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# Report of the Working Group on Phytoplankton and Microbial Ecology (WGPME)

19-21 March 2013

Helgoland, Germany



Conseil International pour l'Exploration de la Mer

## International Council for the Exploration of the Sea Conseil International pour l'Exploration de la Mer

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#### **Executive summary**

WGPME was appointed in 2010 and has since then concentrated on the acquisition of relevant time-series data. A comprehensive set of phytoplankton and microbial time-series together with accompanying physico-chemical data has now been assembled. WGPME has therefore now entered a new phase where these datasets are being explored with a view to establishing the degree of comparability between time-series which can be limited due to methodological constraints.

Based on the WGPME ToRs concepts are now being developed for further more detailed investigations leading to joint publications. For ToR B for instance a list of species has been established that covers different foodweb components, that are comparable across those time-series and that would facilitate additional time-series data on these species to be integrated rapidly. In a next step these data will now be analysed with respect to long term trends in species ranges.

Similarly for ToR A, addressing the range of analytical methodologies used in phytoplankton/microbial sample collection and analysis. The scope of these methods will be further reviewed and summarized. The resulting product will be made available either online or in a hard copy publication (Manual?), the extent of which has yet to be developed. This would be particularly useful for two categories of methods: 1. Those that have been established for a long-time but for which many different 'sub-routines' exist that hamper comparability, 2. Relatively novel techniques such as flow cytometry or molecular tools, for which we still hope to be able to achieve some true harmonization of methodologies.

In summary WGPME is in the final stages of consolidating existing knowledge to then move on towards more detailed and large-scale analyses of long-term patterns in phytoplankton and microbial time-series and to relate these to underlying drivers by linking the time-series data to hydrodynamic models.

Importantly WGPME is not only pursuing scientific questions of great importance but will also seek to make the results available not only via peer-reviewed publications but also through different media such as online and other multimedia resources such as apps.

#### 1 Administrative details

#### Working Group name

Working Group on Phytoplankton and Microbial Ecology (WGPME)

Year of Appointment

2010

Reporting year within current cycle (1, 2 or 3)

1 **Chair(s)** 

Xosé Anxelu G. Morán, Spain

Alexandra Kraberg, Germany

Meeting venue

Helgoland, Germany

**Meeting dates** 

19-21 March 2013

#### 2 Terms of Reference a) – f)

a) Examine current marine microbial time-series sampling techniques with an effort towards harmonization if required

b) Examine distribution and range patterns of microbial taxa and functional groups to discern significant change over time and to identify potential drivers.

c) Report progress on discovery of novel lineages and cryptic taxa of phytoplankton and marine microbes

d) Explore the use of hydrographic models and other statistical analyses to provide further understanding of distributional patterns of phytoplankton and microbial assemblages

e) Discuss and prepare sections for the second Cooperative Research report on ICES phytoplankton and microbial plankton status to be completed for June 2015

f) Prepare peer-reviewed manuscripts using extant phytoplankton and microbial time-series

ToR	Description	Background	Science Plan topics addressed	Duration	Expected Deliverables
a	Examine current marine microbial time-series sampling techniques with an effort towards harmonization if required.	WGPME can provide a summary of current methodologies used in microbial plankton time-series with the goal of achieving better comparability between sites.	112	3 years	Best practise recommendations for microbial plankton time- series provided in the WGPME website (wgpme.net); in 2015 with regular updates; to biological oceanographers but especially phytoplankton and microbial ecologists.
b	Examine distribution and range patterns of microbial taxa and functional groups to discern significant change over time and to identify potential environmental drivers.	After finding examples of taxa and/or functional groups that have actually changed their distribution we need to know the environmental drivers underlying these changes before we can make sound projections.	113	2 years	Interim WG report; in 2014; to SSGEF
с	Report progress on discovery of novel lineages and cryptic taxa of phytoplankton and marine microbes.	By providing state-of- the-art knowledge of novel microbial biota we will be able to better understand unexplained variation of current time-series datasets.	121	2 years	Interim WG report; in 2014; to SSGEF
d	Explore the use of hydrographic models statistical analyses to provide further understanding of distributional patterns of phytoplankton and microbial assemblages	We need to incorporate other perspectives and the expertise of researchers from different fields and ICES WGs in order to disentangle the factors causing changes of distribution in microbial plankton groups.	111, 114, 115	2 years	Interim WG report; in 2014; to SSGEF
e	Prepare sections for the second Cooperative Research Report on ICES	The CRR needs to be updated regularly to better establish the	11, 12	3 years	Second ICES CRR Phytoplankton and Microbial

