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Defense Responses Induced by Ulvan in Wheat Against Powdery Mildew Caused

- by Blumeria graminis f. sp. tritici
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19 ABSTRACT

- 20 Ulvan is a water-soluble sulfated heteropolysaccharide extracted from the cell walls of
- 21 the green seaweeds *Ulva* spp. This polysaccharide is known to induce resistance and
- 22 protect plants against a broad range of plant pathogenic fungi, such as Blumeria
- 23 graminis f. sp. tritici (Bgt), the causal agent of powdery mildew in wheat. We aimed to
- study the defense mechanisms induced by ulvan against Bgt in susceptible wheat by
- 25 investigating the defense-related gene expression, enzymes activity, accumulation of
- 26 phenolic compounds and hydrogen peroxide (H₂O₂), as well as the development of Bgt
- 27 infection structures in vitro and in planta. Symptoms were reduced by 42% in ulvan-
- treated plants. *In vitro*, ulvan did not inhibit conidial germination of *Bgt* but *in planta*,
- 29 increased the appressorial germ tubes without haustorium. Ulvan increased the presence
- of fluorescent papillae and accumulation of H_2O_2 at the penetration sites of Bgt, as well
- as the content of phenolic compounds. POX, PAL and LOX activities were stimulated

in ulvan-treated plants during the first 48 h after inoculation. However, few of defense-related genes studied were differentially expressed in infected plants after ulvan treatment. By contrast, in non-infected conditions, ulvan up-regulated the expression of genes involved in phenylpropanoid metabolism, *i.e.* PAL, CHS, COMT, ANS and FLS, genes encoding pathogenesis-related proteins, *i.e.* PR1, PR9, PR15, and LOX during the first 96 h after treatment. This study provides new insights about the multiple ulvan effects on wheat defense responses, and especially the elicitation of the phenylpropanoid pathway leading to phenolic compounds accumulation, which could be involved in cell wall reinforcement.

Keywords: algal polysaccharides, *Blumeria graminis*, induced resistance, *Triticum aestivum* L., *Ulva fasciata*.

1. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the most widely cultivated cereal in the world (Kang et al., 2020). This crop is affected by a wide range of fungal diseases, and among them, powdery mildew has been considered one of the most important (Jankovics et al., 2015; Kang et al., 2020).

Powdery mildew causes severe yield losses in many wheat-growing regions and the infection is favored by mild temperatures (15-22°C) and high humidity (above 70%). This disease is caused by the ascomycete *Blumeria graminis* f. sp. *tritici* (*Bgt*), a biotrophic fungus widely distributed throughout the world. *Bgt* produces asexual spores known as conidia, and sexual ascospores in cleistothecia, which enable the fungus to survive under adverse weather conditions (Jankovics et al., 2015). Disease symptoms on wheat appear between 7-10 days after infection and are characterized by the presence of white or grayish powdery colonies on leaves and stems. These colonies have abundant conidia that are easily spread by wind to long distances and promote secondary infections throughout the wheat cropping (Jankovics et al., 2015). After infection, the fungus exclusively colonizes the cell walls of the epidermal cell layer of leaf tissues and forms haustoria, the only fungal structures developing within the host tissues, but without breaking the cell membrane. Haustoria are at the center of the biotrophic

interaction of *Bgt* by taking up nutrients from the host and by delivering effectors in the invaded cells to impair plant immunity (Jankovics et al., 2015).

Due to the rapid evolution of the pathogen and the emergence of new virulent isolates, many race-specific (R) resistance genes introduced in wheat cultivars have become ineffective for controlling powdery mildew development (Kang et al., 2020). In this case, synthetic fungicides are commonly used to control this disease in wheat, which are not healthy and environmentally friendly. For this reason, using alternative control strategies that are compatible with a more sustainable agriculture have been required (Renard-Merlier et al., 2007). In this scenario, oligo- and polysaccharides obtained from marine macroalgae are interesting sources of active molecules to control powdery mildew on various crops (Paulert et al., 2010; Jaulneau et al., 2011; Stadnik and de Freitas, 2014). Algae extracts are a source of a wide range of chemically active metabolites. These molecules possess various biological properties including antimicrobial, antioxidant, antifungal effects, and resistance inducer capacity via the elicitation or priming of plant defense responses (Siah et al., 2018). In addition to metabolites, polysaccharides from brown, red, and green seaweeds have been the most studied ones. Among them, carrageenans, fucans, laminarins, and ulvans (Cluzet et al., 2004; Jaulneau et al., 2011; Stadnik and de Freitas, 2014; de Borba et al., 2021) can be used in plant protection.

Plants are able to defend themselves during pathogen attacks, and the activation of an effective plant immunity depends on pathogen recognition *via* the perception of exogenous elicitors highly conserved and considered as essential structures for pathogens survival (Newman et al., 2013), which are referred as pathogen-/microbe-associated molecular patterns (PAMPs or MAMPs). In addition to these molecules, fragments of plant cell walls released by the action of hydrolytic enzymes secreted by the pathogens, named damage-associated molecular patterns (DAMPs), represent a class of endogenous elicitors (Trouvelot et al., 2014). As a consequence of PAMPs, MAMPs, or DAMPs recognition by pattern recognition receptors (PRRs) occurring in the plant cell membrane, plants induce a broad range of defense reactions: transient oxidative burst, alkalinization of the extracellular medium, influx of calcium, reinforcement of the plant cell wall, production of antimicrobial compounds such as phytoalexins, and induction of pathogenesis-related (PR) proteins (Trouvelot et al., 2014).

The extent of plant defense induction can lead to an increased resistance against subsequent pathogen attack. In this sense, various compounds acting as elicitors have been identified, consisting of lipids, glycopeptides, glycoproteins, and notably

carbohydrates. Depending on their characteristics, oligo- and polysaccharides tend to act as non-specific plant defense elicitors, mimicking the pathogen attack (Paulert et al., 2010). For example, laminarins, the β 1,3 glucans from *Laminaria digitata*, are thought to mimic structurally fungal cell wall polysaccharides.

