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Distinct branches of the N-end rule pathway modulate the plant immune response

Jorge Vicente1, Guillermina M. Mendiondo1, Jarne Pauwels2,3, Victoria Pastor4, Yovanny Izquierdo5, Christin Naumann6,7, Mahsa Movahedi8, Daniel Rooney1, Daniel J. Gibbs1, Katherine Smart9, Andreas Bachmair10, Julie E. Gray8, Nico Dismeyer6,7, Carmen Castresana5, Rumiana V. Ray1, Kris Gevaert2,3 and Michael J. Holdsworth1

1School of Biosciences, University of Nottingham, Nottingham, LE12 5RD, UK; 2VIB-UGent Center for Medical Biotechnology, Albert Baertsoenkaai 3, B-9000 Ghent, Belgium; 3Department of Biochemistry, Ghent University, Albert Baertsoenkaai 3, B-9000 Ghent, Belgium; 4Area de Fisiología Vegetal, Departamento de Ciencias Agrarias y del Medio Natural, Universitat Jaume I, Castellón E-12071, Spain; 5Centro National de Biotecnología CSIC, C/Darwin, 3, Campus de Cantoblanco, E-28049 Madrid, Spain; 6Leibniz Institute of Plant Biochemistry (IPB), Weinberg 3, D-06120 Halle (Saale), Germany; 7Science Campus Halle – Plant-Based Bioeconomy, 06120 Halle (Saale), Germany; 8Department of Molecular Biology and Biotechnology, University of Sheffield, Sheffield, S10 2TN, UK; 9SABMiller Plc, SABMiller House, Church Street West, Woking, GU21 6HS, UK; 10Department of Biochemistry and Cell Biology, Max F. Perutz Laboratories, University of Vienna, Dr. Bohr Gasse 9, Vienna A-1030, Austria

Authors for correspondence: Michael J. Holdsworth
Tel: +44 1159516046
Email: michael.holdsworth@nottingham.ac.uk

Jorge Vicente
Tel: +44 1159516046
Email: Jorge.Vicente_Conde@nottingham.ac.uk

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Introduction

The regulation of protein stability through the ubiquitin proteasome system (UPS) is a central component of cellular homeostasis, environment interactions and developmental programmes (Varshavsky, 2012), and an important component of the plant immune system (Zhou & Zeng, 2017). Plants have evolved to recognize the presence of a pathogen in two main ways. Basal (primary) defence is characterised by the recognition of pathogen elicitors called pathogen associated molecular patterns (PAMPs) by protein receptors known as pattern recognition receptors (PRR), activating PAMP-triggered immunity (PTI) (Boller & Felix, 2009). When this response is effective, pathogens can deliver effector molecules into the host cells to weaken PTI and facilitate infection triggering a second layer of defence (effector triggered immunity; ETI). ETI is typically a qualitative response based on interference with pathogen effector activity by plant resistance (R) gene products, localized inside the cell (Dangl & Jones, 2001). Both PTI and ETI induce similar immune responses but of different amplitude, with ETI often resulting in a hypersensitive response (HR). The specific set of mechanisms activated also depend to a large extent on the life strategy of the pathogen and how adapted they are to the host. Typically, the plant hormones jasmonic acid (JA) and ethylene (ET) mediate responses to nonadapted necrotrophs that cause host cell death to acquire nutrients from dead or senescent tissues (Grant & Jones, 2009; Pieterse et al., 2009) whilst salicylic acid (SA) plays a crucial role in activating defence against adapted biotrophs and hemibiotrophs. Recently, regulation of protein stability by the Arg/N-end rule pathway of ubiquitin-mediated proteolysis has been demonstrated to play a role in plant responses to biotic stress. The pathway is associated with increased development of...
clubroot caused by the obligate biotroph *Plasmodiophora brassicae* (Gravot et al., 2016). Induction of components of the hypoxia response, controlled by Group VII ETHYLENE RESPONSE FACTOR (ERFVII) transcription factor substrates (ERFVIIs), enhanced clubroot development, indicating that the protist hijacks the N-end rule ERFVII regulation system to enhance infection. In another study, inactivation of different components of the Arg/N-end rule pathway was shown to result in greater susceptibility of Arabidopsis to necrotrophic pathogens and altered timing and amplitude of response to the hemibiotrophic *Pseudomonas syringae* pathovar *tomato* (*Pt*) AvrRpm1 (de Marchi et al., 2016). A correlation between Nt-Acetylation and the stability of a Nod-like receptor, Suppressor of NPR1, Constitutive 1 (SNC1) was also reported (Xu et al., 2015). Whilst these reports provide evidence that the N-end rule pathway is involved in the regulation of plant defence responses, the mechanisms, substrates or their function in resistance have not been investigated previously (Gibbs et al., 2014a). The N-end rule pathway of ubiquitin-mediated proteolysis is an ancient and conserved branch of the UPS (Gibbs et al., 2014a). This pathway relates the half-life of substrates to the amino-terminal (Nt-) residue, which forms part of an N-degron (Gibbs et al., 2014a). Destabilizing residues of the Arg/N-end rule are produced following endo-peptidase cleavage and may be primary, secondary or tertiary (Fig. 1a). Basic and hydrophobic primary destabilizing residues are recognized directly by N-recognin E3 ligases, in plants represented by two proteins, PROTEOLYSIS(PRT)6 and PRT1 (Gibbs et al., 2014a). Secondary destabilizing residues (Glu, Asp and oxidized Cys) can be N-terminally arginylated by arginyl-transferases (ATEs), and tertiary destabilizing residues (Gln, Asn and Cys) can undergo modifications to form secondary destabilizing residues (Gibbs et al., 2014a). Oxidation of Cys was shown in *vitro* to occur both nonenzymically (Hu et al., 2005) or enzymatically (Weits et al., 2014; White et al., 2017), whereas in higher eukaryotes deamidations of Gln and Asn are carried out by residue-specific N-terminal amidases (NTAQ1 (Wang et al., 2009) and NTAN1 (Grigoryev et al., 1996), respectively). This hierarchical structure is conserved in eukaryotes, and physiological substrates with N-terminal residues representing these destabilizing classes have been identified (Piatkov et al., 2014). The Usp1 deubiquitylase is targeted for degradation through the deamidation branch of the Arg/N-end rule via NTAQ1 as a consequence of auto-cleavage, that reveals N-terminal Gln (Piatkov et al., 2012). Proteins with similarities to mouse NTAN1 and NTAQ1 are encoded in higher plant genomes, in Arabidopsis by AT2G44420 (putative NTAN1) and AT2G41760 (putative NTAQ1). Expression of these in a deamidation deficient *Saccharomyces cerevisiae* could functionally restore degradation of the N-end rule reporters Asn-β-galactosidase (β-Gal) and Gln-β-Gal, respectively. ATE activity was required for this destabilization in yeast (Graciet et al., 2010). Although the Arg/N-end rule pathway is evolutionarily highly conserved in eukaryotes, few substrates or functions for different branches have been shown. In plants the Cys branch of the Arg/N-end rule pathway controls homeostatic response to hypoxia (low oxygen) and NO sensing through the Met-Cys initiating ERFVII transcription factor substrates (Gibbs et al., 2011, 2014b; Licausi et al., 2011).

