The Helminth Antimicrobial Peptidome: a novel opportunity for parasite control?

Allister Irvine, Sharon Huws, Louise Atkinson, Angela Mousley

Microbes & Pathogen Biology, The Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast

Antimicrobial Peptides (AMPs) are ancient innate immune components that play key roles in defending against diverse microbial pathogens including bacteria, fungi and viruses. AMPs are ubiquitous in nature and act as the first line of defense against pathogens. Whilst AMPs are known to be critical for the survival of many invertebrates, the role of AMPs in helminth biology remains uncharacterised. Parasitic helminths, living in specific host niches, likely produce a diverse AMP arsenal with bioactivity against host microbiota. Indeed, many gastrointestinal helminths have been shown to modify the host gut microbiome, causing some aspects of disease pathology. Characterisation of helminth derived AMPs is key to deciphering their role in host-worm-microbiome interactions and may reveal novel targets for parasite control.

In this study we characterised the pan-phylum AMP profiles of nematodes and flatworms through homology directed approaches. Here we reveal that phylum Nematoda is AMP-rich and -diverse, where >5000 genes encode AMPs. The data demonstrate that some nematode species e,g. *Trichinella/Trichuris* genera and the filarial parasites, possess a reduced AMP profile, whereas others encode more expanded AMPs cohorts. Using public transcriptomic datasets, we also show that nematode AMPs are transcriptionally active and are upregulated in key parasitic life stages. In contrast, flatworms do not appear to be as AMP-rich or -diverse. In this study we also employed machine learning tools to mine helminth genomic datasets for novel AMPs that are not detectable via homology-based approaches. These data reveal eight novel helminth AMPs which possess variable antibacterial properties against key gram-negative and gram-positive bacterial pathogens.

This study provides valuable insights into the complexities of the Helminth Antimicrobial Peptidome and expose the system as a novel target for helminth control.