

Transcriptomic analysis of *Ascaris suum* larvae during their hepatopulmonary migration.

Wang T.¹ & Vlamincck J.¹, Jex A.², Gasser R.², Geldhof P.¹

¹Faculty of veterinary medicine, Department of virology, parasitology & immunology. Salisburylaan 133, 9820 Merelbeke, Belgium.

²Faculty of Veterinary Science, The University of Melbourne, Australia.

* Corresponding Author: Johnny.vlamincck@ugent.be

Introduction

Infections with the intestinal parasitic nematode *Ascaris sp.* present a problem in pig and human hosts all over the world. During the initial stage of infection, the invading stage three larvae (L3) pass through the intestinal tissue, liver and lungs to eventually grow into adulthood in the small intestine of its host (See Fig 1). During this migration, larvae have to continuously adapt to the changing environmental conditions as well as prevent possible fatal attack by the host's immune defences. All of this is likely to require tightly regulated transcriptional changes in the parasite.

Aim of the study

The intent of this project was to offer researchers an extra tool to investigate parasite biology, host-parasite interaction processes, and potential novel drug- or vaccine targets by producing the complete transcriptome of the *Ascaris suum* larvae during the different stages of their hepatotracheal migration using next generation sequencing.

Results

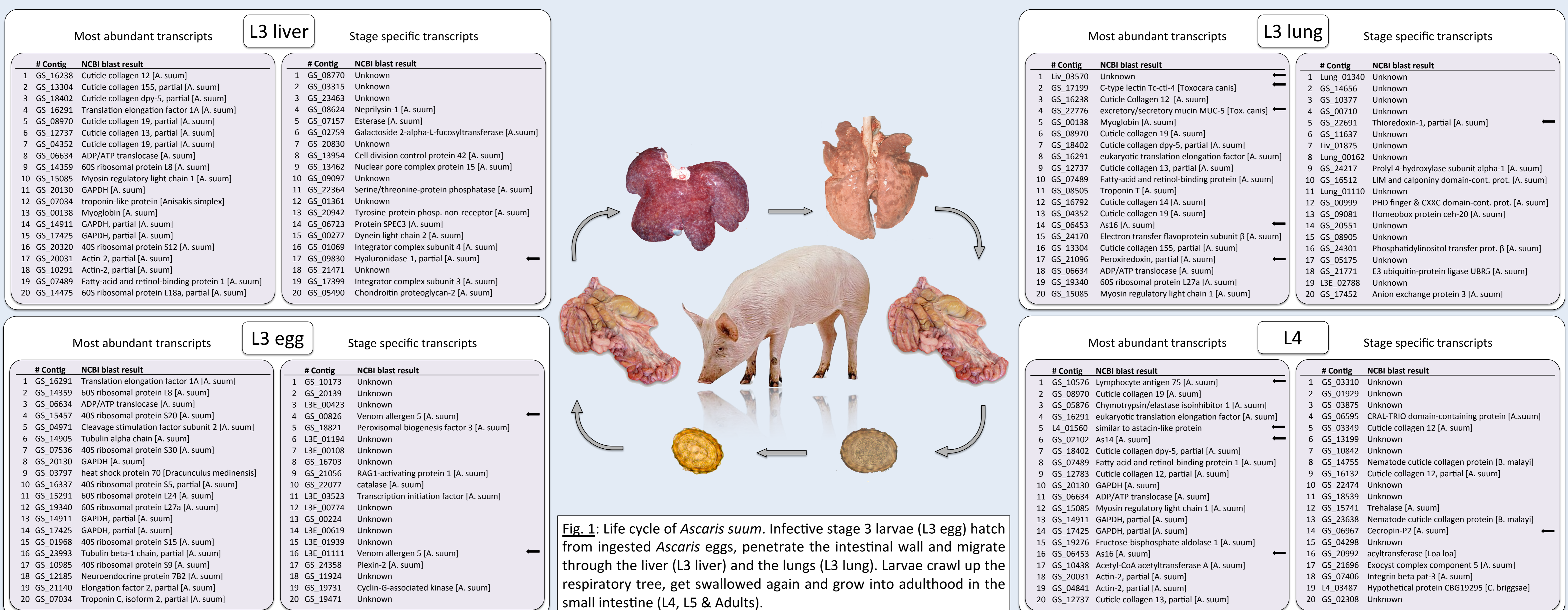


Fig. 1: Life cycle of *Ascaris suum*. Infective stage 3 larvae (L3 egg) hatch from ingested *Ascaris* eggs, penetrate the intestinal wall and migrate through the liver (L3 liver) and the lungs (L3 lung). Larvae crawl up the respiratory tree, get swallowed again and grow into adulthood in the small intestine (L4, L5 & Adults).