In this paper, we investigated the role of distinct branches of the Arg/N-end rule pathway in the immune response in Arabidopsis and barley (*Hordeum vulgare*). We demonstrate that two branches of the pathway, Glu-deamidation and Cys-oxidation, regulate resistance to the hemibiotroph *Pst* and the biotroph *Blumeria graminis* f. sp. *hordei* (*Bgh*). We also show a significant role for Nt-Gln amidase NTAQ1 in the regulation of molecular components associated with basal responses to infection, and a role for both NTAQ1 and the known Nt-Cys ERFVII substrates in resistance related to stomatal function.

### Materials and Methods

**Plant material, growth conditions and experimental design**

*Arabidopsis thaliana* seeds were obtained from NASC, UK unless otherwise stated, including *pro6-1* (SAIL 1278_H11), *ntaq1-1* (SALK_075466), Mutant *ntan1-1* (Q202* mutation (CAA to TAA)) was obtained from the Seattle TILLING project (http://tilling.fhcrc.org). Mutant *ntaq1-3* was obtained from the GABI-Kat T-DNA insertion collection (GK_306F08). The *pad3-1* null allele was described previously (Glazebrook & Ausbel, 1994). Mutants are in the Col-0 (wild type, WT) accession. Plants were grown and assayed performed in controlled-environment rooms under the following conditions: 12 h of light (23°C) and 12 h of dark (18°C), 60–70% relative humidity. Plants were treated between 3 and 4 wk after germination. barley plant genotypes and growth conditions were as previously described (Mendiondo et al., 2016).

**Construction of transgenic Arabidopsis lines ectopically expressing NTAQ1**

To generate Arabidopsis NTAQ1 overexpressing lines, full-length cDNA sequence (with and without the STOP codon) was amplified from 7-d-old seedling cDNA and recombined into pDONR221. The constructs were mobilized into *Agrobacterium tumefaciens* C58C1 (pSoup) containing the binary vector pH7m34G, pH7m34G*, expressing the rhino tag (strain GV3101 pMP90) and Arabidopsis *ntaq1-3* using standard protocols (Clough & Bent, 1998).

