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Tansley review
Chloroplast immunity illuminated

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Summary
The chloroplast has recently emerged as pivotal to co-ordinating plant defence responses and as a target of plant pathogens. Beyond its central position in oxygenic photosynthesis and primary metabolism – key targets in the complex virulence strategies of diverse pathogens – the chloroplast integrates, decodes and responds to environmental signals. The capacity of chloroplasts to synthesize phytohormones and a diverse range of secondary metabolites, combined with retrograde and reactive oxygen signalling, provides exquisite flexibility to both perceive and respond to biotic stresses. These processes also represent a plethora of opportunities for pathogens to evolve strategies to directly or indirectly target ‘chloroplast immunity’. This review covers the contribution of the chloroplast to pathogen associated molecular pattern and effector triggered immunity as well as systemic acquired immunity. We address phytohormone modulation of immunity and surmise how chloroplast-derived reactive oxygen species underpin chloroplast immunity through indirect evidence inferred from genetic modification of core chloroplast components and direct pathogen targeting of the chloroplast. We assess the impact of transcriptional reprogramming of nuclear-encoded chloroplast genes during disease and defence and look at future research challenges.

II. Introduction
A plant’s initial response to a broad spectrum of different stresses, including pathogens, is through integrated signalling modules that recognize a common set of second messengers (calcium, reactive oxygen species (ROS), nitric oxide (NO) and lipid molecules), often incorporating kinase-based signal transduction cascades. Understanding how cells specify the timing, amplitude and duration of signal outputs, and decode and integrate these signals locally and distally remains a key challenge in plant biology. What is
often neglected is that these signals are perceived not only at the cell surface and/or in the nucleus, but also by other organelles, which collectively contribute to orchestrating an effective response.

1. Plant immunity, more than membrane to nuclear signalling

Put simply, plant immunity comprises three core modules. Predominately membrane-localized pattern recognition receptors (PRRs) perceive pathogen-associated molecular patterns (PAMPs) activating PAMP-triggered immunity (PTI). Pathogens deliver effectors (generally proteinaceous but also small molecules) directly or indirectly into the cell to collectively suppress PTI, often targeting the PRRs and their coreceptors. This effector triggered suppression (ETS) can be successfully overcome by intracellular plant disease resistance (R) proteins which activate effector-triggered immunity (ETI) effectively containing and eliminating the invading pathogen through a programmed cell death process known as the hypersensitive response (HR) (Jones & Dangl, 2006). However, there is a growing acceptance that PTI and ETI are not two distinct processes but are somewhat interdependent and contribute as a continuum to host immune responses (van der Burgh & Joosten, 2019). Superimposed on ETI is the initiation and establishment of broad-spectrum systemic immunity known as systemic acquired resistance (SAR) (Shine et al., 2019). Because of the localization of PRRs and signalling components of ETI, most of the innate immunity research has been focused on the cell membrane, the nucleus and the role of MAPK (mitogen-activated protein kinase) signalling cascades in unravelling plant immunity mechanisms.

2. The chloroplast is a key hub in coordinating effective plant immune responses

Aside from oxygenic photosynthesis, chloroplasts act as both environmental signal integrators and metabolic hubs. Chloroplasts not only link to primary metabolism but synthesize phytohormones, fatty acids, amino acids and a plethora of other secondary metabolites. This therefore provides unprecedented flexibility in fine tuning complex signalling to specific environmental stresses, and the capacity to rapidly modulate and redeploy metabolic signalling. This review will focus on the role of the chloroplast in disease and defence and seek to provide the reader with an overview of current knowledge of chloroplast immunity. We will examine evidence of a pivotal role for chloroplasts both in orchestrating an effective immune response and as a pathogen target, to suppress immunity. Pathogens probably also reconfigure primary metabolism for nutrition, although experimental insight into this is limited. We will additionally touch on current concepts in retrograde signalling and draw parallels with other stress processes that impact chloroplast homeostasis to explore commonalities in signalling responses.

3. Chloroplasts in plant immunity: an historical overview

In the past decade, the chloroplast has emerged as a central player in plant defence, initially in the context of its identification as a genuine effector target but more recently in recognition of its contribution to defence. The importance of the chloroplast in immunity has been known for a long time. Kupeevicz (1947) first reported that viruses and other plant pathogens alter chlorophyll (Chl) accumulation during infection. By the 1990s, viral proteins, such as the coat protein of Tobacco Mosaic Virus (TMV), were identified within the chloroplast (Banerjee & Zaitlin, 1992). In comparison to virus research (which we only use here as exemplars), studies on how bacteria, fungal and oomycete pathogens target the chloroplast were limited until the emergence of ‘effector biology’ in the early 2000s.

4. The complexity of chloroplast immunity: where to begin?

We aim to leave readers with two key messages, the first being that chloroplast-derived reactive oxygen species (cROS) play a pivotal role in establishing effective plant immunity and, secondly, that pathogen effectors directly and indirectly target chloroplast processes to suppress immunity. Obviously, to effect these changes a plethora of processes are activated or suppressed. While recognising this is still an embryonic field, we will draw on relevant examples to provide insight into current state-of-knowledge of the complexity of chloroplast processes modified and known components targeted. We first briefly overview phytohormone modulation of immunity, and the contribution of the chloroplast to PTI, ETI and SAR in the context of cROS, and how effectors modulate/facilitate this.

We next document potential processes contributing to chloroplast immunity that have been revealed using genetic approaches, with a strong focus on the role of cROS. We then provide a comprehensive overview of proteinaceous pathogen effectors targeted to the chloroplast and their targets, if known. Finally, we examine transcriptional control of nuclear-encoded chloroplast genes in PTI and ETI and touch on the emerging role of subcellular reorganization. Chloroplast retrograde signalling has recently been comprehensively reviewed (Chan et al., 2016; de Souza et al., 2017), including possible roles for metabolites in immune signalling (Fernandez & Burch-Smith, 2019) and hence this is not addressed here, other than to highlight specific examples.

We have tried to illustrate a variety of key immune processes that impact the chloroplast throughout the review. A powerful technique to visualize the impact of pathogens on chloroplast physiology is through $F_o/F_m$ measured by Chl fluorescence imaging (Baker, 2008). $F_o/F_m$ provides sensitive quantitative temporal–spatial measurements of changes in the maximum (dark-adapted) quantum efficiency of photosystem II (PSII; a sensitive indicator of damage/downregulation of photosynthesis), while simultaneously enabling imaging of pathogen challenges in real time and, thus, is increasingly being used to monitor pathogen infection dynamics (de Torres Zabala et al., 2015). Fig. 1 illustrates suppression of PTI by the virulent phytopathogenic pathogen Pseudomonas syringae pv. tomato strain DC3000 (Pst) both visually (Fig. 1a) and quantitatively (Fig. 1b) and its relationship to in planta bacterial multiplication (Fig. 1c). $F_o/F_m$ can also effectively capture changes in chloroplast physiology caused by fungal challenges (Fig. 1d).
Photosystem II quantum efficiency ($F_v/F_m$) captures early chloroplast changes in response to virulent and avirulent pathogens. (a,b) Challenge with the virulent apoplastic bacterial phytopathogen *P. syringae* pv. *tomato* DC3000 (*Pst*) but not mock (MgCl$_2$) or the disarmed *hrpA* mutant results in reduced $F_v/F_m$ 7–8 hpi (h post-infection) as illustrated visually (a) or quantitatively during disease establishment (b). (c) *Pst* multiplication significantly increase above initial inoculation levels at 8 h post-infiltration, coincident with reduction in $F_v/F_m$. Error bars, ± SD. (d) Spray infection with spores of the virulent rice pathogen *Magnaporthe oryzae* Guy11 similarly induces localized decreases in $F_v/F_m$. (e) Challenge with the vascular pathogen *Xanthomonas campestris* pv. *campestris* (*Xcc*) or *P. syringae* pv. *maculicola* suppresses $F_v/F_m$ during infection, the extent of which is directly correlated with virulence of the strains. Pretreatment with ABA, which is rapidly induced de novo following virulent bacterial infections, dramatically enhances suppression of $F_v/F_m$ in both *Xcc* and *Pst*. (f) ETI induced either by RPM1 or RPS4 following challenge with *Pst* carrying the respective avirulence genes, *AvrRpm1* or *AvrRps4*, causes a rapid suppression of $F_v/F_m$, the timing of which is unique to the specific R protein and correlates with speed of HR development. Kindly provided by: (a–c, f) M. Grant & S. Breen; (d) G. Littlejohn; (e) de Torres et al. (2015: Fig. S4).
III. Hormones and chloroplasts, a well-established link in plant immunity

