The AtrbohD-Mediated Oxidative Burst Elicited by Oligogalacturonides in Arabidopsis Is Dispensable for the Activation of Defense Responses Effective against Botrytis cinerea

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Oligogalacturonides (OGs) are endogenous elicitors of defense responses released after partial degradation of pectin in the plant cell wall. We have previously shown that, in Arabidopsis (Arabidopsis thaliana), OGs induce the expression of PHYTOALEXIN DEFICIENT3 (PAD3) and increase resistance to the necrotrophic fungal pathogen Botrytis cinerea independently of signaling pathways mediated by jasmonate, salicylic acid, and ethylene. Here, we illustrate that the rapid induction of the expression of a variety of genes by OGs is also independent of salicylic acid, ethylene, and jasmonate. OGs elicit a robust extracellular oxidative burst that is generated by the NADPH oxidase AtrbohD. This burst is not required for the expression of OG-responsive genes or for OG-induced resistance to B. cinerea, whereas callose accumulation requires a functional AtrbohD. OG-induced resistance to B. cinerea is also unaffected in powdery mildew resistant1, despite the fact that callose accumulation was almost abolished in this mutant. These results indicate that the OG-induced oxidative burst is not required for the activation of defense responses effective against B. cinerea, leaving open the question of the role of reactive oxygen species in elicitor-mediated defense.

Plants need to recognize invading pathogens in a timely manner to mount appropriate defense responses. Specific molecules associated with different microbial pathogens can be perceived by plant cells at early stages of infection and trigger inducible defenses that include phytoalexin accumulation, expression of pathogenesis-related proteins, production of reactive oxygen species (ROS), and, at least in some cases, programmed cell death. Many of these molecules, traditionally called general elicitors, are secreted or are present on the surface of all strains of a given microbial taxonomic group and activate defense responses effective against a wide range of pathogens (Nurnberger et al., 2004). For this reason, they are also referred to as microbe-associated molecular patterns or pathogen-associated molecular patterns (PAMPs; Parker, 2003; He et al., 2007). PAMPs (for review, see Nurnberger and Brunner, 2002) are often structural components of the pathogen cell wall (e.g. chitin, glucan) or other macromolecular structures (e.g. bacterial flagellin).

Hahn and colleagues (1981) first showed that structural components of the plant cell wall, released during pathogen infection as a consequence of microbial enzymatic activities, can also induce defense responses. In particular, oligogalacturonides (OGs) with a degree of polymerization (DP) between 10 and 15 can accumulate when fungal polygalacturonases (PGs) degrade the homogalacturonan component of plant pectin (Hahn et al., 1981). OGs elicit a variety of defense responses, including accumulation of phytoalexins (Davis et al., 1986), glucanase, and chitinas (Davis and Hahlbrock, 1987; Broekaert and Pneumas, 1988). Exogenous treatment with OGs protects grapevine (Vitis vinifera) and Arabidopsis (Arabidopsis thaliana) leaves against infection with the necrotrophic fungus Botrytis cinerea (Aziz et al., 2004; Ferrari et al., 2007), suggesting that production of this elicitor at the site of infection, where large amounts of PGs are secreted by the fungus, may contribute to activate defenses responses. For these reasons, OGs can be considered as danger

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signals derived from an altered self (host-associated molecular patterns).

A prominent feature of the plant defense response is the oxidative burst, a common early response of plant cells to pathogen attack and elicitor treatment (Lamb and Dixon, 1997). ROS such as superoxide anion (O$_2^-$) and hydrogen peroxide (H$_2$O$_2$) are toxic intermediates resulting from reduction of molecular O$_2$. ROS are important signals for defense responses and phytoalexin accumulation in several species. It is generally thought that ROS contribute to plant resistance by directly exerting a cytotoxic effect against pathogens, by participating in cell wall reinforcement (cross-linking of structural protein and lignin polymers), or by inducing hypersensitive cell death, expression of defense genes, or the accumulation of antimicrobial compounds (Levine et al., 1994). Generation of ROS can be induced by a variety of elicitors (Apostol et al., 1989; Legendre et al., 1993; Bolwell et al., 2002; Aziz et al., 2003; Kasparovsky et al., 2004; Pauw et al., 2004; Xu et al., 2005) and in many plant systems ROS production is biphasic (e.g. Dorey et al., 1999; Yoshioka et al., 2001).

