZ: Biogeographic patterns

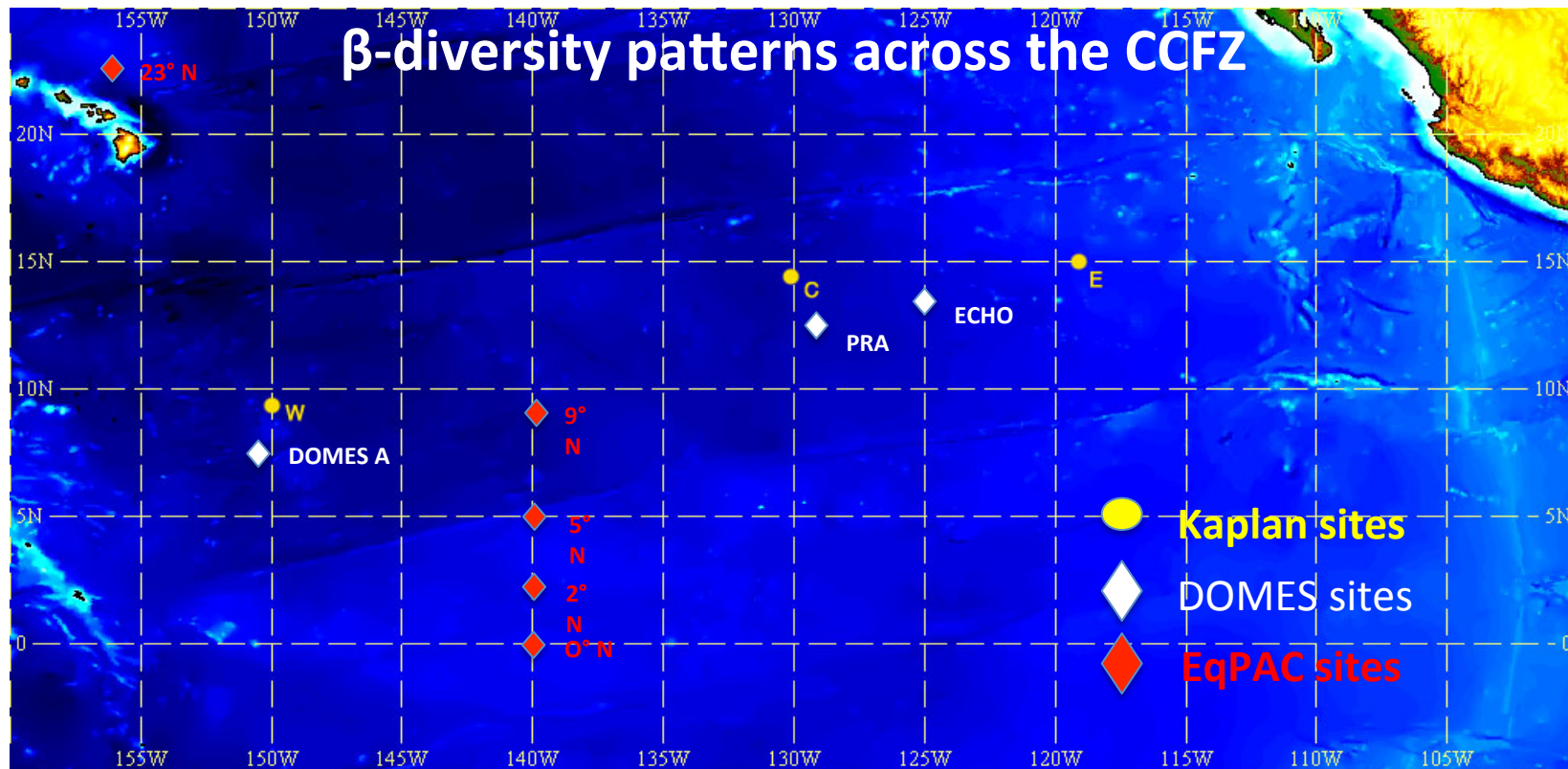
Two examples to demonstrate why greater understanding of the biogeography of the macrofauna is important.