Being the main site of phytohormone precursor synthesis, the chloroplast is central to integrating signals from PTI and ETI and an obvious target for effector modulation. Hormonal crosstalk in plant–microbe interactions is now well established (Robert-Seilaniantz et al., 2011; Burger & Chory, 2019). Thus, here we only briefly overview the core roles of, or selected new insights into, the three key immunity modulating hormones salicylic acid (SA), jasmonic acid (JA) and abscisic acid (ABA) to provide context for further reference in later sections.

1. Salicylic acid

Salicylic acid (SA) is the archetypal defence hormone effective against biotrophic and hemibiotrophic pathogens (Ding & Ding, 2020). Rapid SA biosynthesis in response to pathogens occurs through formation of isochorismate by the chloroplast-localized isochorismate synthase (ICS). The decades long challenge to understand how isochorismate was converted to SA was recently resolved. EDS5 (ENHANCED DISEASE SUSCEPTIBILITY 5) exports isochorismate to the cytosol where the amidotransferase PBS3 (avrPphB SUSCEPTIBLE3), originally identified in a genetic screen for loss of RPS5-specific resistance (Warren et al., 1999), catalyses its conjugation to glutamate, forming isochorismate-9-glutamate, which spontaneously decomposes into SA (Rekhter et al., 2019; Torrens-Spence et al., 2019). SA may directly interfere with pathogen virulence strategies through its interaction with nonexpressor of pathogenesis-related gene (NPR) SA receptors. Increases in SA inhibit ROS scavenging enzymes such as catalase and ascorbate peroxidases (Durner & Klessig, 1995; Zhang et al., 2016). More recently, SA was proposed as a retrograde signal generated by impaired PSII proteostasis (Duan et al., 2019), although whether biotic stress leads to sufficient accumulation of photodamaged proteins to instigate SA retrograde signalling remains to be demonstrated.

2. Jasmonates

Classically, jasmonates are associated with core biotrophic pathogen virulence strategies to suppress SA signalling. JA also acts synergistically with ethylene in defence against necrotrophic pathogens and ABA during herbivory (Robert-Seilaniantz et al., 2011; Zhang et al., 2017; Yang et al., 2019). Linolenic and linoleic acid, derived from chloroplast galactolipids, provide the 18-carbon fatty acid substrate which is oxidized at the C-13 position by chloroplast lipoxygenase then cyclized to 12-oxo-phytodienoic acid (OPDA) via the consecutive activities of allene oxide synthase and allene oxide cyclase. OPDA is exported to the peroxisome where it is converted, via a series of beta oxidation steps, to JA which is conjugated to isoleucine to form bioactive JA-Ile. JA may undergo alternative modifications, although biological understanding of their significance is currently limited (Wasternack & Hause, 2013). With a predominant focus on jasmonate antagonism of biotrophic defences, it is often overlooked that jasmonates are also produced de novo during ETI (Andersson et al., 2006; Zoeller et al., 2012) and have been implicated in both SAR (Truman et al., 2007) and induced systemic resistance (ISR) (van Wees et al., 2000).

3. The role of ABA in repressing chloroplast immunity

While early studies revealed that ABA treatment suppressed resistance to biotrophic and hemibiotrophic bacterial, fungal and oomycete pathogens (Henfling et al., 1980; Mohr & Cahill, 2003), it was not until subsequent, transcriptomic and genetic studies with ABA biosynthetic and signalling mutants demonstrating that pathogens hijack host ABA signalling to promote virulence that ABA became universally recognized as a key player in suppression of biotrophic immunity. De novo ABA synthesis induced by virulent Pst is remarkably rapid, occurring within 6 h of challenge, significantly preceding bacterial multiplication (de Torres-Zabala et al., 2007, 2009). Pathogen-induced ABA requires transcriptional upregulation of genes encoding the chloroplast-localized 9-cis-epoxycarotenoid dioxygenase (NCED) and cytosolic abscisic aldehyde oxidase (AAO) – key enzymes in the final steps of ABA biosynthesis (Truman et al., 2006; de Torres-Zabala et al., 2007, 2009; Peng et al., 2019). Concomitantly, transcripts encoding protein phosphatase 2Cs (PP2C), negative regulators of ABA signalling, are suppressed (Truman et al., 2006) (see Fig. 4c later for a summary).

Carotenoid intermediates provide the precursors for ABA biosynthesis. Zeaxanthin, derived from β-carotene – whose oxidation products are themselves potential chloroplast signalling molecules (reviewed by Hawaux, 2014) – is converted to violaxanthin, and then via trans-neoxanthin into 9-cis-neoxanthin and 9′-cis-violaxanthin. These substrates are converted by NCED to the 15-carbon xanthoxin which is transported to the cytosol where it is converted into abscisic aldehyde and finally to ABA via AAO (Seo & Koshiba, 2002). De novo ABA induced by Pst is proposed to suppress PTI-induced cROS (de Torres-Zabala et al., 2015) as well as antagonizing later SA signalling (de Torres-Zabala et al., 2009). ABA biosynthetic mutants (aao3) are more resistant to Pst and other biotrophic pathogens. Notably, pretreatment with ABA abolished PTI, enhanced the decrease of Fv/Fm (Fig. 1e) and, analogous to ABA suppression of ROS in imbibed seeds (Ye et al., 2012), induced ROS (de Torres-Zabala et al., 2015). As ABA can repress transcription of many plastid genes through PP2C-dependent activation of nuclear genes (Yamburenko et al., 2015), the recent demonstration that Xanthomonas effectorss of both rice and Arabidopsis pathogens promote virulence by suppressing transcripts encoding chloroplast-localized PP2Cs (Akimoto-Tomiyama et al., 2018) reinforces the complex role of ABA in effector modulation of chloroplast immunity.

