Running title: Glutathione reductase in H$_2$O$_2$ responses

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Arabidopsis GLUTATHIONE REDUCTASE 1 plays a crucial role in leaf responses to intracellular H$_2$O$_2$ and in ensuring appropriate gene expression through both salicylic acid and jasmonic acid signaling pathways[1][W]

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Abstract

Glutathione is a major cellular thiol that is maintained in the reduced state by glutathione reductases (GR), which is encoded by two genes in *Arabidopsis thaliana* (*GR1* and *GR2*). This study addressed the role of *GR1* in H$_2$O$_2$ responses through a combined genetic, transcriptomic, and redox profiling approach. To identify the potential role of changes in glutathione status in H$_2$O$_2$ signaling, *gr1* mutants, which show a constitutive increase in oxidized glutathione (GSSG), were compared with a catalase-deficient background (*cat2*), in which GSSG accumulation is conditionally driven by H$_2$O$_2$. Parallel transcriptomics analysis of *gr1* and *cat2* identified overlapping gene expression profiles that in both lines were dependent on growth daylength. Overlapping genes included phytohormone-associated genes, in particular implicating glutathione oxidation state in the regulation of jasmonic acid signaling. Direct analysis of H$_2$O$_2$-glutathione interactions in *cat2 gr1* double mutants established that *GR1*-dependent glutathione status is required for multiple responses to increased H$_2$O$_2$ availability, including limitation of lesion formation, accumulation of salicylic acid, induction of pathogenesis-related genes, and signaling through jasmonic acid pathways. Modulation of these responses in *cat2 gr1* was linked to dramatic GSSG accumulation and modified expression of specific glutaredoxins and glutathione S-transferases, but little or no evidence of generalized oxidative stress or changes in thioredoxin-associated gene expression. We conclude that *GR1* plays a crucial role in daylength-dependent redox signaling and that this function cannot be replaced by the second *Arabidopsis* glutathione reductase gene or by thiol systems such as the thioredoxin system.
Thiol-disulfide exchange plays crucial roles in protein structure, the regulation of enzymatic activity, and in redox signaling, and is principally mediated by thioredoxin (TRX) and glutathione reductase (GR)/glutathione systems (Buchanan and Balmer, 2005; Jacquot et al., 2008; Meyer et al., 2008). Arabidopsis lines identified in independent screens for alterations in heavy metal tolerance, meristem function, light signaling, and pathogen resistance have been shown to harbor mutations in the gene encoding the first enzyme of glutathione synthesis (Cobbett et al., 1998; Vernoux et al., 2000; Ball et al., 2004; Parisy et al., 2007). Studies on the rml1 mutant, which is severely deficient in glutathione synthesis, define a specific role for glutathione in root meristem function (Vernoux et al., 2000). However, shoot meristem function is regulated in a redundant manner by cytosolic glutathione and TRX (Reichheld et al., 2007), providing a first indication for functional overlap between these thiol-disulfide systems in plant development.

Modifications of cellular thiol-disulfide status may be important in transmitting environmental changes that favor the production of oxidants such as H$_2$O$_2$ (Foyer et al., 1997; May et al., 1998; Foyer and Noctor, 2005). The glutathione/GR system is involved in H$_2$O$_2$ metabolism by reducing dehydroascorbate generated following the (per)oxidation of ascorbate (Asada, 1999). This pathway is one way in which H$_2$O$_2$ reduction could be coupled to NADPH oxidation, with the first reaction catalyzed by ascorbate peroxidase (APX) and the last by GR, though ascorbate regeneration can occur independently of GSH through NAD(P)H- or (in the chloroplast) ferredoxin-dependent reduction of monodehydroascorbate (MDAR) (Asada, 1999). Additional complexity of the plant antioxidative system has been highlighted by identification of several other classes of antioxidative peroxidases that could reduce H$_2$O$_2$ to water. These include the TRX fusion protein CDSP32 (Rey et al., 2005) and several types of peroxiredoxin (PRX), many of which are themselves TRX-dependent (Dietz, 2003). Plants lack animal-type selenocysteine-dependent glutathione peroxidase (GPX), instead containing cysteine-dependent GPX (Eshdat et al., 1997; Rodriguez Milla et al., 2003). Despite their annotations as GPX, these enzymes are now thought to use TRX rather than GSH (Iqbal et al., 2006). However, H$_2$O$_2$ could still oxidize GSH via peroxidatic glutathione S-transferases (GSTs) and/or glutaredoxin (GRX)-dependent PRX (Wagner et al., 2002; Jacquot et al., 2008). Metabolism of H$_2$O$_2$ may occur through APX or through ascorbate-independent GSH peroxidation, both of which potentially depend on GR activity, as well as through TRX-dependent pathways. The relative importance of these pathways remains unclear.
The major sites of intracellular H$_2$O$_2$ production in most photosynthetic plant cells are the chloroplasts and peroxisomes (Noctor et al., 2002). Despite this, Davletova et al. (2005) demonstrated a crucial role for cytosolic APX1 in redox homeostasis in *Arabidopsis*. This finding implies that the cytosolic ascorbate-glutathione pathway is important in metabolizing H$_2$O$_2$ originating in other organelles, thus marking out this compartment as a key site in which redox signals are integrated to drive appropriate responses. Cytosolic metabolism of H$_2$O$_2$ could be key in setting appropriate conditions for thiol-disulfide regulation through cytosolic/nuclear signal transmitters such as NPR1 and TGA transcription factors (Després et al., 2003; Mou et al., 2003; Rochon et al., 2006; Tada et al., 2008). Because peroxisomal reactions can be a major producer of H$_2$O$_2$, a related issue that remains unresolved is to what extent reductive H$_2$O$_2$ metabolism overlaps with metabolism through catalase, which is confined to peroxisomes and homologous organelles. Intriguingly, double antisense tobacco lines in which both catalase and cytosolic APX were down-regulated showed a less marked phenotype than single antisense lines deficient in either enzyme alone (Rizshky et al., 2002). This observation implies that if the major role of the GR-glutathione system is indeed to support reduction of DHA to ascorbate, down-regulation of cytosolic GR capacity should produce a similar effect to APX deficiency.

Two genes are annotated to encode GR in plants. Pea chloroplast GR was the first plastidial protein shown also to be targeted to the mitochondria (Creissen et al., 1995). Dual-targeting of this protein also occurs in *Arabidopsis* (Chew et al., 2003), where the plastidic/mitochondrial isoform is named GR2. The second gene, *GR1*, is predicted to encode a cytosolic enzyme. In pea, cytosolic GR has been well characterized at the biochemical level (Edwards et al., 1990; Stevens et al., 2000) but the functional significance of the enzyme remains unclear. Under- or overexpression studies in tobacco and poplar have reported significant effects of modifying chloroplast GR capacity (Aono et al., 1993; Broadbent et al., 1995; Foyer et al., 1995; Ding et al., 2009). Less evidence is available supporting an important role for cytosolic GR. In insects, GSSG reduction can also be catalyzed by NADPH-TRX reductases (NTR; Kanzok et al., 2001) and it has recently been shown that *Arabidopsis* cytosolic NTR can functionally replace GR1 (Marty et al., 2009).

Key outstanding issues in the study of redox homeostasis and signaling in plants are therefore (1) the importance of GR/glutathione in H$_2$O$_2$ metabolism and/or H$_2$O$_2$ signal transmission
and (2) the specificity of GSH and TRX systems in H$_2$O$_2$ responses. In this study we sought to address these questions by a genetically based approach in which the effects of modified H$_2$O$_2$ and glutathione were first analyzed in parallel in single mutants then directly through the production of double mutants. This was achieved using gr1 insertion mutants and a catalase-deficient Arabidopsis line, cat2, in which intracellular H$_2$O$_2$ drives accumulation of GSSG in a conditional manner (Queval et al., 2007). Our study provides in vivo evidence for a specific irreplaceable role for GR1 in H$_2$O$_2$ metabolism and signaling.