Over the past few decades, ulvan, a water-soluble sulfated heteropolysaccharide extracted from the cell walls of green macroalgae *Ulva* spp., has shown promising effects on plant resistance induction as well as priming agent (Paulert et al., 2010). In this way, treatments with ulvan are able to protect various crops against a wide range of fungal diseases (Paulert et al., 2010; Stadnik and de Freitas, 2014). Previous studies have shown that ulvan are effective in controlling powdery mildew in monocots like wheat and barley (Paulert et al., 2010; Jaulneau et al., 2011), and dicots crops, such as common bean (de Freitas and Stadnik, 2012; de Borba et al. 2019), cucumber and grapevine (Jaulneau et al., 2011). Treatments with extracts of Ulva spp. provided protection to alfalfa against subsequent infection by Colletotrichum trifolii, which was related to the biosynthesis of phytoalexins and the expression of defense-related genes encoding PR-proteins, such as PR1, PR3, and PR10 in plant tissues (Cluzet et al., 2004). Ulvan appeared also to stimulate various enzymes of defense responses, like peroxidase (POX) or glucanase (GLU) in bean and Arabidopsis, which may lead to the resistance of these plants against various fungal pathogens, such as Colletotrichum lindemuthianum (de Freitas and Stadnik, 2012), C. higginsianum and Alternaria brassicicola (de Freitas and Stadnik, 2015), respectively.

So far, studies to investigate the ulvan effect on wheat were restricted to the evaluation of the efficacy of this polysaccharide in controlling powdery mildew caused by *Bgt*. However, few studies have been carried out in order to clarify the mode of action and the defense pathways involved in wheat resistance against this biotrophic pathogen in response to foliar application of ulvan.

Thus, the present work aimed to study the defense mechanisms induced by ulvan against Bgt in bread wheat by investigating the activation of plant defense-related gene expression, enzymes activity, and the evolution of phenolic compounds in leaves. A microscopic study was also performed to monitor the development of infection structures *in planta* and the accumulation of defense compounds such as phenolics and hydrogen peroxide (H_2O_2) at the site of Bgt penetration attempts in response to ulvan treatment. Finally, *in vitro* assay allowed to assess the ability of ulvan to inhibit directly Bgt conidial germination.

2. MATERIAL AND METHODS

2.1 Biological material

Bread wheat (*Triticum aestivum* L.) cv. Pakito, provided by RAGT (Rodez, France), was used in this study. This cultivar was considered highly susceptible to *Blumeria graminis* f. sp. *tritici* (*Bgt*), exhibiting an estimating field resistance level at 4 on a 1-9 scale. Seeds were water soaked overnight in order to facilitate their germination and then 24 seeds were sown in 30×12 cm plastic trays with a commercial substrate (Floradur® - Floragard, Germany). Plantlets were grown for 10 days in a growth chamber with a 12 h photoperiod (light intensity 250 μ mol m⁻² s⁻¹), 18°C day temperature, 12°C night temperature, and 70% relative humidity.

Blumeria graminis f. sp. tritici isolate MPEbgt1 was provided by M.P. Latorse (Bayer CropScience, France). The fungus was inoculated and maintained on wheat plants cv. Alixan (Limagrain, Saint-Beauzire, France) in a growth chamber under constant light at 20°C.

2.2 Ulvan obtention

Ulvan was obtained as described by Paulert et al. (2010) and de Borba et al. (2021). Briefly, dried algae (*Ulva fasciata* Delile) was suspended in distilled water (w:v, 1:10) and autoclaved at 110°C for 2 h. The resulting aqueous solution was filtered through a cotton cloth and the polysaccharide precipitated with ethanol absolute (v:v, 1:3) for 48 h at -20°C. The polysaccharide obtained from the first precipitation was collected, dried at 40–45°C, and ground to a fine powder. Thereafter, the polysaccharide was dissolved in distilled water at 10 mg ml⁻¹, dialyzed in a 3600 Da Mw cutoff dialysis membrane for 72 h, and then lyophilized. The product was stored at -20°C in a desiccator or silica until use.

2.3 Plant treatment

Ulvan treatment was previously dissolved in ultrapure water at 1 mg mL⁻¹. For each tray, 10 mL of ulvan was applied on ten-day-old wheat plantlets using a sprayer connected to an air compressor (ITW Surfaces et Finitions, Valence, France) until all leaf area was covered. Plants sprayed with ultrapure water were used as control.

2.4 Inoculation and disease evaluation

Wheat plants were inoculated with a suspension of 5×10⁵ conidia mL⁻¹ at 48 h after ulvan treatment. Conidia of Bgt were harvested from fifteen-day-old infected wheat plantlets and immediately suspended in Fluorinert FC43 (heptacosafluorotributhylamine 3M, Cergy-Pontoise, France) (Randoux et al., 2006). For each tray, 5 mL of inoculum was sprayed using a sprayer (ITW Surfaces et Finitions, Valence, France) connected to an air compressor. After inoculation, plants were kept under the same growth conditions described above. Disease symptoms were evaluated at 10 days after inoculation by counting the number of Bgt colonies on the fully expanded first leaf of plants, on both adaxial and abaxial surfaces. The ulvan effect on protection against powdery mildew was determined by assessing the number of Bgt colonies per leaf in comparison with the control group (water sprayed).

2.5 Conidial germination of B. graminis f. sp. tritici (Bgt) in vitro

In order to evaluate the ulvan effect on conidial germination, plastic Petri plates (5 cm) containing agar medium (12 g L^{-1}) in presence of water (control) or amended with ulvan solution (1 mg m L^{-1}) were prepared. Then, conidia of *Bgt* were gently tapped above the plates to allow a uniform conidia deposition and evaluated after 24 h of incubation at 18°C. The germination was randomly determined on 400 conidia per plate, being that divided into four quadrants, using a light microscope (Olympus BX 40). The conidia were classified into five categories: non-germinated conidia (NG), conidia with aborted germ tubes (AGT), with a single short germ tube (SGT, length < $10\mu m$), a single long germ tube (LGT, length > $10\mu m$) and multiple germ tubes (MGT) (Fig. 2).

2.6 Cytological observations of *Bgt* infection process

In order to monitor the development of infection structures of *Bgt*, segments (1.5 cm length) from the 1st expanded wheat leaves treated and non-treated with ulvan were excised at 24, 48, and 72 h after inoculation (hai). Leaf tissues were cleared in an acetic acid: ethanol solution (v:v, 1:3), stained with trypan blue (w:v 0.1%) for 30 min, mounted on glass slides with lactoglycerol, and observed with a light microscope (Olympus BX 40). Different developmental stages were evaluated in epidermal leaf cells and classified into six categories: non-germinated conidia, germinated conidia with a primary germ tube (PGT), with an appressorial germ tube (AGT) without haustorium (HS), AGT with HS in an early stage of development, AGT with fully formed HS and AGT with branched hyphae (BH) (Table 1).