IV. cROS in immunity and insights from disruption of chloroplast components

Specificity in ROS signalling is achieved via the spatiotemporal control of production and scavenging at different organelar and
subcellular locations. During plant defence, recognition of PAMPs by PRRs activates plasma membrane-localized NADPH oxidase (Zhou et al., 2019) and apoplastic type III peroxidases (Daudi et al., 2012) generating, within minutes, a rapid burst of $H_2O_2$ comprising synthesis of short-lived superoxide and its more stable dismutation product hydrogen peroxide in the apoplast (Smirnoff & Arnaud, 2019). Hydrogen peroxide can enter the cytosol via plasma membrane aquaporins (Rodrigues et al., 2017). ROS are also produced in organelles by oxygen reduction during electron transport and by oxidase enzymes in peroxisomes (Asada, 2006; Mullineaux et al., 2018; Waszczak et al., 2018; Smirnoff & Arnaud, 2019). The prominent routes for cROS generation are oxygen photoreduction at PSI (Mehler reaction) and possibly via the PSII electron acceptor plastoquinone (Dietz et al., 2016; Vetoshkina et al., 2017). Singlet oxygen ($O_2^*$), a highly reactive species, is formed in PSII by transfer of excitation energy from triplet-state Chl (Mullineaux et al., 2018a; Dogra et al., 2019) and is the major ROS involved in ETI-induced lipid peroxidation (Zoeller et al., 2012).

1. PTI and cROS

As part of PTI, chloroplasts of Arabidopsis leaves challenged with virulent $Pst$ generate reactive species (as determined by 2′,7′-dichlorodihydrofluorescein diacetate (H$_2$DCFDA) oxidation) which are suppressed within 4 h by Pst effectors (de Torres Zabala et al., 2015). DCMU (3-(3,4-dichlorophenyl)-1,1-dimethylurea), which blocks photosynthetic electron transport between PSII and plastoquinone (Metz et al., 1986), also blocks 2′,7′-dichlorodihydrofluorescein oxidation, indicating that this burst is probably generated by oxygen photoreduction producing superoxide/$H_2O_2$ downstream of PSII (Mubarakshina et al., 2010; Exposito-Rodriguez et al., 2017). Interestingly, $Pst$ ROS suppression coincides with a decrease in $F_v/F_m$ (Fig. 1a,b) and photosynthesis (de Torres Zabala et al., 2015) and an increase in bacterial growth (Fig. 1c) indicating that effectors (some of which are targeted to the chloroplast) interfere with critical photosynthetic components that have yet to be identified. Notably, ABA mimics DCMU application, suggesting that $Pst$-induced de novo ABA biosynthesis may play a key role in suppressing ROS production. Indeed, pretreatment of leaves with ABA strongly enhances the $Pst$-induced decrease in $F_v/F_m$ and this is common to other, less virulent pathogens such as Xanthomonas campestris pv. campestris (Fig. 1c).

At the same time, $Pst$ (and other pathogens) suppress the expression of a large set of nuclear-encoded chloroplast genes including photosynthesis-related and antioxidant enzyme transcripts (Bilgin et al., 2010; de Torres Zabala et al., 2015; Su et al., 2018). The signalling mechanism driving PTI-generated cROS is unclear but may involve calcium and/or retrograde signalling as discussed below.

2. cROS and ETI

The interaction between high light, phytochrome and pathogen responses has been documented (Bechtold et al., 2005; Ballare, 2014). Light is required for, or enhances, ETI-triggered HR (Torres et al., 2006; Nomura et al., 2012). These observations suggest the interaction of cROS with photosynthesis, SA production (Chaubch et al., 2010, 2012) and additionally NO (Zaninotto et al., 2006; Yun et al., 2011; Yun et al., 2016). The development of an HR is rapid and effectively contains the pathogen. The HR is widely thought to be triggered by $O_2^*$ generation, which leads to lipid peroxidation (Havaux, 2014). Pioneering analytical studies of the temporal accumulation of oxidation products derived from unsaturated fatty acids during the HR strongly support a $O_2^*$ burst. Notably, the HR leads to an early and massive accumulation of both enzymatic and nonenzymatic chloroplast galactolipid-derived oxylipins (Andersson et al., 2006; Zoeller et al., 2012) with huge increases in JA measured within 5 h of infection with PstavrRpm1 (Zoeller et al., 2012). This timing is consistent with the earlier biophoton production following PstavrRpm1 challenge (Bennett et al., 2005), which is indicative of lipid oxidation (Havaux et al., 2006). For example, HR in Arabidopsis inoculated with PstavrRpm1 is enhanced by increased light intensity and associated with disruption of the PSII light harvesting complex, decreased $F_v/F_m$ (Fig. 1f) and accumulation of the Chl catabolite phaeophorbide, a potent photosensitizer that generates $O_2^*$ (Mur et al., 2010). Indeed, $F_v/F_m$ provides a powerful readout to accurately capture and quantify the timing of specific R protein activation, before visible symptoms, as illustrated for the RPM1–AvrRpm1 and RPS4–AvrRPS4 interactions (Fig. 1f; for a recent review see also Perez-Bueno et al., 2019).

Further evidence that chloroplast-sourced ROS are involved in ETI and mediated by MAPK pathways are provided by studies in Nicotiana benthamiana (Liu et al., 2007) and Arabidopsis (Su et al., 2018). PstavrRps2 (like PstavrRpm1, Fig. 1f) causes a much larger and earlier decrease in PSII quantum efficiency than $Pst$ (Fig. 1a) (de Torres Zabala et al., 2015), and a more prolonged activation of MAPKs (Su et al., 2018). This response is mirrored by conditional induction of MAPKs (MPK3/6) leading to cell death. Both PstavrRps2 and MAPK activation increase cROS within 6 h in a light-dependent manner (consistent with biophoton generation at c. 7 h post-inoculation (hpi); Bennett et al., 2005), accompanied by visible disruption of PSI. Comparison of apparent chloroplast-sourced ROS between PTI and ETI in this system indicates that chloroplast-targeted effectors decrease photosynthesis and suppress cROS production (de Torres Zabala et al., 2015) whereas ETI involves a more aggressive effect on photosynthesis, as illustrated by rapid decreases in $F_v/F_m$ and an increase in ROS (Su et al., 2018), consistent with extensive chloroplast galactolipid oxidation recorded during early ETI (Andersson et al., 2006; Zoeller et al., 2012).

3. A role for cROS in systemic immunity?

The chloroplast is becoming increasingly linked to effective SAR, a process conferring broad-spectrum and lasting immunity to pathogens of diverse lifestyles (Fernandez & Burch-Smith, 2019). Classic SAR is established following successful ETI leading to the HR. Chloroplast lipids and cROS appear to be central to generation of SAR inducing signal(s) following ETI-activated HR (Wendehenne et al., 2014; Shire et al., 2019), supported by the SAR-deficient phenotypes of fatty acid desaturase (fads2;
SUPPRESSOR OF FATTY ACID DESATURATION DEFICIENCY2) mutants. The chloroplast galactolipid mutants mgd1 and dgd1 (monogalactosyl synthase 1, digalactosyl synthase 1), responsible for monogalactosyldiacylglycerol (MGDG) and digalactosyldiacylglycerol (DGDG) synthesis respectively, function nonredundantly in initial SAR signal perception (Gao et al., 2014; Shah et al., 2014). As noted above, ETI-generated ROS modify fatty acids on chloroplast galactolipids leading to rapid JA accumulation (Andersson et al., 2006; Zoeller et al., 2012). Although JA is classically associated with suppression of SA signalling in biotrophic interactions, jasmonates have been implicated in both SAR (Truman et al., 2007; Liu et al., 2016) and ISR (van Wees et al., 2000). While somewhat speculative, interesting parallels are emerging between the role of ROS in signalling pathways that regulate SAR and systemic acquired acclimation (SAA) and wounding, where a wave of ROS signalling appears to be a common early mediator of systemic signalling responses although on different time scales (Zandalinas et al., 2019).