1) Analyses of β -diversity across the CCFZ.

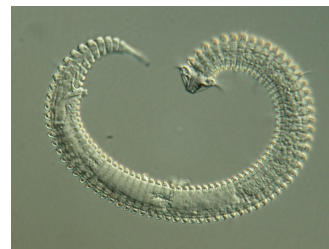
Using polychaetes what does existing data tell us about species distribution patterns across the CCFZ?

2) Assessment of rarity.

Are species really rare or just undersampled?



Polychaetes – Domes, Kaplan
and EqpAC



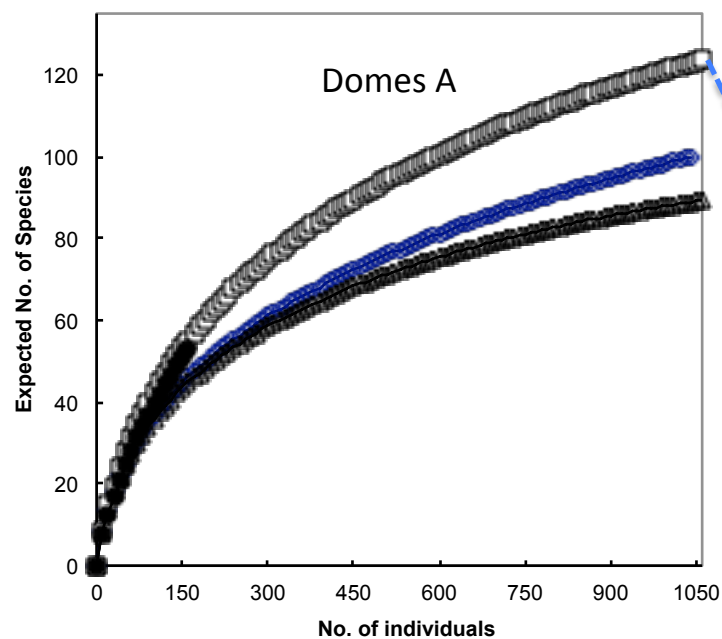
Nematodes – EqpAC

Looking at three transects across the CCFZ.
East to West : DOMES, KAPLAN
South to North: EqpAC

