

Development of a bioassay with *Drosophila melanogaster* as an alternative model for studying the effect of various pollutants exposure

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Contamination of environment by toxic pollutants has become commonly recognized as an environmental concern. Those compounds are often present at low concentrations making them difficult to detect. They could also cause ecological issues according to their nature (heavy metals, pesticides, endocrine disruptors...). Therefore, ecotoxicity risks are evaluated with various types of organisms, from cell-lines and microorganisms to plants, invertebrates and vertebrates. Most of them allow the detection of a phenotype, thus indicating a toxic effect and some of them can also highlight the modification of molecular actors involved in the toxic response. However, few models offer the opportunity to perform integrated study with multiple approaches, from molecular variations to physiological consequences. *Drosophila melanogaster* is a proven model organism in genetic and biology research. The fruit fly has been further considered as an emerging and suitable model in toxicology and ecotoxicology in the past few years. *Drosophila* has a short and well described development; reproduction and maintenance do not require sophisticated equipments and are rather economical. Furthermore, there are a lot of amenities available to study genetic actors involved in stress or toxic response compared with other models (i.e. open access of online molecular database, gene inhibition or over-expression, mutant production, coupling of fluorescence with gene expression...). Moreover, the fruit fly's development is under hormonal control making endocrine disruptors studies possible. To develop this "tool box" as an alternative model, we focused firstly on the impact of two heavy metals, cadmium and mercury on post embryonic development of *Drosophila melanogaster*. The first results indicate that mercury is more toxic than cadmium, and has different kind of effects on post embryonic development. We also analyzed the expression of various genes, as biomarkers, involved in different defense and detoxification mechanisms to establish a response profile that could be used in future works.