2.7 Papilla autofluorescence at Bgt penetration sites

Autofluorescent papillae were assessed using the same leaf segments collected to evaluate the infection structures development. Leaf tissues were observed using an Eclipse E600 microscope (Nikon) using a blue exciter filter, excitation 450–490nm, dichroic mirror 505, and barrier filter 20 nm with transmittance range 500 to 800 nm. The fluorescence beneath AGTs on epidermal cells was classified according to Randoux et al. (2006) as no fluorescence, fluorescent papilla, and whole fluorescent cell (Fig. 4).

2.8 Cytochemical detection of hydrogen peroxide (H₂O₂) accumulation

Detection of H₂O₂ was carried out using the DAB staining method according to Thordal-Christensen et al. (1997). For H₂O₂ visualization, leaf segments treated or nontreated with ulvan were collected at 24, 48, and 72 hai and immediately submerged in 3,3-diaminobenzidine (DAB) solution (1 mg mL⁻¹, pH 3.8) for 4 h. Thereafter, tissues were completely bleached in acetic acid: ethanol (v:v, 1:3) solution and stored with lactoglycerol in the darkness at room temperature. H₂O₂ accumulation was identified by visualization of reddish-brown staining in all epidermal cells caused by oxidative polymerization of DAB. Reactions were evaluated using a light microscope (Olympus BX 40) and classified into three classes according to their frequencies: no DAB staining, staining localized at the penetration sites, and whole-cell DAB staining (Fig. 5).

2.9 Extraction and quantification of total phenolic compounds

Total phenolic compounds were determined using the Folin-Ciocalteu method (Singleton and Rossi 1965) downscaled to a 96-well plate with minor modifications. For this, leaves (treated or non-treated \times inoculated and non-inoculated) were collected at 24, 48, and 72 h after inoculation (hai). Powdered fresh leaf tissues (200 mg) were mixed with 1 ml of methanol (MeOH) and the mixture was shaken for 1 h at 40°C under 180 rpm in dark condition before two centrifugations at 13,000 \times g for 5 min. The supernatants were stored at -20°C until analysis. An aliquot (30 μ L) of methanolic extract was mixed with 150 μ L of Folin-Ciocalteu reagent (10-times diluted) and after 5 min of incubation at room temperature, 120 μ L of sodium carbonate solution (w:v 10%) was added. The mixture was incubated at room temperature for 2 h, and the absorbance was read at 750 nm. Total phenolic compounds were expressed as mg of Gallic acid equivalents (GAE) per g of fresh tissue.

2.10 Enzyme activities

Three plant enzyme activities involved in defense mechanisms were assessed 24, 48, and 72 h after inoculation with *Bgt* in wheat leaves treated and non-treated with ulvan.

Peroxidase (POX, EC 1.11.1.7) activity was assayed according to Mustafa et al., (2017) and was determined by monitoring the increase in absorbance at 412 nm for five min. The activity was defined as the amount of enzyme that reduced the electron donor at 1 mol s⁻¹ using ABTS (2, 2-azino-bis 3-ethylbenzothiazoline-6-sulfonic acid) as substrate ($\mathcal{E} = 32400 \,\mathrm{M}^{-1} \,\mathrm{cm}^{-1}$).

Lipoxygenase (LOX, EC 1.13.11.12) was measured according to Randoux et al. (2010) using linoleic acid as substrate. LOX activity was determined by monitoring changes in absorbance at 234 nm for five min, and one unit was defined as the amount of enzyme that catalyzes the conversion of the substrate (linoleic acid) at 1 mol s⁻¹ (ϵ = 23000 M⁻¹ cm⁻¹).

Phenylalanine ammonia-lyase (PAL, EC 4.3.1.24) was assayed according to Reignault et al. (2001). Enzyme activity was monitored by an increase in absorbance at 290 nm and one unit was defined as the amount of enzyme that catalyzes the formation of cinnamic acid at 1 mol s⁻¹ (ε = 10000 M⁻¹ cm⁻¹).

Protein content was measured using the method of Lowry et al. (1951). The standard curve was established with bovine serum albumin (BSA). POX, LOX, and PAL activities were expressed as nanokatal mg⁻¹ protein, where 1 kat represents the amount of enzyme that converts 1 mol of substrate s⁻¹ or forms 1 mol of product s⁻¹.

2.11 RNA extraction and RT-qPCR gene expression analysis

First wheat leaves (treated and non-treated \times inoculated and non-inoculated) were collected at 0, 24, 48, 60, 72, and 96 h after treatment, snap-frozen in liquid nitrogen, and kept at -80 °C until processing. Total RNA was extracted from 100 mg of plant tissue using RNeasy Plant Mini Kit (Qiagen, Germany). Genomic DNA contaminating the samples was removed by treatment with DNase using RNase-Free DNase Set (Qiagen, The Netherlands). In total, 2 μ g of RNA was reverse-transcribed using the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, USA) according to the manufacturer's protocol.

The expression of 10 selected target genes was tracked by quantitative RT-PCR using the primers reported in Supplementary Table 1 (phenylalanine ammonia-lyase -

PAL, chalcone synthase - CHS, flavonol synthase - FLS1, dihydroflavonol-4-reductase -DFR, anthocyanidin synthase - ANS, caffeic acid 3-O-methyltransferase - COMT, lipoxygenase - LOX, pathogenesis-related protein 1 - PR1, oxalate oxidase - PR8, and peroxidase - PR9). Among them, eight genes (PAL, CHS, FLS, ANS, LOX, PR1, PR8, PR9) and the housekeeping genes (ATPAAA, ATPase AAA Family. PetA, class A Apetala 2) were selected from previous studies performed on wheat–pathogenic fungus interactions (Khong et al., 2013; Tayeh et al., 2013, 2014 and 2015; Ma et al., 2014; Sharma et al., 2016; Giménez et al., 2011; Ors et al., 2018; de Borba et al., 2021). Primers pairs of two targeted genes (DFR and COMT) were newly designed using the Oligo Explorer 1.1.0 software and Primer3Plus website (Supplementary Table 1).

