Genetic basis of non-host disease resistance

Plant immunity against the majority of microbial pathogens is conveyed by a phenomenon known as non-host resistance (NHR) (Heath, 2000). This defence mechanism affords durable protection to plant species against given species of pathogens. This contrasts with the well-studied host resistance, mediated by the products of plant resistance (*R*) genes, which establish pathogen race- or cultivar-specific resistance. Whereas NHR routinely provides durable crop protection in the field, the effectiveness of host-resistance is characteristically transient.

The broad-spectrum nature of NHR closely parallels that exhibited by the innate immune system of animals. NHR, however, has proved difficult to characterise as a result of the absence of a tractable genetic system. It is thought to be genetically complex, involving the deployment of both constitutive and inducible defence responses, in combination with a host physiology that may be routinely incompatible with pathogenesis.

To initiate the genetic dissection of NHR we have developed a pathosystem employing the wheat powdery mildew pathogen, *Blumeria graminis* f.sp. *tritici* (*Bgt*) and the model plant species, *Arabidopsis thaliana* (Yun et al. 2003). Work in our laboratory has shown that NHR against *Bgt* is established via a sequential series of defence responses which are deployed at specific steps during attempted *Bgt* infection. Furthermore, we have discovered that by simultaneously disabling key plant defence responses *Arabidopsis* can support the growth and asexual reproduction of *Bgt*, despite a divergence time of approximately 150 million years between wheat and *Arabidopsis*. Therefore, effective defence responses rather than an incompatible cellular physiology may protect plants against pathogens that characteristically colonise distantly related host species.
3-D confocal imaging showing bilateral haustorium and secondary hyphae of *Blumeria graminis f.sp tritici* on *eds1* cytochalasin E treated *Arabidopsis* plants.

Network of hyphae produced by *Blumeria graminis f.sp tritici* on *Arabidopsis eds1* plants.

To further uncover the genetic basis of NHR we have initiated an extensive gene discovery programme utilising forward and reverse genetics and exploiting natural variation. For example, forward screens have identified a novel series of NHR mutants by exploiting a luciferase imaging approach. The isolation and characterisation of uncovered genes will provide significant insights into the genetic basis of non-host resistance, which may have significant agricultural utility in the rationale design of crops expressing durable disease resistance.

**References**
