

CANDIDATE SECRETED PROTEINS AND EFFECTORS OF PRATYLENCHUS SPP. Jones<sup>1</sup>, M.G.K., J.C.H. Tan<sup>1</sup> and J. Fosu-Nyarko<sup>2</sup>. <sup>1</sup>Plant Biotechnology Research Group, School of Veterinary and Life Sciences, Western Australia, Australia; <sup>2</sup>State Agricultural Biotechnology Centre, Murdoch University, Perth, Western Australia 6150, Australia. Root lesion nematodes (*Pratylenchus* species) are a group of economically important migratory endoparasitic plant pathogens that attack host roots of major crops. We have used Roche 454 deep sequencing of RNA extracted from mixed stages of *Pratylenchus thornei* and *Pratylenchus zae* to generate reads, which following assembly and annotation, have provided transcriptomic data on sequences of genes expressed by these nematodes. Using this data to provide target sequences we have shown that both *P. thornei* and *P. zae* are amenable to gene silencing (RNAi). By applying bioinformatics tools we have interrogated the transcriptome data for the presence of sequences that encode candidate secreted proteins, and from these about 30 candidate genes for such proteins have been identified. Some of these are common to sedentary endoparasitic nematodes, in particular genes encoding wall degrading enzymes, some found in the sedentary endoparasites are absent, and some candidate sequences have no known function. In silico comparative analysis of proteins and putative effectors present in the migratory and sedentary endoparasites will be provided as well as functional characterisation of some identified effectors using RNAi. Since *Pratylenchus* spp. do not reprogram cell identity and metabolism to form giant cells or syncytia, it would be expected that classes of effectors involved in those activities by root knot and cyst nematodes would be lacking, whereas the types of proteins secreted to aid entry and migration