

Application of a coordinated OMICS research program and data into regulatory frameworks: case-studies and perspectives

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Wednesday May 25, 8:15 AM - 10:15 AM, Salle 150

During the past decade, governments from around the world are reassessing the effectiveness of current regulations at protecting human and environmental health against the potential harmful effects of chemical and nano compounds. These are critical and complex rules that are either based on the observed adverse effects of compounds, or based on precautionary principles. Most recently, the Adverse Outcome Pathway (AOP) framework is proposed to consolidate mechanistic information on how compounds disrupt biological processes that result in adverse outcomes. This latest approach to understand toxicity thresholds (useful for regulation) can potentially also bridge the artificial divide between toxicology applied to human and the environment. However, persistently huge scientific constraints remain at determining the environmental and human health risks for an ever increasing number and diversity of consumer products introduced to the market, primarily because toxicity testing fails to keep pace with modern biology. This has created an enormous backlog of chemicals that have yet to be experimentally assessed for potential health hazards (especially as mixtures), combined with inadequate methods at monitoring for the presence of contaminants in the environment and determining the level of risk so policy makers and regulators can make informed decisions, balancing economic priorities with the need to protect vital ecosystems and public health.

Recognizing that the main challenge of implementing proposed methods to improve environment and health protection stems from the lack of useful experimental data, an innovative and coordinated scientific approach is underway. This approach pursues toxicology as foundational science, having the same effect that genetics and genomics have at revealing fundamental principles useful for understanding and treating human disease. This proposed session and discussion among investigators and stakeholders begins by forecasting that a big data scientific enterprise - using high-throughput toxicity testing with data-rich OMICS (e.g. genomics, transcriptomics, proteomics, metabolomics) in non-mammalian model organisms and in vitro cell models - will deliver fundamental principles of how genes and their products functionally associate into responsive networks. In parallel, systems biology approaches are in development that utilize this vast amount of information and are able to extract key components central to the AOP framework.

Closing the gap between these approaches and the regulatory application is therefore a key component of this session. We invite presentations of case studies and perspectives using OMICS that result in (or lead towards) better understanding of regulatory decisions. These may include examples of OMICS-based predictions of apical endpoints, approaches for AOP identification, cross-validation studies, supporting categorisation, selection/de-selection of alternative substances, supporting toxicity assessment contributions for faster screening and prioritization and weight-of-evidence contributions. We also seek contributions from industry and regulators, presenting visions, objectives or hurdles on the way towards a Knowledgebase of new toxicological understanding and principles. We propose to bring together science, industry and policy makers to discuss present usages of these technologies, increasing the value and robustness of this data-driven knowledge and its applications to meet the requirements of industry and regulators, in order to make a step forward in environmental protection, while supporting the needs of cost-effective industrial innovation.

Epigenetic and evolutionary effects of pollutants: new challenges for long-term ERA

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Wednesday May 25, 10:50 AM - 12:50 PM, Salle 150

Many organisms, populations and species are currently facing severe degradation of their environment due to global change. Human activities, among which the continuous release of potentially toxic substances into the environment, contribute significantly to this pervasive change. There is growing evidence that environmental change may affect organisms beyond exposed generations, as a result from non-genetic transmission mechanisms or from rapid evolutionary processes. At the population level, these phenomena may give rise to either adaptation or aggravated and unexpected stressful effects with adverse consequences. With regard to transgenerational effects, environmental stressors, including chemicals, biocides and plant protection products, may contribute to the de-regulation of epigenetic mechanisms. Yet, their disruptive potential in environmental toxicology is largely unknown due to a limited knowledge of epigenetic effects in ecotoxicological model organisms. Epigenetic disruptors may act by directly impacting on components of epigenetic regulation pathways, like DNA methylases or histone modification enzymes, or may even irreversibly alter the "epigenetic code". Epigenetic effects represent a new challenge for risk assessment as their adverse outcomes may still be detected long after the actual exposure occurred. As for genetic processes, the probability of adaptive evolution depends on population standing genetic variation and evolutionary history, and on phylogenetic constraints. The difficulty to assess pollutant driven selection in the field is still increased by confounding factors that also shape the distribution of genetic diversity. However, evidence for evolutionary (genetic) and trans-generational (non genetically inherited) impact of pollutants is accumulating across a diversity of systems, and this reality cannot be ignored in future assessment procedures (see SETAC Meeting sessions from 2008, see Ecotoxicology Special Issues; see top research questions selected by the SETAC-Horizon Scanning Workshop, held in Barcelona, 6-7 May 2015). Therefore, it becomes urgent to acquire tools and methods to measure, anticipate, and even predict epigenetic and evolutionary ecotoxicological effects, the genetic and non-genetic basis of adaptation/maladaptation to environmental stress and the adaptive potential of natural populations, as well as to understand their consequences for ecosystems, including species distribution and persistence. These tools should provide scientific guidance to support optimized decision making, through a sustainable trade-off between human demand on, and conservation of natural resources.

This session is proposed by the EVOGENERATE workgroup (SETAC, ERA-AG).

MetaOMICs in ecotoxicology: evaluation of alterations in the structure and functions of ecosystems

Susana Cristobal, Martin Eriksson, Mechthild Schmitt-Jansen

Wednesday May 25, 2:00 PM - 4:00 PM, Salle 150

MetaOMICs in ecotoxicology play a new role in the evaluation of alterations in the structure and functions of ecosystems. Metagenomics, metaproteomics and metametabolomics analyses respectively the DNA sequences of a community, the translated proteins and the metabolites resulting from cellular processes. Therefore "meta-omics" data could capture the functional interactions occurring in a given ecosystem and provide community analysis tools that could link ecology, physiology and functional analysis.

By discovering a huge novel prokaryote and eukaryote biodiversity in terrestrial and aquatic ecosystem, metaOMICs is having a profound impact on our understanding of how the biosphere is organised and how it functions, and will be leading to a true paradigm shift in ecotoxicology. Metagenomics has been used in community ecotoxicology and field studies describing effects of contaminants and selection pressures in the environment. Metaproteomics has been applied to define the role that microbial species have in an ecosystem, or understanding the microbial community response and adaptation to environmental stressors. The metametabolomics studies provide complementary data for the functional characterization of a community and generate indirect measurement of the molecular phenotype.

This session welcomes research focus on meta-omics data analysis and its application to aquatic and terrestrial ecotoxicology. The metadata analysis from environmental samples could cover several levels of biological complexity from metagenetics (amplicon sequencing of specific genes), metagenomics and functional proteins in communities, or genetics, genomics or proteomics of populations and metametabolomics, expression the community at the metabolic level. The session will present studies that assess how toxicants or other anthropogenic stressors change the diversity and/or function of communities or populations, studies presenting metagenome mining, metaproteome characterization of relevant environmental samples, methodological implementation for data analysis and functional characterization, and novel environmental assessment methodologies. The robustness and capability from meta-omics data is highlighting importance of understanding the microbial population dynamics and community ecology to safeguard our environmental for future generations.