V. Immunity insights from perturbation of chloroplast metabolism and cROS production

The following sections describe components of the photosynthetic electron transport system and the main sources of ROS occurring in the chloroplast. The reader is referred to the schematic in Fig. 2 for context. The removal of H₂O₂ in chloroplasts is carried out by a diverse set of enzymes providing robustness to PTI. These include ascorbate peroxidases localized to the stroma or attached to the thylakoid membrane along with glutathione and associated enzymes to regenerate oxidized ascorbate: glutathione peroxidase-like and peroxiredoxins (Smirnoff & Arnaud, 2019) (Fig. 2). Oxidized peroxiredoxins are regenerated by thioredoxin with involvement of NADPH-dependent thioredoxin reductase C (NTRC) (Perez-Ruiz et al., 2017). While mutants of individual peroxiredoxins (Prx) in Arabidopsis (there are four chloroplast Prx isoforms in Arabidopsis; Tripathi et al., 2009), have normal Pest responses, an NTRC mutant (ntrc) shows increased cell death and increased peroxide production as determined by 3,3′-diaminobenzidine staining (Ishiga et al., 2011) but no difference in Pest growth compared to wild-type Col-0. Interestingly, the authors also showed that NTRC-silenced tomato plants showed accelerated necrotic cell death and enhanced symptom development in response to the necrotrophic soil pathogen Sclerotinia sclerotiorum. A similar response was elicited by nonhost P. syringae, although pathogens varied in specific responses (Ishiga et al., 2016). Notably, these symptoms were absent in plants inoculated with a coronatine (COR)-deficient Pest strain, implicating a role for COR in cROS-induced disease-associated necrosis (Ishiga et al., 2016). Antisense knockdown of two chloroplast GPX-like enzymes in Arabidopsis increases H₂O₂ and high light-induced SA. These plants had elevated PTI to Pest and P. syringae pv. maculicola (Psm), and more extensive HR following PestavrRpm1-initiated ETI (Chang et al., 2009). Manipulation of chloroplast APX also impacts pathogen response. Rice lines overexpressing thylakoid membrane-bound APX exhibited increased initial tolerance to rice bacterial blight conferred by Xanthomonas oryzae pv. oryzae, whereas RNAi lines were more susceptible, and this was correlated with H₂O₂ levels, presumably chloroplast-derived (Jiang et al., 2016). In Arabidopsis, conditional silencing of thylakoid-bound APX showed that accumulation of chloroplastic H₂O₂ triggered retrograde signalling leading to induction of nuclear-encoded pathogen defence genes in the absence of any pathogen challenge (Maruta et al., 2012). While not confined to chloroplasts, the concentration of the antioxidants ascorbate and glutathione, which are involved in H₂O₂ removal and redox regulation, influence pathogen responses. Ascorbate-deficient mutants have increased H₂O₂ PR levels, camalexin and SA accumulation and have increased basal resistance to Pest and the oomycete Hyaloperonospora (Barth et al., 2004; Pavet et al., 2005; Colville & Smirnoff, 2008; Mukherjee et al., 2010). Consistent with these observations, glutathione-deficient mutants have decreased resistance to PestavrRpm1 (Ball et al., 2004; Parsiy et al., 2007).

Expressing the cyanobacterial electron transport protein flavodoxin in tobacco chloroplasts improves robustness of photosynthesis to various stresses including methyl viologen (MV: a redox cycling compound that generates superoxide at PSI) and high light. This appears to be associated with decreased cROS production (Tognetti et al., 2006) and altered pathogen responses (Zurbriggen et al., 2009; Rossi et al., 2017). The reason that flavodoxin, which has a flavin cofactor, improves stress resistance and decreases cROS production is not immediately apparent. It functionally replaces the plant PSI electron acceptor ferredoxin (Tognetti et al., 2006) which has a 2Fe–2S reaction centre. One possibility is that electron transfer through flavodoxin decreases oxygen photoreduction at PSI (the Mehler reaction) (Fig. 2). Alternatively, because Fe–S proteins are a target for superoxide and H₂O₂, which can demetallate them (Imlay, 2013), chloroplastic ferredoxin may be sensitive to inactivation by ROS. Indeed, superoxide inactivates spinach ferredoxin (Fisher et al., 2016), consistent with the marked increase in resistance to MV (Tognetti et al., 2006). This may account for the significant reduction in localized cell death induced by the nonhost pathogen Xanthomonas campestris pv. vesicatoria (Xco) in flavodoxin-expressing tobacco leaves, which was associated with decreased cROS production (Zurbriggen et al., 2009). Similarly, infection of flavodoxin-overexpressing tobacco with the necrotrophic fungus Botrytis cinerea significantly restricted hyphal growth, lesion development, Pathogenesis Related (PR) gene expression and phytoalexin accumulation (Rossi et al., 2017). Expression of flavodoxin in Arabidopsis chloroplasts decreases ROS production and disassembly of PSI in response to PestavrRpt2, attenuating ETI (Su et al., 2018). These studies highlight a central role for cROS in effective PTI and ETI. A mutant in the main chloroplast ferredoxin (fd2) (Fig. 2) exhibiting altered pathogen responses provides additional evidence linking electron transport from PSI with PTI (Wang et al., 2018). fd2 was more susceptible to Pest, possibly as a direct result of the elevated JA observed. By contrast, ETI elicited by AvrRpt2 was stronger, with twice as much H₂O₂ generation. This result is part of a growing body of evidence for possible photosystem-specific roles for ROS generation during ETI and PTI, with ROS generated by ETI being primarily derived from PSI whereas PTI may generally require electron transport to PSI, which is compromised in fd2 plants. This is also consistent
with PSI being the source of H$_2$O$_2$ for PTI (de Torres Zabala et al., 2015).

In conclusion, various lines of evidence show that cROS is induced by PTI and ETI, and we speculate that H$_2$O$_2$ derived from PSI may be the primary ROS underpinning PTI whereas ETI elicits rapid accumulation of 1O$_2$ (Fig. 2). The intensity and duration of the response, and hence the eventual pathogenic outcome is dictated by a complex interaction, its outcome being dictated by the specific pathogen virulence strategy and host resistance protein complement. Higher H$_2$O$_2$ levels can improve basal immunity, but effectors collaborate to directly or indirectly repress cROS production, probably by inhibiting electron transport to PSI. By contrast, and somewhat counterintuitively, ETI appears to elicit an extensive disruption of photosynthesis, including breakdown of PSII leading to greater ROS production and the HR. This is likely to be driven by 1O$_2$. However, at this point a fuller understanding of these mechanisms is limited by the poor specificity of the ROS assays (Smirnoff & Arnaud, 2019). New genetically encoded reporters (Nietzel et al., 2019) and nanosensors (Lew et al., 2020) offer better specificity and temporal spatial resolution to better dissect these processes.

VI. Direct targeting of pathogen effectors to the chloroplast

The previous sections show that pathogen effectors modulate chloroplast function, either directly or indirectly, which implies that effectors may themselves localize to the chloroplast and directly interact with chloroplast-located targets. Here we summarize direct and indirect experimental evidence for effector localization to the chloroplast.

