GENERA: Use of genomic and proteomic tools for the development of contaminant specific biomarkers for the environmental risk assessment of aquatic ecosystems.

Measuring the effects of pollution in the environment is becoming an important priority as the number of discharged synthetic chemicals grows continuously. People and the environment are exposed to thousands of chemical substances every day through use of consumer products (e.g. shampoo, washing powder) and involvement in industrial activities (e.g. oil lubricants, farming pesticides). More than 100,000 synthetic chemicals are used in commerce today and society expects that these chemicals are safe for use. Risk Assessors within companies and regulatory agencies assess the relative risk of specific uses of chemicals to human health and/or the environment. The classic approach to measure these effects is laboratory-controlled exposure of selected test organisms and to record the effects in survival or other physiologic responses such as growth and reproduction. Moreover, these higher level responses are preceded and thus caused by alteration in the expression of related genes and proteins.

However, this is an unviable, time- and cost intense process and alternatives to the current risk assessment strategies are required. In this context, the recent EC Scientific Committee report 'Making Risk Assessment More Relevant for Risk Management', highlighted that current human health and environmental risk assessment approaches for chemicals are not sufficiently transparent or evidence-based to inform today's complex risk management decisions. Moreover there is considerable fragmentation both within and across the ecological and human health risk research communities meaning that we may not be best utilizing the many cutting-edge approaches that are available to different fields.

The availability of new high-through-put techniques (transcriptomics and proteomics) for holistic gene expression profiling, together with the availability of potent bioinformatic tools, has provided a generic platform with enormous potential for the acquisition of knowledge on the mechanistic processes involved in toxic events at gene- of protein level.

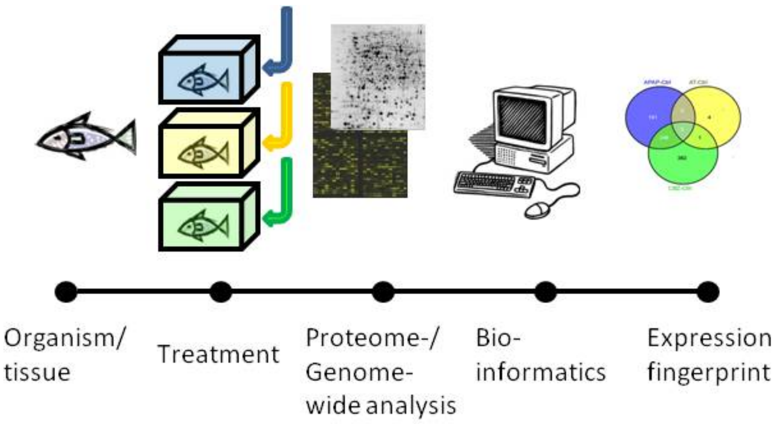

Figure 2. Work-flow in moleculat high-through-put techniques.

The use of genomic tools is rapidly increasing in ecotoxicology, and results from transcriptomic and proteomic studies of the effects of environmental pollutants are becoming more and more available. The knowledge of the processes occurring at molecular and cellular level helps to understand the mechanisms of action involved in toxicity. Current risk assessment (of aquatic ecosystems) faces the problem of dealing with thousands of chemical contaminants already on the market with still unknown ecotoxic effects. And there are also those industrial chemicals that are continuously being developed for commercialization. Thus, there is a need for a shift in current risk assessment procedures able to streamline toxicity testing of compounds by being able to predict toxicity of untested compounds by extrapolation from already obtained results. This is only possible with an in-depth-understanding of the molecular events of involved pathways elucidated by the different classes of pollutants.

However, even if important information is gathered on differential gene and proteome expression, the application of species specific high through put techniques in non-model target organisms is still a task to be tackled in order to progress in this field. In this context, an attempt to join efforts for the discovery and development of susceptible genes and proteins to be employed in routine environmental risk assessment is highly desirable. In this project, we selected several marine species from different organizational and trophic levels to be tested for the genomic and proteomic effects of the exposure to priority contaminants. Obtained responses are being analyzed for similarities at different organizational levels with the aim to identify contaminant-category specific mechanisms of actions and to develop interspecies relevant biomarkers for environmental risk assessment of the most important contaminants.

Through the IRSES Action GENERA, it was possible to strengthen already existing collaborations between the participating organizations and to expand these collaborations into a network that is very likely to continue in the future. This is evidenced in a series of actions and projects that are currently being jointly submitted or planned. The expertise of the partners in their fields and their complementarities to produce high quality data for risk assessment is evidenced in the high number of scientific manuscripts and congress contributions produced throughout this project and as result of the performed exchanges.

The work performed in the framework of the project GENERA is not only important from a fundamental point of view; it has also a significant socio-economic impact. Integrity or deterioration of natural environments has important implications on human life quality and health. Not only in relation to food production and consumption of products from contaminated sites, but also the continuous contact with a contaminated environment (exposure to contaminants via air and water) affects human health directly. Quality of human life is reduced in contaminated environments with poorer ecosystem services, both from a health as well as recreational point of view. In fact part of the studied organisms constitutes important natural resources which in some of the partner countries are mainly devoted to exportation to EEC countries. This sector involves an important number of employees. A better quality of these products will also help to guarantee these employments.