## 3 Summary of Work plan

	Phytoplankton and Microbial Plankton Status to be completed for June 2015.	climatologies and long-term trends for phytoplankton and other planktonic microbes as well as introduce new analyses, providing the basis for informed assessments of distributional changes at all organizational levels.			Plankton Status Report; in 2015; to research community and policy-makers.
f	Prepare peer-reviewed manuscripts using existing phytoplankton and microbial plankton time- series to describe large-scale and long-term patterns in the distribution and seasonality of phytoplankton communities and chosen key species	WGPME is currently entering the position to provide multi datasets comparisons of microbial time- series to a wider scientific community, potentially of use also by policy-makers.	11, 12	3 years	Joint peer- reviewed articles with data across North Atlantic coastal waters on at least two of these issues: a) macroecological patterns of cyanobacteria, b) ratios of diatoms to dinoflagellates and c) comparison of drivers causing temporal dynamics of diatom species; in 2015; to oceanographic and marine ecology scientific community.

#### 4 List of Outcomes and Achievements of the WG in this delivery period

- **ToR A:** It was decided to explore the possibility to produce a searchable and downloadable document comparing different methods on the ICES website. It has also been decided to produce a species list of taxa used within WGPME and to store image metadata for these species in the PLANKTON\*NET database (<u>http://planktonnet.awi.de</u>). This process will take some time and will not be complete before 2015, but the result will be a species resource that can serve as a Gold Standard for future comparative studies by WGPME and beyond.
- **ToR B:** A list of species that is reliably identified in all time-series available to us was chosen for further analyses of long-term temporal and spatial trends.
- **ToR C:** The coverage of taxa in the WGPME was discussed and several gaps identified, including bacteria and oomycetes. An external collaboration with the Senckenberg institute in Germany to carry out a joint study on oomycete diversity using molecular methods is currently explored. A list of potential collaborators has now been drawn up and these will be contacted in the next few months.
- **ToR D:** A range of possible analyses with respect to hydrography was reviewed. In a breakout group the CoastDat database was introduced as a potential tool for carrying out these studies as it provides hindcasting of past environmental conditions and therefore facilitates an analysis of potential environmental drivers that might have caused past events in the WGPME time-series. Its further use is now being discussed.
- **ToR E:** A discussion of this ToR was deferred to the meeting in 2014, as this will depend on the data integration steps now in progress and on the resulting data analyses and manuscripts
- **ToR F:** 3 potential manuscripts were discussed: For the first onlarge phytoplankton, the species to be examined and sites to be used were already determined and an outline of the manuscript written during the workshop in Helgoland. A second manuscript on the spatial and temporal dynamics of *Synechococcus* was also discussed. A list of sites and variables will be decided upon well before the 2014 meeting in Plymouth. Third a review on molecular methods and their benefits and drawbacks when used for the generation of time-series data were considered. This will need to be discussed further when extending the collaboration on molecular methods to external partners (see ToR C).

#### 5 Progress report on ToRs and workplan

The following summary provides a detailed summary of discussions and results of the results of the Helgoland meeting on a ToR by ToR basis:

#### 5.1 ToR A: Examination of current time-series analytical techniques

Session 1 (March 19, 2013, 11:30 - 13:00)

Leads: Glen Tarran

Rapporteur: Xelu Morán

The session started with a short presentation of the ToR. The major question can be summarized as to whether we can safely compare whether we can safely compare the time-series contributing to the WG or whether a harmonization of current methods is necessary. Prior to the meeting at Helgoland, a questionnaire had been sent to all contributors to our first Phytoplankton and Microbial Plankton Status Report 2009/2010 (ICES CRR No. 313), getting response from approximately 25% of the people.

Glen Tarran identified two major areas of data collection, one being organisms smaller than 2  $\mu$ m in size (including small eukaryotes, prokaryotes (bacteria and archaea) and viruses and the other being the traditionally surveyed organisms (phytoplankton and microzooplankton). Accordingly, the questionnaire had 2 sections. Once completed by a significant fraction of researchers, we could look at comparability and differences between methods, which should be based on well justified reasons. A possibility for this ToR would be to include a workshop in one of our future WGPME meetings in which to discuss and make decisions. The best approach would be to run extant and recommended new protocols in parallel.