RESULTS

Characterization of gr T-DNA Mutants

While T-DNA insertions in the coding sequence of dual-targeted chloroplast/mitochondrial GR2 are embryo-lethal (Tzafrir et al., 2004), homozygous gr1 mutants were readily obtained. RT-PCR confirmed the absence of GRI transcript while total extractable GR activity was decreased by 40% relative to Col-0 (Supplemental Figure S1). Despite these effects, repeated observations over a period of five years showed that the mutation produced no difference in rosette growth rates from Col-0 in either short days (SD) or long days (LD) or in flowering timing and leaf number (data not shown). Thus, our analysis is in agreement with the report of Marty et al. (2009) that absence of cytosolic GR activity caused a measurable decrease in leaf GR activity but that this did not cause phenotypic effects. Moreover, analysis of the response to two abiotic stresses showed that the gr1 mutation did not affect root growth in either high salt or cadmium (data not shown).

Comparative Analysis of Glutathione and H$_2$O$_2$-dependent Changes in Gene Expression

Because gr1 mutants are aphenotypic in typical growth conditions, the present study analyzed the potential role of the enzyme in H$_2$O$_2$ metabolism and signaling. First, we performed parallel microarray analysis of GSSG-accumulating gr1 and the catalase-deficient mutant cat2, which conditionally accumulates GSSG triggered by photorespiratory H$_2$O$_2$ production (Queval et al., 2007). To compare effects on transcript abundance while minimizing possible interference of long-term developmental effects due to oxidative stress in cat2 grown from seed in air, plants were sampled following initial growth at high CO$_2$, where the cat2 mutation is silent (Queval et al., 2007). This experimental design was chosen to allow comparison of
the effects of modified glutathione status in gr1 with similar H2O2-induced effects triggered in cat2 after transfer from high CO2 to air. Our rationale was that while H2O2 may modify gene expression through a number of signaling mechanisms, any effects mediated via glutathione should also be observed in gr1, even in the absence of the oxidative stress that drives GSSG accumulation in cat2 (Fig. 1A).

As previously reported, cat2 showed a wild-type phenotype at high CO2. The consequences of the cat2 mutation for gene expression and phenotype in air are strongly influenced by growth photoperiod (Queval et al., 2007). Thus, measurements of transcripts and antioxidant were performed after transfer of gr1 and cat2 from high CO2 to air in both SD (8h photoperiod) and LD (16h photoperiod). In both photoperiods (and at high CO2), the glutathione reduction state was lower in gr1 than in Col-0 (Fig. 1B). In cat2, however, this factor was only lower than in Col-0 after transfer to air, where it was decreased below the values observed in gr1. In both mutants, leaf ascorbate contents were much less affected than glutathione. The only significant difference was observed in ascorbate reduction state in cat2 in LD (Supplemental Fig. S2).

Analysis of microarray data was performed by considering as being differentially expressed genes with a Bonferroni P-value ≤ 0.05, as described in Gagnot et al. (2008). An additional selection criterion was introduced by considering only genes that showed statistically significant same-direction change in both biological replicates. The analysis showed that H2O2-regulated gene expression (in cat2) was highly daylength-dependent (Fig. 1C). More genes were significantly induced in cat2 transferred to air in SD than in LD, whereas the reverse was true for significantly repressed genes. Fewer genes were affected in gr1 but effects were also daylength-conditioned. Of genes induced in gr1 in SD only three were also induced in LD, together with another four LD-specific genes. The number of repressed genes in gr1 in LD was similar to that in SD (Fig. 1C) but of these only two were common (Supplemental Table S2). Thus, as for genes regulated by an H2O2 signal, gene expression dependent on a drop in glutathione reduction state was strongly determined by photoperiod context. Of the 58 genes showing significantly modified expression in response to a mild perturbation of glutathione redox state in gr1, most showed significant same-direction changes in at least one cat2 replicate (Supplemental Table S2). It should be noted that Figure 1C provides a conservative estimate of overlap between gr1 and cat2 transcriptomes because
only genes that showed statistically significant same-direction changes in all four dye-swap repeats (two gr1/Col-0 and two cat2/Col-0) are considered.

Several genes whose expression was modified in gr1 encoded stress-related proteins, notably cadmium-, salt- and cold-responsive genes, as well as two glutathione S-transferases (GSTU7 and GSTU6) and three multidrug resistance-associated proteins (Supplemental Table S2). This is consistent with the roles of glutathione in redox homeostasis, heavy metal resistance, cold acclimation, and metabolite conjugation and transport (May et al., 1998; Cobbett et al., 1998; Kocsy et al., 2000; Wagner et al., 2002; Gomez et al., 2004).

Sixteen of the 58 gr1-sensitive genes are annotated as phytohormone-associated. In all cases, induction or repression of these genes was dependent on daylength context (Table 1). A putative monoxygenase with similarity to SA-degrading enzymes was among induced genes whereas other differentially expressed genes in gr1 were associated with auxin, gibberellin, ABA, and ethylene function (Table 1). The most striking impact of the gr1 mutation was on the expression of genes involved in jasmonic acid (JA) synthesis and signaling. Of the 18 genes repressed in gr1 in LD, eight have been shown to be early JA-responsive genes (Yan et al., 2007). These genes encoded, among others, LIPOXYGENASE3 (LOX3), MYB95, GSTU6, and two of the 12 JASMONATE/ZIM-DOMAIN (JAZ) proteins recently characterized as JA-inducible repressors of JA signaling (Staswick, 2008; Browse, 2009). All but one of the JA-dependent genes repressed in gr1 in LD showed the same response in the GSSG-accumulating cat2 mutant (Table 1).

Two induced stress-associated genes and four JA-dependent genes that showed similar responses in gr1 and cat2 were selected for qPCR analysis. This confirmed the induction in gr1 of the cold-regulated COR78 in SD and of the cadmium-responsive At3g14990 in both daylength conditions (Fig. 2). For the JA-associated genes, qPCR revealed that in addition to repression in gr1 and cat2 in LD, three of the four genes (LOX3, MYB95, and JAZ10) were also induced in SD (Fig. 2). Thus, GR1-dependent glutathione status influences expression of genes involved in JA synthesis and signalling in a daylength-dependent manner.

**Genetic Analysis of GR1 Function in Responses to H₂O₂**
To directly explore the role of GRI and glutathione status in the H₂O₂ response, the gr1 mutation was crossed into the cat2 background. Preliminary analysis of F2 seeds grown in air failed to identify double cat2 gr1 homozygotes. Thus, F3 seeds from a cat2/cat2 GRI/gr1 genotype were germinated and grown at high CO₂ where, as noted above, the cat2 mutation is phenotypically silent because photorespiratory H₂O₂ production is largely shut down. Genotyping of these seeds identified several plants with cat2/cat2 gr1/gr1 genotypes, suggesting selection against cat2 gr1 double homozygotes in the presence of photorespiratory H₂O₂ production (air) but not in its absence (high CO₂).

When F4 seeds obtained from F3 cat2 gr1 double homozygotes identified at high CO₂ were sown on agar plates in air, germination was similar to Col-0, gr1, and cat2, but growth was severely compromised in all cat2 gr1 plants from the cotyledon stage onwards (Fig. 3A). Although cat2 gr1 was able to grow on soil at moderate irradiance, all plants with this genotype showed a dwarf rosette phenotype that was much more severe than that observed in cat2 (Fig. 3B).