Reactions were carried out in a real-time PCR detector CFX Connect (Bio-Rad) using the following thermal profile: 15 s at 95°C (denaturation) and 1 min at 60°C (annealing/extension) for 40 cycles. PCR reactions were performed in duplicate with the SsoAdvanced Universal SYBR Green Supermix (Bio-rad, USA) according to the manufacturer's protocol. Melting curve assay was performed from 65° to 95°C at 0.5°C/s. Melting peaks were visualized for checking the specificity of each amplification. The data were analyzed using the CFX Manager software, and the relative levels of gene expression were determined following the method of Hellemans et al. (2007) with *ATPAAA* and *PetA* serving as two internal reference genes. The results were expressed relative to the respective control, for each sampling time, corresponding to a fixed value of 1.

2.12 Experimental design and statistical analyses

The experiments were arranged in a completely randomized design using three replicates for each treatment and repeated three times. Each replication corresponded to one plastic tray with 24 wheat plants. All data were subjected to analysis of variance (ANOVA) in order to determine the significance of differences. Means were compared by Student's t-test ($p \le 0.05$) using the SAS program (v.9.1 SAS Institute, Inc., Cary, NC). Total phenolic compounds were analyzed using the Tukey test ($p \le 0.05$).

For the relative expression of targeted genes, three replicates corresponded to three independent leaves for each condition and each sampling time. The experiments were conducted three times and only results that were repeated at least twice were considered. Bonferonni's multiple comparison test ($p \le 0.05$) was used for gene expression analysis. The expression was considered as up- or down-regulated to the 1x controls, when changes in relative expression were >2x or >0.5x, respectively.

3. RESULTS

3.1 Disease protection

At ten days after inoculation, the disease symptoms on wheat leaves were visually evaluated and characterized by the presence of white to grayish powdery colonies on the total surface of both faces of the first leaf of each plantlet. Control plants exhibited on average 77 colonies per leaf, while ulvan-treated plants showed about 45 colonies, corresponding to a significant 42% reduction of infection (Fig. 1a and 1b).

3.2 Ulvan effect on conidial germination of Bgt in vitro

Conidial germination of *Bgt* was slightly affected by ulvan treatment *in vitro*. In the control condition, 52.8% of conidia were non-germinated (NG), 20% presented a single short germ tube (SGT), 19% multiple germ tubes (MGT), 6.5% a single long germ tube (LGT), and 1.8% of aborted germ tubes (AGT). Ulvan treatment significantly decreased the percentage of NG conidia by 34% and stimulated the development of MGT by 81% in comparison to control. No significant effect of ulvan was observed for conidia with AGT, SGT, or LGT (Fig. 2).

3.3 Ulvan effect on the development of Bgt infection structures

In our conditions, during the first 24 h after inoculation, the conidia deposited on the leaf surface germinated and formed one short germ tube, named primary germ tube (PGT) (Fig. 3a). This step was rapidly followed by the emergence of a secondary germ tube, which swells at the tip and this was then named appressorial germ tube (AGT) (Fig. 3b). Subsequently, AGT produced a penetration peg, which breaks through the subjacent cell wall. Between 24 h and 48 h, the first haustorium was formed without disrupting the plasma membrane of the invaded epidermal cell (Fig. 3c). Once the haustorium was successfully developed (Fig. 3d), a secondary epiphytic hypha emerged from AGT, and thereafter branched hyphae (BH) were formed (Fig. 3e).

No impact of ulvan treatment on *Bgt* conidial germination was observed on wheat leaves at 24, 48, and 72 h after inoculation (Table 1). Concerning the infection process of the fungus on leaf tissues, a similar percentage of conidia with only a PGT was observed in ulvan-treated plantlets and non-treated ones. However, the percentage of conidia with an AGT but without HS was 42, 36, and 75% higher at 24, 48, and 72 hai on leaves of ulvan-treated wheat plants when compared to non-treated ones,

respectively. In contrast, the percentage of conidia with an AGT and with HS at an early stage of development decreased by 34, 25, and 13% at 24, 48, and 72 hai, respectively, on ulvan-treated wheat leaves in comparison to the control ones. No conidium with an AGT and a fully formed HS was detected before 48 hai, in treated and non-treated leaves, and no significant difference was found in the percentages observed in both cases at 48 and 72 hai. Conidia with AGT and BH were observed only at 72 hai. The percentage of these structures decreased by 76% on epidermal cells of ulvan-treated plants in comparison to the control ones (Table 1).

3.4 Autofluorescence at Bgt penetration sites

The occurrence of autofluorescence at the penetration sites of the fungus was evaluated and the frequency of fluorescent papillae and whole fluorescent cells were recorded (Fig. 4a-4c). The ulvan treatment significantly increased the presence of fluorescent papillae by 13% in comparison to control plants (water-sprayed) at 72 hai (Fig. 4d). In contrast, no significant effect of ulvan was observed for whole fluorescent cells (Fig. 4e).

3.5 Cytochemical detection of H₂O₂ accumulation at Bgt penetration sites

Upon *Bgt* infection of wheat leaves, H₂O₂ accumulation in the epidermal cell wall beneath AGT was monitored by reddish-brown staining *via* DAB at 24, 48, and 72 hai. DAB staining was classified into three categories, no DAB staining (Fig. 5a), staining localized at the penetration site of the fungus (Fig. 5c), and whole-cell DAB staining (Fig. 5e). In control plants (water-sprayed), most penetration events led to no visible DAB staining in the epidermal leaf cells. At 24 hai, the percentage of events with no DAB staining was significantly lower by 30% in ulvan-treated plants than in control ones (Fig. 5b). In contrast, ulvan-treatment increased the events with localized DAB staining by 90% in comparison to control at 24 hai (Fig. 5d). Ulvan treatment also increased the percentage of whole-cell DAB staining by 400, 83, and 48% at 24, 48, and 72 hai, respectively (Fig. 5f).

