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### **An ex vivo abomasal ovine model to study the immediate immune response in the context of *Haemonchus contortus* larval-stage**

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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 and 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 upregulated in response to the addition of L4inoculum 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.

**Keywords:** *Haemonchus contortus*; Illumina HiSeq 4000 platform; immediate immune response; Gene Ontology, Kyoto Encyclopedia of Genes and Genomes; Ovine abomasal explants; galectin-1