

## **Identification of some novel biomarkers for assessment of copper sulphate toxicity in liver of *Puntius javanicus* through proteomic analyses**

### **ABSTRACT**

Copper is extensively released into the environment, affecting the natural habitat of surrounding organisms especially the aquatic life. The aim of this study is to explore the different protein expressions on different concentrations of CuSO<sub>4</sub>. *Puntius javanicus* liver was used as a tool to investigate the biomarkers and mechanisms of copper toxicity to *P. javanicus* through proteomic assessment after being exposed with different concentrations of CuSO<sub>4</sub> (0, 0.1, 0.3, 0.5, 1.0 and 5.0 mg/L). *P. javanicus* liver was extracted (TCA-acetone extraction) and electrophoresed (IEF and 2D PAGE). Ten protein spots were found to be significantly different in their expression and subsequently identified via matrix assisted laser desorption/ionization tandem time-of-flight (MALDITOF). Three protein spots were further identified as new alternative biomarkers for copper toxicity namely, zinc finger C4H2 domain-containing protein, insulin gene enhancer protein isl-2a and synaptic vesicle membrane protein VAT-1 homolog-like. The present study could provide an additional understanding on the hepatotoxic mechanisms of copper as well as enhance the development of biomarkers for an efficient monitoring of the contamination level in the environment based on proteomic assessment.

**Keyword:** Proteomic; Copper; Liver; Biomarker; *Puntius javanicus*; Proteins