3.6 Total phenolic compounds

The total phenolic compounds were analyzed in wheat leaves of ulvan-treated or water-sprayed plants and inoculated or not with *Bgt*. Under non-inoculated conditions, the content of phenolic compounds was slightly higher in leaves of ulvan-treated plants when compared to the control. The levels of phenolics in ulvan-treated plants were

about 13, 26, and 23% higher than control at 24, 48, and 72 h after inoculation (*i.e.* 72, 96, and 120 h after treatment). Under inoculated conditions, significant differences were also observed, but only at 24 and 48 hai, when ulvan treatment increased total phenolic compounds by 9 and 11%, respectively (Fig. 6)

3.7 Enzyme activities

Two days after ulvan-treatment or water-spraying (control) and before the *Bgt* inoculation in wheat plants (48 hat or 0 hai), the activity levels of POX, LOX and PAL were measured. At this sampling time, no significant stimulation of the three enzymatic activities was observed in ulvan-treated plants compared to control ones (Fig. 7).

Under inoculated conditions, ulvan treatment led to an increase of POX activity by about 60% and 55%, at 24 and 48 hai, respectively when compared to the control (Fig. 7a). Similarly, LOX activity in ulvan-treated plants was 45% and 63% higher than controls at 24 and 48 hai, respectively (Fig. 7b). Concerning PAL activity, a significant increase was observed at 48 hai in leaves of ulvan-treated plants by about 2.5-fold in comparison to control (Fig. 7c).

3.8 Induction of molecular defense markers in wheat leaves pre-treated with ulvan

The impact of ulvan-treatment on the expression of genes involved in defense was evaluated under non-inoculated and inoculated conditions. These genes were involved in the phenylpropanoid pathway (*PAL*, *CHS*, *COMT*, *ANS*, *DFR*, and *FLS*), the octadecanoid pathway (*LOX*) or encoded for pathogenesis-related proteins (*PR1*, *PR9*, and *PR15*).

Under non-inoculated conditions, ulvan induced the expression of 5 of the 6 genes involved in phenylpropanoid metabolism, *i.e. PAL*, *CHS*, *COMT*, *ANS*, and *FLS* at 72 h and/or 96 h after treatment (hat) in comparison to the non-treated and non-inoculated wheat plants (Table 2). Concerning *CHS*, its expression was transiently down-regulated at 60 hat. In the case of *LOX*, a first and transient induction was observed at 24 hat (3.8-fold) when a second up-regulation of this gene was observed at 96 hat (8.5-fold) (Table 2). The expression of genes encoding PR-proteins appeared also to be modulated by the ulvan treatment. For *PR9*, an up-regulation was observed at 24 and 72 hat (5- and 7.5-fold, respectively), whereas the induction of *PR15* expression was observed from 60 to 72 hat (5.6- and 3.6-fold, respectively) (Table 2). Finally, the expression of *PR1* was clearly impacted by ulvan, with a down-regulation of the gene

from 24 to 48 h (0.2-fold), followed by an up-regulation from 60 to 96 hat (29-, 127- and 8-fold at 60, 72 and 96 hat, respectively) (Table 2).

Bgt infection of the control plants (water-sprayed) clearly modulated the expression of the targeted genes (Table 3). Concerning the genes encoding proteins involved in the phenylpropanoid pathway, the Bgt infection transiently induced an upregulation of ANS (2.6-fold) at 24 hai and COMT (2.9-fold) at 48 hai in comparison to control (non-inoculated). In the case of PAL and CHS, the gene appeared to present a different pattern with an induction at 24 and 48 hai (11.6- and 4.2-fold, 14- and 12-fold, respectively). No significant modulation of DFR and FLS was observed on the kinetic points studied (Table 3). The expression of LOX was induced from 24 hai, reaching a higher accumulation at 48 hai (4.7-fold) (Table 3). Concerning the PR-proteins, various patterns were observed according to the type of PR genes analyzed. Two peaks of high transcripts accumulation of PR1 were observed, with a first transient peak at 12 hai (7,341-fold) and a second one at 48 hai (22,566-fold). The expression of PR9 was induced on all points of the kinetic (from 12 to 48 hai, by about 1,600-, 2,300- and 3,300-fold, respectively). Similar to PR9, PR15 was induced on all points of the kinetic, with the higher transcript accumulation at 12 hai (60-fold) (Table 3).

In general, under inoculated conditions, similar patterns were observed in leaves of ulvan-treated and control plants, except for *CHS*, *COMT*, and *PR1* wherein the expression was significantly lower in infected leaves of ulvan-treated than in control ones at 48 hai (Table 3). For *ANS* and *PR15*, the expression appeared to be significantly higher in leaves of infected plants pretreated with ulvan than in infected control at 12 hai (Table 3).

4. DISCUSSION

In this study, ulvan treatment showed to be effective in reducing powdery mildew infection in wheat. The pre-treatment of whole plants significantly reduced the disease severity, but also induced numerous defense responses, such as an up-regulation of defense-related genes, an increase in some enzyme activities involved in defense, and the amount of total phenolic compounds. Moreover, at the microscopic scale, we observed more autofluorescence in papillae, suggesting phenolic compounds accumulation, and an accumulation of H_2O_2 in whole-cells at the site of Bgt penetration attempts.

Ulvan has been known to show systemic effect in various plants and its effectiveness is dependent on the time interval between applications, the dose, the number of treatments, environmental conditions, and fungal species (Paulert et al., 2010; Jaulneau et al., 2011; Stadnik and de Freitas, 2014). In cucumber and grapevine, a reduction of powdery mildew severity was also observed when a crude extract of *Ulva* was applied once at 3 days or twice at 3-6 days before fungal inoculation (Jaulneau et al., 2011). In alfalfa, two ulvan treatments were more effective against *C. trifolii* than one single treatment because some plant defense genes were particularly induced after two consecutive ulvan applications (Cluzet et al., 2004). In common bean, one, two, or three applications of ulvan were able to reduce the *Fusarium oxysporum* f. sp. *phaseoli* colonization at earlier, but not at later phenological stages. Furthermore, higher protection in bean was found when ulvan was applied onto leaves but not *via* seed soaking or soil irrigation (de Borba et al. 2019).