O$_2^-$-generating NADPH oxidases are generally considered to be a major enzymatic source of ROS in the oxidative burst of plant cells challenged with pathogens or elicitors (Torres and Dangl, 2005; Torres et al., 2006). Two different NADPH oxidase genes in potato (Solanum tuberosum) are responsible for the elicitor-induced biphasic oxidative burst (Yoshioka et al., 2001). In Arabidopsis, several genes encoding proteins with high similarity to the mammalian NADPH oxidase gp91phox subunit have been characterized. Among them, AtrbohD is required for the production of ROS during infection with different bacterial and fungal pathogens, including B. cinerea (Torres et al., 2002, 2005). Besides NADPH oxidases, other enzymes appear to be important in the elicitor-mediated oxidative burst, including apoplastic oxidases, such as oxalate oxidase (Dumas et al., 1993), amine oxidase (Allan and Fluhr, 1997), and pH-dependent apoplastic peroxidases (Bolwell et al., 1995; Frahry and Schopfer, 1998), which generate either O$_2^-$ or H$_2$O$_2$.

We have recently shown that OGs and an unrelated elicitor, the synthetic 22-amino acid peptide flg22 derived from bacterial flagellin (Felix et al., 1999), activate defense responses against B. cinerea both in wild-type Arabidopsis and in mutants impaired in salicylic acid (SA), jasmonate (JA) or ethylene (ET)-mediated signaling (Ferrari et al., 2007). Elicitor-induced protection against B. cinerea requires the PHYTOALEXIN DEFICIENT3 (PAD3) gene (Ferrari et al., 2007). PAD3 encodes the cytochrome P450 CYP71B15, which catalyzes the last step of the biosynthesis of the phytoalexin camalexin (Schuhegger et al., 2006). Camalexin is known to contribute to Arabidopsis basal resistance to B. cinerea (Ferrari et al., 2003a; Klieberstein et al., 2005). Notably, the expression of PAD3, as well as that of another defense-related gene, AtPGIP1, which encodes a PG-inhibiting protein effective against B. cinerea, is induced by OGs independently of SA-, JA-, and ET-mediated signaling (Ferrari et al., 2003b, 2007). It is therefore likely that multiple defense responses are induced by OGs independently of SA, ET, and JA.

Transient accumulation of extracellular H$_2$O$_2$ was previously observed in tobacco (Nicotiana tabacum) leaf explants and grapevine cells treated with OGs (Bellincampi et al., 1996; Aziz et al., 2004). Because PAD3 expression and camalexin accumulation can be induced by chemicals that generate oxidative stress (Zhao et al., 1998; Denby et al., 2005), we have investigated the hypothesis that H$_2$O$_2$ mediates the induction of defense responses effective against B. cinerea in Arabidopsis plants treated with OGs. Here, we show that OGs induce an oxidative burst in Arabidopsis that is AtrbohD-dependent; however, we also show that H$_2$O$_2$-dependent responses are not required for OG-induced resistance against B. cinerea.

RESULTS

Early Activation of Genes in Response to General Elicitors Is Independent of SA, ET, and JA Signaling

To establish the degree of specificity of early gene expression in response to OGs and other general elicitors, we monitored the expression of AtPGIP1, PAD3, and several other early elicitor-induced genes (Ferrari et al., 2007; Denoux et al., 2008) in response to a pool of OGs with a DP between 10 and 15 (hereafter referred to as OGs), to purified oligodecaglacturonic acid (DP10), to flg22, and to a B-glucan elicitor from Phytophthora megasperma f. sp. Glya (Cheong et al., 1991). In addition to AtPGIP1 and PAD3, we tested the expression of AtWRKY40 (At1g80840), encoding a transcription factor that acts as a negative regulator of basal defense (Xu et al., 2006; Shen et al., 2007); CYP81F2 (At5g57220), encoding a cytochrome P450 with unknown function; and RetOx (At1g26380), encoding a protein with homology to reticulin oxidases, a class of enzymes involved in secondary metabolism and in defense against pathogens (Dittrich and Kutchan, 1991; Carter and Thornburg, 2004). These genes were selected because they are rapidly and strongly up-regulated upon exposure to elicitors, as previously demonstrated by whole-genome transcript profiling and real-time quantitative PCR analyses (Ferrari et al., 2007; Denoux et al., 2008). As negative controls, we treated seedlings with water or α,1,4-trigalacturonic acid (DP3; Hahn et al., 1981; Cervone et al., 1989; Bellincampi et al., 2000; Navazio et al., 2002).

