

ing similarities between the molecular organization of animal and plant systems for non-self recognition and antimicrobial defence. Like animals, plants have acquired the ability to recognize invariant pathogen-associated molecular patterns (PAMP) that are characteristic of microbial organisms, but which are not found in potential host plants. PAMPs that trigger innate immune responses in various vertebrate and non-vertebrate organisms include peptidoglycans (PGN) from Gram-positive bacteria, lipopolysaccharides from Gram-negative bacteria, eubacterial flagellin or fungal cell wall-derived glucans, chitins, mannans and proteins.

PGNs which are located on the surface of virtually all bacteria constitute excellent targets for recognition by the innate immune system. In animals PGN is recognised via the plasma membrane-located toll-like receptor 2 (TLR2) and the cytoplasmic receptors Nod1 and Nod2. Our data provide evidence that PGN mediates the activation of innate defence responses in the model plant *Arabidopsis thaliana*. Treatment with PGN from the phytopathogenic Gram-positive bacterium *Staphylococcus aureus* results in an induction of typical plant defence responses, such as medium alkalization, NO-production and activation of MAPKs. Moreover, microarray analysis (ATH1 chip) performed with RNA prepared from PGN-treated *Arabidopsis* leaves revealed enhanced (>2-fold) transcript levels for approximately 240 genes, many of which are also altered upon administration of the well characterized PAMP flagellin.

#### PS 6-328

##### CHARACTERISATION OF *BDPH1*, A MEMBRANE LOCALISED RECEPTOR LIKE PROTEIN INVOLVED IN BASAL DEFENCE OF *ARABIDOPSIS THALIANA*

Benjamin KEMP<sup>1</sup>, Kathy MITCHELL<sup>2</sup>, Alec FORSYTH<sup>2</sup>, Volkan ÇEVİK<sup>1</sup>, Bart THOMMA<sup>3</sup>, Eric HOLUB<sup>1</sup>, John MANSFIELD<sup>2</sup> and Mahmut TÖR<sup>1</sup>

<sup>1</sup>Warwick HRI, University of Warwick, Wellesbourne, Warwick CV35 9EF, UK. <sup>2</sup>Imperial College at Wye, Wye, Ashford, Kent TN25 5AH, UK <sup>3</sup>Wageningen University, P.O. Box 8025 6700 EE Wageningen, The Netherlands

Basal defence against bacterial pathogens of plants is orchestrated by the perception of Microbe Associated Molecular Patterns (MAMPs) such as the conserved subunits of bacterial flagellin, the flg22 peptide and elongation factor EF-Tu. Plant cells perceive and respond to MAMPs using membrane bound Toll-related receptors including extracellular LRR containing receptor-like proteins (RLPs) and receptor-like kinases (RLKs). There are 56 RLP encoding genes in *Arabidopsis* and we have identified homozygous T-DNA insertion lines for each of these genes in the Columbia background. *BDPH* (basal defence against *Pseudomonas syringae* pv. *phaseolicola*) gene family were revealed from screening these T-DNA insertion lines with the bacterial pathogen of bean, (*P. s. pv. phaseolicola*) which fails to multiply in *Columbia*. Col-*bdph1* support a high level of bacterial growth compared to wild type, still perceives flg22, thus *BDPH1* is likely to detect a different MAMP from *P. s. phaseolicola*. *BDPH1* is predicted to be a 87 kDa protein with a signal peptide, a region of Leucine Rich Repeats, a single transmembrane domain and a short (25 amino acid) cytoplasmic tail. When fused to YFP *BDPH1* localises to the plasma membrane in transgenic *Arabidopsis* plants.

#### PS 6-329

##### ANALYSIS OF PEN2-MEDIATED PATHOGEN ENTRY CONTROL IN *ARABIDOPSIS* NONHOST RESISTANCE TO FUNGAL PATHOGENS

Christine KUHNS, Rene FUCHS, Volker LIPKA

The Sainsbury Laboratory, John Innes Centre, Colney, Norwich, NR4 7UH, UK

Nonhost resistance describes the immunity of an entire plant species against all genetic variants of a particular parasite and represents the most robust and durable plant disease resistance type in nature. Recently, three molecular components of *Arabidopsis* nonhost resistance, *PENETRATION 1* (*PEN1*), 2 and 3 were identified which control entry success of non-adapted fungal pathogens into epidermal leaf tissue (Collins et al., 2003; Lipka et al., 2005; Stein et al., 2006). The *PEN2* gene encodes one out of 47 predicted *Arabidopsis* family 1 glycosyl hydrolases (FIGHs). FIGHs are required for the catalytic activation of small molecules from inactive glycosidic precursor metabolites. Phylogenetic analyses suggest that *PEN2* forms a monophyletic side branch with 9 other *Arabidopsis*-FIGHs and represents an evolutionarily recent acquisition of the *Arabidopsis* genome. To assess functional diversification within the *PEN2*-FIGH subfamily we are currently conducting reverse genetics and complementation experiments with transcriptional and structural chimeras. On the protein sequence level *PEN2* exhibits a unique C-terminal extension which is required for protein function in nonhost resistance. Transgenic expression of functional GFP-fusions revealed an association of *PEN2* with (possibly functionally specialized) peroxisomes, which are subject to pathogen-induced cell polarisation. To address the question which intrinsic structural features are required for *PEN2* function and subcellular localisation we are employing site directed mutagenesis and expression of truncated variants. This approach is complemented by experiments aiming at isolation of putative *PEN2* protein interactors by means of Y2H and pull down assays. Moreover, we are developing strategies for the isolation of *PEN2*-decorated peroxisome (sub-) populations from pathogen-challenged and non-challenged leaf tissue which will subsequently be used for comparative organelle proteomics. Together these strategies will help to understand the exact biological role and mode(s) of action of *PEN2*.

#### PS 6-330

##### EXOCYTOSIS-MEDIATED NON-HOST RESISTANCE TO FUNGAL PARASITES IN *ARABIDOPSIS*

Chian KWON<sup>1</sup>, Hye Sup YUN<sup>1</sup>, Volker LIPKA<sup>2</sup>, Christina NEU<sup>1</sup>, Simone PAJONK<sup>1</sup> and Paul SCHULZE-LEFERT<sup>1</sup>

<sup>1</sup>Department of Plant Microbe Interactions, Max-Planck Institute for Plant Breeding Research, D-50829, Cologne, Germany; <sup>2</sup>Sainsbury Laboratory, John Innes Centre, Norwich Research Park Colney Lane, Norwich NR4 7UH, UK.

Plants and phytopathogens have co-evolved and elaborated multiple defense and counter-defense systems, respectively. We have previously identified *PEN1*, a syntaxin, as key component in *Arabidopsis* non-host resistance to parasitic powdery mildew fungi. *PEN1* becomes focally concentrated in lipid raft-like plasma membrane microdomains at fungal entry sites. However, its exact function is unclear since *NtSyr1*, a tobacco homolog of *PEN1*, has been implicated in ABA signaling. Here we report how *PEN1* acts in immune responses to attack by the non-adapted powdery mildew, *Blumeria graminis*. *PEN1* interacts with synaptosome-associated protein 33 (SNAP33),