1. Bacterial effectors

Evidence for physical targeting of chloroplasts by bacterial effectors did not emerge until the mid-2000s (Jelenska et al., 2007; Lee et al., 2008) yet remarkably and more than 10 of Pseudomonas syringae’s core effector repertoire of 30–40 proteins have been predicted or experimentally shown to localize to the chloroplast (Table 1). More recently, a number of effector proteins from Ralstonia solanacearum have been shown to localize to the chloroplast (Table 1), although knowledge of their host targets is limited (Jelenska et al., 2007; Lee et al., 2008; Rodriguez-Herва et al., 2012).

Pseudomonas syringae The recently described P. syringae pan genome (Laflamme et al., 2020) has provided a rich resource to further expand our knowledge of effectors targeted to the chloroplast.

HopI1 One of the first bacterial effectors found to target the chloroplast was HopI1 from Psm. HopI1 has a redundant chloroplast-targeting sequence and contains P/Q-rich repeats (to facilitate protein folding) and a J domain, through which it directly

Fig. 2 An outline of the photosynthetic electron transport system showing the main sources of reactive oxygen species (ROS; singlet oxygen (1O$_2$), superoxide (O$_2$^-) and hydrogen peroxide (H$_2$O$_2$)) at photosystems I and II. Proteins that are validated effector targets are shown in red. APX, ascorbate peroxidase; 2-Cys Prx, 2-cysteine peroxiredoxin; Fd, ferredoxin; FNR, ferredoxin-NADPH reductase; GPX, glutathione peroxide-like; NTRC, NADPH-dependent thioredoxin reductase; PQ, plastoquinone; PC, plastocyanin; SOD, superoxide dismutase; Trx, thioredoxin.
### Table 1 Pathogen effectors predicted to be chloroplast localised.

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<td>pisi</td>
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| Chloroplast, nucleus, mitochondria | Chloroplast, nucleus, mitochondria | Chloroplast associated cytosolic Heat shock protein 70 (Hsp70). While \textit{in planta} interaction with the Hsp70 chloroplast isomer has yet to be demonstrated, Hop1 induces altered thylakoid structure and reduced SA accumulation (Jelenska et al., 2007), although how Hop1 enters the chloroplast remains to be determined. **HopN1** HopN1 suppresses ROS accumulation, callose deposition and HR cell death (López-Solanilla et al., 2004; Rodríguez-Herva et al., 2012), these activities being dependent on its cysteine protease activity. HopN1 localizes to the thylakoid membrane, interacting with and degrading PsbQ from PSII, reducing oxygen production, electron transport and attenuating cROS. Collectively, these studies have shown that PsbQ quantitatively contributed to both PTI and nonhost HR. **AvrRps4/HopK1** AvrRps4 is more commonly associated with triggering ETI when recognized by RPS4 in \textit{A. thaliana}. However, AvrRps4 localizes to both the nucleus and the chloroplast and has high N-terminal sequence homology to another effector protein, HopK1. Both AvrRps4 and HopK1 target the chloroplast via a cleavable transit peptide (Li et al., 2014) and their chloroplast localization is required to suppress the classical PTI responses, ROS production and callose deposition, and to enhance bacterial growth. The generation of combinations of chimeric effectors between C- and N-terminal domains of AvrRps4 and HopK1 demonstrated that AvrRps4 contributes to bacterial virulence in \textit{Pst} lacking HopK1, although the chloroplast targets of these effectors remain to be determined. HopK1\textsuperscript{N-AvrRps4C} but not AvrRps4\textsuperscript{N-HopK1C} chimeras induced a strong HR delivered through \textit{Pseudomonas fluorescens} (Halane et al., 2018). However, AvrRps4\textsuperscript{N} not only directly interacted with EDS1 but also contributed to bacterial virulence in \textit{Pst} lacking HopK1, establishing AvrRps4 as an evolved bipartite effector with dual nuclear and chloroplast functions (Halane et al., 2018). **HopM1** \textit{Pst} HopM1 localizes to the trans-Golgi network where it interacts with the ADP-ribosylation factor guanine nucleotide exchange factor, AtMIN7, to suppress vesicle-trafficking (Nomura et al., 2011). However, HopM1 from \textit{P. syringae pv. actinidiae} with 67% amino acid identity to \textit{Pst} HopM1, localizes to the chloroplast (Choi et al., 2017), suggesting an intriguing evolution of alternative functions for these proteins. Of the remaining \textit{P. syringae} effectors that are known to localize to the chloroplast, the predicted ADP-ribosyl transferase HopO1-2 and HopR1 translocate into isolated chloroplasts (de Torres Zabala et al., 2015) although further functional insight is lacking. HopR1 and HopO1-2 were amongst a number of effectors identified to interact with predicted chloroplast-localized proteins in yeast two-hybrid screens, including HopU1, HopZ1, HopW1 and HopBB1 (Lee et al., 2008; Mukhtar et al., 2011). **Other bacterial effectors** Evidence for effectors targeting to the chloroplast is emerging from other bacterial pathogens. The chloroplastic phospholipase A1 RipAL (\textit{Ralstonia}-injected proteins) from \textit{Ralstonia solanacearum} (Nakano & Mukaihara, 2018)
shares homology with DEFECTIVE IN ANOTHER DEHISCENCE1 (Ishiguro et al., 2001), which catalyses the release of linoleic acid, a critical precursor of JA biosynthesis, from chloroplast membranes. RipAL localizes to the chloroplast and wild type, but not a lipase active site mutant, suppressed PTI in N. benthamiana via enhanced JA signalling and JA/JA-isoleucine content, with a concomitant decrease in SA and associated SA-signalling genes (Nakano & Mukaihara, 2018). The F-box domain RipG effector family comprises seven members, of which RipG3 and RipG7 interact with chloroplast proteins – possible targets for ubiquitination and proteasomal degradation (Dahal et al., 2018). RipAD is also localized to chloroplasts, although its host target(s) remain unknown (Jeon et al., 2020). Notably, both RipAL and RipAD interfere with flg22-triggered ROS production presumably from the chloroplast (Nakano & Mukaihara, 2018; Jeon et al., 2020).

2. Effectors from filamentous pathogens

Chloroplast-localized effector proteins from fungi and oomycetes are now being identified, indicating that filamentous pathogens have also evolved to target the chloroplast (Table 1).

Rusts  Transient expression in N. benthamiana has localized eight effector proteins from rusts (Table 1) (Petre et al., 2015; Petre et al., 2016; Sperschneider et al., 2017). Notably, the program LOCALISER has proved useful for in silico prediction of chloroplast and other cellular effector addresses (Sperschneider et al., 2017), identifying a further two chloroplast-localized effectors from the biotrophic rust Puccinia graminis f. sp. tritici, PG1_00164 and PG1_06076, which were experimentally validated.

Given the dearth of experimentally validated chloroplast-localized effector proteins from other fungi, this may reflect a rust virulence strategy or lack of experimental endeavour.

Oomycete  Oomycete effectors are largely of the ‘RXLR’ class. RXLRs are defined by a secretion signal peptide followed by a conserved N-terminal domain comprising the RXLR (Arg–Xaa–Leu–Arg) consensus sequence, where X is any amino acid that shares a conserved structural fold (Win et al., 2012). A high-throughput screen of 83 candidate RXLR effectors of the obligate biotrophic oomycete Plasmopara viticola (Liu et al., 2018) identified four effectors localized to the chloroplast (Table 1). Only one contained a cleavable N-terminal transit peptide and was specifically targeted to the chloroplast, PvRXLR86, whereas the others had multiple organellar addresses (Liu et al., 2018). PvRXLR61 and PvRXLR161 localized to the chloroplast and nuclei whereas PvRXLR54 additionally targeted the mitochondria (Liu et al., 2018). A chloroplast-localized effector was also identified from the related sunflower powdery mildew, Plasmopara halstedii. PhRXLR-C20, expressed during pathogen colonization, was observed in the chloroplast and stromules (Pecrix et al., 2019). Notably, PhRXLR-C27 targeted plastid-associated membranes (Pecrix et al., 2019). The host targets of these two effectors remain unknown.