As shown in Figure 1, OGs, DP10, flg22, and B-glucan activated the expression of all tested genes in Arabidopsis seedlings, whereas water and DP3 failed to induce the expression of any of the genes analyzed. The expression of PAD3, RetOx, CYP81F2, AtWRKY40, and AtPGIP1 was also compared across a set of 322 publicly available Arabidopsis microarray datasets using the Arabidopsis Coexpression Tool (Manfield
et et al., 2006). The Pearson correlation coefficient between PAD3 and RetOx expression was the highest ($r = 0.78$) among the tested genes (Supplemental Fig. S1), followed by RetOx and CYP81F2 ($r = 0.71$). The AtWRKY40 expression pattern appeared to correlate moderately with that of PAD3 and RetOx ($r = 0.58$ in both cases), whereas no significant correlation between AtPGIP1 and any of the other genes was observed, suggesting that the expression of this gene is regulated differently from that of PAD3, RetOx, and CYP81F2. Despite the fact that AtPGIP1 does not significantly correlate with any other analyzed gene, it was included in subsequent analyses because of its established role in plant defense (Ferrari et al., 2003b, 2006). Transient expression of PAD3, RetOx, CYP81F2, and AtWRKY40 was also observed in rosette leaves infiltrated with OGs (Supplemental Fig. S2) with kinetics comparable to those occurring in seedlings, indicating that these genes can be considered markers of early elicitor-induced responses both in seedlings and in adult plants.

To determine whether RetOx, CYP81F2, and AtWRKY40 are expressed after elicitor treatment independently of SA, ET, or JA, as previously shown for AtPGIP1 and PAD3 (Ferrari et al., 2003b, 2007), we analyzed their expression in the npr1 ein2 jar1 (nej) genetic background harboring mutations in the NON-PR1 EXPRESSOR1 (NPR1; Cao et al., 1997), JASMONATE RESISTANT1 (JAR1; Staswick et al., 1992), and ETHYLENE INSENSITIVE2 (EIN2; Guzman and Ecker, 1990) genes, and therefore impaired in all three signaling pathways (Clarke et al., 2000). No major difference in expression of RetOx, CYP81F2, and AtWRKY40 was observed, either in terms of kinetics of induction or in transcript levels, in wild-type or nej plants treated with OGs (Fig. 2, A–C), or in npr1, ein2, and jar1 single mutants (Supplemental Fig. S3A). Expression of AtPGIP1, that was previously shown to be independent of JAR1, EIN2 or NPR1, based on data obtained with single mutants (Ferrari et al., 2003b), was also unaffected in the triple mutant (Fig. 2D).

Because some reports have suggested that the jar1-1 mutation is leaky (Staswick et al., 1998; Kariola et al., 2006), the expression of marker genes in response to elicitors was determined. Arabidopsis seedlings were treated at the indicated time (h) with water (H2O), OGs, purified oligodecagalacturonic acid (DP10), flg22, trigalacturonic acid (DP3), or β-glucan (GLU). Expression of the indicated genes was analyzed by semiquantitative RT-PCR, using the UBQ5 gene as internal standard. This experiment was repeated twice with similar results.
we also analyzed the coronatine insensitive1 (coi1) mutant, which is severely impaired in JA-mediated responses (Xie et al., 1998). Induction of RetOx and CYP81F2 by OGs in wild-type and coi1 seedlings was indistinguishable, whereas AtWRKY40 expression was slightly reduced in coi1 (Supplemental Fig. S3B), in accordance with a previous report indicating that AtWRKY40 gene can be induced by JA in a COI1-dependent manner (Wang et al., 2008). Similarly, to further rule out an effect of SA on OG-induced gene expression, we treated sid2-2 seedlings, which carry a mutation in the isochorismate synthase gene ICS1 required for pathogen-activated biosynthesis of SA (Wildermuth et al., 2001). Also, in this case, no significant reduction of OG-induced gene expression was observed compared to the wild type (Supplemental Fig. S3C). These results indicate that expression of the OG-induced marker genes tested is independent of SA, ET, and JA.