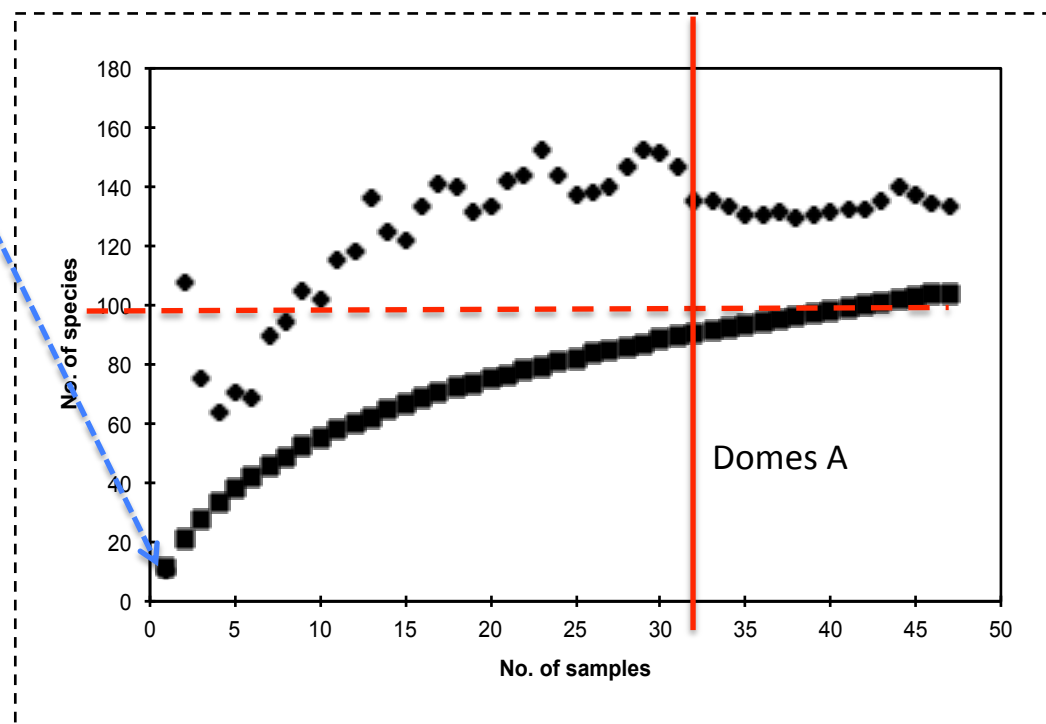
Importance of taxonomy

To be able to determine species distribution need to be able to accurately identify what those species are.

And there are lot of them...



Rarefaction of CCFZ DOMES sites



Estimate of the number of species present in an area of the CCFZ

Importance of taxonomy

So there may be high species richness in each area >200 spp.

But are the same species found in all areas?

Are we looking at one regional species pool? - Nesteresss

Potential extinction risk – low to moderate

Or

Does the species composition change with increasing distance? – Species Turnover

Potential extinction risk—moderate to high

Table 4. β -diversity measures for the CCFZ stations based on polychaetes – PRA, ECHO and DOMES A; Polychaetes and Nematodes–EqPac 0N, 2N, 5N, 9N and HOT station 23N, Kaplan polychaetes. SIM=Simpson's multiple site dissimilarity; SOR = Sorensen's pairwise dissimilarity–measure of turnover, NES = nestedness measure.

	Spatial turnover: Dissimilarity Beta.SOR	β -diversity \$beta.SIM	nestedness: beta.NES
Polychaetes CCFZ	0.511	0.487	0.024
Polychaetes Kaplan	0.806	0.625	0.181
Polychaetes EqPac	0.783	0.626	0.156
EqPac nematodes	0.629	0.460	0.168

β -diversity patterns across the CCFZ

Summary

Results suggest that the fauna changes with distance

The fauna maybe different from one area to another

Risk of causing species extinction is potentially high

Caveats

This analysis is based on a fairly limited sample set

Taxonomy has not been unified so based on a limited understanding of species distribution