**In vitro assay for NTAQ1 activity**

The Arabidopsis NTAQ1 coding sequence was cloned from cDNA and flanked by an N-terminal tobacco etch virus (TEV) protease recognition sequence (ENLYFQ-X) using primers *ss_ntaq1_te* and *as_ntaq1_g*, followed by a second PCR with *as_ntaq1_g* and adapter tev attaching a Gateway attB1 site for sub-cloning into pDONR201 (Invitrogen). An LR reaction into pVP16 (*Thao et al., 2005*) leads to an N-terminal 8xHis:MBP double affinity tag. An assay for NTAQ1 activity was performed as described previously (Wang et al., 2009) with slight modifications. The assay was performed in three technical replicates from three

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independent NTAQ1 protein expressions. The activity of NTAQ1 towards QKGSGAW was used as the 100% reference value.

Analysis of pathogen growth in plant material
The bacterial suspension was injected with a needleless syringe into the abaxial side of leaves or sprayed on the surface of the leaves of 3.5-wk-old plants. *Pst* DC3000 *avrRpm1*, *Pst* DC3000 and *Pst* DC3000 *hrpA−* were grown overnight at 28°C in Petri dishes on King’s B medium. For analysis of bacterial growth, three leaves per plant of at least seven plants were injected with a bacterial suspension of $10^6$ CFU ml$^{-1}$ (OD$_{600}$ nm 0.1 = $10^8$ CFU ml$^{-1}$) or sprayed with a suspension of $10^8$ CFU ml$^{-1}$. A disc of 0.28 cm$^2$ from each infected leaf was
excised at 96 h, pooled in triplicate, homogenized, diluted and plated for counting. Inoculation of *Botrytis cinerea* was performed by pipetting a drop of 10 μl of a suspension of 5 × 10^7 spores ml⁻¹ onto the surface of the leaves. The response was analyzed by measuring the diameter of the symptoms produced in three leaves of at least 20 independent plants.

Barley plants were infected with *Fusarium* spp. and *Blumeria graminis* f. sp. *hordei* as previously described (Ajigboye et al., 2016). Leaf material of 25-d-old barley plants grown under controlled conditions (20°C: 15°C; 16-h photoperiod; 80% RH, 500 μmol m⁻² s⁻¹ metal halide lamps (HQL) and supplemented with tungsten bulbs) were syringe infiltrated with 0.1 OD 910°C of a suspension of *Pseudomonas syringae pv. tomato* DC3000 (AT2G41760) (Fig. S1a). Bacterial growth in leaves of DC3000 pv *tomato* DC3000 and T-DNA insertion null mutants of the putative Gln-specific amino-terminal amidase NTAQ1 (AT2G41760) (Fig. 1a) was visualized by staining with 3,3′-diaminobenzidine tetrachloride as described (Thordal-Christensen et al., 1997; Moreno et al., 2005).

**Stomatal aperture analyses**

For stomatal aperture in response to *Pst* assays, leaves from 3.5-wk-old plants were used. In the morning after 2 h the lights were switched on and peels from the abaxial side of the leaves were placed in Petri dishes containing 10 mM MES/KOH pH 6.1, 50 mM KCl and 0.1 mM CaCl₂ for 2 h in continuous light. Then the buffer was replaced with a solution of *Pst* DC3000 (OD 0.2: 2 × 10⁹ CFU ml⁻¹). Stomatal aperture was measured after 0, 1 and 3 h of incubation with the bacteria. Stomatal aperture measurements for ABA sensitivity assays were carried out on detached leaf epidermis as described previously (McAinsh et al., 1991; Chater et al., 2011).

**Protein extraction and Immunoblotting**

Protein extractions and immunoblotting were carried out as described previously (Gibbs et al., 2011).

**Gene expression analysis**

RNA extraction, cDNA synthesis, semiquantitative and quantitative RT-PCR were performed as previously described for Arabidopsis (Gibbs et al., 2011, 2014b) and barley (Mendiondo et al., 2016). For primers used see Supporting Information Table S1.

**Analysis of nitrate reductase activity**

Nitrate reductase was assayed as previously (Vicente et al., 2017) with modifications described elsewhere (Kaiser & Lewis, 1984).

**Analysis of protein, RNA and metabolites**

Protein extraction, immunoblotting and histochemistry were carried out as described previously (Gibbs et al., 2011). Quantitative RT-PCR was performed as previously described for Arabidopsis (Gibbs et al., 2014b) and barley (Mendiondo et al., 2016). Proteomics (Vu et al., 2016) and metabolomics (Gamir et al., 2012; Sánchez-Bel et al., 2018) analyses were carried out as previously described.

**Experimental statistical analyses**

All experiments were performed at least in triplicate. Statistical comparisons were conducted using GraphPad Prism 7.0 software. Horizontal lines represent standard error of the mean values in all graphs. For statistical comparisons we used Student’s t-test, where statistically significant differences are reported as: ***, P<0.001; **, P<0.01; *, P<0.05; and one-way analysis of variance (ANOVA) with Tukey’s multiple comparisons test, where significant differences (α<0.05) are denoted with different letters.