Fig. 3 Convergent targeting of Thylakoid formation 1 (Thf1), a negative regulator of cell death, by diverse pathogens. Thf1 plays an important role in photosystem II (PSII) – light harvesting complex II dynamics and is targeted by necrotrophs, biotrophs and viruses. (a) The effector protein ToxA found in a variety of necrotrophic wheat fungal pathogens, Pst, Pyrenophora triticci-repentis (Pt) and Bipolaris sorokiniana (Bs), targets the wheat Thf1 orthologue, ToxA Binding Protein 1 (ToxABP), inducing necrosis via ROS accumulation through reduction in PSI and PSI–protein complex abundance. The wheat sensitivity protein, Tsn1, is required for ToxA-dependent necrosis and may monitor binding of ToxA to ToxABP1. (b) The hemibiotrophic bacterium Pseudomonas syringae pv. tomato (Pst) delivers effectors (yellow circles) which appear to disrupt Thf1 function, again leading to enhanced lesion formation, although it remains to be determined whether this is by direct or indirect interaction. (c) The Tphomamovirus (TBV) N’ virus resistance protein, belongs to the conserved Solanaceae I2 class of CC-NBS-LRR resistance protein. That can confers resistance to Phytophthora and Fusarium sp. TBV’s CC domain physically targets and destabilizes TBV-coat protein in a light-dependent manner to enhance resistance. Based on analogy to the cyanobacterium Synechocystis Thf1 orthologue, Psb29, Thf1 destabilization affects accumulation of the FtsH ATP-dependent zinc metalloproteases, FTSH2 and FTSH5 (also known as VAR2 and VAR1 respectively), which are involved in the selective degradation of PSII subunits, such as D1 during PS repair. This would lead to PSI disassembly and increased ROS production.
Nectrophic fungal effectors  ToxA, a 178 amino acid secreted nectrophic effector protein was first isolated from the fungus *Pyrenophora tritici-repentis* (Sarma et al., 2005) and was more recently identified in *Parastagonospora nodorum* and *Bipolaris sorokiniana* (McDonald et al., 2017). ToxA targets the chloroplast ToxA Binding Protein 1 (ToxABP1), inducing ROS accumulation through decrease in PSI and PSII protein complex abundance (Manning et al., 2007; Faris et al., 2010). The sensitivity in wheat to ToxA is governed by the *Tnl1* locus, encoding classical nucleotide binding, leucine rich repeat disease resistance proteins, suggesting these may monitor ToxA activity. The severity of necrosis can be restricted by preventing ROS accumulation or silencing ToxABP1 (Manning et al., 2007). The *A. thaliana* homologue of the wheat ToxABP1, known as Thylakoid formation 1 (Thf1), is also targeted by multiple pathogens (see below), suggesting convergent evolution of effector targets. The *S. sclerotiorum* effector SsITL has recently been shown to localize to the chloroplast and interact with the chloroplast-localized calcium-sensing receptor (CAS, see below) (Tang et al., 2020). The interaction of SsITL with CAS interferes with the SA signalling pathway to reduce SA accumulation during early infection while overexpression of CAS increased resistance to *S. sclerotiorum* (Tang et al., 2020).

3. Convergent targeting of Thf1, a negative regulator of cell death, by diverse pathogens

Aside from being a target of ToxA, chloroplast-localized Thf1 is involved in a range of host–microbe interactions (nectrotrophic, biotrophic, viral), mediating both PTI and ETI (Fig. 3). Thf1 is an orthologue of ToxABP1 which binds ToxA (see above, Fig. 3a) and plays a central role in controlling PSII–light-harvesting complex II (LHCII) dynamics during dark-induced senescence and light acclimation (Huang et al., 2013). It has also been linked to DC3000 virulence and virus infection (Fig. 3b,c). Both virus-induced gene-silenced *SALC*, the tomato Thf1 orthologue, and *Arabidopsis thf1* mutants exhibited accelerated lesion formation upon DC3000 challenge, and *SALC1* chloroplast localization was affected by coronatine (Wangdi et al., 2010). Interestingly, Thf1 was additionally identified as an interactor with the CC domain of the *Solanaceae* I2-like class of CC-NLRs (Ori et al., 1997), which recognize *Tomovirus* coat protein. Using N’, an I2 CC-NLR which recognizes *Tomovirus* coat protein (Hamel et al., 2016) demonstrated that Thf1 functions as a negative regulator of cell death, and activation of N’ results in the destabilization of Thf1 in a light-dependent manner (Fig. 3c). Notably, like the TMV N protein interaction with chloroplast-localized NRIP protein (see below (Caplan et al., 2008)), the N’–Thf1 interaction appears to take place in the cytosol. Possible insight into how Thf1 destabilization impacts chloroplast immunity is provided by the demonstration that a cyanobacterial Thf1 homologue Psb29 is required for the accumulation of the FtsH ATP-dependent zinc metalloproteases, which function in selective degradation of PSII subunits during repair (Beckova et al., 2017). Normally, inactivation of PSII is restored through a repair cycle replacing damaged...
protein subunits, mainly the D1 reaction centre subunit, with functional copies. Damaged D1 repair is usually mediated through proteolysis by members of the Arabidopsis FTSH family. Thf1 is required for normal accumulation of FTSH2 and FTSH5 (also known as VAR2 and VAR1 respectively; Wu et al., 2013). Thus N’ destabilization of Thf1 would diminish FTSH2/5 levels, impacting PSII repair, and lead to the production of ROS and presumably HR cell death (Fig. 3c).

4. Getting the message across: is calcium signalling involved?

There are common and distinct roles for ROS and calcium signalling in activating and uncoupling chloroplast immunity. Calcium signalling, like ROS signalling, is probably via a propagative wave, initiated at the plasma membrane upon PRR activation and transmitting to the chloroplast and nucleus, although current knowledge of this remains sparse. Twenty years ago, rapid transient cytosolic calcium (Ca$^{2+}$) increases in response to PTI (Pst, PshrpA and Pst avrRpm1 challenges) were recorded using the calcium-sensitive reporter aequorin (Grant et al., 2000). PstavrRpm1 (ETI) elicited an additional slow, sustained increase in Ca$^{2+}$ yet it is still unclear whether this is a signal perceived by other organelles, or indicative of loss of Ca$^{2+}$ homeostasis coincident with HR development.

A role for calcium in establishment of chloroplast immunity is evidenced from studies on the thylakoid-membrane-localized Ca$^{2+}$-sensing protein (CAS), which generates stromal Ca$^{2+}$ spikes via Ca$^{2+}$ release from thylakoid membranes (Fig. 4a). The cas-1 mutant was strongly compromised in resistance to virulent and avirulent Pst (Fig. 4b). Additionally, classical PTI responses such as callose deposition and stomatal closure were attenuated in cas-1. Biochemical characterization of CAS-silenced N. benthamiana plants positioned CAS downstream of activated MAPK signalling cascades and upstream of ROS signalling (Nomura et al., 2012). Recently, the S. sclerotiorum integrin-like effector SsITL was shown to directly target CAS to suppress immunity (Fig. 4b) (Tang et al., 2020). SsITL-expressing transgenic plants were more susceptible and CAS overexpression enhanced resistance to S. sclerotiorum, consistent with the previously reported role of SsITL in suppression of JA/ethylene signalling (Zhu et al., 2013). Thus, stromal calcium signalling appears important in mediating broad-spectrum immunity.

