

Omic approaches in environmental risk assessment

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Conventional environmental health risk assessment implies the measurement of a limited set of biological responses supposed to be elicited by the compound, the so called biomarkers. Hence, many other responses of similar or even higher importance can be ignored and the prediction of risk to susceptible populations of pollutants result underestimated. Integration of genomic-based methodologies into ecotoxicology using transcriptome, proteome and metabolome analyses, has permitted (i) to maximize the information obtained from limited testing species; (ii) to reduce the future level of routine ecotoxicity testing; (iii) to allow identification and understanding mechanisms of toxicity of existing and emerging pollutants that may aid developing predictive simulation models of toxic effects; (iv) to link molecular and cellular biomarkers with higher level population and ecosystem responses; and (v) to anticipate potential ecological risks for new chemicals and emerging technologies.

This work aims to provide a working scheme for the use of combined transcriptomic, proteomic and metallomic methodologies in environmental biomonitoring. Among others, we have used the *Mus spretus* mouse and the *Procambarus clarkii* crayfish as sentinel organisms. *M. spretus* is an unprotected rodent that typically inhabits marshlands. The red swamp crayfish, *P. clarkii*, is one of the most important freshwater decapods farmed for consumption. It is well established that both bioindicators are good sentinels for assessing the effects of contaminants in terrestrial and aquatic environments, respectively. Animals were collected at different zones in the SW region of Spain, mainly Huelva city and its polluted industrial parks (Punta del Sebo and the Domingo Rubio Stream), and the boundaries of the Doñana National Park, where industrial and intensive agriculture activities generate a big amount of pollutants that reach the Park, one of the most important European biological reserves, and its inhabitants.

The difficulties of working with non-model organisms as bioindicators have been solved by combining several omic approaches. As a whole, our results with heterologous microarrays in *M. spretus* and suppressive subtractive hybridization (SSH) in *P. clarkii* indicated that animals sustaining a heavy pollution burden exhibited enhanced immune, oxidative and xenobiotic stress responses. The proteomic studies provided a holistic insight regarding the manner by which pollution shifts protein amounts in two-dimensional gel electrophoresis, and the peptide amounts in iTRAQ. The metallomic analysis revealed the presence of low molecular mass metallothionein-like proteins in animals captured at polluted areas, according to the high metal levels found in these animals tissues. This integration of metallomics with proteomics and transcriptomics can be useful in further studies for assessment of environmental issues. (Grants: CTM2009-12858-C02-02 and CVI-3829)