**Results**

Nt-Gln amidase and Cys oxidation branches of the Arg/N-end rule pathway increase basal resistance against *Pst* DC3000

The role for the Arg/N-end rule pathway in the plant immune response was assessed using the model bacterial pathogen *P. syringae pv. tomato* DC3000 and T-DNA insertion null mutants of the putative Asn-specific amino-terminal amidase NTAQ1 (AT2G41760) (Fig. 1a–d) and N-recognin E3 ligase PRT6 (AT5G02310) genes, and a premature termination allele of the putative Asn-specific amino-terminal amidase NTAN1 (AT2G44420) (Q202*) (Fig. 1a). The entire effect of NTAQ1, NTAN1 and Cys branches of the Arg/N-end rule pathway on response to pathogen challenge can be assessed by analysis of the *prt6* mutant, as this removes E3 ligase activity, thus stabilizing all substrates of NTAQ1, NTAN1 and substrates with Nt-Cys (Fig. 1a). Bacterial growth in leaves of *prt6* was significantly lower by 4 d post-infiltration with virulent (*Pst* DC3000) or avirulent (*Pst* DC3000 *avrRmp1*) strains, indicating that substrates destabilized by PRT6 action contribute to the immune response (Figs 1b, S2a). In comparison, *ntaq1* alleles also showed significantly lower bacterial growth (comparable with that of *prt6*) compared with both the *ntan1*-1 mutant or the wild type (WT) Col-0 for plants grown from seed in soil under neutral days (12 h : 12 h, light : dark). These results are opposite to those obtained by de Marchi et al. (2016), who found enhanced sensitivity to *Pst* DC3000 of N-end rule mutants *prt6* and *ate1 ate2* (which removes ATE Nt-arginylation activity, Fig. 1a). To investigate this difference, we assayed bacterial growth under conditions used by de Marchi et al. for plant growth and infection. In their case, germination and initial 7 d growth of seedlings was carried out on agar containing MS medium and 0.5% sucrose before transfer to soil and, following transfer, plants were grown under short-day conditions (9 h : 15 h, light : dark). We grew Col-0, *prt6* and *ate1 ate2* under these conditions and assayed bacterial growth at 2 d and 4 d post-infiltration. For plants grown under neutral days, we found that by 4 d post-infection, bacterial growth was significantly lower in N-end rule mutants than in the
WT (Fig. S2b). All subsequent reported experiments were carried out using plants grown from seed under neutral-day conditions.

Tissue cellular leakage measured 4 d following infection was significantly lower in prt6 and ntaq1 mutants (Figs 1c, S1d). Expression in WT of NTAQ1 and PRT6 was not strongly affected by infection with either bacterial strain (Fig. S2c). Inoculation with the PTI inducer Pst DC3000 hrpA- (with a compromised type-three secretion system), resulted in reduced susceptibility of prt6 and ntaq1 mutants compared with WT or ntaq1 (Fig. 1d). Ectopic expression of either N- or C-terminally tagged NTAQ1 removed enhanced resistance of ntaq1-3 (Fig. 1e), and the double mutant prt6-1 ntaq1-3 did not show significant difference compared with the single mutants prt6-1 or ntaq1-3 (Fig. 1f). It was previously suggested that formation of N-terminal pyroglutamate by glutaminyl cyclase (GC) might compete with NTAQ1 for Nt-Gln substrates (Wang et al., 2009), implying that a lack of GC activity could lead to enhanced susceptibility. We observed a similar response to Pst DC3000 of WT and a mutant of GLUTAMINYL CYCLASE1 (GC1) (Schilling et al., 2007) (Fig. S2d), indicating that competition for Nt-Gln substrates between NTAQ1 and GC1 is not relevant for the regulation of bacterial growth following infection.

To define the biochemical action of NTAQ1, we analysed the Nt-deamidation capacity of recombinant Arabidopsis NTAQ1 that showed high specificity for Nt-Gln in comparison with Nt-Asn, -Gly and -Lys (Fig. 1g).

![Graphical representation of data](image-url)