The cat2 gr1 phenotype was completely reverted by growth at high CO₂ (Fig. 4A). Together with the aphenotypic nature of the single gr1 mutant, this observation indicates that the functional importance of GR1 is highly correlated with conditions of increased intracellular H₂O₂ availability. To further investigate this point, we analyzed the phenotypic responses of cat2 gr1 grown at high CO₂ after transfer to air in either SD or LD. Lesions developed in cat2 at 5-6 days after transfer to LD but did not develop in SD (data not shown). Four days after the transfer to LD, few or no lesions were apparent on cat2 leaves (Fig. 4B). By contrast, extensive bleaching was observed on cat2 gr1 leaves as early as two days after the transfer to air in LD (Fig. 4B). In both photoperiods, photorespiratory H₂O₂ induced slower growth in cat2 and this effect was exacerbated by the absence of GRI function (Fig. 4C). Remarkably, however, bleaching was limited or absent in cat2 gr1 transferred to air in SD.

To verify the conditional genetic interaction between the cat2 and gr1 mutations, a second allelic gr1 T-DNA line was obtained and crossed with cat2. F2 plants from this cross were grown at high CO₂ then transferred to air in LD, and lesions were quantified and plants were genotyped (Supplemental Fig. S3). Neither F1 CAT2/cat2 GRI/gr1 double heterozygotes grown in air nor any F2 plants grown at high CO₂ showed any apparent phenotype (data not shown). Of 93 F2 plants transferred from high CO₂ to air in LD, seven displayed readily
visible lesions within four days (Supplemental Fig. S3). Genotyping confirmed that all plants showing substantial lesions were cat2/cat2 gr1/gr1 double homozygotes, and lesion quantification and rosette fresh mass distinguished these plants from the eight other genotypes (Supplemental Fig. S3).

**Microarray Analysis of the H2O2-GR1 Interaction**

To identify H2O2-regulated genes whose expression is dependent on GR1, transcript profiling of cat2 and cat2 gr1 was performed after transfer of plants grown at high CO2 to air. In view of the above phenotypic observations and the daylength-dependent transcript profiles for cat2 and gr1 single mutants (Fig. 1, Supplemental Table S2), the analysis was performed after transfer to both SD and LD. A full list of significantly different genes and signal intensities is given in Supplemental Table S3.

Clustering analysis of significantly different transcripts delineated two major patterns of H2O2-induced gene expression (Fig. 5). The first was largely composed of genes that were induced by photorespiratory H2O2 in cat2 and cat2 gr1 (cluster 1) while the second comprised genes that responded in a daylength-dependent manner (cluster 2). The most striking impact of the gr1 mutation in the cat2 background was to annul or impair induction of genes by photorespiratory H2O2 in SD, an effect exemplified by a sub-cluster of genes in cluster 2. Of 62 genes in this sub-cluster, 33 are annotated as involved in JA- or wounding-dependent responses (Taki et al., 2005; Yan et al., 2007; http://www.arabidopsis.org) and are highlighted yellow in Figure 5. Data mining of all significantly different genes using the above datasets revealed that, in all, 47 genes inducible by JA or wounding, or encoding proteins involved in JA synthesis, conjugation or signaling, were differentially expressed in cat2 and/or cat2 gr1 (Supplemental Table S4). Twenty-five of these were among 35 genes recently shown to be induced by wounding in a JA-dependent manner (Yan et al., 2007) while among the others were established JA-associated genes such as LOX2, LOX3, OPR3, JAZ1, JAZ3, JAZ7, JAZ9, JAR1, and JMT1.

In the cat2 single mutant, the predominant effect of H2O2 on genes involved in JA synthesis and signaling was induction in SD and/or repression in LD. This daylength-dependent regulation was strongly modulated by the absence of GR1 function in cat2 gr1. Of the 47 JA-associated transcripts whose abundance was significantly modified in cat2 and/or cat2 gr1
relative to Col-0, only 10 did not show differential expression between the two lines in at least one photoperiod (Supplemental Table S4). The overwhelmingly predominant effect of the gr1 mutation in the cat2 background to cause or enhance repression (eg, LOX2, JMT1, JAZ3), to oppose induction in SD (eg, RAP2.6, JAZ10, AOS), or both (LOX3, TAT3, OPR3).

Profiling of Glutathione and Associated Gene Expression in cat2 gr1

Consistent with the absence of phenotype at high CO2 (Fig. 4A), cat2 glutathione status was similar to wild-type (95% GSH) whereas in cat2 gr1 the glutathione pool was only about 70% reduced (Fig. 6A), ie, similar to the gr1 single mutant in air or at high CO2 (Supplemental Fig. S2). These observations are consistent with the silent nature of the cat2 mutation at high CO2 and with a constitutive oxidation of glutathione in the gr1 genotype. The impact of the gr1 mutation on glutathione in conditions of increased H2O2 was assessed under the same conditions as for the microarray analysis. A time course following transfer to air revealed that leaf glutathione (1) became progressively oxidized and accumulated in cat2; (2) became much more rapidly oxidized and accumulated more strongly in cat2 gr1; and (3) was most oxidized and most strongly accumulated in cat2 gr1 in SD. The changes in glutathione involved a fall in the GSH:GSSG ratio to below 1 in cat2 and cat2 gr1, with the lowest ratio observed in cat2 gr1 in SD (Fig. 6A).

Mining of the transcriptome data for glutathione-associated genes showed that modified glutathione status in cat2 and cat2 gr1 was associated with induction of genes encoding three GSTs of the tau class (GSTU7, GSTU8, GSTU19) and two of the phi class (GSTF2, GSTF8), two multidrug resistance associated protein (MRP2 and MRP14), a glutathione/thioredoxin peroxidase (GPX6), a glyoxylase I family protein, two members of the glutaredoxin (GRX) family, and a GRX-like expressed protein (Fig. 6B). These genes were equally or more strongly induced in cat2 gr1 compared to cat2, though the effect depended on daylength. In no case did the gr1 mutation oppose induction of these genes in cat2, which were all found to be grouped in cluster 1 on the heatmap shown in Figure 5.

Five glutathione-associated genes showed a different expression pattern (Fig. 6B, bottom) and were all found within cluster 2 shown in Figure 5. While one GRX (At5g18600) showed a tendency to repression in all conditions, repression was only significant in cat2 gr1 in SD. GSTU5 and GSTU6 were both induced in cat2 but not in cat2 gr1 in SD, and repressed in
both genotypes in LD (Fig. 6B). The gr1 mutation in the cat2 background also produced repression of GGT1 and GRX480, specifically in LD. Thus, the expression patterns of these five genes were similar to those of JA-dependent genes (Fig. 5, Supplemental Table S4). In contrast to the differential expression of these glutathione-dependent genes, the expression of cytosolic thioredoxins and associated genes involved in thiol-disulfide exchange reactions was little or not affected in either cat2 or cat2 gr1 genotypes (Supplemental Table S5).

Analysis of Oxidative Stress and the Ascorbate-Glutathione Pathway

Catalase-independent pathways of H₂O₂ metabolism depend on ascorbate, which is considered to be partly regenerated by glutathione, while NADPH is required for reduction of GSSG. Despite this, the effects of gr1 and cat2 mutations on glutathione pools were not associated with marked perturbation of leaf ascorbate pools, which remained more than 80% reduced in all plants. In LD conditions, ascorbate was decreased in cat2 and cat2 gr1, though this small effect was only statistically significant for cat2 (Fig. 7A). Like ascorbate, the NADP reduction state was not greatly affected in any of the samples (Fig. 7B). The only significant effects were observed in cat2 gr1, which in SD had more NADPH than Col-0 and in LD less NADP⁺. Because of these effects, the most reduced NADP(H) pools were observed in cat2 gr1. Assay of lipid peroxidation products using thiobarbituric acid also showed no significant effect between any of the samples in either condition (Fig. 7C).

