

Signal transduction in response to excess light: getting out of the chloroplast

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Plants are continually in danger of absorbing more light energy than they can use productively for their metabolism.

Acclimation to environmental conditions therefore includes the development of mechanisms for dissipating or avoiding the accumulation of such excess excitation energy. Acclimation could be controlled by many signal transduction pathways that would be initiated by the perception of excess excitation energy both inside and outside the chloroplast. Recent studies in related areas provide models of how these signalling pathways could operate in acclimation to excess light. Components of photosynthetic electron transport chains, reactive oxygen species, redox-responsive protein kinases, thiol-regulated enzymes, chlorophyll precursors and chloroplast-envelope electron transport chains all have roles in these models.

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Abbreviations

ABA	abscisic acid
APX1	ASCORBATE PEROXIDASE1
EEE	excess excitation energy
FMN	flavin mononucleotide
JA	jasmonic acid
LHC	light-harvesting complex
LHCP	LHC protein
NADPH	reduced form of nicotinamide adenine dinucleotide phosphate
NPH1	NONPHOTOTROPHIC HYPOCOTYL 1
NPL1	NPH1-like1
PET	photosynthetic electron transport
PSII	photosystem II
PsbS	gene encoding the PSII subunit S protein
ROS	reactive oxygen species
TAK1	THYLAKOID-ASSOCIATED KINASE1

Introduction

The amount of light energy encountered by plants in excess of that which they need for photosynthetic productivity is termed excess excitation energy (EEE) [1*,2–4]. The amount of EEE that plants experience may also be dictated by additional environmental and developmental factors that cause the amount of light energy required for cellular processes to vary. Disease, nutrient and water limitation, and rapid changes in temperature can promote EEE even at light intensities that would not pose a problem under benign conditions.

The possibility of generating EEE is ever-present for land plants, which cannot move away from adverse environmental conditions. Failure to dissipate or avoid accumulating EEE leads to photooxidative damage to the photosynthetic apparatus, which is often manifested as bleaching, chlorosis or bronzing of leaves [1*,2–5]. Many mechanisms have evolved that serve to dissipate EEE and act as ‘safety valves’ to ensure that the harvesting of light energy does not inadvertently lead to cellular damage [1*]. Acclimation to a range of adverse environmental conditions might include increasing the number and efficiency of dissipatory mechanisms and developing physiological, biochemical and structural changes that avoid the accumulation of EEE.

Immediate responses to the conditions that promote EEE must initiate signalling pathways that lead to whole-plant acclimation. In this review, we draw on a wider literature to suggest ways in which such signalling pathways might be initiated and function.

Dissipation and avoidance of EEE

Several excellent reviews have been written recently that describe the protective mechanisms of dissipation and avoidance of EEE [1*,2,3,6,7]. Briefly, dissipation of EEE in plants is achieved by a combination of so-called non-photochemical and photochemical quenching processes.

Non-photochemical quenching processes include the transfer of triplet-state chlorophyll excitation energy to carotenoids that, in turn, dissipate the excess energy as heat during their return to a non-excited ground state [1*,3,6]. In *Arabidopsis*, a chlorophyll-pigment-binding protein, photosystem II (PSII) subunit S protein (which is encoded by the nuclear gene *PsbS*), has no effect on photosynthetic efficiency but is absolutely required for non-photochemical quenching [8**].

Photochemical quenching of EEE is the collective term for processes that increase the consumption of electrons by the deployment of additional metabolic sinks. These include the reduction of O₂ by electrons fed directly from PSII or PSI (i.e. the Mehler reaction), increased rates of photorespiratory and chlororespiratory metabolism, and perhaps increased C, N and S metabolism [2,7,9–12]. An increase in the production of reactive oxygen species (ROS) is an inevitable by-product of the reduction of O₂ in many of these processes. This increases further the dissipatory value of such reactions, as both electrons and energy are required to maintain an extensive network of antioxidants that prevent the accumulation of ROS [7]. Although potentially damaging, ROS also play a part in other protective responses, such as the reversible photoinhibition of PSII

activity [13], and induce acclimation to conditions that promote EEE both locally and systemically [5].