Production of H2O2 But Not Gene Expression, in Response to OGs Is Mediated by AtrbohD

Analysis of the publicly available expression data using Genevestigator (https://www.genevestigator.ethz.ch) indicates that PAD3, RetOx, AtWRKY40, and CYP81F2 transcript levels increased after treatment with H2O2, suggesting that their expression may be mediated by ROS (data not shown). Transient accumulation of extracellular H2O2 was previously observed in tobacco leaf explants and grapevine cells treated with OGs (Bellincampi et al., 1996; Aziz et al., 2004). To investigate whether OGs are also able to induce an apoplastic oxidative burst in Arabidopsis, we measured the release of H2O2 in the culture medium of seedlings treated with these elicitors. A significant oxidative burst was observed in response to OGs and DP10, whereas H2O2 accumulated to a much smaller extent in response to flg22, β-glucan, or DP3 (Fig. 3A).

We then investigated the source of H2O2 generated after treatment with OGs. Previous reports suggest that the oxidative burst observed after inoculation with virulent and avirulent pathogens is generated in Arabidopsis by the NADPH oxidase AtrbohD (Torres et al., 2005). To determine whether this enzyme is also the source of the extracellular burst observed in response to OGs, we analyzed an Arabidopsis knockout (KO) line containing a T-DNA insertion in the AtrbohD gene (Torres et al., 2002). This line failed to accumulate extracellular H2O2 after elicitation (Fig. 4A), indicating that AtrbohD is necessary for the OG-induced oxidative burst.

To determine the role of the oxidative burst in OG-triggered early gene expression, we analyzed the expression of PAD3, RetOx, CYP81F2, and AtWRKY40 in elicited wild-type and atrbohD mutant seedlings. Strikingly, despite the absence of a functional AtrbohD gene and of an oxidative burst, no significant differences in the mRNA levels of all tested marker genes could be detected (Fig. 5). Similar results were obtained in wild-type and atrbohD adult plants infiltrated with OGs (Supplemental Fig. S2). To conclusively rule out a role of NADPH oxidases in OG-induced marker gene expression, before application of OGs, we treated seedlings with diphenylene iodonium (DPI), which, at low concentrations, specifically inhibits this class of enzymes (Bolwell et al., 1995; Frahry and Schopfer, 1998). DPI completely blocked the OG-induced oxidative burst (Fig. 6A), but had no effect on the expression of PAD3, RetOx, CYP81F2, and AtWRKY40 (Fig. 6B), confirming that NADPH oxidases are not required for early OG-induced transcriptional changes.

To conclusively demonstrate that extracellular H2O2 is not involved in OG-induced gene expression, we elicited Arabidopsis seedlings in the presence of catalase at a concentration that almost completely abolished the oxidative burst (Fig. 3A). Coincubation of
OGs with catalase had no significant effect on the expression of PAD3, AtPGIP1, RetOx, CYP81F2, and AtWRKY40 (Fig. 3B), confirming that H$_2$O$_2$ is not required for OG-induced marker gene expression. Furthermore, treatment of seedlings with Glc and Glc oxidase (G/GO) at concentrations that induced H$_2$O$_2$ levels in the same order of magnitude observed after OG treatments (Fig. 4B), failed to induce the expression of the same set of genes (Fig. 5).

Taken together, our results indicate that OG-mediated early gene expression is independent of the extracellular oxidative burst.

**Basal and OG-Induced Resistance to *B. cinerea* Infection Are Independent of AtrbohD and of PMR4/GSL5**

To determine whether defense responses that occur relatively late after treatment with OGs are also independent of H$_2$O$_2$, we analyzed callose deposition and induced resistance in wild-type and atrbohD KO plants. Callose is a high-M$_r$ β-1,3-glucan deposited at the site of infection by pathogens, probably acting as a physical barrier against colonization of the intercellular space (Ryll, 1996; Donofrio and Delaney, 2001). It was previously shown that flg22 induces callose deposition in Arabidopsis seedlings (Gomez-Gomez et al., 1999) and that callose accumulation induced by flg22 is impaired in leaf strips of atrbohD KO plants (Zhang et al., 2007). Similarly, infiltration of OGs in wild-type rosette leaves resulted in a significant accumulation of callose (Denoux et al., 2008), which was reduced of about 50% in atrbohD leaves (Fig. 7A), indicating that the oxidative burst contributes to callose synthesis also in response to OGs. As expected, infiltration of leaves of the powdery mildew resistant4 (pmr4) mutant, which has a mutation in the callose synthase gene GLUCAN SYNTHASE-LIKE5 (GSL5; Nishimura et al., 2003), resulted in a dramatic decrease of callose deposition (Fig. 7B).