Potential problems that must be taken into account in measuring H₂O₂ include low assay specificity, interference, and extraction efficiency (Wardman, 2007; Queval et al., 2008). In this study, we used three different techniques to assess H₂O₂ or ROS levels in cat2 and cat2 gr1. In situ staining using DAB did not produce evidence for generalized accumulation of H₂O₂ in gr1, cat2, or cat2 gr1 leaves in SD or LD (Supplemental Fig. S5A). Likewise, assays of extractable peroxides using luminol chemiluminescence did not find increased contents in cat2 or cat2 gr1 in either daylength condition (Supplemental Fig. S5B). Semi-quantitative ROS visualization within the mesophyll cells in vivo also revealed that the cat2 mutation caused only minor increases in dichlorofluorescein fluorescence (Fig. 8). The cat2 gr1 double mutant showed an appreciably stronger fluorescence signal, but this effect was specific to plants in SD (Fig. 8).
To further assess the impact of the mutations on the ROS-antioxidant interaction, we measured the extractable activities and expression of APX, catalase, GR, and dehydroascorbate reductase (DHAR), the enzyme linking glutathione and ascorbate pools. The only one of these enzyme activities that was significantly different between Col-0 and grl was GR (Fig. 9A). Similarly, the grl mutation in the Col-0 background produced no significant change in transcripts other than GRL (Fig. 9C). Decreased catalase activity in cat2 was associated with an increase in APX activity in both conditions (Fig. 9A). Increased APX activity was accompanied by induction of transcripts for APX1, encoding the cytosolic isoform (Davletova et al., 2005). Of eight APX transcripts present on the chip, only APX1 was significantly increased in cat2 and, as for APX activity, this effect was similar in both SD and LD (Fig. 9C). Induction of APX1 in cat2 was accompanied by induction of a cytosolic DHAR (DHAR2) though this effect was stronger in SD than in LD and was not associated with a marked increase in the overall activity of this enzyme. Compared to Col-0, effects in cat2 grl were similar to those observed in cat2, ie, induction of APX1 in both SD and LD, an increase in extractable APX in the two conditions, and induction of DHAR2 transcripts, particularly in SD (Fig 9). Overall, the presence of the grl mutation in Col-0 or cat2 backgrounds did not greatly affect responses of these antioxidative systems relative to the respective controls.

Despite the oxidation of the glutathione pool in cat2 and its very marked oxidation in cat2 grl (Fig. 6A), neither genotype showed compensatory induction of GR2 transcripts, encoding the chloroplast/mitochondrial isoform (Fig. 9C).

**Salicylic Acid Signaling and Pathogen Responses**

Given the observed effects on JA associated genes (Fig. 5, Table 1, Supplemental Table S4), and the opposition between JA signaling and SA-dependent pathways (Dangl and Jones, 2001; Koorneef et al., 2008), we analyzed SA and expression of SA marker genes in grl, cat2 and cat2 grl in both daylength conditions. SA-dependent PR genes (PR1, PR2) were both significantly induced in cat2 in LD but less strongly or not at all in SD (Fig. 10A). Induction of SA-dependent PR genes in cat2 in LD was antagonized by the grl mutation, producing significantly lower expression in cat2 grl. Leaf SA contents were similar in all samples in SD, though slightly decreased in cat2 grl, whereas in LD H2O2-induced SA accumulation was observed in cat2 but not in cat2 grl (Fig. 10A). The grl mutation also decreased basal SA levels in the Col-0 background in LD (Fig. 10A).
We investigated the response of gr1 to infection with the virulent bacterium P. syringae DC3000 (Fig. 10B). Bacterial growth in gr1 leaves was intermediate between that observed in Col-0 and the npr1-1 mutant, in which cytosolic redox-modulated NPR1 function is lacking (Mou et al., 2003). In agreement with the data of Fig. 10A, increased sensitivity to bacteria in gr1 was associated with lower total SA levels than in Col-0 (Fig. 10B).

DISCUSSION

Recent data have highlighted the functional overlap between glutathione and TRX systems (Reichheld et al., 2007; Marty et al., 2009). A key question therefore concerns the specificity of cytosolic GR-glutathione and NTR-TRX functions. Glutathione has been proposed to play a role in H2O2 signaling (Foyer et al., 1997; May et al., 1998). Here, we present a targeted, genetically based study of such a role by using cat2 and gr1 mutants in combination.

GLUTATHIONE REDUCTASE 1 Plays a Non-redundant Role in H2O2 Metabolism and Signaling

In this study, the cat2 mutant was used both as a reference GSSG-accumulating H2O2 signaling system and as a genetic background in which to directly explore the GR1-H2O2 interaction. Because daylength-dependent effects have been described for redox signaling during pathogen and oxidative stress responses (Dietrich et al., 1994; Karpinski et al., 2003; Queval et al., 2007; Vollnes et al., 2009), we analyzed the importance of GR1 in Col-0 and cat2 backgrounds in two growth daylengths.

Our analysis of gr1 in the Col-0 background confirm the results of Marty et al. (2009) that GR1 is not required for growth in optimal conditions. However, GR1 plays an important role when intracellular H2O2 production is increased and during pathogen challenge. The effect of gr1 on the cat2 phenotype contrasts with results in which plants were exposed to exogenous H2O2 present in agar, where no difference was found between gr1 and Col-0 phenotypes, even at highly challenging H2O2 concentrations (Marty et al., 2009). This suggests that the site of H2O2 production is crucial. Enhanced H2O2 availability in cat2 leaves placed in air occurs intracellularly through the photorespiratory enzyme, glycolate oxidase, which is located in peroxisomes. In these conditions, redox perturbation in cat2 produces similar effects to those observed in stress conditions, notably oxidation and accumulation of glutathione and changes
in the abundance of many stress-related transcripts. GR activity has been detected in pea leaf peroxisomes and it is likely that GR1 is found in Arabidopsis peroxisomes as well as in the cytosol (Jiménez et al., 1997; Kaur et al., 2009). It is therefore possible that GR1 is important in peroxisomal ascorbate- and/or glutathione-dependent H$_2$O$_2$ metabolism. At least one (APX3) and possibly as many as three (APX4, APX5) Arabidopsis APXs are targeted to peroxisomes or the peroxisomal membrane (Narendra et al., 2006) but the corresponding transcripts were not significantly induced in gr1, cat2 or cat2 gr1 (Fig. 9). Most of the antioxidative genes that were induced in cat2 and cat2 gr1 encoded cytosolic enzymes, including APX1, DHAR2, and MDAR2 (Supplemental Table 3). The present analysis thus point to tight coupling between H$_2$O$_2$ produced in the peroxisomes and cytosolic antioxidative systems.

The dramatic accumulation of GSSG in cat2 gr1 placed in air shows that GSH regeneration through alternative pathways is rapidly exceeded under conditions of enhanced intracellular H$_2$O$_2$ availability. To our knowledge, the accumulation of GSSG in cat2 gr1 (up to 2 µmol GSSG g$^{-1}$ fresh weight: Fig. 6A) exceeds previously reported values for this compound in leaf tissues. Further work is required to identify the compartments in which such marked accumulation of GSSG occurs. Analysis of the gr1 single mutant in air and the cat2 gr1 double mutant at high CO$_2$ show that mild perturbation of the glutathione pool is not sufficient to produce marked phenotypic effects, while effects produced by the more severe perturbation of glutathione in cat2 gr1 in air were dependent on growth daylength. Lesions were not observed in cat2 gr1 in SD, even though these plants showed the most dramatic GSSG accumulation and the lowest GSH:GSSG ratios. Oxidized glutathione pools are considered to be among cellular factors underlying dormancy and cell death (Kranner et al., 2002, 2006). However, the present data show that although growth arrest was linked to glutathione perturbation in both daylengths, leaf cells can tolerate extreme perturbation of intracellular thiol-disulfide state without undergoing bleaching (Fig 5). Analysis of ascorbate, TBARS and ROS also provided little evidence that oxidative stress was stronger in LD compared to SD.

