

O1200 Potential diagnostic biomarkers identified from plasma proteome for *Opisthorchis viverrini*

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Background: *Opisthorchis viverrini* is responsible for Opisthorchiasis and the aggressive bile duct cancer cholangiocarcinoma in Thailand and Southeast Asia. In order to prevent cholangiocarcinoma, patients infected with *O. viverrini* have to be diagnosed early and effectively treated with the anthelmintic drug. Detection of parasite antigen, antibody, or DNA for diagnosing Opisthorchiasis still remains controversial. Fecal examination remains the gold standard, despite its poor sensitivity and specificity. The alternative approach to detecting active *O. viverrini* infections includes host proteins which respond to infection. Therefore, the aim of this study is to identify potential diagnostic biomarkers from plasma proteomes which specifically found in *O. viverrini* infected patients.

Materials/methods: The pooled plasma proteome from 48 *O. viverrini* (OV) infected patients was investigated and compared with the pooled plasma proteome from 48 non-infected patients (non-OV). The plasma proteins were denatured, carbamidomethylated, digested with trypsin, and analysed by LC-MS/MS. The obtained LC-MS/MS data was analysed (DeCyder MS) and matched with the database (NCBI). A Venn diagram (<http://jvenn.toulouse.inra.fr>) was used to identify OV-specific proteins. The GI number was used for PANTHER (www.pantherdb.org) and the uniprot ID (<http://www.uniprot.org>) for STITCH (<http://stitch.embl.de>) to predict the Gene Ontology (GO) and functions, respectively.

Results: A total of 1,795 plasma proteins were retrieved from the LC-MS/MS database. The 1,663 proteins were shared in non-OV and OV. Interestingly, 46 proteins were found exclusively in the plasma of OV patients. The GO of these OV-specific proteins was related to the gonadotropin-releasing hormone receptor pathway as well as several cell signalling pathways such as VEGF, FGF, EGF, and TGF-beta. By using STITCH, OV-specific proteins were linked to the MAP kinase signalling pathway and coatamer protein complex.

Conclusions: Based on GO and protein-protein interactions, the specific upregulated proteins in OV infected plasma was found to involve several cell signalling pathways and secreted vesicles. The relationship between these upregulated proteins found in *O. viverrini* and the development of cholangiocarcinoma should be investigated. Furthermore, these OV-specific proteins will prove useful for the diagnosis of *O. viverrini* infected patients whether patients are currently experiencing an active or inactive infection.

