

PLANT BIOLOGY SEMINAR SERIES

INVITED SEMINAR: 18th August 2010



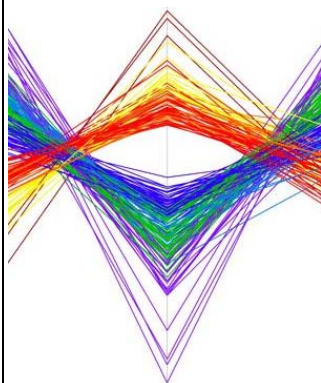
THE AUSTRALIAN NATIONAL UNIVERSITY

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Deducing plant biology from the genome of a parasitic nematode



by

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<http://www.cals.ncsu.edu/plantpath/people/faculty/bird/>

Root-knot nematodes (RKN: *Meloidogyne* spp.) are widely distributed throughout temperate and tropical regions and are responsible for major yield losses on food and fiber crops. They render plants more susceptible to drought stress and are a significant contributing factor to a looming world food crisis. Our recently completed genome sequence of the 54 Mbp diploid RKN, *M. hapla*, provides a research platform to study the genetic and biochemical basis for parasitism. One key feature the *M. hapla* genome is that it encodes a large cadre of genes apparently acquired during evolutionary history from bacteria, perhaps representing the legacy of ancient nematode-bacterial symbioses. These genes, many of which have seemingly obvious roles in plant-parasitism, have been amplified into families with diverse sub-specialties and at least partial redundancy. The RKN genome also includes sets of genes encoding small proteins with sequence similarity to at least three distinct classes of plant peptide hormones. Unlike the canonical plant proteins, which are expressed as pre-pro-proteins, the RKN genes encode simple pre-proteins, likely reflecting direct secretion by the nematode into the apoplast. We are using bioassays to assess the functional role of these apparent ligand mimics in the host-parasite interaction. Based on initial computational analyses it appears that these mimics may have evolved by convergent evolution. Like genes acquired horizontally, ligand mimic genes in RKN appear to be expanding and diversifying into families. Collectively, RKN genes with strong inter-kingdom analogues appear to lie at the core of the parasitic armory.

Seminar at 2pm in the Robertson Seminar Room, RSB, ANU

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