The dramatic perturbation of glutathione pools in cat2 gr1 compared to cat2 provides direct evidence for the role of GR1 in intracellular H$_2$O$_2$ metabolism. Analysis of ROS suggests that H$_2$O$_2$ accumulation in cat2 is localized and/or minimized by metabolism through ascorbate- and/or glutathione-dependent pathways. Little or no detectable increase in H$_2$O$_2$ in cat2 compared to wild-type is consistent with previous studies of catalase-deficient tobacco and
barley lines (Willekens et al., 1997; Noctor et al., 2002; Rizhsky et al., 2002). Although certain antioxidative enzymes and transcripts were up-regulated in cat2 and cat2 gr1, these effects were at least as marked in SD as in LD. ROS signal intensity was increased in cat2 gr1 in SD, but increases were less evident in this genotype in LD (Fig. 8), conditions in which bleaching occurred (Fig. 5). An alternative explanation of the requirement of LD conditions for leaf bleaching is that other daylength-linked signals are required in addition to oxidative stress intensity.

The phenotype of cat2 gr1 in LD contrasts with observations of tobacco plants deficient in both cytosolic APX and catalase, which showed an ameliorated phenotype compared to parent lines (Rizhsky et al., 2002). One explanation of the different effects of GR and APX deficiency in catalase-deficient plants is that some proportion of H2O2 is metabolized through GR-dependent but ascorbate-independent pathways. Hence, as well as GSH oxidation by DHA, glutathione perturbation in cat2 may occur both through enzyme-catalyzed peroxidation of GSH, eg, catalyzed by certain GSTs (discussed further below). Although increases in APX activities in cat2 and cat2 gr1 were associated with induction of APX1 (Fig. 9), several glutathione-associated genes with potential peroxidative functions were also induced in these lines (Fig. 6).

**H2O2 and Glutathione Modulate the Expression of Specific Glutathione-associated Genes in a Daylength-dependent Manner**

Although there was no evidence of oxidative stress or phenotypic effects in the gr1 single mutant, transcriptomes in this line partly overlapped with that of the H2O2 signaling reference system, cat2. Both transcriptomes was found to be highly dependent on daylength. This observation suggests that modulation of redox-linked gene expression by growth daylength is not restricted to oxidative stress or is a secondary consequence of stress-induced phenotypes.

Fewer genes were affected in gr1 than in cat2. Genes affected in cat2 but not gr1 could reflect H2O2 signaling that occurs independently of changes in glutathione (Fig. 1A). The difference could also be related to the stronger perturbation of the glutathione pool in cat2 (Fig. 1B). If the difference can be partly explained by weaker changes in glutathione in gr1, then the overlap in transcriptomes we report could provide a minimum estimate of the importance of glutathione in H2O2 signaling.
Many TRX-linked components play roles in oxidative stress (Dietz, 2003; Rey et al., 2005; Pérez-Ruiz et al., 2006) but none of these transcripts was induced by increased H$_2$O$_2$ availability in cat2 or cat2 gr1. A lack of response was also observed for chloroplast ferredoxin-thioredoxin reductase subunit genes and for the two cytosolic NTRs and cytosolic TRXs (Supplemental Table S5). The only TRX-linked gene that was significantly induced by H$_2$O$_2$ was GPX6, and this effect was largely independent of both daylength and the gr1 mutation (Fig. 6).

In contrast to the lack of response of TRX systems, H$_2$O$_2$ or gr1-driven perturbation of glutathione triggered changes in the abundance of transcripts of several glutathione-associated genes, notably GSTs and GRXs. Analysis of GST functions is complicated by the number of genes in plants, notably due to the presence of large plant-specific phi and tau sub-classes, as well as substrate overlap between the different enzymes. The present transcript profiling analysis showed that H$_2$O$_2$ modified transcript levels for two phi class (GSTF2, GSTF8) and three tau class (GSTU7, GSTU8, GSTU19) enzymes, and that in all cases these effects were further modulated by daylength and/or the gr1 mutation. Type F GSTs exhibit both conjugase and peroxidase activities, with GSTF8 showing considerable activity against cumene hydroperoxide (Wagner et al., 2002; Dixon et al., 2009). As well as GSTFs, some GSTUs, including GSTU8, show quite high peroxidase activity (Dixon et al., 2009).

Analysis of GRX function is also complicated by the number of genes, notably due to a large sub-class that is specific to higher plants. At least 30 GRX genes have been described in Arabidopsis (Lemaire, 2004; Meyer et al., 2008). Based on active-site sequences, these are sub-classified into CPYC, monothiol CGFS, and CC-type GRX, with the last sub-class being specific to land plants (Lemaire, 2004). Although at least one CGFS GRX is implicated in oxidative stress (Cheng et al., 2006), no CPYC or CGFS GRXs showed differential expression in gr1, cat2 or cat2 gr1 in either photoperiod condition (Supplemental Table S5). All differentially expressed GRX genes observed in our analysis belong to the CC-type sub-class, consisting of 20 identified members that are thought to encode cytosolic proteins. The functions of most CC-type GRXs remain obscure, but two have been implicated in the regulation of gene expression by interacting with TGA transcription factors. GRX480 overexpression represses the JA marker gene, PDF1.2, while ROXY1 is required for petal development (Ndamukong et al., 2007; Li et al., 2009). The predicted protein encoded by the
GRX-like sequence (Fig. 6B) has an active-site CCMS motif that is shared with nine annotated GRX proteins, and BLAST analysis revealed that the protein has 58-60% amino acid identity with five of these CCMS GRXs. The \( \text{H}_2\text{O}_2 \) and/or \( \text{gr}1 \)-dependent changes in CC-type GRXs suggest that the encoded proteins may play roles in the redox regulation of gene expression.

**GR1 is Required for Salicylic Acid Responses and for Expression of Genes Involved in Jasmonic Acid Signaling**

The \( \text{cat}2 \) mutation causes accumulation of SA and induction of SA responses in LD but not SD (Chaouch et al., 2010; Fig. 10). \( \text{GR1} \) function appears to be required for optimal SA production, as this was compromised in the \( \text{gr}1 \) single mutant relative to Col-0 and in \( \text{cat}2 \ \text{gr}1 \) relative to \( \text{cat}2 \) (Fig. 10). Further, \( \text{gr}1 \) showed decreased resistance to bacteria while induction of \( \text{PR} \) genes in \( \text{cat}2 \ \text{gr}1 \) was compromised compared to \( \text{cat}2 \). As well as effects on SA production itself, the \( \text{gr}1 \) mutation could interfere with SA-dependent gene expression by altered redox regulation of NPR1 (Mou et al., 2003; Tada et al., 2008). Because loss of GR1 function in an \( \text{H}_2\text{O}_2 \) signaling context produces accelerated lesion formation, the enzyme appears to be required both to restrict leaf bleaching and to enable induction of SA and \( \text{PR} \) genes.

