As the leader of a research team motivated by new knowledge, scientific angles and international collaborations, Dr Jeremy Murray of the John Innes Centre, UK explains why the intracellular accommodation of mycorrhiza and rhizobia within plants is something worth getting excited about.

Could you begin by briefly summarising your research project and its overall aims?

The aim of my research programme is to understand the key molecular components of the plant host during infection by rhizobia and arbuscular mycorrhiza. We are doing this by first identifying the genes involved and then studying the function of the proteins they encode.

What drew you to studying intracellular accommodation of mycorrhiza and rhizobia by plants?

I think the idea of one organism living inside another is intriguing. I want to understand how this works. During my first postdoc in Krzysztof Szczyglowski’s lab we studied alternate modes of infection by rhizobia, and we also discovered a role for the phytohormone cytokinin in nodulation; it really was an exciting time.

After that, I joined Michael Udvardi’s group where we used genomic approaches to discover Vapyrin which controls infection of both rhizobia and mycorrhiza; this discovery sparked my interest in the shared infection mechanisms of these two symbioses.

Why is it important to identify novel plant genes involved in rhizobial and arbuscular mycorrhizal fungi (AMF) invasion?

Identifying the genes involved in symbiotic infection will allow us to answer questions like, ‘How is plant development coordinated with bacterial infection?’ and ‘How do plants send signals to and receive signals from the rhizobia? Why are defence responses not triggered during infection?’. I think if we can answer these questions we will be able to improve agriculture and better understand plant-microbe interactions in general.

Could you describe the deep sequencing technologies you have used to define the ‘infectome’ or the transcriptional expression domain of infected cells?

One of the most powerful tools we have at our disposal is next-generation or deep-sequencing technologies. These technologies allow us to sequence entire plant genomes or transcriptomes in a single experiment. These can be combined with genetic studies to allow us to rapidly identify the plant genes required to establish these symbioses. One of the most exciting aspects of this technology is that it enables us to carry out genetic studies in crops and less well-studied organisms so that we are no longer limited to working with established plant model systems.

Your approach revealed many new genes whose expression increased in root hairs during infection. What is the significance of these findings?

The ability to isolate root hair cells from plants infected by rhizobia separate from other plant tissues allowed us to monitor the expression of genes that would otherwise be undetectable. With this approach we have identified several new genes involved in nodulation, and have also made some surprising connections between nodulation and the older arbuscular mycorrhizal symbiosis. We are now carrying out functional genetics studies on these genes to determine their roles.

How effective are current seed formulations or spray applications of inoculants containing rhizobia, mycorrhiza and other growth promoting microbes? In what way could your research lead to more efficient inoculants for industry?

Commercial inoculums can be more or less effective depending on their composition, what crop they are being used on, and the conditions in which the plants are grown. I am now engaged in a collaborative research project with Dr Phil Poole of the John Innes Centre (JIC) to identify the plant factors that determine successful rhizosphere colonisation. With a better understanding of the host factors that contribute to rhizosphere competitiveness it will be possible to improve inoculant formulations so that they are more robust across different environmental conditions.

Why is it beneficial for plant breeders to develop crops that mycorrhize and nodulate better?

Below-ground traits like nodulation and mycorrhization are often overlooked by plant breeders. Our understanding of the molecular-basis of these symbioses has been advancing in leaps and bounds over the last decade, but this knowledge has not yet been applied to crop improvement. Since these two symbioses have such a major impact on plant nutrient uptake, this represents a major opportunity for yield gains in many crops.
With an international outlook and a commitment to enhancing our agricultural industry, a team based in the UK is exploring the role of the protein Vapyrin in aiding symbiotic processes within the roots of plants.

**WHEN IT COMES** to maximising agricultural productivity, we are not fully utilising the knowledge to which we have access. Plant breeders have focused their attention on the yield, disease resistance and drought resistance. While these are important subjects, they are often pursued at the expense of less conspicuous traits, such as the plant nutrient uptake that results from symbiotic associations with soil microorganisms. Thankfully, a team at the John Innes Centre at the Norwich Research Park in the UK is undertaking an enthusiastic exploration of the genetic issues that significantly affect these important plant-microbe interactions.