As a group we should seek for deliverables not a new, printed book but a document accessible and downloadable from the ICES website that includes a search engine. It was suggested to start exploring this now as a potential deliverable for 2015. It should be updated regularly.

Rowena Stern also presented some examples from the Plymouth Marine Laboratory and suggested to improve collaborative sampling effort, especially on molecular aspects such as parallel DNA assays for deep-level species detection. Katja Metfies said that comparability should be ensured and she stressed the need to harmonize analysis. Norbert Wasmund noted that there are many different groups, a whole European community, already concerned with this issue, for instance, chlorophyll measurements of phytoplankton, so we should be careful not to duplicate work.

Karen Wiltshire mentioned the problems sometimes found within the same institute, using again chlorophyll as an example. It is not possible to change an already stardandized method when it suits their analysis. Probably the most we may get is to run parallel methods. In any case, changes in methods are themselves a long-term process such as in the North and the Baltic Sea, where phaeopigments are no longer considered.

Xosé Anxelu (Xelu) G. Morán suggested that we should seek to advise on variables not long established like chlorophyll, but for instance on flow cytometry methods Karen and Katja agreed that we may pose ourselves some small objective for molecular tools. Karen went on to argue that probably a joint study without conclusions about the wrongness of a method could be attempted. Rowena suggested that a collaborative joint analysis of the same samples could be done in order to make recommendations on what we can.

Claire Widdicombe asked for the availability of guides for flow cytometric methods since microscopic analysis frequently have to do with an inherited species list. Alex Kraberg stressed that we should be aware that we all make mistakes in taxonomy but as long as we are consistent we could probably fix them in future. Pictures, such as the visual guides of Helgoland phytoplankton and zooplankton recently published books, can greatly help, and especially in the case of a species claimed new for a given environment.

The discussion then moved forward to our need to produce some species list, as Glen suggested. It would provide links to recommended databases with images such as PLANKTON\*NET (www.planktonnet.awi.de) and indeed a collection of 'WGPME agreed reference images could be stored in the database. However, any species list will require long-term maintenance we may have different levels, for the public and for internal users. For any given species, we might provide a "gold standard", include images from different sites and have a discussion forum. Alex Kraberg agreed to take care of that as a 2015 milestone. In the process, we should give it some name and progress as a joint WGPME initiative. Rowena Stern raised the issue to not only harmonize species lists but to suggest joint molecular protocols. An issue could be to do our own analysis, e.g. determining the DNA concentration and sequencing of 10 samples per institute, with the same sampling volume. This would be an important exercise as there are many confounding issues when doing comparative molecular analyses, e.g. nucleic acid extractions, primers, PCR conditions. However being at an early stage of methods development this exercise might facilitate a true harmonization of methods.

So far, Glen Tarran identified 4 key points to improve on existing methodological concepts:

- 1) To have links to good picture libraries.
- 2) To endorse existing recommendations (e.g. HELCOM manual).
- 3) To progress the newer techniques, such as flow cytometry, which essentially shares the same methods (e.g. D. Marie's protocol for fixed samples) among the still small community of researchers (Bill, Glen, Xelu and Josep M. Gasol among the WGPME members). The point was made that Flow-CAM is a dif-ferent question, with many problems.
- 4) To explore the potential for intercomparison and cross-calibration studies, and ultimately make analysis techniques more uniform among us for providing better estimates of abundance.

Norbert Wasmund argued that the time and effort needed for fully carrying an extended workshop or a ring test such as the ones in which he participates probably is not worth the final result since frequently people go on doing the analysis their own way. A long-lasting question is how to measure the cells and which factor use for carbon content estimates. Alex Kraberg said that still workshops are very useful for taxonomic purposes since taxonomic expertise greatly differs from person to person and different groups (dinoflagellates, diatoms, cryptophytes, etc). If a test should be done then we better restrict it to a small amount of samples. The problem with species checklists (mostly inherited) and any unusual finds was discussed by Rowena Stern, Alex Kraberg and Claire Widdicombe, who agreed again that images are very useful for any rare species. With regard to molecular methods within the WG, Katja Metfies suggested to get a sample and see where we are with annotation, without the need to get at the genus level. Rowena warned against the frequent biases in taxonomic and molecular methods. She suggested as a way forward to run a standard assay with specific genes for eukaryotes, perhaps sequencing 5 samples with the same DNA concentration at 5 different laboratories. We might be suitably happy with where we are now.

