



Modeling feeding-site formation by root-knot nematodes

Tuesday 17 June 2 - 3pm

Speaker

David McK. Bird

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Location

Slatyer Seminar Room

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This lecture is free and open to the public

PSS event information:

biology.anu.edu.au/News/events-ps.php

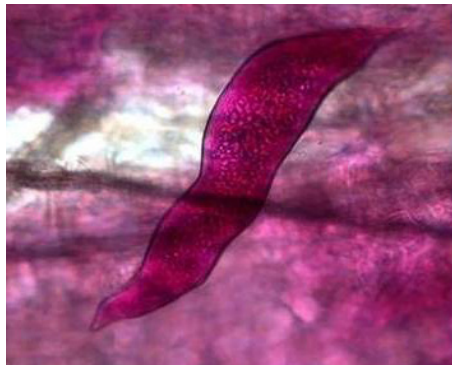


Photo of nematode courtesy of Lauren Venugoban.

As a genus, root-knot nematodes (RKN: *Meloidogyne* spp.) are amongst the world's most economically-important plant pathogens. Stereotypical of the parasitic interaction is the induction of Giant Cells (GC) in host roots. We have been mining the genetic basis for the natural variation of parasitism-attributes observable between wild isolates of *M. hapla*. To this end, we have integrated Mendelian genetics,

QTL analysis, and structural biochemistry. Interrogation of whole genome sequences revealed that RKN encode suites of peptides (including CEP and CLE) that bio-assay confirms are biologically-active in vascular plants. CEP link environmental sensing pathways to the regulation of root architecture. They also control the number of RKN feeding sites. We postulate that RKN-encoded CEP interact with the same molecular machinery as do endogenous peptides. CLE function to control meristem identity, and is likely responsible for the transcriptional overlap we observe between GC and meristems. We postulate that endogenous CEP and CLE function as intermediaries between global hormonal signals (e.g., cytokinin) and individual responsive cells. Importantly, direct cell-to-cell signalling permits the necessary analogue-to-digital transformation of inductive signals necessary to avoid cellular or tissue chimeras. Based on computational docking experiments we have explored the kinetics of various receptor/ligand pairs, and based on those data, we propose a model for GC formation.

About the speaker

The primary focus of Dr Bird's research group is to understand the mechanisms underlying parasitic interactions between nematodes and plants. David was a pioneer in framing the key questions in the context of nematode and host development. Together with collaborators world-wide, his group has been instrumental in establishing the root-knot nematode, *Meloidogyne hapla*, as the preeminent genetic system to model less-tractable nematode-host interactions, and as a platform for comparative genomics. His current program also emphasizes vaccine development for malaria-like diseases of cats and dogs.

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