High number of rare species makes improved sample coverage really important

Future needs

Better spatial coverage

Unified taxonomy



MANAGING IMPACTS OF DEEP
SEA RESOURCE EXPLOITATION

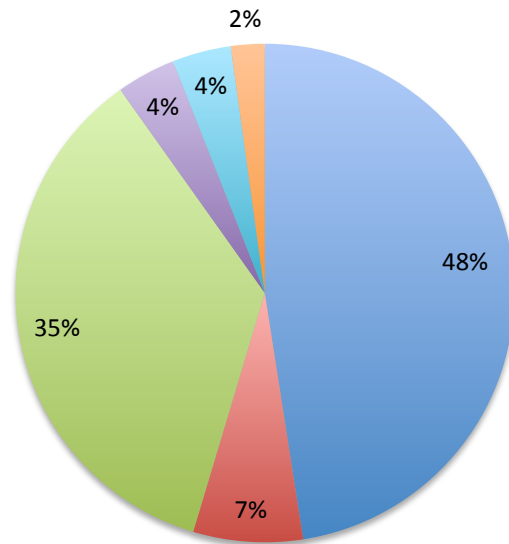


ISA-KOIST Macrofauna Workshop,
Korea, November 2014

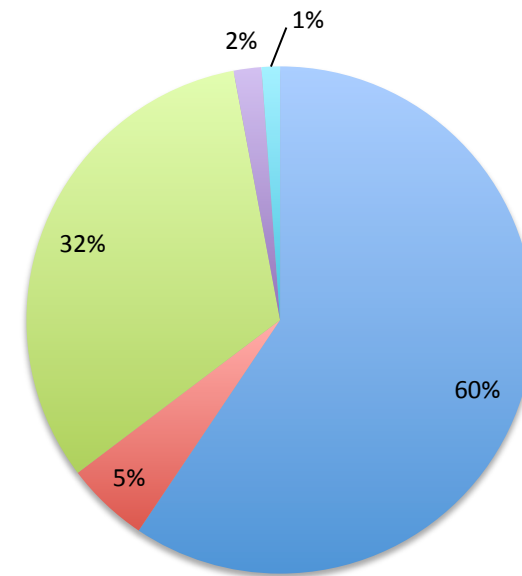


RARITY & ENDEMISM

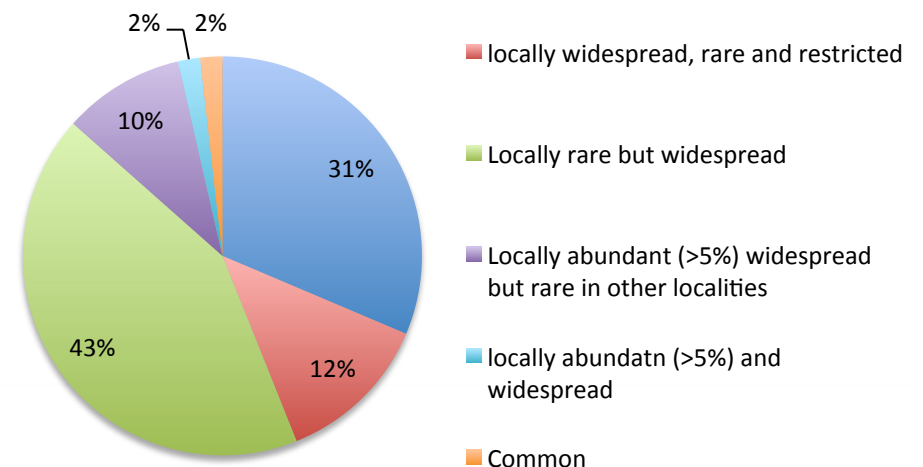
CCFZ polychaetes



EqPAC Polychaetes



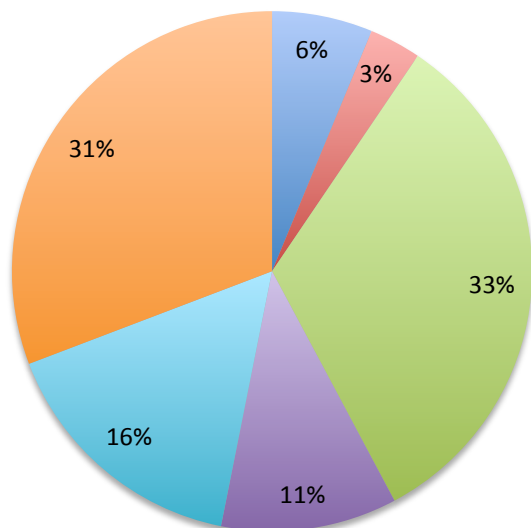
EqPac Nematodes



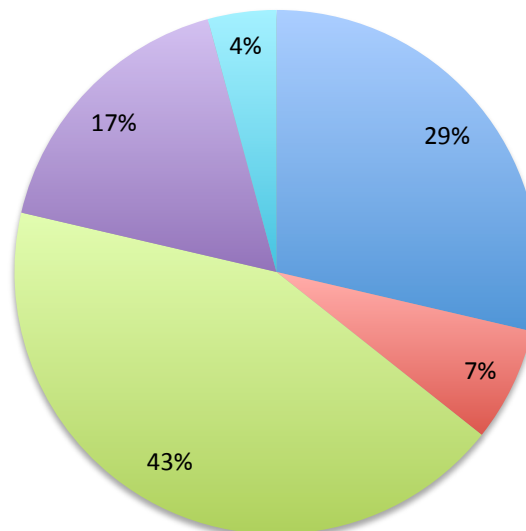
Percentage of species

Rare species are the most common in abyssal samples

CCFZ Polychaetes
% abundance



EqPac Polychaetes
% abundance

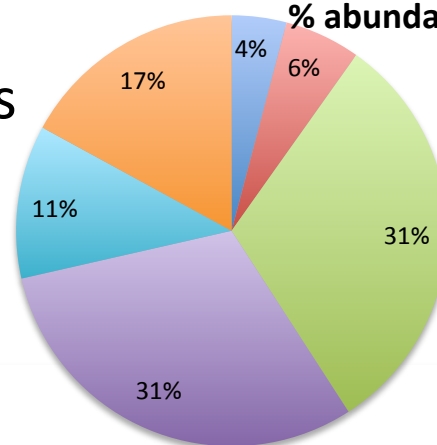


- rare
- locally widespread, rare and restricted
- Locally rare but widespread
- Locally abundant widespread but rare in other localities
- Common

