Sreening of novel biomarkers to detect environmental toxicity using toxicogenomic and proteomic methods in *Daphnia magna* exposed by heavy metals

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In our industrialized society, many anthropogenic activities have generated multiple pollution and waste streams that have endangered the health of humans and biota. Many researchers are performing risk assessments and toxicological studies of heavy metals with the organisms by means of physical and chemical measurements, but such the classical "dead" or "alive" endpoint may not be sufficient to provide detailed information on how heavy metals affect the cells on a molecular level. We performed −omics analysis of *Daphnia magna* in response to Sodium arsenite [$NaAsO_2$], Sodium arsenate [Na_2HAsO_4], and Cadmium nitrate [$Cd(NO_3)_2$] as a heavy metal, by using −omics such as Reverse transcriptase Polymerase Chain Reaction, microarray and two−dimensional gel electrophoresis, and found that candidates of biomarker from *Daphnia magna* were shown distinct expression patterns for the each heavy metals. Therefore, the systematic approach to the analysis of −omics responses used in this result as well as the detailed analysis results reported herein would be useful in screening of the novel biomarkers for heavy metals−induced hazardous effects and designing the systemic strategies for the new biomonitoring tools to detect heavy metals toxicity.