MICROBIAL COMMUNITY-BASED INDICATOR OF WATER QUALITY TO INTEGRATE IN A MODELING SCENARIO

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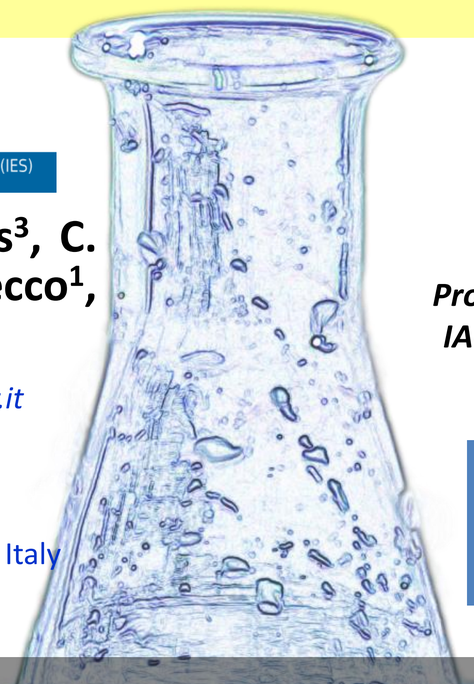

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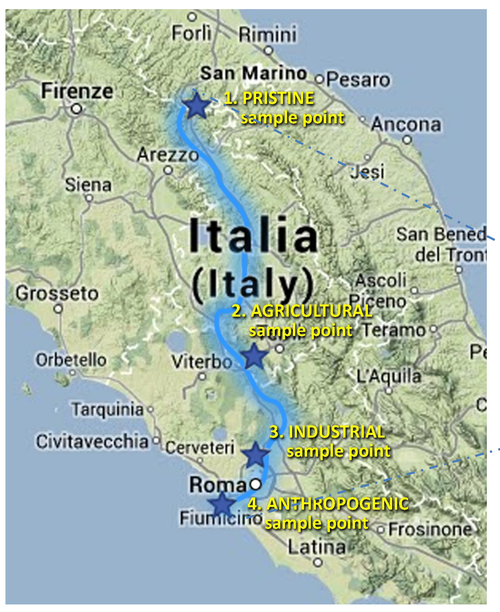
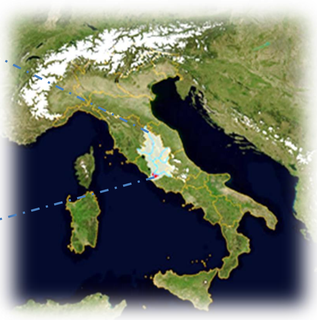
Microbial communities are the base of the food web pyramid, representing about 50% of the total biomass on Earth. They are responsible for the geochemical cycles and bio-removal of organic compounds, including xenobiotics, playing a key-role in ecosystem functioning and providing several ecosystem services.
They are able to adapt promptly to environmental changes and the presence of a natural microbial community is a necessary prerequisite for an effective response to the various chemicals that can contaminate an ecosystem. However, the recovery from contamination is only possible if toxicity does not hamper microbial activity. The knowledge of natural remediation capacity of a microbial community allows to assess the contaminant availability to higher levels (including man) in the ecosystem food web.

MicroCokit is a Marie Curie Industry-Academia Partnerships and Pathways (MC-IAPP) project entitled "Microbial Community-based sequencing analysis linked to anthropogenic pressures: MicroCoKit to address the water quality".
It involves a close cooperation between academic groups with pan-European academic laboratories and leading private enterprises, and is coordinated by CNR-IRSA.
Its main aims are:
-investigate and identify aquatic complex stressor indicators based on microbial communities;
-foster the transfer of knowledge among the partners with the final goal to bring to market faster, more sensitive and robust tools as bioindicators of water quality.





The river Tiber has been chosen as a pilot case study and four areas, including Emilia Romagna, Umbria and Lazio region, have been selected on the basis of various kinds of anthropogenic pressures

Water sampling points are:
1) Monte Fumaiolo, the river source which is in the pristine area;
2) Attigliano, an agriculture area affected by widespread pesticide use;
3) Aniene, which udergoes Industrial contamination before enter the river Tiber in the city of Rome;
4) Scafa, which is an anthropogenic area downstream from the Magliana WWTP of Southern Rome, and is very close to the sea.

At each sampling (one in Autumn and one in Spring for two consecutive years) chemical and microbiological analyses will be performed in order to assess:
i) Microbial community structure by Fluorescence In Situ Hybridization (FISH) and microbial sequencing by metagenomics; so it means all the microorganisms present in the water sample will be sequenced
ii) Main physical-chemical parameters (oxygen, pH, temperature, nutrients);
iii) Chemical analyses of main inorganic and organic pollutants, including emerging ones
iv) Microbial targets enriched for specific bioindicators (pathogens or ecological indicators).

The aim will be to link the microbial communities in terms of species and/or metabolic pathways to the water quality (e.g. chemical pollutants, nutrients) in order to extrapolate "universal indicators" of the water quality which will be used to develop tools such as ready to use plate for qPCR and probes for FISH. Additionally in the project, it will be tested the DNA microarray, develop in the project FP7 µAQUA, to identify freshwater pathogens.

The figure shows the final goal of MicroCokit project which will be to generate two tools for water quality assessment, one based on quantitative real time (qPCR) and the other one on Fluorescence in situ Hybridization (FISH).