Percentage abundance

But widespread species are the most abundant in abyssal samples

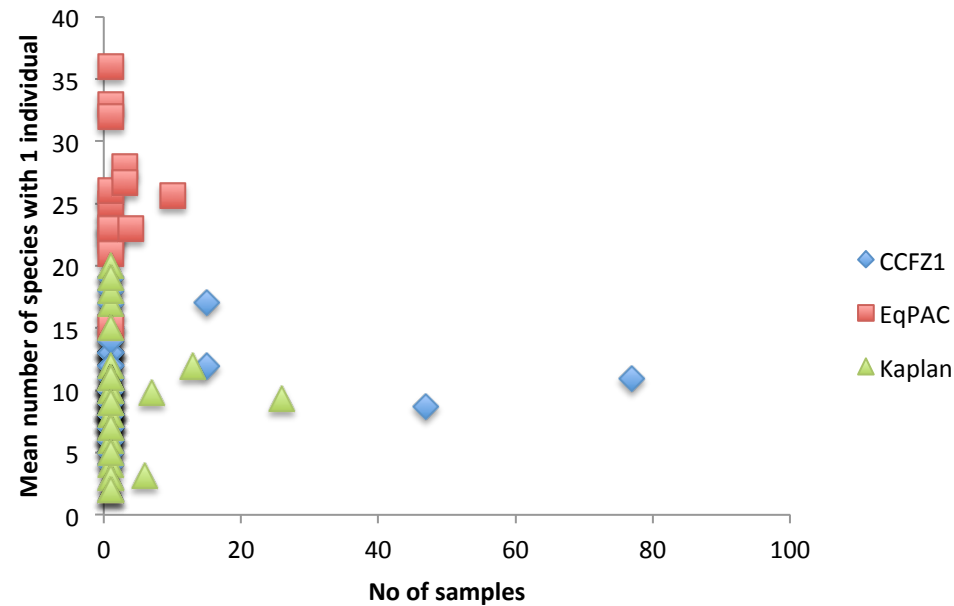
EqPac Nematodes
% abundance



- rare
- locally widespread, rare and restricted
- Locally rare but widespread
- Locally abundant (>5%) widespread but rare in other localities
- locally abundant (>5%) and widespread
- Common

RARITY

There is some indication that increased sampling effort reduces the number of rare species



But the numbers appear to level off. There remains a high proportion of rarity species in a sample.

Table . Rarity and relevance at different scales			
	Locally rare	Basin-scale rare	Globally rare
Impact	Local extinction threat	Loss of genetic diversity – potential impact on functioning and gene flow	Serious threat of extinction
Relevance to deep sea	Detailed sampling across the claim and preservation areas is essential to be able to determine whether refugias contain functioning populations	Need to know the distribution of all size class elements at regional scales	Difficult to establish as the likely distribution and occurrence are often unknown due to lack of appropriate sampling
Knowledge Gap	Insufficient knowledge of small scale distributions and how this is related to scales of physical heterogeneity Insufficient molecular data to establish population genetics	Insufficient information of biogeography and connectivity basin scale studies Understanding of species distributions and population connectivity is poor to non-existent	Lack of synthetic studies bringing together information on distribution of different taxa
Consequences	Unable to determine whether refugias or set aside areas will provide sufficient protection	Unable to determine basin scale impacts and to determine efficacy of regions of special interest.	Unable to determine extinction levels on a global scale because of poor baseline data
Reasons why	Detailed sampling is resource heavy There is no regulatory mandate to do this type of study Taxonomic and ecological expertise is in short supply Funding is not sufficient to support this intensive approach	Concentration by different contractors of groups in selected areas Lack of exchange of data Molecular data are needed but often difficult to get for certain faunal elements	Lack of data Large-scale studies, particularly taxonomic ones are time-consuming and require financial support Need taxonomic support and co-ordination
Current mitigation proposals	Local areas of refuge and no activity areas	Regional reserved areas and no activity zones	Restrictions on activity in zone where endemic species are found

Rarity

Increased sampling suggests that the proportion of rare or 'endemic' species reduces in area.

