



*How to Use the Online Abstract Submission System for
28th Conference of the World Association for the Advancement of
Veterinary Parasitology 2021*

Important Information

- Abstracts are submitted via an [online submission system](#). Register with the abstract submission website and establish your user name and password.
- If you are submitting more than one abstract you **must** use the same login for each abstract.
- The maximum length of an abstract is **300 words**. **Please ensure that your findings are described to a level sufficient for reviewers to make an informed decision on quality. Abstracts that fail to meet these criteria will be rejected.**
- Do not include author names in the title or body of your abstract – these are entered online during the submission process.
- You can alter your abstract at any time up to the submission deadline of **15th January 2021**.
- Abstracts will be reviewed and any abstract that was submitted for consideration as an oral presentation, but was unsuccessful in that regard, will be considered for poster presentation.
- Each author may present **a maximum of two presentations** at the Congress.
- Please note that at least one author **must** register in full to attend and present the abstract at the Conference.

1. Congress Topics

WAAVP 2021 will accept abstracts under the following topics:

- Anti-parasitic drugs and drug development
- Arthropods
- Co-infection
- COMBAR session
- Education
- Epidemiology
- EVPC residents' corner
- EVPC session
- Genetics
- Genomics
- Helminths
- Immunology
- ISP session
- One Health
- Parasite vaccines
- Parasites of companion animals
- Parasites of farmed ruminants
- Parasites of fish
- Parasites of horse
- Parasites of wildlife
- Protozoa
- Science and policy



2. The Submission Process

Submitting an abstract is a **3-step process**. We strongly recommend that you complete your submission at one time.

Step 1: Register on the system

We are using a dedicated website for abstract submission and you must [first register on the system](#). The website is accessible by username and password. Please note that you will need to create your own username and password to access the system.

You only need to register once - each subsequent time that you visit this page, you will log in with your e-mail and chosen password.

Step 2: Submit your abstract

- Once you have registered and created your profile, you must log in to the dedicated submission [webpage](#), when you have prepared your abstract - enter your email address and the password you chose when you registered.
- Submitting an abstract requires that you complete a questionnaire for each abstract. Some questions are mandatory (marked with an asterisk) and you will not be able to complete your submission until these questions have been answered. You will be required to provide the **names and affiliations of all authors, confirmation that all authors have approved the submission and the topic to which you are submitting your abstract**. You will also be able to indicate if you wish your abstract to be considered for oral presentation.
- It is strongly recommended that you complete your submission once started. However, if you decide to start your submission for completion at a later point, you must ensure to “Submit” your incomplete abstract. It will then be available for you to finish at a later stage. **Failure to “Submit” your incomplete abstract will result in it being lost and you will have to start again.**
- Mandatory questions are marked with an asterisk (*) and must be answered. Your submission will not be complete if a mandatory question is left unanswered. Incomplete submissions will not go for review.
- If you exceed the word count for either the title or abstract, your submission will be marked as incomplete in our system. Incomplete submissions will not go for review.

Step 3: Confirmation e-mail

You will receive an e-mail confirming that your submission has been received. The subject of the mail will indicate if your submission is complete or incomplete. An incomplete submission may have an answer that is unfinished or you may have exceeded the word limit for the abstract. Incomplete



submissions will not go for review. You **must** log back into the submission system, click on the title of the abstract and complete it. Once complete you will receive the confirmation e-mail.

If you wish to make another submission, please click on New Submission and a new blank submission form will open.

3. Amending a Submission

You may wish to change your submission. You can do this at any time up to the deadline of **15th January 2021**.

- [Log in to the abstract submission system.](#)
- You will see the abstract(s) that you have submitted. Click on the abstract title to open the file.
- Amending an abstract is just the same as the original submission process except that the online form will be automatically filled in with the answers that you gave previously. You don't have to change an answer if you don't want to.
- Once you click "Submit", your changes will be saved and you will be sent an email confirming that your abstract has been amended. **Your changes will not be recorded if you fail to click "Submit"**. You will also receive an e-mail confirming that an amendment has been made to your abstract.

4. Queries

If you have any queries about the submission process or you want to withdraw an abstract, please contact the congress administrator at abstracts@waavp2021.com



5. Sample Abstract

This is for information only – you must not enter your abstract as below as the abstract system captures the abstract in a series of steps. However, you may use the section headings (Introduction, Methods etc.) if you wish and the output will be similar to the following.

***Fasciola hepatica* Infection in Cattle: Analysing Responses of Peripheral Blood Mononuclear Cells (PBMC) Using a Transcriptomics Approach.**

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Abstract

The parasitic helminth *Fasciola hepatica* (liver fluke) causes economic loss to the livestock industry globally and also represents a zoonotic disease. New control strategies such as vaccines are urgently needed, due to the rise of drug resistance in parasite populations. Vaccine development requires a comprehensive understanding of the immunological events during infection. Previous *in vivo* studies by our group have investigated global differentially expressed genes (DEGs) in ovine peripheral blood mononuclear cells (PBMC) in response to both acute and chronic *F. hepatica* infection. This work demonstrated that pathways involved in the pathogenesis of ovine fasciolosis included inhibition of macrophage nitric oxide production, fibrosis, and antibody isotype switching, among others. Transcriptomic changes in PBMC populations following *F. hepatica* infection in cattle, in which the disease phenotype is quite different, have not yet been examined. Using RNA sequencing we investigated gene expression changes in PBMC isolated from 9 non-infected and 11 *F. hepatica*-experimentally-infected calves at the day of infection, at 1 week and at 14 weeks post-infection. Longitudinal time-course comparisons among groups revealed 21 and 551 DEGs driven exclusively by *F. hepatica* infection in cattle at acute and chronic stages, respectively. In addition, significant numbers of DEGs related to growth and maturation were detected in both groups at week 14. These results show that fewer DEGs at the acute stage of infection can be identified in cattle, as compared with sheep. Our results reflect the major differences in the disease phenotype between cattle and sheep and may implicate pathways to target in vaccine development. It also highlights the importance of including an uninfected group in the experimental design for transcriptomics-based infection time-course studies to control for physiological changes due to growth and development. The significant differences in DEGs, immunological pathways, and their relevance for the development of anti-liver fluke vaccines are discussed.