Acclimation to conditions that promote EEE not only includes an increase in the number and activity of dissipatory processes, but also may involve protective strategies that avoid the absorption of excitation energy. These include the movement of chloroplasts away from high light sources [14^{••}], a decrease in the number of photosynthetic reaction centres per unit leaf area [15], leaf curling [16], an increase in the thickness of cuticular wax or other EEE-protective screens [17] and changes in leaf and whole-plant morphology [2]. The dynamic balance of ROS and antioxidant systems has been suggested to play a crucial role in determining how quickly plants react and acclimate to changes in their environment [5,18]. This suggests that the regulatory and signal transduction pathways involved in establishing whole-plant acclimation must contain individual components that are sensitive to this ROS/antioxidant balance.

Signal transduction pathways that respond to EEE

An emerging literature clearly indicates that signalling pathways are integrated into a regulatory network, such that many pathways may share common routes or interact with one another [19–21]. We could predict, therefore, that a major part of an EEE-responsive signalling pathway(s) may well join such a regulatory network in order to effect acclimation at the whole-plant level. The remainder of this review focuses on those features of EEE signalling responses that pose the following questions: How are the conditions that promote EEE perceived and transduced into a signal, especially but not exclusively within the chloroplast? And how does a chloroplast-derived signal exit the chloroplast to join a cellular regulatory network?

The perception of EEE and the initiation of signal transduction

The photosynthetic apparatus is a prime candidate for the perception of EEE. In principle, any increase in the activity of dissipatory processes could initiate signalling pathways. In response to EEE, increases in electron transport rates and consequent redox changes in photosynthetic electron transport (PET) components would be almost instantaneous. The regulation of both nuclear and chloroplast genes that encode components of photosynthesis and antioxidant metabolism have been associated with redox changes in PET [5,22,23[•],24]. Examples of such nuclear-encoded genes include *Cab* (which encodes a chlorophyll a/b binding protein), *Lhc* (the gene encoding the light-harvesting complex protein [LHCP]; [23[•]]), *RbcS* (which encodes the small unit of ribulose-1,5-bisphosphate carboxylase/oxygenase; [23[•]]), *ASCORBATE PEROXIDASE1* (*APX1*) and *APX2* [5,22]. Chloroplast-encoded genes that have been associated with redox changes in PET include *psbA* (the gene encoding the D1 protein of the PSII reaction centre) and *psaAB* (which encodes the PSI reaction centre protein; [24]). Redox changes in the

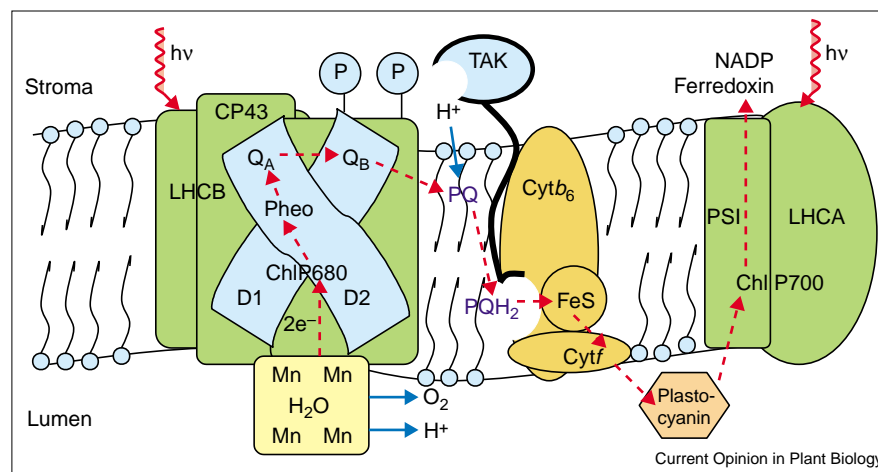
vicinity of Q_A (the primary quinone electron acceptor), Q_B (the secondary quinone electron acceptor) or plastoquinone (Figure 1) have been suggested to be key starting points for signalling [5,22,23[•],24,25]. Equally, it is likely that changes in the redox state of PET components could be coincident with, rather than determine, changes in gene expression. For example, increased rates of PET could lead to the channelling of electrons into other routes, such as the chlororespiratory pathway, which in turn could initiate a signalling pathway. Alternatively, changes in pH across thylakoid membranes upon an increase in EEE could be a rapid and powerful signal initiator [3].