**Fig. 2** Genetic characterization of the role of the N-end rule pathway in the Arabidopsis stomatal response to Pst DC3000. (a-d) Quantification of Pst DC3000 growth in wild type (WT) and mutant plants 4 d after bacterial infiltration by injection (10^6 colony forming units (CFU) ml^-1) or bacterial foliar spray application (10^6 CFU ml^-1). (c) Stomatal aperture response to applied Pst DC3000 in WT and mutants. (e) Total NR enzyme activity following foliar application of Pst DC3000 (10^6 CFU ml^-1). (f) Expression of NIA1 and NIA2 RNA following leaf infiltration with Pst DC3000. (g) Stabilisation of C^4H^4GUS protein and expression of MC^4H^4GUS and ACTIN RNA in WT Arabidopsis plants sprayed with Pst DC3000 (10^6 CFU ml^-1). (h) Stabilisation of C^4H^4GUS 24 h after injection with flg22 (1 µM) or H_2O. CBB, Coomassie Brilliant Blue. Data represent means ± SEM. Statistical differences were analyzed by ANOVA followed by Tukey test (* P < 0.05), significant differences are indicated with letters, or Student’s t-test: * P < 0.05; ** P < 0.01; *** P < 0.001.
Using mutants in which ERFVII activity was removed (Abbas et al., 2015) (rap2.12 rap2.2 rap2.3 bre1 bre2 pentuple mutant, hereafter erfVII, and the prt6 erfVII sxtuple mutant), analysis of infections of Pst DC3000 following infiltration showed no significant influence of ERFVIIIs in affecting apoplastic growth of either virulent or avirulent Pst strains (Figs 2a, S3a). Bacterial growth 4 d following foliar spray application of Pst DC3000 revealed greater resistance of both prt6-1 and ntaq1-3 mutants compared with WT or ntaq1-1 (Figs 2b, S3b), which for both foliar spray and injection required SA, analysed in double mutant combinations of prt6-1 or ntaq1-3 with sid2-1. SID2 is an isochorismate synthase required for SA synthesis (Nawrath & Metraux, 1999) (Fig. S3c). Stomatal closure is a key component of early defence response following pathogen attack (Arnaud & Hwang, 2015). We found that, in response to Pst, WT initially closed and then, induced by the pathogen, reopened its stomata, as did prt6-1 and ntaq1-3. The erfVII and prt6 erfVII mutants failed to close stomata at any point (Fig. 2c). ERFVIIIs have previously been shown to regulate stomatal ABA sensitivity via the N-end rule pathway (Vicente et al., 2017), and we also found ntaq1-3 stomata were hypersensitive to ABA (Fig. S3d). In response to Pst DC3000 infection following foliar spray application, resistance was significantly lower in the absence of ERFVII transcription factors (either erfVII or prt6 erfVII) compared with WT or prt6 (Fig. 2d), respectively. Response to the foliar spray application of Pst DC3000 was associated with a large decrease in activity and expression of NITRATE REDUCTASE (NR) (Fig. 2e,f). This reduction has been previously linked with increased basal resistance against Pst (Park et al., 2011), whereas expression of ADH1, a marker for hypoxia, was only increased immediately following pathogen challenge (Fig. S3e). Infection with Pst DC3000 was associated by 24 h with increased stabilization of an artificial Cys-Arg/N-end rule substrate derived from the construct 35S:MC-1HA-GUS, that following constitutive MetAP activity is expressed as C-1HA-GUS (Gibbs et al., 2014b; Vicente et al., 2017) (Fig. 2g). To clarify whether plant-derived factors were solely responsible for the control of the stability of C-1HA-GUS, we injected the PAMP peptide flg22, and showed that injection of flg22 was able to stabilize C-1HA-GUS (Fig. 2h).

The Arg/N-end end rule pathway has a conserved function in the immune response

To determine the conservation of Arg/N-end rule pathway role in the immune response, we tested responses to pathogens in barley, a monocot species distantly related to Arabidopsis, in which the expression of the PRT6 orthologue gene HvPRT6 was reduced by RNAi (Mendiondo et al., 2016). Following inoculation with a strain of P. syringae pv japonica with known pathogenicity to barley (Dey et al., 2014), significantly lower bacterial load was observed in HvPRT6 RNAi leaves compared with the WT (Fig. 3a). Similarly, HvPRT6 RNAi plants exhibited reduced development and severity of mildew caused by Bgh (Fig. 3b,c). By contrast, susceptibility of HvPRT6 RNAi to Fusarium graminearum or F. culmorum, tested on detached leaves was increased compared with the WT (Fig. 3d). To assess the response of prt6-1 in Arabidopsis to a necrotroph we inoculated the mutant and WT with the fungal pathogen B. cinerea but we failed to observe any significant differences in disease severity, measured as diameter of necrotic lesions (Fig. S3f). Infection of barley with Ps pv japonica or Bgh also resulted in accumulation of the artificial Nt-Cys substrate CGGAIL-GUS (from pUBI-MCGGAIL-GUS, containing the first highly conserved seven residues of ERFVIIIs; Gibbs et al., 2014b; Mendiondo et al., 2016; Vicente et al., 2017), therefore Nt-Cys stabilization in response to infection is conserved in flowering plants (Fig. 3e).