Several antioxidative genes can be induced by JA, including genes encoding enzymes of glutathione synthesis (Xiang and Oliver, 1998; Sasaki-Sekimoto et al., 2005). Recent reports implicate glutathione-associated components in JA signaling (Ndamukong et al., 2007; Tamaoki et al., 2008; Koornneef et al., 2008). In both Col-0 and \( \text{cat}2 \) backgrounds, the \( \text{gr}1 \) mutation affected a suite of JA-associated genes in a daylength-dependent manner. We observed induction of JA genes in \( \text{cat}2 \) and \( \text{gr}1 \) single mutants in SD but repression in all mutant genotypes in LD. This may indicate (1) an optimum glutathione redox status for induction of JA genes and (2) daylength-dependent signals that operate to modulate the impact of changes in glutathione status on JA signaling. The daylength and \( \text{gr}1 \)-modulated expression of several GRX and GSTs suggests that these components may functionally link glutathione and JA signaling. Such components could include GRX480 (Ndamukong et al., 2007), GSTU8-dependent formation of GS-oxylipin conjugates (Mueller et al., 2008) and \( \text{GSTU}6 \), which is among JA-dependent genes that are rapidly induced by wounding (Yan et al., 2007). In our analysis, similar expression patterns were observed for these glutathione-
associated genes and for a suite of JA-dependent genes. Other genes that link glutathione and JA may include GSTU7, GSTU19, and MRP2, which were induced most strongly in cat2 gr1 in SD and less strongly in cat2 and cat2 gr1 in LD. These genes are up-regulated by phytoprostone or 12-oxo-phytodienoic acid (OPDA) treatment (Mueller et al., 2008). Several of the glutathione-associated genes shown in Figure 6 are rapidly induced by methyl jasmonate, OPDA, phytoprostane, or wounding (Supplemental Fig. S6). Based on JA- or oxylipin-dependent expression patterns, the activities of GSTs against electrophilic metabolites, and interactions of CC-type GRX with transcription factors (Wagner et al., 2002; Ndamukong et al., 2007; Yan et al., 2007; Mueller et al., 2008; Li et al., 2009), it is possible that several GSTs and CC-type GRX could be involved in linking glutathione to JA signaling.

Interestingly, the glutathione-deficient pad2 mutant is compromised in insect resistance (Schlaeppi et al., 2008). Glutathione status is modulated by various stresses, notably biotic challenge, while sulfur deficiency, which can induce JA synthesis genes (Hirai et al., 2003), is an important determinant of glutathione concentration. As well as the influence of glutathione status, the present data also underline the potential importance of daylength context in modulating redox-triggered signaling through the JA pathway.

**Conclusion**

While TRX- and glutathione-dependent pathways have overlapping functions in plants (Reichheld et al., 2007; Marty et al., 2009), the present study shows that GR1 plays specific roles in intracellular H2O2 metabolism, in daylength-linked control of phytohormone gene expression, and in certain responses to biotic stress. The transcriptomic patterns we report also point to glutathione- and TRX-specific pathways in redox signaling, with relatively little crosstalk between the two pathways at the level of gene expression.

Two non-exclusive hypotheses could explain how the GR-glutathione system influences H2O2-linked gene expression. In the first, glutathione turnover would influence H2O2 concentration through its antioxidative function. Most of our observations do not suggest that this is the main cause of the gr1-linked changes in gene expression, though in situ visualisation of ROS suggests that it could contribute to differences between cat2 and cat2 gr1, particularly in SD. In the second hypothesis, glutathione status would be a key part of H2O2-triggered signal transduction. This hypothesis receives support from several of our
observations, notably the partial overlap between *cat2* and *gr1* transcriptomes, but further work is required to confirm the role of glutathione status *per se*.

**MATERIALS AND METHODS**

**Plant Material**

*Arabidopsis thaliana* mutant lines carrying T-DNA insertions in the *GR1* gene (At3g24170) were identified using insertion mutant information obtained from the SIGnAL website at [http://signal.salk.edu](http://signal.salk.edu), and seeds were obtained from the Nottingham Arabidopsis Stock Centre ([http://nasc.nott.ac.uk](http://nasc.nott.ac.uk)). The default *gr1* line was *gr1-2* (SALK_060425). A second *gr1* insertion mutant (SALK_105794), named *gr1-1* by Marty et al. (2009), was used to confirm the phenotypic effects of the *cat2 gr1* interaction. After identification of homozygotes, all further analyses were performed on plants grown from T3 seeds. The *cat2* line was *cat2-2* (Queval et al., 2007), now renamed *cat2-1*.

**Identification of Homozygous gr1 Insertion Mutants**

Leaf DNA was amplified by PCR (30 s 94°C, 30 s 60°C, 1 min 72°C, 30 cycles) using primers specific for left T-DNA borders and the *GR1* gene (Supplemental Table 1). Fragments obtained were sequenced to confirm the insertion site. Zygosity was analyzed by PCR amplification of leaf DNA and RT-PCR analysis of *GR1* transcripts was performed using gene-specific primers (Supplemental Table 1).

**Plant Growth and Sampling**

Seeds were incubated for 2 days at 4°C and then sown either on agar or in soil in 7 cm pots. Plants were grown in a controlled environment growth chamber at the specified photoperiod and an irradiance of 200 µmol.m⁻².s⁻¹ at leaf level, 20°C/18°C, 65% humidity, and given nutrient solution twice per week. The CO₂ concentration was maintained at 400 ppm (air) or 3000 ppm (high CO₂). Samples were rapidly frozen in liquid nitrogen, and stored at -80°C until analysis. Unless otherwise stated, data are means ± SE of three independent samples from different plants and significant differences are expressed using t-test at *p* < *0.1*, **0.05**, and ***0.01.
Pathogen Tests

The virulent *Pseudomonas syringae pv. tomato* strain DC3000 was used for resistance tests in a medium titer of $5 \times 10^5$ cfu mL$^{-1}$. Whole leaves of three week-old plants grown in a 16h photoperiod were infiltrated using a 1-mL syringe without a needle. Leaf discs of 0.5 cm$^2$ were harvested from inoculated leaves at the appropriate time points. For each time point four samples were made by pooling two leaf discs from different treated plants. Bacterial growth was assessed by homogenizing leaf discs in 400 µL of water, plating appropriate dilutions on solid King B medium containing Rifampicin and Kanamycin and quantifying colony numbers after three days.

Microarray Analysis

Microarray analysis was performed using the CATMA arrays containing 24,576 gene-specific tags corresponding to 22089 genes from *Arabidopsis* (Crowe et al., 2003; Hilson et al., 2004) plus 1217 probes for miRNA genes and putative small RNA precursors (information available at [http://urgv.evry.inra.fr/projects/FLAGdb++](http://urgv.evry.inra.fr/projects/FLAGdb++)). This array resource has been used in 40 publications over the last five years using a protocol based on technical repeats of two independent biological replicates produced from pooled material from independent plants (eg, Achard et al., 2008; Besson-Bard et al., 2009; Krinke et al., 2009) and this approach was adopted in the present study. For each biological repeat and each point, RNA samples were obtained by pooling leaf material from independent sets, each of two plants. Samples of approximately 200 mg FW were collected from plants after 3.5 weeks growth in the conditions specified above. Total RNA was extracted using Nucleospin RNAII kits (Macherey-Nagel, Hoerdt, France) according to the supplier’s instructions. For each comparison, one technical replication with fluorochrome reversal was performed for each biological replicate (i.e. four hybridizations per comparison). The labelling of cRNAs with Cy3-dUTP or Cy5-dUTP (Perkin-Elmer-NEN Life Science Products), the hybridization to the slides, and the scanning were performed as described in Lurin et al. (2004).