Cuticle collagen expression during the hepatotracheal migration of *A. suum* larvae

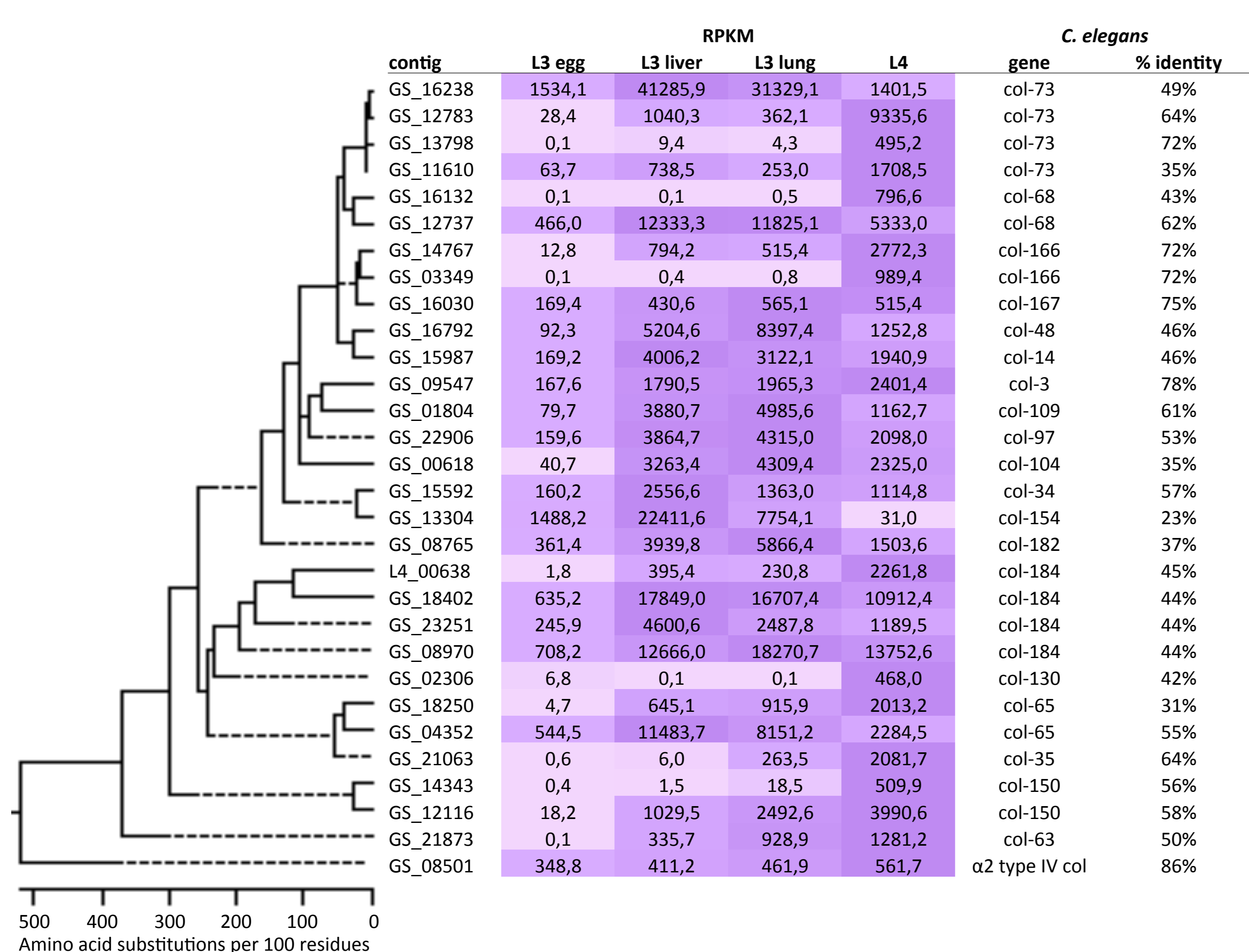


Fig. 2: Phylogenetic relation and expression levels of the different cuticle collagen transcripts detected in the top 1000 most produced transcripts of the L3 egg, L3 liver, L3 lung and L4 of *Ascaris suum*. (RPKM = Reads Per Kilobase per Million reads).

The Top-100 most abundant transcripts per life stage were investigated. Results showed that in the egg L3, transcripts associated with the regulation of translation and transcription, mainly ribosomal proteins, were most abundant. Next to that, several other interesting transcripts were found (see black arrows). Namely, the protective antigens As14 & As16, the antioxidant peroxiredoxin, the astacin-like metalloprotease and the C-type lectin-4, lymphocyte antigen 75 or secretory mucin 5 which might have important functions in host mimicking and/or immune evasion.

From the liver-L3s onwards, high transcription levels were seen for cuticle collagens, indicating the growth of the larvae during their migration. The expression profile of all collagen genes present in the Top 1000 transcripts is represented in figure 2.

Transcripts were also sorted according to their life stage specificity by sorting the transcripts on descending RPKM value and subsequently filtering out the transcripts with at least a 100-fold higher RPKM value in comparison with other life stages. Interesting transcripts were the VAP-5 antigen in the egg L3, the hyaluronidase in the larvae penetrating the liver, the antioxidant thioredoxin in the lung L3 and the anti-bacterial substance Cecropin 2B in the L4. A great number of transcripts did not show any homology to other proteins within the NCBI database (e-value cut-off = 10⁻⁵) implying that many biologically interesting molecules from this parasite remain to be discovered and investigated.

Acknowledgements

This work was financed by the Flemish Agency for Innovation through Science and Technology.