NTAQ1 regulates expression of the camalexin biosynthesis pathway

A shotgun proteomic analysis of total proteins from untreated ntaq1-3 and WT adult leaves revealed 13 proteins which were significantly differentially regulated, 12 exhibited increased and one decreased abundance in ntaq1-3 (Table S2). The functions of most ntaq1 upregulated proteins are related to oxidative, biotic and abiotic stresses, including a 2-OXOGLUTARATE OXYGENASE (AT3G19010) potentially involved in quercetin biosynthesis and targeted by bacterial effectors (Truman et al., 2006) and DJ-1 protein homolog E (DJ1E) involved in response to PAMPs (Lehmeier et al., 2016). Not all ntaq1 upregulated proteins were also upregulated at the level of RNA (Fig. S4). Several ntaq1 over-accumulated proteins are involved in the regulation of reactive oxygen species (ROS). However, analysis of gene expression of a ROS accumulation marker, the antioxidant enzyme CATALASE1 (CAT1), and histochemical analysis of the accumulation of the ROS hydrogen peroxide (H2O2) during infections with Pst failed to reveal significant differences between the mutants ntaq1 and prt6 and WT (Fig. S5). Increased tolerance of the mutants which was associated with less cellular damage required SID2, an isochorismate synthase required for SA synthesis (Nawrath & Metraux, 1999), as double mutant combinations of prt6-1 or ntaq1-3 with sid2-1 showed susceptibility similar to the sid2-1 single mutant (Fig. S3c). Analysis of phytohormone levels indicated that there were no differences between ntaq1-3, prt6-1 or WT in untreated or infected leaves for SA, JA or IAA (Figs 4, S6). These results together suggest a functional redundancy of ntaq1 upregulated proteins with other antioxidant mechanisms, already documented in the case of the GLUTATHIONE S-TRANSFERASEs (GSTs) (Sappl et al., 2009), or alternative roles for ntaq1 upregulated proteins in plant defence.

One of the identified proteins upregulated in ntaq1, the phi class GSTF6, functions in secondary metabolism related to the synthesis of the major Arabidopsis phytoalexin, camalexin (Su et al., 2011), as do the upregulated proteins PUTATIVE ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (involved in the synthesis of the camalexin precursor tryptophan; Zhao & Last, 1996) and IAA-AMINO ACID HYDROLASE (ILL4), that generates indole-3-acetic acid (IAA) from its conjugated form (Davies et al., 1999). Another upregulated protein, GSTF7 was hypothesized to play a role in camalexin synthesis based on its induction in the constitutively active MKK9 mutant.
Our analysis of previously published transcriptome data (de Marchi et al., 2016) comparing gene expression in *ate1 ate2* with WT, and comparing gene expression during *Pst* infection in Col-0 and *ate1 ate2* also showed increased expression of RNAs encoding camalexin synthesis genes (Tables S3, S4). Analysis of transcript expression indicated greater accumulation for most genes of camalexin synthesis in mature uninfected leaves of *ntaq1* and *prt6* compared to WT (Figs 4, S7), including *PAD3* (*CYP71B15*), that catalyzes the final two steps of camalexin synthesis. Interestingly, during a time course following infiltration with *Pst* DC3000, levels of camalexin-associated transcripts, including *GSTF6* and *PAD3*, as well as *GSTF7* increased in WT but to a lesser extent in mutant leaves (Figs 4, S7). Whilst basal levels of camalexin in uninfected leaves were similar in mutants and WT they increased to a greater degree in mutants than WT in response to infection (Fig. 4). Mutant plants showed greater basal levels of indole-3-carboxylic acid (I3CA), a compound synthesized during the defence response and a potential precursor of camalexin through the action of GH3.5 (Forcat et al., 2010; Wang et al., 2012) that was also upregulated at the RNA level in untreated leaves of *ntaq1-3* (Fig. 4). Camalexin synthesis is highly interconnected with other pathways of secondary metabolism, for example it has been reported that *vte2* and *cyp83a1*, mutants of key steps of tocopherol and aliphatic glucosinolate synthesis pathways respectively, show increased levels of camalexin (Sattler et al., 2006; Liu et al., 2016). *VTE2* and *CYP83A1* showed decreased expression in *ntaq1-3* and *prt6-1* in both basal and infected conditions (Figs 4, S8). Combination of a null *pad3* allele with *prt6-1* resulted in a loss of the *prt6* enhanced resistance to injected *Pst* DC3000 (Fig. 5).

The Arg/N-end rule pathway regulates an age-dependent primed state in uninfected plants

Previous work showed that hypoxia-associated genes are ectopically upregulated in *prt6* and *ate1 ate2* mutant seedlings (Gibbs et al., 2011; Licausi, 2013). However, it was recently shown that this is age-dependent, that in mature mutant plants these genes
Fig. 4 Influence of NTAQ1 and PRT6 on camalexin and associated secondary metabolism in Arabidopsis in response to infiltration with *Pst* DC3000 (10^6 colony forming units (CFU) ml⁻¹). Schematic representation of the camalexin synthesis pathway highlighting time courses of changes in RNA expression (qRT-PCR) or metabolites in WT, ntaq1-3 or prt6-1 in response to bacterial infection. IAOx, indole-3-acetaldoxime; IAN, indole-3-acetonitrile; GSH, glutathione; DHCA, dihydrocamalexin acid; IAA, indole-3-acetic acid; I3CA, indole-3-carboxilic acid; GH3.5, IAA-AMIDO SYNTHASE; PAD3, PHYTOALEXIN DEFICIENT 3. Data represent means ± SEM. Student’s t-test: *, P < 0.05; **, P < 0.01; ***, P < 0.001.
Statistical differences were analyzed by ANOVA followed by Tukey test. Arabidopsis apoplastic response to growth in wild type (WT) and mutant plants 4 d after bacterial infiltration of the biotroph Ps japonica was assessed. We observed a large increase in stability of artificial NTAQ1 substrates and ERFVII proteins in untreated plants, and consistent phenotypes between Arabidopsis and barley (Fig. 6c).

