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Comparative proteomic analysis between two haemocyte subpopulations in shrimp *Fenneropenaeus chinensis*

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Abstract: In our previous work, granulocytes and hyalinocytes were successfully separated by immunomagnetic bead (IMB) method using monoclonal antibodies (mAbs) against granulocytes of shrimp (*Fenneropenaeus chinensis*). In order to elucidate the proteomic differentiation between granulocytes and hyalinocytes, in this paper, the differentially expressed proteins were analyzed between non-fixed/un-permeabilized (NFP) haemocytes and fixed/permeabilized (FP) haemocytes using two-dimensional gel electrophoresis (2-DE) combined with mass spectrometry (MS). Then the FP haemocytes were separated into two haemocyte subpopulations using IMB method, and the comparative proteome between granulocytes and hyalinocytes was investigated. The results showed that 10 differentially expressed protein spots were detected and identified as 4 proteins in the NFP haemocytes. Twenty one differentially expressed proteins were successfully identified between granulocytes and hyalinocytes, which include 4 unique expressed proteins in granulocytes, 4 significantly highly expressed proteins in granulocytes, and 13 significantly high expressed proteins in hyalinocytes. According to Gene Ontology annotation, the identified proteins between granulocytes and hyalinocytes were classified into six categories, including binding proteins, proteins involved in catalytic activity, enzyme regulator activity, structural molecule