Increased spatial coverage also suggests that the proportion of rare species declines.

Increased taxonomic resolution is critical to identifying and discriminating species – this can also reduce the numbers of apparently rare species.

To assess the risk of irreversible species loss need to:

Create a consistent taxonomy across the CCFZ

Current state of the art: The Gaps

Biodiversity and biogeographic Information

The EU MIDAS project assessed our current knowledge in the following areas:

Taxonomy

Taxonomic keys and resolution—was the literature comprehensive
Collections—were collections being archived and were they available?
What mechanisms were available to exchange information and data?

Sampling

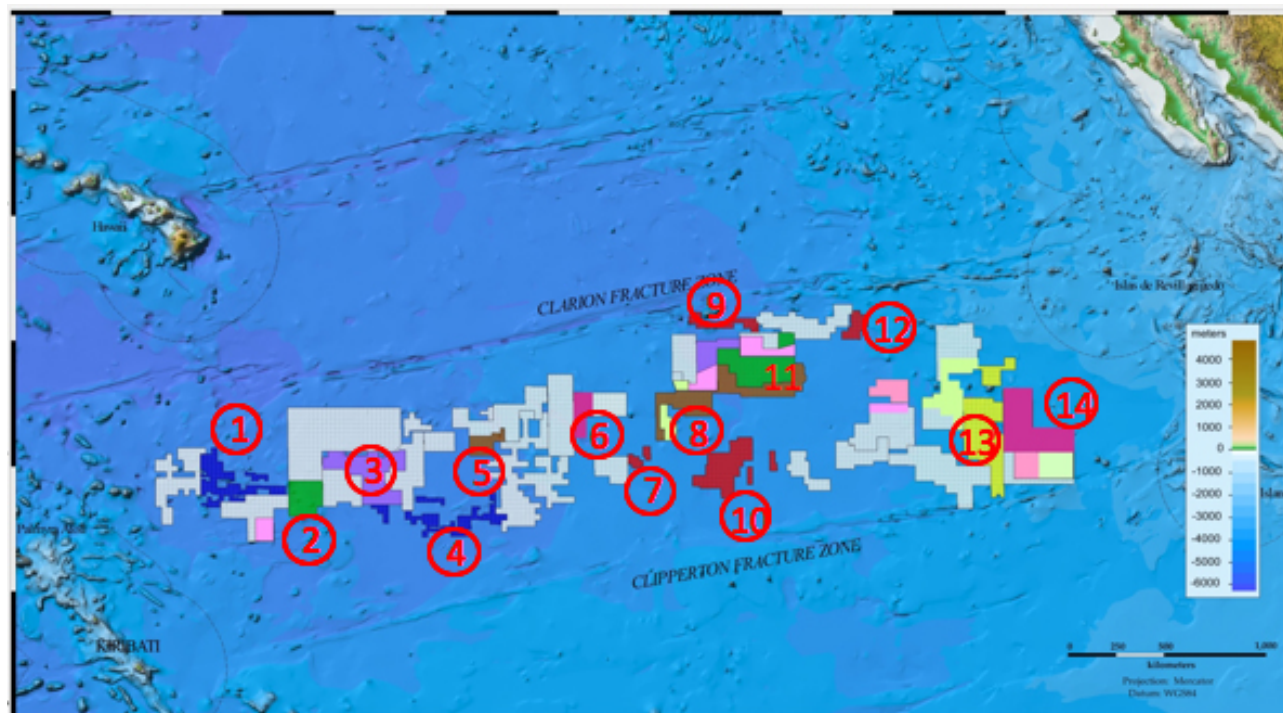
Sample coverage—what was being collected and the spatial coverage
Molecular samples/data—being taken?
Sampling standardisation – are the same approaches being made using comparable protocols and equipment?