We have previously observed that OGs induce protection of Arabidopsis plants against *B. cinerea* and that this protection requires PAD3 expression (Ferrari et al., 2007). To determine the role of AtrbohD in induced resistance, we treated wild-type, atrbohD, and, as a negative control, pad3 plants with OGs, and subsequently inoculated them with *B. cinerea*. As expected, pad3 plants showed increased basal susceptibility, and OG pretreatment did not reduce lesion development (Fig. 8A). In contrast, no significant difference in basal susceptibility and in OG-induced resistance between wild-type and atrbohD plants was observed either in detached leaves (Fig. 8A) or in intact plants (Fig. 9). This indicates that OG-induced activation of defense responses effective against *B. cinerea* does not require AtrbohD.

Furthermore, we investigated the role of callose in OG-elicited resistance to *B. cinerea*. As shown in Figure 8B, lesion development in pmr4 plants inoculated with *B. cinerea* was unaffected or, in some experiments, slightly reduced, compared to wild-type plants. Moreover, OG treatment of the pmr4 mutant resulted in protection against *B. cinerea* infection (Fig. 8B), indicating that callose does not play a major role in either basal or elicitor-induced resistance against this pathogen.

Finally, we infiltrated adult rosette leaves with G/GO at concentrations that in seedlings induced production of H$_2$O$_2$ levels in the same order of magnitude observed after OG treatments (Fig. 10A), but did not alter basal resistance to *B. cinerea* (Fig. 10B). These data indicate that a moderate extracellular oxidative burst, comparable to that observed after OG treatment, is not sufficient to induce defense responses effective against *B. cinerea*.

**DISCUSSION**

One of the earliest responses observed in plants inoculated with a pathogen or treated with an elicitor
is the oxidative burst, characterized by a rapid and transient production of ROS. OGs induce a strong extracellular oxidative burst, initially suggesting that ROS might play an important role in mediating responses to OGs. We therefore adopted both pharmacological and genetic approaches to investigate both the genesis and the role of the oxidative burst elicited by OGs in Arabidopsis plants.

There are a number of potential sources of ROS generated upon pathogen or elicitor perception. Increasing evidence points to superoxide-generating NADPH oxidases as the main sources of extracellular ROS produced during pathogen infection or elicitation (Yoshioka et al., 2001, 2003; Torres et al., 2002; Kobayashi et al., 2006; Nuhse et al., 2007). O2− generated by NADPH oxidases is rapidly dismutated into H2O2, which is much more stable and can accumulate in tissues. Extracellular H2O2 can also be generated by other sources, most notably apoplastic peroxidases (Bolwell et al., 2002), making it sometimes difficult to discern the involvement of specific sources of ROS in the oxidative burst. The data presented here clearly indicate that the NADPH oxidase AtrbohD is necessary for the extracellular burst induced in Arabidopsis by OGs, as previously shown for flg22 (Nuhse et al., 2007). H2O2 produced after OG treatment is therefore likely released by dismutation of O2− directly generated by AtrbohD in accordance with the observation that OGS induce the accumulation of O2− in Arabidopsis leaves (Song et al., 2006). In addition to the extracellular oxidative burst, protoplastic sources of ROS emanating from mitochondrial, chloroplastic, or peroxisomal generating systems have also been documented (Bolwell et al., 2002). However, intracellular generation of ROS has mainly been studied in relation to abiotic stress (Asada, 1999; del Río et al., 2002). There are reports of intracellular accumulation of ROS in response to elicitors, such as cryptogein (Ashtamker et al., 2007), although its role in plant defense response has not been assessed.

OGs activate a very strong extracellular oxidative burst; surprisingly, however, this burst has a minor, if any, role in several downstream responses, based on the following evidence: (1) under our experimental conditions, there is significantly less H2O2 accumulation in response to flg22 and β-glucan than in response to OGS, but the effect of flg22 and β-glucan on the expression of early molecular marker genes is comparable to that observed with OGS; (2) H2O2 generated by G/GO at levels comparable to those observed in OG-treated plants fails to activate the expression of elicitor-activated marker genes or to induce resistance to B. cinerea; (3) scavenging of H2O2 accumulation by catalase or inhibition of the OG-induced oxidative burst either by DPI or by the atrbohD mutation did not affect
early gene expression. Taken together, these results indicate that early changes in gene expression activated by OGs independently of SA, ET, and JA do not require the oxidative burst generated by AtrbohD. Furthermore, OG-triggered resistance against *B. cinerea*, which is also independent of SA, ET, and JA, occurs in the absence of AtrbohD.