VII. Cellular reorganization during infection, stromules and perinuclear chloroplast movement

Subcellular reorganization is well documented during plant–pathogen interactions. In addition to the generation of specialized interfaces between plant cells and invading pathogens (e.g. the extrahaustorial membrane (EHM) and biotrophic interfacial complex (BIC)), cellular components are recruited to sites of infection, often mediated by actin microfilaments or microtubules, as recently reviewed (Park et al., 2018b; Boevink et al., 2020). Chloroplasts move around the cell on actin microfilaments, but
there is compelling evidence which shows that stromule formation (finger-like tubular stroma-filled chloroplast extensions) is mainly microtubule-dependent (Caplan et al., 2015; Erickson et al., 2018). However, treatment with the microtubule-depolymerizing agent oryzalin indicates additional microtubule-independent stromule formation with each type characterized also by its speed of movement (Erickson et al., 2018).

1. Stromules and perinuclear chloroplast movement – ROS as a retrograde immune signal?

Systematic studies of chloroplasts during pathogen challenge are limited. Pioneering work on the TMV N resistance protein/TMV p50 effector demonstrated a cytosolic interaction of N with chloroplastic localized N Receptor Interacting Protein 1 (NRIP1) (Caplan et al., 2008). N-mediated ROS-induced stromules in a CHloroplast Unusual Positioning 1 (CHUP1)-dependent manner (Fig. 5a) (Caplan et al., 2015). While stromules can be induced in vitro, indicating this is a chloroplast autonomous response, actin microfilament remodelling to facilitate perinuclear chloroplast movement appears to be an active ETI strategy to establish a conduit for possible retrograde ROS (or metabolite) signals (Fig. 5a) (Caplan et al., 2015; Kumar et al., 2018; Park et al., 2018a; Park et al., 2018b; Fernandez & Burch-Smith, 2019).

Stromules were observed following flg22 treatment, but not 20 hpi with PsbrcC (Caplan et al., 2015). This apparent anomaly

![Diagram](image-url)
may represent a timing issue as cROS is produced during early PTI (4–5 hpi with PstrhpA; de Torres Zabala et al., 2015 (Fig. 5b)). Strikingly, PTI-induced cROS, as determined by H$_2$DCFDA staining, was only detected in perinuclear chloroplasts or those with stromules that appear to physically contact the nucleus following PstrhpA challenge. Interestingly, chloroplasts staining for ROS were significantly smaller than the others (Fig. 5b), suggesting heterogeneity in chloroplasts as reported for high light responses (Exposito-Rodriguez et al., 2017), possibly a direct consequence of stromule formation. Additionally, there is evidence for chloroplast aggregation late in successful infections, as illustrated in Fig. 5(c) and described by Hutt et al. (2017). As many of these studies use different cell types (epidermal vs mesophyll), the importance of cell type on chloroplast function and chloroplast heterogeneity in specific pathogen immune responses requires further investigation. Chloroplasts also appear to be recruited to the EHM in P. infestans infections of N. benthamiana, where the anchoring of chloroplasts to the EHM is also CHUP1-mediated (Toufexi et al., 2019). Silencing of CHUP1 reduced chloroplast recruitment to the EHM, reduced stromule formation and led to higher levels of P. infestans hyphal growth, reinforcing the importance of CHUP1 and highlighting a role for chloroplast dynamics in establishment of plant immunity.

Thus, organization of chloroplasts during infection is typified by perinuclear chloroplast localization and the CHUP1-dependent extension of stromules toward the nucleus, each of which provide a physical basis for retrograde signalling (Erickson et al., 2018; Mullineaux et al., 2020). Indeed, perinuclear positioning of chloroplasts in immunity appears generic, being reported during viral infections (Fig. 5a) and in both avirulent (Pst), virulent (PsthrpQ1-1) and Agrobacterium tumefaciens challenges of N. benthamiana, transient expression of effectors or viral proteins such as p50, or following exogeneous application of ROS (Erickson et al., 2014; Caplan et al., 2015; Ding et al., 2019). Pathogen effects on stromule formation and chloroplast–nuclear association is remarkably similar to cROS-mediated high light responses (Exposito-Rodriguez et al., 2017) and oxidative stress imposed by silencing of NTRC (Brunkard et al., 2015).

Recent evidence for effector suppression of stromules comes from studies with the Xcv E3 ubiquitin ligase effector XopL. Overexpression of XopL but not an XopL E3 ubiquitin ligase mutant in N. benthamiana abolished stromule formation in lower epidermal cells induced by A. tumefaciens (Erickson et al., 2014; Erickson et al., 2018). By contrast, XopQ, known to elicit ETI in N. benthamiana, increased stromule formation by over 50%. Notably, perinuclear chloroplast localization was still observed with XopL overexpression, implying nuclear recruitment of chloroplasts and formation of stromules to be independent mechanisms in immunity.

VIII. Functional significance of suppression nuclear-encoded chloroplast genes (NECGs)

While suppression of NECGs has been reported previously (e.g. Bilgin et al., 2010), a detailed time course comparing Pst with its type III secretion-deficient hrpA mutant revealed that wholesale suppression of NECGs was a PTI response, with c. 35% of all differentially suppressed genes within 3 hpi representing NECGs (de Torres Zabala et al., 2015; Lewis et al., 2015). This appears to indicate an active defence response to prioritize defence at the expense of growth. Notably, neither hrpA (nor flg22) challenge markedly affected Chl fluorescence parameters (de Torres Zabala et al., 2015), yet within 3 hpi, Pst effectors differentially regulate a subset of hrpA-suppressed NECGs (Fig. 6). These transcriptional changes occur in parallel to suppression of cROS and before measurable differences in Fv/Fm, or decrease in photosynthesis rate (de Torres Zabala et al., 2015).

A meta-analysis of rice transcriptomic datasets also reported extensive downregulation of NECGs under both biotic and abiotic stress (Cohen & Leach, 2019). Considering the 11 diverse datasets and disparate temporal sampling, a core set of 85 photosynthesis-related genes were identified as suppressed across eight experiments. Thus, rapid transcriptional suppression of NECGs is a core response to retrograde stress signals, possibly representing a universal strategy to maximize resource allocation to defence by short-term attenuation of photosynthetic capacity, but possibly collaterally decreasing the capacity to repair effector targets.

