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Dear colleagues,

It is for me difficult to make comments on the discussions started in Palma just because I have the feeling that microbiologists are underrepresented in this very forum of discussions. It is somehow a fight of a David against Goliath. In this regard I have some remarks to the WG1 results and new questions.

1- *Indicators of environmental changes*. The role of microbes in the assessment of environmental changes should not be underestimated. It might be true that changes of the species composition of a given microbial community may not be directly linked to an environmental alteration. Microbial communities are too complex to objectively observe significative changes. However, the metabolic state of a community is directly linked to the environmental factors. A change on the environment leads to a quick response of the community metabolism. Facts like awakening of dormant cells and metabolism relentization of active microbes are common responses to environmental changes. This might not be directly reflected by clear-cut community composition changes. Monitoring the active portion of a given microbial community may lead to the understanding of the factors driving the environment.
2- *The response of microbial communities is fast*. Microbes respond very quickly to environmental changes. Monitoring changes in the active portion of the microbial communities could help to predict long-term changes in higher taxa. Additionally, once a change is observed one can hypothesize what has occurred.
3- *How to distinguish anthropogenic and natural impacts.* The analysis of the microbiota can give clues to the origin of the impacts. Facts like antibiotic resistances or xenobiotic degradation/resistances are directly linked to human activities.
4- *Monitoring changes in the active portion of a microbial community.* As I explained, the analysis of how and in which measure do the microbial communities in a given site react to impacts could help to a fast warning of environmental changes.

Remarks to WG3 Genetic and molecular diversity

In the frame of the WG3 I have concrete answers to the two first new questions.

1- *Which indicator to use*. In microbiology we have a well-established methodology to assess diversity. As we already talked, the sequence analyses of conserved genes are

used for phylogenetic reconstructions. Especially important are the ribosomal RNA genes that are not only used for phylogenetic reconstructions but for the monitorization of microbe populations through e.g. fluorescence in situ hybridisation. At the moment we are very satisfied about the molecular or genetic indicators that can be used to assess diversity. The point is to match such indicators with the species unit. To the date we still cannot assume that each of the phylotypes we recognize respond to a different species. In this regard, in a given environment we can only produce a phylotype inventory but not a species inventory.

2- *Is microbial diversity a reliable indicator of general biodiversity*? I would not say so. Of course it depends of the size of the sample. One cannot talk about global marine microbial diversity as a reliable indicator of general biodiversity. However, it is clear that each of the higher taxa individuals may be colonized (symbiotic, saprophytic or parasitic) by a microbiota that is exclusive of the given organism. We microbiologists are not yet aware about the real dimensions of microbial diversity in marine samples. And this is especially true for benthonic microbes. We expect a very high diversity of prokaryotes because of the ubiquity and high density of microbial communities. However, as you heard in Palma the diversity of the major key players in such environments might not be very huge.

I hope that this is enough for the moment to open a bit your minds into the microbial world.

ramon