Ulvan did not inhibit conidial germination of Bgt in vitro, but increased the formation of multiple germ tubes. Abnormal formation of germ tubes usually can be associated with an atypical source of nutrition or under special conditions that impair conidial germination, i.e. when pre-infection structures did not recognize the surface (Nielsen et al. 2000). Similar effects have been found out for another fungal pathogen as C. fructicola, where ulvan also stimulated the elongation of germ tubes (Gonçalves and Stadnik, 2012). In contrast, in planta ulvan treatment did not affect conidial germination and primary germ tube formation. Nevertheless, the percentage of appressorial germ tubes (AGTs) without haustorium increased. These results suggest that ulvan does not impair the initial germination in planta, but at later stages of infection when Bgt starts the formation of haustorium in epidermal leaf tissues. The treatment therefore indirectly affects the fungal colonization, providing evidence that ulvan is able to induce plant defense mechanisms and acts as a resistance inducer. Similar effects were observed using ulvan in wheat against the hemibiotrophic fungus Zymoseptoria tritici (Zt), where the treatment significantly reduced substomatal colonization and pycnidium formation (de Borba et al., 2021). On the other hand, a commercial product based on Ascophyllum nodosum (Dalgin Active®) did not affect fungal colonization but inhibited Zt sporulation in bread and durum wheat (Somai-Jemmali et al., 2020).

Previous works have shown that algal polysaccharides, as ulvan, are considered as an important source of plant resistance inducers (Paulert et al., 2010; de Freitas and Stadnik, 2012; de Borba et al., 2021). Corresponding induced plant responses include the biosynthesis of phytoalexins, pathogenesis-related (PR) proteins (Cluzet et al.,

2004), induction of enzyme activities as peroxidases, and accumulation of phenolic compounds (Abouraïcha et al., 2015). However, molecular mechanisms underlying the ulvan-induced defense to powdery mildew pathogens are still unknown.

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In the present study, enzyme activity assays, defense-related gene expression analyses, and microscopic observations provided additional information about the defense mechanisms associated with ulvan treatment and probably contributing to the reduction of Bgt symptoms development on susceptible wheat. Concerning the defenserelated enzymes, the activities of POX and LOX increased in ulvan-treated plants in comparison to control at 24 and 48 h after inoculation (hai), whereas PAL activity markedly increased only at 48 hai. A previous study on resistance induction by acibenzolar-S-methyl (benzothiadiazole, Bion®) in wheat against powdery mildew showed a PAL activity peak at 24 hai, which occurred during the formation of AGTs (Stadnik and Buchenauer, 1999). PAL seems to be central for systemic acquired resistance (SAR) because its inhibition suppresses induced resistance (Stadnik and Buchenauer, 2000; Bhuiyan et al., 2009). POX and PAL are involved in the branch of the phenylpropanoid pathway leading to the biosynthesis of lignin but also other secondary metabolites, such as antimicrobial and phenolic compounds (Reignault et al., 2001; Abouraïcha et al., 2015). In our study, the increase of POX and PAL activities may be associated with the increase of phenolic compounds observed in ulvan-treated and inoculated plants at 24 and 48 hai, which could explain the increase of fluorescent papillae at the penetration sites of Bgt at 72 hai and contribute to impair fungal penetration. Papillae are typically formed to overcome pathogen penetration or delay the infection process of powdery mildew fungus, and their autofluorescence in epidermal cells indicates accumulation of phenolic compounds (Hückelhoven et al., 1999; Stadnik and Buchenauer, 1999, 2000; Reignault et al., 2001). Similar results were observed on Bgt-infected wheat pre-treated with natural inducers like Iodus40[®] (a product based on laminarin), trehalose (Renard-Merlier et al., 2007), and acetylated oligogalacturonides -OGAs (Randoux et al., 2010). Thus, PAL and POX activities were stimulated in ulvan-treated plants during the first 48 h after infection probably leading to the accumulation of phenolic compounds and to a cell-wall reinforcement.

Similarly, regarding H_2O_2 accumulation, ulvan-treated plants showed more DAB-stained cells during the 72 h after infection. Some elicitor treatments lead to ROS accumulation, as a result of their recognition by the plant as a pathogen attack (Randoux et al., 2010). The increase in whole-cell DAB staining from 24 hai may suggest that ulvan pre-treatment leads to H_2O_2 accumulation in response to the attachment of PGTs

or AGTs, which helps to avoid pathogen infection. This is corroborated by the upregulation of *PR15*, encoding an oxalate oxidase activity producing H₂O₂, just after inoculation in ulvan-treated plants. Indeed, ulvan is highly associated with enhanced resistance against powdery mildew in wheat and barley plants by priming an oxidative burst in suspension-cultured cells (Paulert et al., 2010). Moreover, the accumulation of ROS, such as H₂O₂, may also play a role in the induction of defense-signaling pathway. Previous studies have clearly shown that the accumulation of H₂O₂ is one of the earliest observable plant defenses strategy. H₂O₂ is also involved in cell wall crosslinking and lignification for strengthening at the infection sites, participating for instance in monolignols oxidation by peroxidases before polymerization into lignin (Bhuiyan et al., 2009; Nguyen et al., 2016). However, H₂O₂ accumulation induced by ulvan treatment can provoke cell death, as an attempt to restrict pathogen growth, since, with the host cell death, the nutrient supply becomes unavailable for biotrophic fungi (Thordal-Christensen et al., 1997).

In contrast to PAL, LOX is involved in the octadecanoid pathway leading to the synthesis of oxylipins and jasmonic acid (JA) accumulation. This enzyme plays an important role in plant response to elicitor treatments and resistance against powdery mildew in wheat (Jaulneau et al., 2011). Similarly, the increase of LOX activity was also associated with a reduction in the number of *Bgt* colonies in wheat plants treated with trehalose, a non-reducing disaccharide found in a wide range of organisms (Tayeh et al., 2014), with Milsana®, an ethanolic extract from the plant *Reynoutria sachalinensis* (Randoux et al., 2006) and with OGAs (Randoux et al., 2010). On the other hand, no significant effect on the regulation of *LOX* was found in wheat treated with the algal-based product Dalgin® and infected with the hemibiotrophic *Z. tritici* (Somai-Jemmali et al., 2021). In alfalfa, ulvan also induced expression of the β-glucuronidase (*GUS*) gene placed under the control of lipoxygenase gene promoter, and as the expression profiling was similar to that observed upon methyl jasmonate treatment (MeJA), the authors suggested for the first time the involvement of the JA-pathway in ulvan-induced immunity (Jaulneau et al., 2010).

