Cellular and molecular profile of liver pathogenesis in the peritoneum during early infection of sheep with Fasciola hepatica

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Abstract

Fasciolosis, an economically important parasitic disease of livestock, is caused by the liver fluke *Fasciola hepatica*. Development of effective vaccines requires an understanding of immune evasion and modulation strategies of the parasite, particularly during early infection. We employed a combination of immunological and proteomic analyses to investigate the peritoneal fluid of sheep infected with *F. hepatica* to characterise early tissue invasion and liver pathogenesis. At 18 days post-infection, we observed a dramatic increase in antibody responses and number of immune cells, with marked eosinophilia. Cytokines such as IL-12, IL-17, IL-23, TGF-β were significantly overexpressed and FoxP3 and iNOS expression greatly increased. Proteomic analysis identified 324 proteins of the peritoneal fluid with 31 proteins uniquely observed in the infected sheep, including periostin and VCAM-1. Immunolocalisation of these molecules in liver indicated that they are signalling molecules relating to liver tissue damage. This study has defined dramatic changes that occur during early *F. hepatica* infection, which can be exploited for future control strategies.

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