In contrast to OGs, flg22 and β-glucan elicited very low levels of H$_2$O$_2$ under our experimental conditions. An extracellular oxidative burst, peaking at about 10 to 15 min, was previously observed using a H$_2$O$_2$-dependent luminescence assay in Arabidopsis leaf explants treated with 1 μM flg22 (Gomez-Gomez et al., 1999). It is possible that the xylene orange-based system used here is not sensitive enough to detect the burst induced by flg22, although previous work indicates the equivalence of this xylene orange and the luminescence assays (Bindschedler et al., 2001). It is possible that the different levels of H$_2$O$_2$ that we observed after treatment with OGs or flg22 could be ascribed to different concentrations of the elicitors. However, at the doses used in this work, flg22 induced the expression of marker genes to levels comparable to OGs, indicating that the gene-activation response does not directly correlate to H$_2$O$_2$ accumulation. The observation that catalase, DPI treatments, or the *atrbohD* mutation block the oxidative burst, but have no significant impact on the expression of the early marker genes, confirms that the induction of these genes is uncoupled to ROS production.

The fact that none of the analyzed marker genes changed expression in response to H$_2$O$_2$ generated by G/GO was unexpected. Previous work showed that *PAD3* expression and camalexin accumulation can be up-regulated by ROS-generating chemicals (Zhao et al., 1998; Denby et al., 2005) and the expression of CYP81F2, RetOx, and *AtWRKY40* has been shown to be induced
by millimolar concentrations of H$_2$O$_2$ (Davletova et al., 2005). However, the concentration of H$_2$O$_2$ measured in our experiments with G/GO was in the same order of magnitude as the concentration measured after elicitation with OGs (in the range of 10–30 μM g$^{-1}$ fresh weight), which is comparable to the concentrations measured in leaves of different plant species under natural conditions (Cheeseman, 2006). This suggests that the relatively high concentrations of H$_2$O$_2$ used in previous expression analyses might be nonphysiological. Similarly, basal resistance to B. cinerea was not affected by treatment with G/GO at the same concentrations used in the seedling experiments. This result is apparently in contrast with a previous report indicating that G/GO infiltration of Arabidopsis leaves increases susceptibility to this pathogen (Govrin and Levine, 2000). However, the concentration of GO used by Govrin and Levine was 10$^4$-fold higher than in our work, suggesting that only very high levels of H$_2$O$_2$, which are not normally induced by elicitors, can affect basal resistance to B. cinerea.

Whereas OG-induced early gene expression and protection against B. cinerea occur independently of AtrbohD, callose accumulation is reduced in atrbohD KO plants. A similar result was obtained in atrbohD leaf strips treated with flg22 (Zhang et al., 2007). Callose deposition is required for β-amino butyric acid-induced resistance against the necrotrophic fungi Alternaria brassicicola and Plectosphaerella cucumerina (Ton and Mauch-Mani, 2004). Our observation that induced resistance to B. cinerea is unaffected in atrbohD plants, despite a reduction in callose accumulation, suggests that callose contributes only marginally to restrict B. cinerea in Arabidopsis. This hypothesis is confirmed by the observation that both basal and OG-induced resistance against B. cinerea are not impaired in the pmr4 mutant, which accumulates very little callose.

Besides callose accumulation, other responses induced by OGs and other elicitors may be dependent on the oxidative burst. Previous reports suggest the existence of both oxidative burst-dependent and independent signaling pathways linking elicitor perception to downstream responses. Treatment of parsley (Petroselinum crispum) cells with DPI blocked both Pep-13-induced phytoalexin production and accumulation of transcripts encoding enzymes involved in their synthesis. In contrast, DPI had no effect on Pep-13-induced PR gene expression (Kroj et al., 2003). In grapevine, the expression of six out of nine defense-related genes responsive to OGs is blocked by DPI (Aziz et al., 2004), and in Arabidopsis Landsberg erecta seedlings treated with OGs, DPI blocks the expression of several defense genes (Hu et al., 2004). It is possible...
that the activation of a subset of late, secondary responses to elicitors is dependent, or at least is amplified by the earlier production of ROS.