Increasing evidence suggests that MAPKs mediate the transcriptional reprogramming of NECGs. MAPKs are rapidly activated following PAMP recognition and the subsequent apoplastic ROS burst (Meng & Zhang, 2013) (Fig. 6a). MAPKs can be induced by ROS but can themselves module ROS production. A body of evidence is emerging that the MPK3/MPK6 pathway also orchestrates ETI responses downstream of R protein activation that contribute to elevated cROS. Conditional activation of tobacco MPK3/6 orthologues SIPK/NtMEK2 DD led to sustained activation of MPK3/MPK6 in Arabidopsis (Fig. 6c). Similarly, conditional induction of AvrRpt2 activated MPK3/MPK6, resulting in a rapid inhibition of PSII and accumulation of singlet oxygen and H$_2$O$_2$ in chloroplasts (Su et al., 2018). How MAPKs impose specificity in modulating chloroplast immunity and transcriptional regulation of NECGs requires further investigation. It has recently been shown that fluctuating light activates local and systemic transcriptional reprogramming, including overrepresentation of genes involved in photoprotection, photosynthesis and photorespiration (Kumar et al., 2018; Schneider et al., 2019). Whether MPK6 integrates the retrograde signals to drive this adaptive, photoprotective response remains to be determined.

1. Emerging examples of indirect transcriptional modulation of ETI- and PTI-mediated chloroplast immunity

Here we review two examples of chloroplast immunity impacted by differential gene regulation. The first involves ETI activation of the P. infestans R protein Rpi-vnt1.1 by its effector AVRvnt1, which depends on light-driven alternative promoter selection. Light is required for expression of full-length tomato and potato glycerate 3-kinase (GLYK) transcripts encoding a chloroplast transit sequence.
AVRvnt1 binds to this chloroplast-targeting sequence and activates resistance (independent of GLYK kinase activity), impairing accumulation of GLYK in both total and chloroplast fractions of potato (Gao et al., 2020). This is somewhat analogous to the TMV N–NRIP1 interaction described above (Caplan et al., 2008), but in this case AVRvnt1 intercepts GLYK’s trafficking to the chloroplast, the depletion of which (probably via proteasomal degradation) is indirectly sensed by Rpi-vnt1.1 activating ETI (Fig. 7a).

The second example requires both differential expression of the rice Light Harvesting Complex of Photosystem II 5 (LHCB5) and its light-dependent phosphorylation. During infection by the rice blast fungus Magnaporthe oryzae, japonica but not indica rice varieties show elevated PTI due to a simple nucleotide polymorphism in the japonica LHCB5 promoter leading to increased expression of LHCB5 (Liu et al., 2019). Cytosolic phosphorylation of LHCB5’s chloroplast transit sequence on Thr24 leads to accumulation of both LHCB5 and superoxide in the chloroplast and enhanced basal immunity. Interestingly, LHCB5 was not phosphorylated during ETI. LHCB5 overexpression lines were more resistant, and RNAi knockdown lines were more susceptible, to M. oryzae. LHCB5 binds PsbS, a thylakoid sensor that is involved in nonphotochemical quenching (NPQ). As phosphorylated LHCB5 accumulating in the chloroplast can form a trimeric complex, the authors predicted that during M. oryzae japonica infection PsbS binding is disrupted, resulting in decreased electron transfer, increased cROS and enhanced basal resistance (Fig. 7b) (Liu et al., 2019). This is supported by studies on Arabidopsis and rice plants deficient in PsbS, which have higher levels of cROS with rice mutants showing enhanced resistance to M. oryzae (Zulfugarov et al., 2014). This may help mechanistically explain the results of
Gohre et al. (2012) where the observed flg22-induced decrease in PsbS abundance may be associated with increased cROS (Gohre et al., 2012).

2. Direct targeting of ‘resistance’ proteins to the chloroplast

Given effector localization to the chloroplast, it is not unreasonable to propose classical R proteins to be associated with the chloroplast to monitor activity, and R proteins have been experimentally predicted to be chloroplast-associated (http://suba.live/). Indeed, the atypical chloroplast-localized Wheat Kinase START 1 (WKS1) confers partial race-non-specific resistance to _P. striiformis_ f. sp. _tritici_ and is encoded at the _YR36_ (Yellow Rust resistance) locus. Terminally processed WKS1 localizes to the chloroplast, binding to and phosphorylating both thylakoid-associated ascorbate peroxidase (tAPX) potentially restricting cROS detoxification (Gou et al., 2015) and PSII component PsbO, decreasing its ability to bind to the supercomplex (Wang et al., 2019) (Fig. 7c). Both _psbo-A1_ mutant and RNAi lines exhibited induction of chlorosis and reduced _P. striiformis_ f. sp. _tritici_ growth (Wang et al., 2019). The authors concluded that WKS1 initially triggers chlorosis by phosphorylating PsbO, and the gradual accumulation of ROS (exacerbated by the phosphorylation of tAPX) induces cell death. It is currently unknown whether WKS1 is a target for _P. striiformis_ f. sp. _tritici_ effectors. Thus, the PSII supercomplex is emerging as a common effector target, as further evidenced by HopN1 targeting of PsbQ (Rodriguez-Herva et al., 2012).

IX. Concluding remarks

Chloroplasts are a central hub in plant metabolism, enabling them to act as environmental sensors and communicate _via a diversity of retrograde signals to the nucleus_. It is now clear that chloroplasts play an essential role in plant immunity, and effectors from diverse pathogens have evolved to directly or indirectly target chloroplast function. At the biochemical level, the underlying mechanisms are complex, involving chloroplast-sourced oxylipins, hormones, hydrogen peroxide and singlet oxygen. An emerging theme is that PTI is associated with simultaneous repression of _NECG_ s and induction of cROS, predominantly generated at PSI. Effector-mediated suppression includes modulating _NECG_ s, and manipulating hormonal balance and various strategies to attenuate cROS via disassembly of the photosystems, although a detailed understanding of this remains elusive. Recent evidence suggests that plant resistance proteins can monitor perturbations to chloroplast homeostasis or recognize chloroplast-targeted effectors to activate ETI. Although further evidence is needed, it appears that in contrast to PTI, ETI drives O_2_ generation via PSII disassembly, the resultant lipid oxidation products contributing to HR. Impairment of photosystem function is potentiated by chloroplast-targeted effectors, some of which have been shown to interact with components of the photosystems likely to affect their function and stability. Furthermore, pathogen infection elicits chloroplast repositioning and formation of stromules that might facilitate retrograde signalling. Not considered in this review, but equally important, are the interacting roles of NO and interorganellar interactions with mitochondria (which have well-known roles in cell death) and peroxisomes.

Further challenges in this relatively embryonic field are multiple. We need to better understand the role of the multiple retrograde chloroplast to nucleus signalling pathways, in addition to ROS, which have been proposed to influence light response, and how these might interact with pathogens (Vogel et al., 2014). Furthermore, in some cases ROS production could be a side reaction associated with other changes that comprise the actual signalling mechanism. This would not be easy to resolve but should be considered when assessing results. The challenge of understanding the relationship between the production of ROS by organelles and from the initial apoplastic PAMP-induced oxidative burst will require the use of probes with high spatial and chemical specificity. It will also require understanding the chloroplast targets manipulated by pathogens to suppress immunity.

Identifying the chloroplast targets of effectors and characterizing their interaction will not only provide important insight into how pathogens have evolved to target chloroplast immunity, but may potentially identify new herbicide leads. Aside from this, other particularly fundamental questions remain. Does the increasingly observed heterogeneity in size and positioning of chloroplasts in the cell reflect different metabolism and signalling roles in response to pathogens? How are PTI-induced cROS generated and how many chloroplasts need to respond to confer effective immunity? How many effectors, both in number and in diversity, need to target a (specific) chloroplast to suppress cROS? That being the case, do R proteins effectively guard chloroplasts?

Answers to these and other questions will not only contribute to fundamental understanding of chloroplast biology, but place the chloroplast at the forefront of endeavours to develop crops with improved pathogen resistance.

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