The exposure of plants to wavelengths of light that favour absorption from PSII over that from PSI triggers the reversible phosphorylation of the LHCP in PSII, which then migrates from PSII towards PSI. This process is termed 'state transition', and is thought to ensure a balance in the light harvesting and, consequently, the functioning of the two photosynthetic reaction centres [24,26^{••}]. THYLAKOID-ASSOCIATED KINASE1 (TAK1) is central to this process [26^{••}]. The simplest model of how the phosphorylation of LHCP is linked to redox changes in PET components is a postulated direct interaction between the cytochrome b_6/f complex and TAK1 (Figure 1); TAK1 then disengages to carry out the phosphorylation of thylakoid proteins including LHCP [26^{••}]. This type of signal-transduction event may well prove to be a model for the type of events that initiate changes in nuclear gene expression in response to EEE.

Changes in the concentrations or rates of production of ROS, from the Mehler reaction or conceivably from chlororespiration, could be additional initiators of signalling pathways inside the chloroplast. Increases in foliar H_2O_2 concentrations have been shown to be important for the induction of *APX2* expression in excess-light-stressed *Arabidopsis* leaves, but the sub-cellular origin of this H_2O_2 was unknown [5]. Conversely, the infiltration of the thiol antioxidant glutathione (γ -glutamylcysteinyl glycine) into *Arabidopsis* leaves [27], or increasing the glutathione biosynthetic capacity of the chloroplasts of transgenic tobacco, increased the sensitivity of the leaves to excess light. Changes in chlorophyll *a* fluorescence parameters in such leaves implied a marked increase in EEE that led to damage to their photosynthetic apparatus. In both studies, this was associated with a failure to increase antioxidant-scavenging capacity in response to EEE-induced oxidative stress [22,28]. Both treatments could have changed the chloroplast redox status by upsetting the balance between ROS and antioxidant levels. This implies that signalling by chloroplast-derived ROS and/or the prevailing redox state of the chloroplast could be important determinants regulating the expression of nuclear-encoded genes [27,28,29^{••}]. The propagation of such signals inside the chloroplast may have parallels to the regulation of the translation of chloroplast-encoded mRNAs and the activity of Calvin-cycle enzymes by protein disulphide

Figure 1

Schematic description of the photosynthetic apparatus and the transport of electrons, abstracted from water, by the different PET chain components. Many of these components may be initiators of signalling in response to excess excitation energy and are discussed in the text. Chl, chlorophyll; CP43, chloroplast protein 43; D1, D1 protein; FeS, iron-sulphur centre; Pheo, pheophytin; PQ, oxidised plastoquinone; PQH₂, reduced plastoquinone; Q_A, primary quinone electron acceptor; Q_B, secondary quinone electron acceptor.



isomerase (PDI) and thioredoxin, respectively [30,31]. Both of these regulatory systems function by carrying out thiol-disulphide exchange reactions on specific redox-sensitive cysteine residues in target proteins and are dependent on the activity of PET to provide reducing equivalents. Their sensitivity to conditions that promote EEE [30,32••] show that these processes are highly responsive to chloroplast redox state.

To our knowledge, neither non-photochemical quenching mechanisms nor highly energised photosynthetic pigments have been directly implicated in any of the signalling mechanisms initiated by EEE. However, *NPH1-like1* (*NPL1*) from *Arabidopsis*, which governs the relocation of chloroplasts within the cell in response to high light intensity, encodes an extraplastidial serine/threonine protein kinase that contains a covalently bound flavin mononucleotide (FMN) moiety that is a blue-light chromophore [14••]. *NPL1* is closely related to the NONPHOTOTROPHIC HYPOCOTYL1 (*NPH1*) class of protein kinases that are involved in other blue-light-mediated responses in plants, such as phototropism [14••,33]. It is postulated that the FMN moiety of both *NPH1* and *NPL1* confers on them redox sensitivity that leads to their activation [14••,33].

The transmission of signals across the chloroplast envelope

It should be noted that many of the hormones or signalling molecules associated with stress, such as jasmonic acid (JA) and abscisic acid (ABA), are synthesised wholly or in part within the chloroplast [34,35]. The involvement of EEE in both abiotic and biotic stresses clearly shows that such molecules could, in effect, signal for EEE. For example, in drought-stressed plants, the recently described mediation of ABA-controlled stomatal closure by H₂O₂ [36••] is a clear indication of the way in which such signalling molecules could interact with the products of EEE. To our knowledge, the routes that these molecules might use to exit the chloroplast are not known.

H₂O₂ is thought to freely diffuse as easily as water across biological membranes [5,37]. Chloroplast-derived H₂O₂ could, therefore, directly influence the functions of extra-plastidial signalling components. The potential for H₂O₂ to act as an intracellular mobile signalling molecule is demonstrated by its role in the systemic responses of plants to excess light [5], pathogens [38] and physical damage [39].