Surprisingly, our findings mainly revealed that ulvan induced the expression of several genes involved in plant defense responses independently of pathogen infection. Most of the genes studied were up-regulated after ulvan treatment, without any challenge by the pathogen, while further inoculation did not activate most of them anymore. First, the expression profiles of PRs exhibited a certain degree of overlap between the activation of both JA and SA pathways. In non-inoculated conditions,

ulvan-treatment up-regulated *PR9* and *LOX* expression 24 h after treatment, and later, the expression of five genes involved in phenylpropanoid metabolism, one in the octadecanoid pathway and three genes encoding PR-proteins, mainly between 60 and 96 h after treatment. The first transient induction of *PR9* and *LOX* could be related to signalization, leading later to the establishment of defense responses. Subsequently, *PR1* was notably induced, which confirms its role in the activation of plant defense. *PR1* is known as a marker for SA signaling pathway and is frequently induced in response to fungal infection by activating SAR, especially against biotrophic pathogens (Cluzet et al., 2004).

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As described above, the phenylpropanoid pathway is known to produce phenolic compounds, which can be involved in many vital processes of plants like lignin biosynthesis and cell wall reinforcement at sites of attempted penetration (Hückelhoven et al., 1999; Stadnik and Buchenauer, 2000; Bhuiyan et al., 2009). Among genes involved in the phenylpropanoid pathway, we studied genes encoding enzymes involved in different branches. PAL is the enzyme acting upstream of the phenylpropanoid pathway, whereas acting downstream, we can find CHS (chalcone synthase), followed by ANS (anthocyanidin synthase) or FLS (flavonol synthase), which are enzymes involved in the flavonoids and isoflavonoid-type phytoalexins biosynthesis pathway. COMT (caffeic acid 3-O-methyltransferase) is a key enzyme for another branch of the phenylpropanoid pathway, leading to monolignol synthesis (Nguyen et al., 2016). Several studies have shown the role of these enzymes in plants under abiotic and biotic stress conditions. According to our results, CHS, ANS, and FLS expressions were upregulated without pathogen challenge and after ulvan treatment in order to help wheat plants to accumulate more flavonoids and probably enhance the resistance to Bgt. For example, CHS and CHI (chalcone isomerase) were also associated with Milsanainduced resistance against powdery mildew in cucumber plants since flavonoids were found in the haustorial complex of the *Podosphaera fuliginea* (Fofana et al., 2002). COMT is also involved in sinapaldehyde synthesis, leading to sinapyl alcohol, one of the main monolignols involved in lignin synthesis in wheat (Nguyen et al., 2016). The up-regulation of COMT in non-infected conditions suggests an accumulation of monolignols, which could be rapidly oxidized and polymerized for lignin synthesis in the case of pathogen attack. Interestingly, monolignol biosynthesis genes have been known to be induced in both susceptible and resistant wheat cultivars after Bgt attack (Bhuiyan et al., 2009). The concomitant up-regulation of PR15, encoding an oxalate oxidase producing H₂O₂, and PR9 encoding a peroxidase using H₂O₂ for lignification seems to confirm this hypothesis. Moreover, we observed that global phenolic compounds already accumulated in wheat in non-infected conditions, which confirms the importance of the elicitation of the phenylpropanoid pathway in wheat for defense.

Our study clearly indicates that ulvan treatment first elicits plant defense responses independently of fungal infection. The phenylpropanoid pathway seems to be largely involved in the protection conferred by ulvan against *Bgt* in wheat. Nevertheless, further investigations, including different genotypes, and non-targeted approaches like metabolomics and global hormonal signaling pathways could be an exciting challenge for future research.

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AUTHOR'S CONTRIBUTION

Aline C. Velho performed all experiments and wrote the manuscript. Pamela Dall'Asta and Maryline Magnin-Robert contributed to gene expression analysis, phenolic compounds assay and manuscript writing. Marlon C. de Borba contributed to enzyme activities and manuscript writing. Philippe Reignault, Ali Siah, Marciel J. Stadnik and Béatrice Randoux supervised this study and contributed to manuscript writing.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