It was agreed that Glen Tarran should continue to lead this ToR while we develop the methods topic further. Karen Wiltshire stated that any final product should not be personalized since we have many different interests, but could give a nice overall picture of all the problems we face. It was suggested that we should concentrate of only one of the many possible issues, a milestone or overarching question everybody would be happy with. This could be the production of a new multi-author manuscript that or the creation of a smartphone application.

Bill brought the question that this group is constituted within ICES and delivers to ICES, so everything should be pointed towards ICES Science Plan and considering annual meetings. Yet, it is now easier for us to advance ToRs on a 3 years basis facilitating the tackling of larger projects such as a book or a phytoplankton App similar to what has already. Bresnan suggested that the range expansion of species could be a nice idea to get the public involved in WGPME efforts e.g by allowing them to report blooms. Enhancements should also be made to the website, for example by linking it to PLANKTON\*NET.

# 5.2 ToR B: Examine distribution and range patterns of microbial taxa and functional groups to discern significant change over time and to identify potential environmental drivers.

Session 2 and 3 (March 19, 2013, 14:00-15:00 and 15:30-17:00

Leads: Alex Kraberg, Claire Widdicombe

Rapporteur: Bill Li

Broadly speaking, the task is to consider examples of taxa and functional groups whose spatial and/or seasonal distributions have changed over the years, and to examine the possible environmental factors that are driving such change. An example comes from the CPR record in the Northeast Atlantic and North Sea showing a change in dominance from dinoflagellates (e.g. *Ceratium furca, Protoperidinium* spp.) to diatoms (e.g. *Thalassiosira* spp., *Pseudo-nitzschia seriata*) that is purportedly caused by an interaction effect of both increasing sea surface temperatures combined with increasingly windy conditions in summer.

The wide scope of this topic was made tractable by a focus on data available to WGPME. In particular, the patterns of change in various diatoms and dinoflagellates at Helgoland Roads and at Plymouth L4 were used as illustrative case studies. A striking example of apparent change is the diatom *Guinardia delicatula*. In recent years at Helgoland Roads, this species has begun to appear as early as March, and is often still quite abundant in October. It is possible that the seasonal extension of this species might be related to its capacity to grow faster under current prevailing warming conditions in these waters. On the other hand, both the seasonality and the multiyear trend for *G. delicatula* at Plymouth L4 are notably different from those at Helgoland. Another diatom that might be useful for cross-site comparison is *Leptocylindrus danicus*. As a starting point, the following criteria might be used to base a comparison: the mean annual abundance of cells, the periods of time during a year

when the species is noted to occur, and the time of year when cell abundance attains its maximum value.

In examining phytoplankton time-series to discern environmentally driven change, various unrelated factors may be inherent in the data that could complicate the interpretation of change. Problems associated with taxonomy are common. For example the revision of names for the same organism may result in the apparent addition of new entities over time. Problems associated with the sampling strategy are also common. For example, uneven sampling frequency over the annual cycle or low sampling frequency during highly dynamic periods can introduce large uncertainties to the statistical analyses. In this regard, there may be opportunities to consider alternate indicators of change that integrate the dynamic signal. Thus, for example, the overall depletion of silicate over time from the start to the end of a diatom bloom might be an informative way to indicate the magnitude of the bloom.

#### Questions and tasks going forward:

- 1) Considering the statistical weakness of a straight line fit to some of the time-series, it may be useful to investigate other statistical measures of trend that better describe non-linearities such as reversals or abrupt transitions. (Action: Todd O'Brien to lead).
- 2) Considering the possible weaknesses (taxonomic and otherwise) in some of the diatom and dinoflagellate datasets, the ratio of these two groups would amplify such weaknessess. At best, the ratio may be useful in a particular context (e.g. Hinder et al. 2012); at worst, it may be a meaningless quantity. Might it not be more useful to consider possible change in diatoms and dinoflagellate separately? (Action: Alex Kraberg to lead).
- 3) Considering that some phytoplankton taxa are relatively prevalent in the WGPME compilation, several were selected for in-depth comparative analysis of seasonal patterns and multiyear trends, as follows:

Guinardia (Alex Kraberg to lead)

Leptocylindrus (Claire Widdicombe to lead)

Synechococcus (Xelu Morán to lead)

Protoperidinium (Rowena Stern to lead)

Ceratium (Lead TBA)

Chaetoceros socialis and Phaeocystis (co-occurrence, Claire Widdicombe to lead)

Analysis support of this task (Todd O'Brien to lead): where available, data of taxa by month, by season, by year, and by location.