We show here that a role for Arg/N-end rule pathway-mediated immunity is conserved in flowering plants. In Arabidopsis we observe a large reduction in expression of hypoxia genes in older plants compared to WT. It has previously been shown that in the NR null mutant nia1 nia2, which produces very low NO levels, the NO burst in response to infection is highly reduced (Modolo et al., 2006; Chen et al., 2014). Further experiments would be required to determine a causative role of reduced NR activity leading to enhanced stabilization. Regardless of the mechanism of stabilization, the observation of increased stability of Nt-Cys substrates following infection in both Arabidopsis and barley indicates a conserved role for modulation of the Cys-Arg/N-end rule pathway, and function for Nt-Cys substrates, in response to pathogen infection that deserves further investigation. Enhanced ABA sensitivity and stomatal response to Pst infection in ntaq1 and erfVII mutants suggest that independently of other mechanisms activated, an increase in camalexin in prt6 may not reach a level necessary for reduction in fungal growth. A recent report showed N-end rule mutants, including alleles of prt6, ate1 ate2 and ntaq1 to be in general equal or more sensitive than WT Arabidopsis to a wide range of bacterial and fungal pathogens with diverse infection strategies and lifestyles (de Marchi et al., 2016). Our results, in which plants were grown under either neutral days or under the short-day condition used by de Marchi et al. showed the opposite results (of increased resistance). Our results provide a consistent pattern across different levels of expression (including enhanced defence gene transcripts and increased levels of camalexin synthesis proteins in untreated plants, and consistent phenotypes between Arabidopsis and barley) that indicate a role for NTAQ1 substrates and ERFVII as components of the immune response that enhance resistance. Therefore, differences observed in the expression of N-end rule mutants in response to infection between our studies remain to be resolved.

A specific effect for ERFVII was observed in the stomatal response to Pst. ABA is an important component of stomatal response to pathogens (McLachlan et al., 2014) and stabilized ERFVII enhance ABA sensitivity of stomata (Vicente et al., 2017). We observed a large increase in stability of artificial Nt-Cys reporters in both Arabidopsis and barley. Stabilisation could be caused by shielding of the Nt, or a reduction of either NO or oxygen. We did not observe an increase in hypoxia-related gene expression (of ADH1) at the same time as GUS stabilization, however we did observe a decline in NR activity. Seemingly contradictory to this assertion is the well known burst of NO in response to Pst infection (Delledonne et al., 1998). However, this burst occurs early following infection, well before the reduction in NR activity and stabilization of artificial Nt-Cys reporters in both Arabidopsis and barley. It has previously been shown that in the NR null mutant nia1 nia2, which produces very low NO levels, the NO burst in response to infection is highly reduced (Modolo et al., 2006; Chen et al., 2014). Further experiments would be required to determine a causative role of reduced NR activity leading to enhanced stabilization. Regardless of the mechanism of stabilization, the observation of increased stability of Nt-Cys substrates following infection in both Arabidopsis and barley indicates a conserved role for modulation of the Cys-Arg/N-end rule pathway, and function for Nt-Cys substrates, in response to pathogen infection that deserves further investigation. Enhanced ABA sensitivity and stomatal response to Pst of the ntaq1 mutant also suggests that Nt-Gln substrate(s) contribute to the stomatal ABA response to pathogens, and explains why erfVII is more sensitive to Pst than prt6 erfVII (where NTAQ1 substrates are still stabilized). An opposite effect of ERFVII was shown for interactions of Arabidopsis with the biotroph P. brassicae, as ERFVII-enhanced infection indirectly by influencing fermentation (Gravot et al., 2016).
These observations and others (Gibbs et al., 2015) indicate an important role for ERFVIs in the plant immune response. Analysis of the response to Pst DC3000 hrpA/C0, together with increased expression of SA-associated defence genes and increased camalexin synthesis, suggests a role for NTAQ1 in the onset of general and inducible PTI defence. An age-related increase in SA-related defence gene expression in N-end rule mutants was not matched by increased SA levels. This suggests a possible role for immune-related MAPK cascade activating MPK3/6 that are sufficient for SA-independent induction of most SA-responsive genes.