Statistical Analysis of Microarray Data
Experiments were designed with the statistics group of the Unité de Recherche en Génomique Végétale. Normalization and statistical analysis was based on two dye swaps (i.e. four arrays, each containing 24,576 GSTs and 384 controls) as described in Gagnot et al. (2008). To determine differentially expressed genes, we performed a paired t-test on the log ratios, assuming that the variance of the log ratios was the same for all genes. Spots displaying extreme variance (too small or too large) were excluded. The raw P-values were adjusted by the Bonferroni method, which controls the Family Wise Error Rate, (with a type I error equal to 5%) in order to keep a strong control of the false positives in a multiple-comparison context (Ge et al., 2003). We considered as being differentially expressed the genes with a Bonferroni P-value \( \leq 0.05 \), as described in Gagnot et al. (2008). Only genes that showed same-direction statistically significant change in both biological replicates of at least one sample type were considered as statistically significant.

**Data Deposition**

According to the “Minimum Information About a Microarray Experiment” standards, microarray data from this article will be deposited at Gene Expression Omnibus and can be consulted at CATdb (http://urgv.evry.inra.fr/cgi-bin/projects/CATdb/consult_expce.pl?experiment_id=256).

**qRT-PCR Analysis**

RNA was extracted using the kit NucleoSpin® RNA plant (Macherey-Nagel, Hoerdt, France) and reverse transcribed with the SuperScript™ III First-Strand Synthesis System (Invitrogen™, Paisley, UK). ACTIN2 transcripts were measured as a control. cDNAs were amplified using the conditions described above for analysis of genomic DNA except that the number of cycles was 50. RT-qPCR was performed according to Queval et al. (2007). Gene-specific primers are listed in Supplemental Table 1.

**Enzyme assays, metabolite and ROS analysis**

Extractable enzyme activities were measured as described previously (Veljovic-Jovanovic et al., 2001). Oxidized and reduced forms of glutathione, ascorbate, and NADP were measured by plate-reader assay, as described in Queval and Noctor (2007). Salicylic acid was measured
according to the protocol of Langlois-Meurinne et al. (2005). Thiobarbituric acid-reactive substances were assayed and calculated as described in Yang et al. (2009). *In situ* visualisation of ROS was performed using dichlorodihydrofluorescein-diacetate (DCFH$_2$-DA) by a protocol modified from Oracz et al. (2009). Leaves were vacuum-infiltrated twice for 15 min at room temperature with DCFH$_2$-DA, carefully rinsed, and kept in the dark. DCF fluorescence at 510-550 nm was visualised on a confocal microscope, simultaneously with red chlorophyll autofluorescence, using argon laser excitation at 488 nm.
Supplemental Material

Supplemental Figure S1. Characterization of the gr1 mutant.

Supplemental Figure S2. Glutathione and ascorbate status in gr1 and cat2 mutants grown at high CO2 and then transferred to air in 8h or 16h days

Supplemental Figure S3. Analysis of the conditional genetic interaction between cat2 and gr1 in an allelic double cat2 gr1 mutant.

Supplemental Figure S4. qPCR confirmation of changes in JA-linked genes in cat2 and cat2 gr1.

Supplemental Figure S5. H2O2 visualisation in leaves of Col-0, gr1, cat2, and cat2 gr1 in short day and long day conditions.

Supplemental Figure S6. Genevestigator analysis (Hruz et al., 2008) of responses of glutathione-associated genes showing significantly different expression in cat2 and/or cat2 gr1 (Figure 6).

Supplemental Table S1. PCR primers used in this study.

Supplemental Table S2. Summary of modified daylength-dependent gene expression in gr1 and overlap with cat2 transcriptomes.

Supplemental Table S3. Complete dataset of significantly modified genes in gr1, cat2, and cat2 gr1 in two daylength regimes.

Supplemental Table S4. List of jasmonic acid-associated genes showing differential expression in cat2 and cat2 gr1 and relative expression values.

Supplemental Table S5. Summary of expression of glutaredoxins, cytosolic thioredoxins and related genes in cat2 and cat2 gr1.
ACKNOWLEDGMENTS

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REFERENCES


FIGURE LEGENDS

**Figure 1.** Comparison of $\text{H}_2\text{O}_2$ and glutathione-regulated changes in gene expression. A, Scheme depicting experimental strategy. B, Glutathione reduction states (100 GSH/total glutathione) in Col-0, *gr1* and *cat2* in high CO$_2$ or in air in 8h (SD) or 16h (LD) growth photoperiods. Different letters indicate significant difference between genotypes at $p < 0.05$. The numbers show the GSH/GSSG ratios. Data are means ± SE of 5-7 independent extracts. C, Overlap in significantly induced or repressed genes in *cat2* or *gr1* following induction of glutathione oxidation in *cat2* after transfer from high CO$_2$ to air.

**Figure 2.** Verification of selected genes repressed or induced in *gr1* by RT-qPCR. Data are means ± SE of two independent extracts.

**Figure 3.** Germination and growth phenotype of *cat2 gr1* double mutants. A, Germination and growth on agar. B, Plants grown on soil from germination in a 16h/8h day/night regime. Black*, significant difference of mutant from Col-0. Red*, significant differences between *cat2* and *cat2 gr1*.

**Figure 4.** Rescue of a wild-type phenotype in *cat2 gr1* at high CO$_2$ and rapid daylength-dependent induction of leaf bleaching following transfer to air. A, Plants were germinated and grown for 25 days at high CO$_2$ (3000 µL L$^{-1}$). FW, fresh weight. B, Plants transferred from high CO$_2$ to air in either short-day (SD) or long-day (LD) conditions. False-color imaging of lesions (red) are shown under each photograph. C, Rosette fresh weights of plants transferred to air in either SD or LD. Histograms show means ± SE of at least six plants. Black*, significant difference of mutant from Col-0. Red*, significant differences between *cat2* and *cat2 gr1*.

**Figure 5.** Comparison of gene expression in *cat2* and *cat2 gr1* following transfer from high CO$_2$ to air in either 8h (SD) or 16h (LD) growth conditions. Hierarchical clustering was performed using MEV (MultiExperimentViewer) software. The exploded heatmap at the right shows a sub-cluster of 62 genes that includes 33 jasmonic acid or wounding-associated genes (highlighted yellow).
Figure 6. Glutathione contents and glutathione-related gene expression in cat2 and the cat2 gr1 double mutant. A, Time course of changes in % glutathione reduction and total glutathione in the different lines following transfer from high CO2 to air. Black circles, Col-0. White circles, cat2. White triangles, cat2 gr1. Top, 100 x GSH/total glutathione (the numbers indicate GSH:GSSG ratio for the final time-points). Bottom, total glutathione (GSH + 2 GSSG). Error bars that are not apparent are contained within the symbols. B, Expression values of significantly different glutathione metabolism transcripts in cat2 and cat2 gr1 relative to Col-0. Black bars, cat2. White bars, cat2 gr1. SD, short days. LD, long days. The top two panels show genes that were induced while the bottom panel shows genes that were significantly repressed in at least one sample type. GST, glutathione S-transferase. GPX, glutathione (thioredoxin) peroxidase. GRX, glutaredoxin. MRP, multidrug resistance-associated protein.

Figure 7. Leaf ascorbate, NADP(H), and thiobarbituric acid-reactive substances (TBARS) in the four genotypes placed in short days (left) and long days (right) in air following growth at high CO2. A, Ascorbate (white bars) and dehydroascorbate (black bars). B, NADP+ (white bars) and NADPH (black bars). C, TBARS. For A and B, numbers above each bar indicate % reduction states (100 ascorbate/(ascorbate+dehydroascorbate) in A and 100 NADPH/(NADP+ + NADPH) in B). Samples were taken 4d after transfer to air. All data are means ± SE of three independent leaf extracts. *within blocks indicates significant differences from Col-0 values in the same condition.