#### 5.3 ToR C: Novel lineages

Session 4 (March 19, 2013, 9:00 - 11:00)

Leads: Rowena Stern

Rapporteur: Katja Metfies

#### Microbial Time-series from Genetic Data

In this session we discussed the taxonomic coverage of the participants' time-series and gaps that we might be able to fill in the future using techniques such as flow cytometry or molecular techniques. Rowena Stern gave a detailed review on the potential benefit of molecular methods for marine time-series. Molecular methods were identified to have potential to support time-series in the assessment of understudied or taxonomically difficult taxa such as protozoa, certain phytoplankton groups (e.g. picoeukaryotes or the diatom *Pseudo-nitzschia* sp.), oomycetes, bacteria, and marine viruses. Sequencing approaches (sequencing of clone libraries or next generation sequencing of marker genes) provide comprehensive overviews of the diversity in a sample, but they are expensive and time delayed. Therefore, targeted approaches (e.g. quantitative PCR or fluorescent *in situ* hybridization) that focus on a particular taxon are proposed.

Currently there are only a few time-series (Western English Channel, Roscoff, and Gulf of Naples) that apply molecular methods for more than five years. Considering this, we discussed the possibility of taking additional samples at the time-series sites represented by the group to carry out molecular analyses in the future. However, at the same time the need for standardized protocols and methods to ensure a comparability of molecular time-series data in the future has been identified. This involves the development of a protocol for sampling and preservation, preservation methods and standardized analyses methods for different taxa and marker genes.

It still needs to be determined however who would have what capacities to carry out such analyses (discussion of next steps: see breakout groups). A potential collaboration with an external partner at the Senckenberg Institute was also discussed and A. Kraberg will investigate the scope for this collaboration, which would be beneficial for the more detailed analysis of one group (the oomycetes) in our time-series.

#### 5.4 ToR D: Links between species distributions and hydrography

Session 5 (March 19, 2013, 9:00 – 11:00)

Leads: Karen Wiltshire

Rapporteur: Alexandra Kraberg

Karen Wiltshire presented a detailed review of the analyses carried out on the Helgoland Roads time-series. The basic measured parameters were introduced.

Following this ecological studies were described. This included a description of species shifts over time, but also autecological studies e.g. on the diatom *Paralia sulcata* which seems to have undergone a niche shift. The mean diatom day was also introduced. This is a simple index for the timing of the spring diatom bloom. While initially showing a delay in the spring bloom, this trend has now reversed.

Long-term trends in the prevailing current regimes were then outlined. The analyses used the Coastdat database for hindcasts of past conditions. Empirical orthogonal function analysis has been carried out to analyse the long-term variability and trends in 2 predominant current regimes (the influence of waters entering the North Sea from the English Channel vs. waters entering from the North, bringing in more saline Atlantic waters. The analyses showed that in recent times current patterns are such that the North Sea is more strongly influenced by open Atlantic water rather than coastal sources.

The scarcity of time-series in the North Sea makes modelled data vital. However it was also discussed whether high frequency measurements from automated sensors could help in sensor arrays such as COSYNA and a range of ferrybox systems could help. These are towed across the North Sea by ships of opportunity and should provide detailed information on a host of different parameters. However, the reliability of theses sensors was still seen as an issue. The comparability between different ferrybox systems is also not a given. Data management systems, QA standards and metadata protocols for these complex devices are still in a process of being developed.

#### 5.5 ToR F: Preparation of manuscripts

Session 7 (March 19, 2013, 9:00 - 11:00)

Leads: Rowena Stern, Alex Kraberg, Xelu Morán

Rapporteur: see session 8 (summary of the activities in the breakout groups

The preparation of manuscripts was discussed in several breakout groups:

# 5.5.1 Species distributions and hydrography (A. Kraberg, C. Widdicombe, E. Capuzzo, A. Ameryk, N. Wasmund)

This group discussed in more details which species are amenable for this type of analysis. One important factor is that the chosen species have are easy to identify so that the chance of ID errors is small and the comparability of data from different regions is high. However, this would not be a sufficient basis for a manuscript and therefore species were chosen so as to include different trophies and habitats as well.