Biogeographic data

Current knowledge on evolution and ecological drivers of biogeographic patterns (is it supported by molecular and phylogeographic approaches?)

Knowledge Grid: CCFZ

	Megafauna	Macrofauna	Metazoan meiofauna	Protozoan meiofauna	Microbial Bacteria	Microbial Archaea
Taxonomic knowledge	Good general knowledge	Limited to a few taxa. Mostly OTU	Limited to a few taxa	Foraminifera and Xenophyophores	Limited	Limited
Keys, literature	Available for many groups	Some available, mostly primary literature	None available	None	N/a	N/a
Collections	Many	Few, not available	Some	Some	Sequences	Sequences
Mechanism to exchange taxonomic information	little exchange of information between contractors	No exchange or intercalibration	No exchange or intercalibration	Mostly academic exchange	No. Data available via external databases such as GenBank	No. Data available via external databases such as GenBank
Sampling – type	Mostly Video and still imaging	Quantitative and qualitative samples	Quantitative samples	Quantitative	Quantitative	Quantitative
Molecular sampling	Little	Only some contractors and research teams	Some but limited	Some but limited	All molecular	All molecular
Sampling - standardisation.	For video and stills but not for specimens.	No. Use of gear is based on ISA standards but new gear being introduced	Possibly ISA have standards which apply	Limited	Limited	Limited
Biogeographic data	Some but based on morphotypes not actual specimens	Some but scattered in scientific literature. Spatial coverage insufficient	Some taxa –	Some	Some but limited to a few areas	Some but limited to a few areas



Area	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Macrofaunal samples	X	X	X	X				X		X	X		X	X
Abundance (m-2)	X	X	X					X		X	X		X	X
Taxonomic level	X	X, M I, Ga, P, Ta	X, M	X, M Most taxa				X, M, Some I		X some I, P	X (some)		X, M P, Ta, Bi	X
Molecular samples		x		X nwu										x
Sequence data		X												X
Epifauna		X		X				X					X	X
































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Keys, literature	Available for many groups	Some available, mostly primary literature				
Collections	Many	Few, not available				
Mechanism to exchange taxonomic information	little exchange of information between contractors	No exchange or intercalibration				
Sampling – type	Mostly Video and still imaging	Quantitative and qualitative samples	Quantitative samples	Quantitative	Quantitative	Quantitative
Molecular sampling	Little	Only some contractors	<p>Standardise sampling</p> <p>Cruises focused on biology</p> <p>Sample areas beyond the exploitation zone – seamounts, areas with low nodule number</p> <p>Make sure molecular samples are taken</p>			
Sampling - standardisation.	For video and stills but not for specimens.	No. Use of gear is based on ISA standards but new gear being introduced				
Biogeographic data	Some but based on morphotypes not actual specimens	Some but scattered in scientific literature. Spatial coverage insufficient				
			Collate and co-ordinate data from all regions.			

Biogeographic knowledge: current stat of the art

RAG Analysis	Vents	Off-Vents	CCFZ	Arctic Seeps	Black Sea
Megafauna					N/A
Macrofauna					N/A
Metazoan meiofauna					
Protozoan meiofauna					
Microbiology: Bacteria					
Microbiology: Archaea					
<div><div></div><div>Little or primary information only – significant gaps in knowledge</div></div> <div><div></div><div>Some useful data available. Still some fundamental gaps</div></div> <div><div></div><div>Good knowledge with ability to make informed predictions</div></div>					

Workshop overview

Why is taxonomy important?

Pivotal in determining environmental risk

It is not just about identification – its about making identifications available.

Why do we need to have any sort of intercalibration between areas?

To assess risk of extinction

The area is so big we haven't the resources to survey accurately all the species which live there.

Need to pool resources and data to answer key questions.

What role will new technologies and approaches make?

In the molecular–digital age we need to incorporate all available tools.

Where do we go from here?

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Korea, November 2014

