## CIESM Congress Session : Megasequencing projects Moderator : Frank Oliver Glöckner, Max Planck Inst. & Jacobs Univ., Bremen, Germany

## Moderator's Synthesis

The introduction outlined the huge interest worldwide in exploring the marine ecosystem in terms of fundamental biodiversity and functional research, as well as biotechnology and applications. Following the footsteps of the Global Ocean Sampling (GOS) expedition to "shotgun the ocean" the Tara Expeditions and Malaspina cruise have opened the black box of microbial diversity through all size classes as well as from the surface to the deep sea. As a recent addition Ocean Sampling Day (OSD) and the citizen science project MyOSD, complemented the circumnavigations by excluding the time parameter in restricting sampling to the 21st of June 2014, 2015, 2016. This resulted in a worldwide snapshot of microbial diversity and function on a single day. With over 90% of the sampling sites being costal, OSD has pioneered addressing the Nagoya protocol on "Access to Genetic Resources and the Fair and Equitable Sharing of Benefits (ABS) Arising from their Utilization". By creating the CIESM charter on ABS, a morally binding, light-weight solution for the fair and equitable exchange of results and expertise has been filed and signed by the Mediterranean OSD participants.

Five communications were presented and followed by an intense discussion. Three of the talks focussed on the functional site of the marine metagenome researched by comparatively exploring the OSD and Tara Oceans attasets. A striking result is the fact that the microbiomes of OSD and Tara Oceans are distinct but complementary. This shows that the coastal influence on the microbial communities is strongly reflected in their genomic repertoire. The dynamic and heterogeneous nature of the coastal environments is underlined by their high amounts of genes for transport, replication, translation and energy production. Research on the nitrogen biogeochemical cycle showed a wide distribution of genes involved in N-fixation and denitrification. Research on Biosynthetic Gene Clusters in the marine environment revealed a common distribution and that they can lead as indicators for anthropogenic influences. This is in line with the contribution researching changes in phytoplankton assemblage structure in the Mediterranean Sea by human pressure. The 18S rRNA analysis shows that sites under heavier human impact expose significantly lower diversity but higher abundances of e.g. single species like *Skeletonema*. Finally, the last talk showed that the involvement of citizen scientists in the production of data and knowledge is advantageous by significantly expanding not only the amount but also quality of samples.

The discussion started with practical aspects of handling the Nagoya protocol and what needs to be done as a researcher to get the corresponding permits from the governments. It expanded towards exchange, comparability and interoperability of data. It finally turned back to the added value of OSD for the participants as a stimulated self-organisation of marine stations to exchange and comply with protocols and standards to allow getting the "big picture" of microbial actions in the marine environment. The wish to continue OSD was mentioned in this respect.

In the debriefing session ample interest was expressed, since many participants from the north and south shore of the Med (Croatia, Italy, France, Turkey, Tunisia, Portugal) see an added value of continuing the

exchange of expertise, protocols as well as data and results to explore continuing OSD in the Mediterranean as "OSD-Med". The open spirit of OSD has turned to be a strong incentive to generate excellent science together. It was therefore suggested to organise a workshop under the umbrella of CIESM to that effect, in particular with the goal to explore a scientific common objective for OSD-Med.

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