These included:

Autotrophic pelagic species: *Guinardia delicatula, G. flaccida, G. striata, Leptocylindrus danicus, L. minimus, Cerataulina pelagica* 

Mixotrophic pelagic species: Ceratium spp., Dinophysis

Heterotrophic pelagic species: Protoperidinium spp.

Autotrophic benthic/tychoplanktonic species: *Odontella aurita, O. sinensis, Cylindrothe- ca* 

As these species also include harmful species, it was decided to also contact the ICES HAB group. A brief outline of the manuscript was written during the meeting and it was decided to produce at least an introduction and methods section by the time of the next meeting. The intervening time will be used in particular to develop a statistical framework for the treatment of the delivered data. The sites to be used were also discussed:

The CoastDat database (http://coastdat.org), a model-based database which facilitates environmental hindcasts of past conditions in the North Sea which be used to investigate particular events in our time-series e.g. a possible regime shift 1998.

#### 5.5.2 Spatio-temporal distribution and variability of Synechococcus (Glen Tarran, Bill Li and Xelu Morán)

The idea is to produce a manuscript on the spatio-temporal distribution and variability of *Synechococcus*, an important, widespread cyanobacterium which can be used as a tracer of the trophic status of pelagic ecosystems, using the extant time-series across the Atlantic and the Mediterranean. As a brief summary of our progress, in September 2011 Bill asked Todd O'Brien to send him all Synechococcus data that he had compiled for the WGPME Status Report. Bill has already done some exploratory plots with the data, including the annual cycles of Synechococcus abundance based on climatological monthly values at 7 sites with the longest records (Plymouth L4 station, Bedford Basin, Booth Bay, Gijón/Xixón, A Coruña, Blanes Bay and Thau Lagoon, see full details in ICES CRR No. 313 downloadable from http://info.ices.dk/products/cooperative.asp), correlations with environmental variables and identification of multiyear trends taken from the Status Report. Our immediate steps are to look for potential additional sites contributing to the paper and have a full dataset with ancillary variables available well in advance of our WGPME

2014 annual meeting, in which we would try to produce a first draft of the manuscript.

#### 5.5.3 Novel lineages (R. Stern and K. Metfies)

The "group" discussed the potential of using molecular methods like sequencing of marker genes etc. on a regular basis in time-series. During the past decades molecular methods became an indispensable tool in marine biology. There is great potential that certain molecular methods could contribute to the assessment of taxa in time-series e.g. of so far understudied groups. However, currently the use of molecular methods is mainly restricted to isolated studies with low temporal resolution. In respect to this the group identified the need to get more information from the scientific community on the premises that need to be fulfilled if molecular method should be used synergistically in time-series. Thus, a questionnaire with 10 questions was prepared, that will be send out to a list of well-established marine molecular ecologists and time-series by the end of this year.

#### 5.5.4 March 21<sup>st</sup>: Meeting summary

As a final meeting item a summary from the breakout groups was produced. The main points are:

- For the manuscript on the long-term shifts in species distributions, all relevant data will be collected and integrated into a single analysable dataset (to be finished by the time the next annual meeting takes place)
- 2) For the group that discussed the use of molecular tools in the generation of time- series data, a list of potential external collaborators was produced. These will be contacted and collaborations will be discussed during the course of the next year
- 3) For the *Synechococcus* manuscript a list of sites with appropriate *Synechococcus* data and accompanying environmental data will be set up before the meeting in 2014. This will include if possible additional datasets not yet part of the WGPME data resources.

## 6 Revisions to the work plan and justification

None

### 7 Next meeting

The next meeting will be held in Plymouth, UK from 18 to 20 March 2014 at the kind invitation of Claire Widdicombe and Glen Taran of the Plymouth Marine Laboratory.

Annex	1:	List	of	par	ticip	ants
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Recommendation	Adressed to
1. Development of more comprehensive web resources to inform the public of our activities but also to facilitate integration of existing data and resources and to encourage public involvement ('people science').	WGPME

#### Annex 2: Recommendations