Led by Dr Jeremy Murray, the research group focuses on topics such as nodulation and mycorrhization, shedding significant light on the role of a protein called Vapyrin in these particular interactions. Occurring as a result of symbiotic relationships, both nodulation and mycorrhization have a powerful influence over the life of plants, with Murray describing them as: “Two very widespread symbioses that are particularly important to agriculture.” With this in mind, it is clear that by gaining a greater understanding of how these processes function on a genetic level, one can learn a lot more about how to optimise crop yields. The practical implications of researching what such interactions bring are clear: “The symbiotic acquisition of nitrogen and phosphate from the environment underpins sustainable agricultural practice,” Murray states. Consequently, the researchers have developed sophisticated methods for isolation of the individual cell types involved in the process and have applied advanced techniques to study gene expression in these cells.

**STUDYING THE BAD WITH THE GOOD**

The work at Norwich’s John Innes Centre addresses a number of clear gaps in scientific knowledge. The first concerns how symbiosis functions on a molecular level. Most research on plant-microbe interactions has centred on pathogens which engage in an ‘arms race’ with the host. By studying beneficial interactions with microbes, Murray’s team gains a unique perspective on plant-microbe interactions. “In a symbiotic interaction the plant has to open all the doors that must normally be kept shut to pathogens. Some pathogens have learned tricks to open these doors,” he observes. To exploit this knowledge, Murray has entered into collaboration with Dr Sebastian Schornack, who has just taken up a position at the new Sainsbury Laboratory, University of Cambridge, to study a pathogen that shares some features of infection with arbuscular mycorrhiza. It is Murray’s wholehearted belief that studying these systems collaboratively will harness a better understanding of both these types of interactions.

**LESSONS FROM LUPINS**

In order to further broaden their knowledge of the two symbiotic processes, Murray’s team intends to look beyond the model systems to other plant species. Certain members of the lupin family of legumes have proved to be particularly interesting, with unusual features that may provide new insights into the evolution of nodulation. Murray and his colleagues have noted that, unlike most other legumes, some lupins do not get infected through their root hairs and also do not support mycorrhizal infection. The researchers have inferred that these lupins must lack one or more of the shared genes necessary for rhizobial and mycorrhizal infection. They have interpreted this as a clue that will help to solve a larger mystery by helping to pinpoint the facilitating elements that are necessary for both symbioses. While Murray admits that this mystery is still unsolved, he expects that emerging data, the sequencing of the lupin genome, will lead to breakthroughs in this area.

Just as the behaviour of lupin legumes brings Murray’s team closer to fully mapping out legume evolution, studies of mutants with defects in infection, such as the *vapyrin* mutant, have enabled the group to develop their studies of standard cell behaviour. For instance, insights into the early stages of infection will be gained from a mutant recently discovered by the Murray group. While in this case the specific gene involved is yet to be identified, the discovery has enabled the team to explore the interdependent nature of infection and nodule organogenesis.

**A COLLABORATIVE APPROACH**

Fittingly, in a study of symbiosis, Murray’s group thrives on collaboration. One of the most recent achievements resulted from work with Dr Michael Udvardi’s group at the Samuel Roberts Noble Foundation, Oklahoma. Working alongside the American team, researchers in Norwich identified a gene necessary for the infection thread formation that
JOEY MURRAY received his PhD from the University of Guelph (Guelph, Canada) in the lab of Dr K Peter Pauls, followed by postdoctorate positions in the labs of Krzysztof Szczyglowski (London, Canada), and Michael Udvardi (Ardmore, USA). He now holds a David Phillips Fellowship at the John Innes Centre (Norwich, UK).

INTRODUCTION

INTRACELLULAR ACCOMMODATION OF MYCORRHIZA AND RHIZOBIA BY PLANTS: MOLECULAR MECHANISMS AND EVOLUTION

OBJECTIVES

To understand the role of the Vapyrin protein in symbiotic interactions by identifying interacting proteins and studying its subcellular localisation during different stages of arbuscular mycorrhizal and rhizobial infections.

KEY COLLABORATORS

Dr Michael Udvardi, Dr Kiran Mysore, Dr Ji He, The Samuel Roberts Noble Foundation (USA) • Dr Joëlle Fournier, Dr Fernanda de Carvalho-Niebel, Dr Andreas Niebel, Laboratoire des Interactions Plantes Micro-Organismes, CNRS-INRA (France) • Dr Giles Oldroyd, Dr Allan Downie; Dr Phil Poole; Dr Tony Miller; Dr Andrew Breakspear; Dr Chengwu Liu; Dian Guan; Donna Cousins; Kirsty Jackson; Sonali Roy; John Innes Centre, (UK) • Dr Sebastian Schornack, Sainsbury Laboratory Cambridge, (UK).

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As the work at the John Innes Centre is conducted by an enthusiastic, dedicated team, it is encouraging to see that Murray has articulated firm plans to continue developing his research.