

Gene and Protein Expression Profiles in *Daphnia magna*: Potential biomarkers in Methidathion Toxicity

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Methidathion, an organophosphate insecticide widely used to control agricultural mite and insect pests, is highly toxic and classified as EPA toxicity class I. The residues of this chemical can contaminate the aquatic environment and have adverse effects on the non-target aquatic organisms. We investigated adverse effects of methidathion on growth and reproduction of *D. magna* through acute and chronic toxicity test. To elucidate the toxicity mechanism on daphnids, molecular responses such as gene and protein expression were examined in organism exposed to different lethal concentrations of chemical. Our results showed that expression of five genes *Dhb*, *Vtg*, *ARNT*, *Cyp4*, and *Cyp314*, biomarkers known for environmental stress, in *D. magna* were alternated in response to methidathion. Except for *Cyp4*, which is not affected by methidathion, expression of other genes are down-regulated. In addition, proteomic analysis using 2-D gel electrophoresis in these exposed animals showed different expression patterns compared to control. An integration analysis of gene and protein expression patterns in *D. magna* exposed to methidathion should be potential to discover novel biomarkers.