Figure 8. In vivo visualization of ROS using dichlorofluorescein fluorescence. Leaf mesophyll cells of plants grown at high CO2 then transferred to air for four days in short days or long days were imaged in intact tissue by confocal microscopy. Each pair of images shows the same area measured for green DCF fluorescence (left) and red chlorophyll autofluorescence (right). Representative examples from three independent experiments are shown. Magnification was the same for all samples.

Figure 9. Major antioxidative enzyme activities and transcript levels in Col-0, gr1, cat2, and cat2 gr1 after transfer to air in short days (gray backgrounds) or long days (white backgrounds). A, Enzyme activities. X-axis numbers refer to Col-0 (1), gr1 (2), cat2 (3), and cat2 gr1 (4). Units are µmol.mg-1prot.min-1 (catalase) and nmol.mg-1prot.min-1 (other enzymes). Means of three independent extracts (*significant difference from Col-0 at p <
0.05). B, Simplified scheme of catalase and ascorbate-dependent H₂O₂ metabolism. C, Abundance (log₂ scale, relative to Col-0) of corresponding transcripts for which probes were present on the CATMA array. *Indicates transcripts that showed significant same-direction difference from controls in both biological replicates. Where no bar is apparent, transcripts were almost identical in abundance in the mutant and the corresponding Col-0 control.

**Figure 10.** Pathogen-associated responses in GR-deficient lines. A, PR gene expression and salicylic acid contents in Col-0, gr1, cat2, and cat2 gr1 in two photoperiods after transfer from high CO₂ to air. Top, 8h days. Bottom, 16h days. Data are means ± SE of two to three biological samples. B, Bacterial resistance and salicylic acid contents in the Col-0 and gr1 grown under standard conditions in air. *Indicates significant difference between mutants and Col-0 while + indicates significant differences between cat2 and cat2 gr1.
Table 1. Annotated phytohormone-associated genes showing significantly modified transcript levels in grl.

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</table>

*significant same-direction response in cat2 in the same condition.
Figure 1. Comparison of H$_2$O$_2$ and glutathione-regulated changes in gene expression. A, Scheme depicting experimental strategy. B, Glutathione reduction states (100 GSH/total glutathione) in Col-0, gr1 and cat2 in high CO$_2$ or in air in 8h (SD) or 16h (LD) growth photoperiods. Different letters indicate significant difference between genotypes at $p < 0.05$. The numbers show the GSH/GSSG ratios. Data are means ± SE of 5-7 independent extracts. C, Overlap in significantly induced or repressed genes in cat2 or gr1 following induction of glutathione oxidation in cat2 after transfer from high CO$_2$ to air.
**Figure 2.** Verification of selected genes repressed or induced in gr1 by RT-qPCR. Data are means ± SE of two independent extracts. Significant difference is indicated at $p < *0.1$, **0.05, and ***0.01.
Figure 3. Germination and growth phenotype of *cat2 gr1* double mutants. A, Germination and growth on agar. B, Plants grown on soil from germination in a 16h/8h day/night regime. Black*, significant difference of mutant from Col-0. Red*, significant differences between *cat2* and *cat2 gr1*. 
Figure 4. Rescue of a wild-type phenotype in cat2 gr1 at high CO2 and rapid daylength-dependent induction of leaf bleaching following transfer to air. A, Plants were germinated and grown for 25 days at high CO2 (3000 µL L⁻¹). FW, fresh weight. B, Plants transferred from high CO2 to air in either short-day (SD) or long-day (LD) conditions. False-color imaging of lesions (red) are shown under each photograph. C, Rosette fresh weights of plants transferred to air in either SD or LD. Histograms show means ± SE of at least six plants. Black*, significant difference of mutant from Col-0. Red*, significant differences between cat2 and cat2 gr1.
Figure 5. Comparison of gene expression in cat2 and cat2 gr1 following transfer from high CO₂ to air in either 8h (SD) or 16h (LD) growth conditions. Hierarchical clustering was performed using MEV (MultiExperimentViewer) software. The exploded heatmap at the right shows a sub-cluster of 62 genes that includes 33 jasmonic acid or wounding-associated genes (highlighted yellow).
Figure 6. Glutathione contents and glutathione-related gene expression in **cat2** and the **cat2 gr1** double mutant. **A**, Time course of changes in % glutathione reduction and total glutathione in the different lines following transfer from high CO₂ to air. Black circles, Col-0. White circles, **cat2**. White triangles, **cat2 gr1**. Top, 100 x GSH/total glutathione (the numbers indicate GSH:GSSG ratio for the final time-points). Bottom, total glutathione (GSH + 2 GSSG). Error bars that are not apparent are contained within the symbols. **B**, Expression values of significantly different glutathione metabolism transcripts in **cat2** and **cat2 gr1** relative to Col-0. Black bars, **cat2**. White bars, **cat2 gr1**. SD, short days. LD, long days. The top two panels show genes that were induced while the bottom panel shows genes that were significantly repressed in at least one sample type. GST, glutathione S-transferase. GPX, glutathione(thioredoxin) peroxidase. GRX, glutaredoxin. MRP, multidrug resistance-associated protein.
Figure 7. Leaf ascorbate, NADP(H), and thiobarbituric acid-reactive substances (TBARS) in the four genotypes placed in short days (left) and long days (right) in air following growth at high CO$_2$. A, Ascorbate (white bars) and dehydroascorbate (black bars). B, NADP$^+$ (white bars) and NADPH (black bars). C, TBARS. For A and B, numbers above each bar indicate % reduction states (100 ascorbate/(ascorbate+dehydroascorbate) in A and 100 NADPH/(NADP$^+$ + NADPH) in B). Samples were taken 4d after transfer to air. All data are means ± SE of three independent leaf extracts. *within blocks indicates significant differences from Col-0 values in the same condition.
Figure 8.

In vivo visualization of ROS using dichlorofluorescein fluorescence. Leaf mesophyll cells of plants grown at high CO$_2$ then transferred to air for four days in short days or long days were imaged in intact tissue by confocal microscopy. Each pair of images shows the same area measured for green DCF fluorescence (left) and red chlorophyll autofluorescence (right). Representative examples from three independent experiments are shown. Magnification was the same for all samples.
Figure 9. Major antioxidative enzyme activities and transcript levels in Col-0, gr1, cat2, and cat2 gr1 after transfer to air in short days (gray backgrounds) or long days (white backgrounds). A, Enzyme activities. X-axis numbers refer to Col-0 (1), gr1 (2), cat2 (3), and cat2 gr1 (4). Units are µmol.mg\(^{-1}\)prot.min\(^{-1}\) (catalase) and nmol.mg\(^{-1}\)prot.min\(^{-1}\) (other enzymes). Means of three independent extracts (*significant difference from Col-0 at \(p < 0.05\)). B, Simplified scheme of catalase and ascorbate-dependent H\(_2\)O\(_2\) metabolism. C, Abundance (log\(_2\) scale, relative to Col-0) of corresponding transcripts for which probes were present on the CATMA array. * Indicates transcripts that showed significant same-direction difference from controls in both biological replicates. Where no bar is apparent, transcripts were almost identical in abundance in the mutant and the corresponding Col-0 control.
Figure 10. Pathogen-associated responses in GR-deficient lines. A, PR gene expression and salicylic acid contents in Col-0, gr1, cat2, and cat2 gr1 in two photoperiods after transfer from high CO₂ to air. Top, 8h days. Bottom, 16h days. Data are means ± SE of two to three biological samples. B, Bacterial resistance and salicylic acid contents in the Col-0 and gr1 grown under standard conditions in air. *Indicates significant difference between mutants and Col-0 while + indicates significant differences between cat2 and cat2 gr1.