Oxidative damage to the thylakoid membranes brought about by EEE could lead to the release of oxygenated fatty acid derivatives, including JA, known collectively as oxylipins [39,40••]. The appearance of these compounds in plant tissues is associated with physical damage and disease [39,40••], but there is no reason why such compounds could not be formed under conditions that promote EEE in the chloroplast [19]. Such compounds may be membrane-permeable and, in *Arabidopsis*, have been shown to induce expression of *GLUTATHIONE-S-TRANSFERASE1* (*GST1*), a gene whose expression responds to a wide range of conditions, including those that promote EEE [19,40••].

In *Chlamydomonas*, chlorophyll precursors have been implicated in chloroplast-to-nucleus signalling during dark-to-light transitions [41••]. Exogenous supply of these precursors to cultures mediated the light-induction of the expression of heat-shock genes in mutants otherwise incapable of this response to light [41••]. Kropat *et al.* [41••] hypothesised, therefore, that in higher plants as well as in algae, the release or export of chlorophyll precursors from the chloroplast is an active process that can occur under certain stress conditions and that can initiate defence responses.

Rates of photorespiration increase substantially in response to EEE [9,37,42]. The consequent increase in photorespiratory metabolism in the peroxisome causes increased rates of H₂O₂ formation, brought about by the oxidation of glycolate [37]. Increased levels of photorespiratory H₂O₂ have been shown to elicit cellular antioxidant defences in

transgenic tobacco plants that are deficient in catalase [37], but whether this occurs in wildtype plants remains to be established. Nevertheless, photorespiratory metabolites must be candidates for a means of getting an EEE-responsive signal out of the chloroplast.

The different scenarios described above all depend upon the passage of some molecule out of the chloroplast to propagate a signal leading to nuclear gene expression. Spectroscopic studies have shown, however, that the chloroplast envelope contains a number of constituents that are involved in the transfer of electrons and therefore could provide another exit for a chloroplast-derived signal. These include iron-sulphur proteins, semiquinones, flavins and α -tocopherol [43]. It is possible to draw a scheme in which an electron transport chain starts with NADPH in the stroma, spans the chloroplast envelope and ends with O_2 as the terminal electron acceptor on the chloroplast outer surface [43]. From the stoichiometry of electron transfer from NADPH, there is a clear implication that ROS could be formed outside the chloroplast and could, therefore, act to propagate any signal emanating from it. Exposure to excess light, for example, would at least transiently increase PET rates, which could stimulate the activity of an envelope-spanning electron transport chain.

Joining the mainstream

In many of the schemes outlined above, H_2O_2 or other ROS are the end-products of signalling pathways that emanate directly or indirectly from the chloroplast. There are a number of ways in which one can envisage how such a signal might be propagated further. ROS could directly interact with redox-sensitive transcription factors paralleling OxyR and Sox/RS in *E. coli* or I- κ B:NF- κ B in animals [44,45]. The activation of transcription factors would then lead to change in gene expression.

Intracellular Ca^{2+} fluxes and the action of signalling molecules, such as phosphoinositides and JA, have been shown to respond to oxidative stress and have been suggested as a means whereby cross-talk between pathways is achieved [21,46–48]. The activation of extensive calcium-dependent protein kinase cascades could provide a mechanism whereby a chloroplast-derived ROS signal would merge into a regulatory network. The indirect activation of a mitogen-activated protein kinase cascade in H_2O_2 -treated *Arabidopsis* protoplasts, which induced the expression of genes involved in defence against oxidative stress and suppressed genes that are involved in plant growth [49**], is a clear indication of how such networks might operate.

Conclusions

We have described briefly some of the means whereby EEE can initiate signalling leading to acclimation to changing environmental circumstances. Given the flexibility of plants' responses to environmental change and the importance of protection against EEE, it would not be

surprising to find that all of these possible signalling routes exist, reflecting the simultaneous operation of many different protective mechanisms.

There is a need to understand how wide a range of adverse environmental factors provoke the same changes in cellular metabolism, reflecting the changed expression of a common or overlapping set of genes. The holistic view of cellular metabolism that metabolite, protein and transcript profiling technology could bring to this problem may prove to be seminal. It is to be hoped that a rational and prediction-based understanding of how plants thrive in highly variable and often adverse environments will emerge from such systems analysis.

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