CONCLUSION

In this work, we investigated the role of the extra-cellular oxidative burst in the induction of early and late responses to OGs in Arabidopsis plants. Our results indicate that OGs induce a transient, but robust, production of \( \text{H}_2\text{O}_2 \) that is dependent on the NADPH oxidase AtrbohD. This oxidative burst does not have a major role in the induction of several early OG-responsive marker genes and in the induced protection against \( B. \text{cinerea} \). It was previously observed that early gene expression, in contrast to callose deposition, in response to the bacterial PAMP flg22, is independent of AtrbohD (Zhang et al., 2007). Here, we show that OGs, which are host-associated molecular patterns of a completely different chemical nature, behave in a similar fashion. However, we have demonstrated that defense responses that require the oxidative burst, such as callose deposition, are not involved in OG-induced resistance to \( B. \text{cinerea} \). In contrast, flg22-induced resistance against \( P. \text{syringae} \) infection is dependent on the NADPH oxidase AtrbohD (Zhang et al., 2007). Taken together, these results indicate that the signaling pathway activated by elicitors bifurcates: activation of one branch requires the oxidative burst and is important against bacterial pathogens, whereas the oxidative burst-independent branch regulates defense responses effective against necrotroph fungi.

MATERIALS AND METHODS

Plant Material

Arabidopsis (\textit{Arabidopsis thaliana}) Columbia-0 (Col-0) wild-type seeds were purchased from Leleche Seeds (Glazebrook and Ausubel, 1994) and \textit{eds1-1/eds2-2} (Wildermuth et al., 2001) mutant lines were previously described. Seeds of \textit{ein2-1} and \textit{jar1-1} were obtained from the Arabidopsis Biological Resource Center. The \textit{mprl-1} line and the triple mutant \textit{mpnl} were a kind gift from Xinnian Dong (Duke University). Heterozygous \textit{coi1-1/COI1-1} seeds were a kind gift from John Turner (University of East Anglia). The \textit{atrbokD} KO line was kindly provided by Jonathan G.D. Jones (Sainsbury Center). AtrbohD KO line was kindly provided by Jonathan G.D. Jones (Sainsbury Center). AtrbohD KO line was kindly provided by Jonathan G.D. Jones (Sainsbury Center).

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Growth Conditions and Plant Treatments

Plants were grown on a 3:1 mixture of soil (Einheitserde) and sand (Compo Agricoltura) at 22°C and 70% relative humidity under a 16-h light/8-h dark cycle (approximately 120 \( \mu \text{mol} \text{ m}^{-2} \text{s}^{-1} \)). For OG treatments, leaves from 4-week-old plants were infiltrated with water or 200 mg mL\(^{-1}\) OGs using a needleless syringe and harvested at the indicated times. Generation of \( \text{H}_2\text{O}_2 \) was obtained by adding 0.25 mM Glc and 0.01 unit mL\(^{-1}\) DPI to the culture medium. As a control, dimethyl sulfoxide was added to the medium to a final concentration of 0.2%.

Determination of \( \text{H}_2\text{O}_2 \)

The \( \text{H}_2\text{O}_2 \) concentration in the incubation medium of treated seedlings (about 100–120 mg in 1 mL of medium) was measured by the FOO1 method (jiang et al., 1990), based on the peroxide-mediated oxidation of \( \text{Fe}^2+ \), followed by the reaction of \( \text{Fe}^3+ \) with xylanol orange dye (o-cresolsulfophenolphthalein 3,3' bis[ethylmimino] diacetic acid, sodium salt; Sigma). This method is extremely sensitive and used to measure low levels of water-soluble \( \text{H}_2\text{O}_2 \) present in the aqueous phase. To determine \( \text{H}_2\text{O}_2 \) concentration, 500 \( \mu \text{L} \) of the incubation medium were added to 500 \( \mu \text{L} \) of assay reagent (500 \( \mu \text{m} \) ammonium ferrous sulfate, 50 \( \mu \text{m} \) \( \text{H}_2\text{SO}_4 \), 200 \( \mu \text{m} \) xylanol orange, and 200 \( \mu \text{m} \) sorbitol). Absorbance of the \( \text{Fe}^3+\)-xylanol orange complex (A\text{600}) was detected after 45 min of incubation. The specificity for \( \text{H}_2\text{O}_2 \) was tested by eliminating \( \text{H}_2\text{O}_2 \) in the reaction mixture with catalase. Standard curves of \( \text{H}_2\text{O}_2 \) were obtained for each independent experiment. Data were normalized and expressed as micromol \( \text{H}_2\text{O}_2/g \) fresh weight of seedlings.