Fig. 6 Age-dependent priming of transcriptomic changes during Arabidopsis development and defence. (a) Relative expression of genes of camalexin synthesis in wild type (WT) and mutant plants. (b) Relative expression of transcripts encoding defence-related genes in WT and mutant plants. (c) Relative expression of HvPR1 and Hvβ1-3 glucanase in WT and HvPR76 RNAi barley plants infected with Blumeria graminis f. sp. hordei. Data represent means ± SEM. Statistical differences were analyzed by Student’s t-test. *, P < 0.05; **, P < 0.01; ***, P < 0.001.
genes, including PR1 (Asai et al., 2002). Concomitantly, it has been demonstrated that both MPK3 and MPK6 activation trigger GSTF6, 7 (and DJ1E) protein accumulation, which produces an increase in camalexin (Xu et al., 2008; Su et al., 2011). The observed increased accumulation of camalexin in ntaq1 and prt6 provides one explanation for the increased resistance of these mutants. Although expression of camalexin synthesis genes was ectopically upregulated in uninfected mature leaves of mutants, enhanced camalexin accumulation was only observed in response to infection. This may be the result of shunting of intermediate(s) to other secondary metabolism pathways. In line with this, unchallenged ntaq1 and prt6 plants show greater levels of i3CA. The observation that mutation of pad3 reverts the enhanced resistance of prt6 highlights the role of N-end rule regulated camalexin synthesis in enhancing the immune response.

How might NTAQ1 function during development and in response to pathogen attack? NTAQ1 and PRT6 expression do not change in response to pathogen attack. NTAQ1 function influences defence gene expression and camalexin synthesis. We demonstrate that downstream responses to NTAQ1, measured as responsive gene expression, are modified during development (although the expression of NTAQ1 (and PRT6) transcripts were not affected by ageing), suggesting that NTAQ1 substrate(s) may show an age-dependent increase in abundance. Following protease cleavage their activity would be revealed in the ntaq1 mutant, where they would remain ectopically stabilized. Following protease cleavage to reveal Nt-Gln, NTAQ1 substrates should be degraded in WT plants. In this case, in mature WT leaves down-regulation of NTAQ1-linked protease activity (or NTAQ1 activity) in response to pathogen attack could result in substrate stabilization. Stabilized NTAQ1 substrate(s) (or uncleaved protease targets that provide substrates) may then function to enhance gene expression associated with defence genes and camalexin synthesis, both resulting in an enhanced basal immune response.

Our data support a conserved role of the Arg/N-end rule pathway in influencing plant immune responses. Barley contains one NTAQ1 gene (MLOC_70886) (Mayer et al., 2012). Manipulation of expression or activity of this gene will be required to understand whether NTAQ1 activity is also required for defence in barley. An important goal of future work will be to identify Nt-Gln substrates that influence the immune response. Although NTAQ1-related genes are present in all major groups of eukaryotes, only a single example exists of a biochemical role for this enzyme and its associated substrate (Usp1) (Piatkov et al., 2012). There is already evidence for Nt-Gln-bearing peptide fragments derived from proteins of diverse functions present in the plant METACASPASE-9 degradome (Tsitsiatisi et al., 2013), suggesting that substrates for NTAQ1 exist. Our results establish new components of the plant immune response, and offer new targets to enhance resistance against plant pathogens.

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Author contributions

J.V., G.M.M., K.S., C.N., N.D., D.J.G., R.V.R., C.C., A.B., J.E.G., K.G., M.J.H. designed research; J.V., G.M.M., J.P., V.P., Y.I., C.N., D.R., M.M., R.V.R., A.B. performed research; J.V., G.M.M., R.V.R., N.D., C.C., M.J.H. analyzed data; J.V. and M.J.H. wrote the manuscript.

ORCID

Nico Dismeyer & http://orcid.org/0000-0002-4156-3761
Michael J. Holdsworth & http://orcid.org/0000-0002-3954-9215

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Supporting Information

Additional Supporting Information may be found online in the Supporting Information section at the end of the article:

Fig. S1 Identification of Arabidopsis ntaq1 alleles.

Fig. S2 Influence of N-end rule mutants on bacterial growth.

Fig. S3 Influence of N-end rule mutants on pathogen growth.

Fig. S4 Quantification of RNA expression.

Fig. S5 Influence of N-end rule mutants on oxidative response to infection by Pst.

Fig. S6 Time course quantification of phytohormone levels in response to Pst DC3000 infection of mature leaves in ntaq1 and ntaq1-3.

Fig. S7 Quantification of RNA expression during infection with Pst.

Fig. S8 Quantification of RNA expression in response to Pst DC3000 infection of mature leaves in VTE2 (a key gene for tocopherols biosynthesis) during Pst DC3000 infection following infiltration.

Fig. S9 Age-related changes in gene expression.

Table S1 Oligonucleotide primer sequences used for qRT-PCT, RT-PCR and genotyping

Table S2 Shotgun proteome analysis comparing Col-0 (WT) and ntaq1-3

Table S3 Expression of proteins identified as upregulate in ntaq1 compared with WT in datasets provided by de Marchi et al. (2016)

Table S4 Expression of genes of camalexin synthesis and associated pathways in datasets provided by de Marchi et al. (2016)

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