

August 13-14, 2018
Paris, FranceAm J Pharmacol Pharmacother 2018, Volume 5
DOI: 10.21767/2393-8862-C1-003

AN EX VIVO ABOMASAL OVINE MODEL TO STUDY THE IMMEDIATE IMMUNE RESPONSE IN THE CONTEXT OF HAEMONCHUS CONTORTUS LARVAL-STAGE

Saeed El-Ashram

Foshan University, Guangdong province, China

We have set up an *ex vivo* ovine abomasal model, which can mimic the multicellular process to explore the early steps in haemonchine nematode infection using RNA-seq technology. Ovine abomasal explants were collected for histological and transcriptional analysis, supernatants collected to quantitate lactate dehydrogenase (LDH) enzymes. A total of 233 were substantially induced genes between L4-inoculated and uninoculated-control tissues, respectively. However, a total of 14 were considerably down-regulated genes between the 51 aforementioned tissues. Fifteen pathways were annotated by Kyoto Encyclopedia of Genes, and Genomes pathway analysis accounted for the significant percentage in immediate response to larval-stage of *H. contortus*. Key genes up-regulated in response to the addition of L4-inoculum of *H. contortus* were IL-6, IL-8, C1q, atypical chemokine receptor-3, chemokine ligand-2, manganese superoxide dismutase, integrin alpha-7, -8, -9, integrin subunit beta-1, integrin subunit beta 6, intercellular adhesion molecule-1 and actin alpha-1. This study shows for the first time that galectin-1 is up-regulated in an *ex-vivo* abomasal segment model exposed to L4-inoculum of *H. contortus* following 6 h of incubation. The abomasal segment model has been shown to be a suitable tool to study the haemonchine larval-stage effects on the ovine abomasal tissues prior to *in vivo* assessment.

saeed_elashram@yahoo.com