For in vivo \( \text{H}_2\text{O}_2 \) visualization, leaves were cut from infiltrated adult plants using a razor blade and dipped for 12 h in a solution containing 1 mg mL\(^{-1}\) of 3,3'-diaminobenzidine-HCl, pH 5.0. Chlorophyll was extracted for 10 min with boiling ethanol and for 2 h with ethanol at room temperature prior to photography (Orozco-Cardenas and Ryan, 1999).

Gene Expression Analysis

Treated seedlings or leaves were frozen in liquid nitrogen, homogenized with a mortar and pestle, and total RNA was extracted with Tri-Reagent (Sigma) according to the manufacturer’s protocol. RNA was treated with RQ1 DNase (Promega) and first-strand cDNA was synthesized using ImProm-II reverse transcriptase (Promega) according to the manufacturer’s instructions. Real-time quantitative PCR analysis was performed using an i-Cycler (Bio-Rad). Two microtiter of a 1:5 dilution of cDNA (corresponding to 20 ng of total RNA) were amplified in a 30-\( \mu \text{L} \) reaction mix containing 1:1 IQ SYBR Green Supermix (Bio-Rad) and 0.4 \( \mu \text{m} \) of each primer. Expression levels of each gene, relative to UNQ5, were determined using a modification of the Pfaffi method (Pfaffi, 2001) as previously described (Ferrari et al., 2006). Semiquantitative reverse transcription (RT)-PCR analysis was performed in a
50-μL reaction mix containing 1 μL of cDNA, 1× buffer (Bioline), 3 μM MgCl₂, 100 μM of each of dNTP, 0.5 μM of each specific primer, and 1 unit Taq DNA Polymerase (Bioline). Twenty-five, thirty, and 35 PCR cycles were performed for each primer pair to verify linearity of the amplification. Primer sequences are shown in Supplemental Table S1. PCR products were separated by agarose gel electrophoresis and stained with ethidium bromide.

Pearson correlation coefficients between the expression pattern of selected genes in 322 Affymetrix ATH1 microarray datasets obtained from different Arabidopsis tissues and after different treatments and available in the Genomic Arabidopsis Resource Network/Nottingham Arabidopsis Stock Centre microarray database (Craigon et al., 2004) and scatter plots of the correlation coefficient values were obtained using the Arabidopsis Coexpression Tool (http://www.arabidopsis.leeds.ac.uk/act/index.php; Manfield et al., 2006). The scatter plot allows users to visualize the correlation of all probe sets against two selected probe sets simultaneously. Every probe set is plotted on a scatter graph, where the two axes are the Pearson correlation coefficients against two different query probe sets. Analysis of the expression of single genes in publicly available microarray experiments was performed using Genevestigator (https://www.genevestigator.ethz.ch; Zimmermann et al., 2004).

**Callose Deposition**

Leaves from 4-week-old plants were infiltrated with water or 200 μg mL⁻¹ OGs using a needleless syringe. After 24 h, for each treatment, about eight leaves, from at least five independent plants, were cleared and dehydrated with 100% ethanol. Leaves were fixed in an acetic acid:ethanol (1:3) solution for 2 h, sequentially incubated for 15 min in 75% ethanol, in 50% ethanol, and in 100% ethanol. Leaves were fixed in an acetic acid:ethanol (1:3) solution containing 150 mM phosphate buffer, pH 8.0, and then stained for 1 h at 25°C in 150 mM phosphate buffer, pH 8.0, containing 0.01% (w/v) aniline blue. After staining, leaves were mounted in 50% glycerol and examined by UV epifluorescence using an Axioskop 2 plus microscope (Zeiss). Images were taken with a ProgRes C10 3.3 MegaPixel digital color camera (Jenoptik). Callose quantification was performed by using ImageJ software.

**Supplemental Data**

The following materials are available in the online version of this article.

**Supplemental Figure S1.** Co-correlation between expression pattern of PAD3 and RetOx.

**Supplemental Figure S2.** Expression of elicitor-responsive genes in adult Arabidopsis wild-type and atrbohD plants.

**Supplemental Figure S3.** Expression of selected marker genes in mutants impaired in SA, JA, and ET signaling.

**Supplemental Table S1.** Primers used in this article.

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