

Review of: "Timing of transcriptomic peripheral blood mononuclear cell responses of sheep to *Fasciola hepatica* infection differs from those of cattle, reflecting different disease phenotypes"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

This transcriptomic study was carried out using ovine peripheral blood mononuclear cells (PBMC) of sheep experimentally infected with *Fasciola hepatica* at 0, 2 and 16 weeks post-infection (wpi) and analysed for differentially expressed (DE) genes between infected and control and infected animals at each time point and for each group relative to time 0. The latter analysis is compared and discussed with a previous transcriptomic study on bovine PBMC. The study design is appropriate and the manuscript is well written. It contains novel information since it is the first transcriptomic study in ovine PBMC in chronic fasciolosis (16 wpi) and also contributes to better understanding of the host-parasite interaction in ovine fasciolosis. The authors made an interesting comparison between the results of the present study and those of previous transcriptomic studies on *F. hepatica* infected sheep in acute stages of infection and with the results of a previous transcriptomic study in ovine hepatic lymph nodes from the same sheep used in the present study. As the authors suggests, a variety of factors such as sheep breed, age of animals, strain of *F. hepatica*, infection dose, geographical location, seasonality, etc. may have an effect on DE genes.

Some minor suggestions are:

1. The abstract contains several abbreviations that are not explained and some readers may find them difficult to understand, ie. FDR, PKR.
- 2.- It is surprising that at 16 wpi only 2 DE genes were found. Since the experimental infection was carried out only with 120 mtc, the low number of DE genes at chronic stages of infection (16 wpi) could be related with a relatively low fluke burden?