Identification of genes associated with DDE-induced toxicity in *Mus spretus* by PCR array focused on stress response.

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Chronic exposure to pollutants is a matter of serious concern because of their potential of causing deleterious effects on human and environmental health. Efficient tools for environmental risk assessment, mainly linked to biological responses, are hence necessary. *Omic* methodologies together to conventional biomarkers provide great potential in this regard, as reported in our previous studies using the free living Algerian mouse (*Mus spretus*) as bioindicator of environmental pollution in Doñana National Park (SW, Spain). However, the complexity of the ecosystems and the synergism/antagonism processes among contaminants make quite difficult to establish a clear link between one contaminant and the specific biological responses by it elicited. For this reason it is necessary to carry out laboratory experiments of exposition to a particular contaminant under controlled condition.

This study considers a semi-omic approach for the evaluation of *M. spretus* mice response to a model contaminants, DDE under controlled experimental conditions. DDE (dichlorodiphenyl-dichloroethylene) is the most prevalent breakdown product of DDT (dichlorodiphenyl-dichloroethane). This organochloride pesticide persists in the environment, concentrates up the food chain and is stored in fatty tissues of animals, fish, and humans. We have used PCR-Arrays to analyze the effect of DDE at the transcriptional level in *M. spretus* mice raised in captivity. PCR-Arrays allow quantitative real-time reverse transcriptase PCR in a more high-throughput way, as it quantifies up to 96 different transcripts, usually involved in one metabolic pathway, on one single plate. The rational of using PCR-Arrays designed for *M. musculus* with *M. spretus* is the phylogenetic proximity between both species. By using a PCR-Array focused on stress response, 21 genes were identified in *M. spretus* liver as responsive to DDE treatment. As PCR-Array generate semi-quantitative data, the results have been verified by absolute quantification by qRT-PCR of the transcripts amounts of a group of selected with primers pairs specific for *M. spretus* sequences. The functional analysis showed deregulation of genes involved in the oxidative stress, the immune response and apoptosis (**CTM2012-38720-C03-02, BIO1657**).