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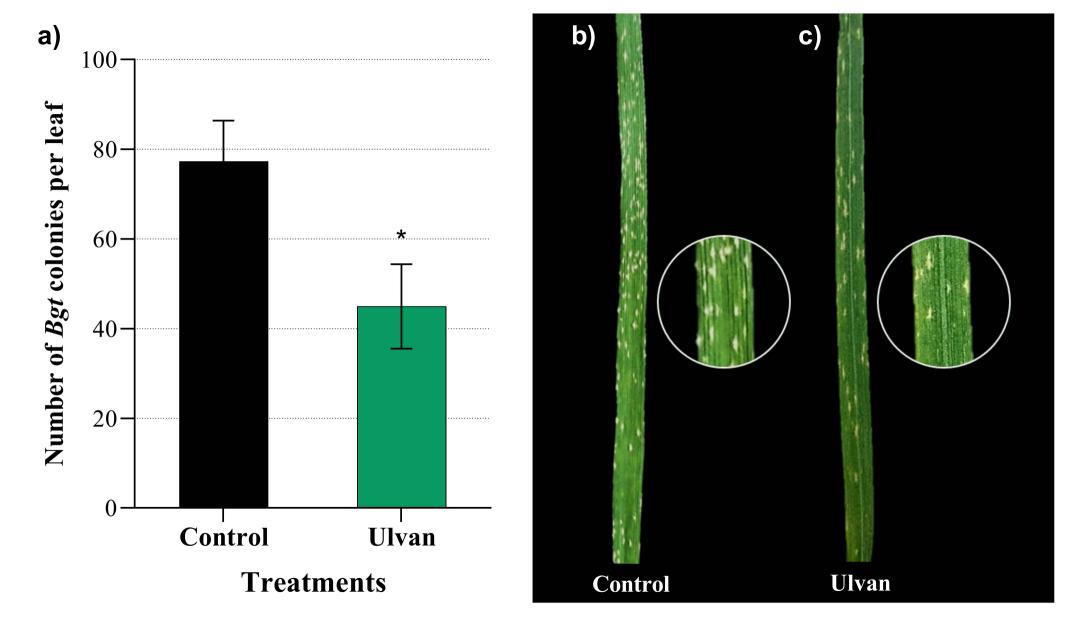
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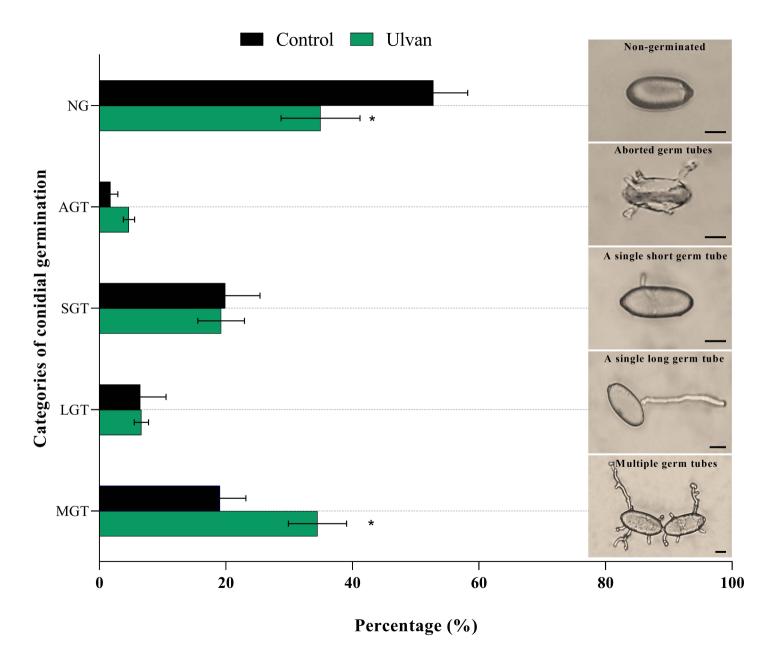
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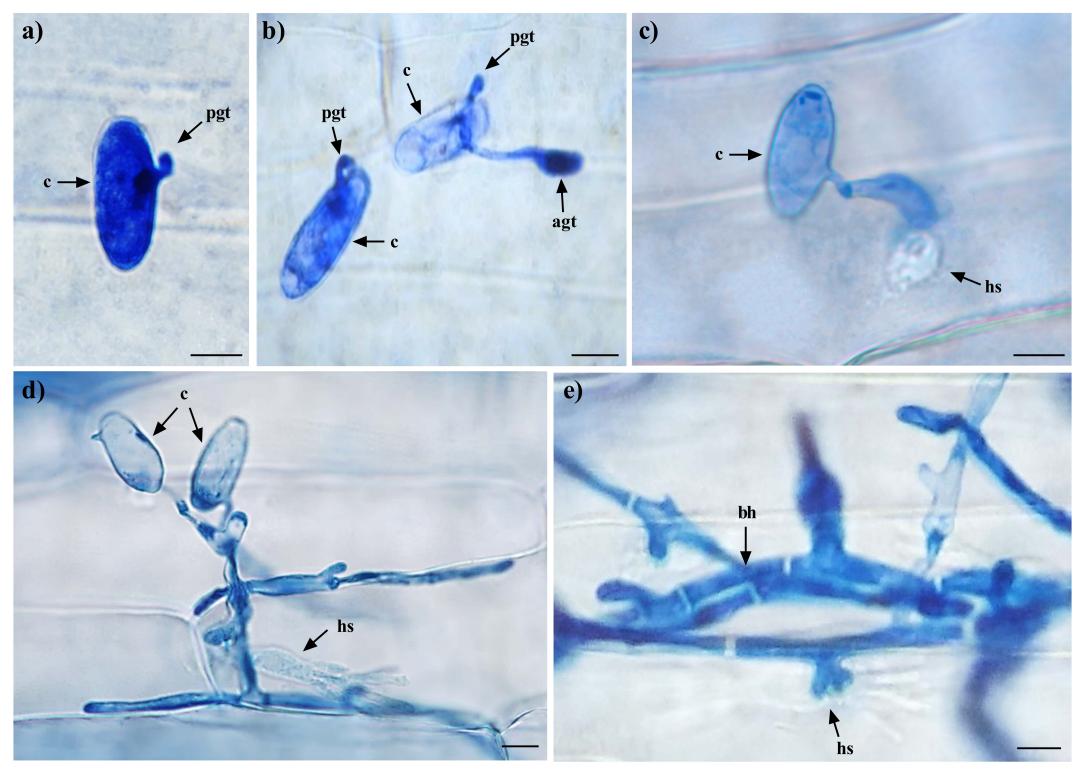
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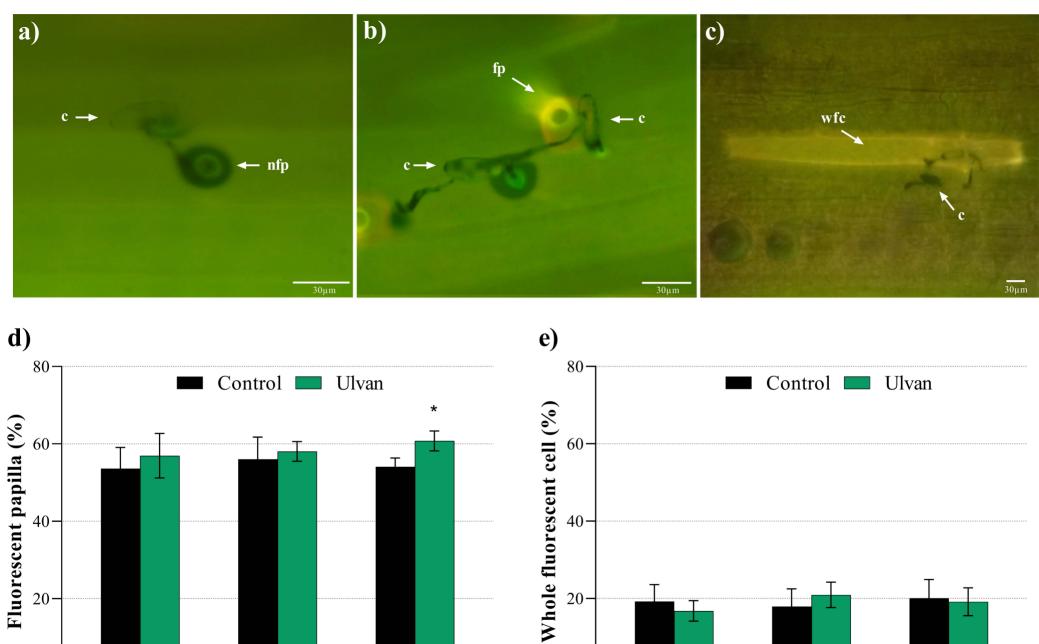
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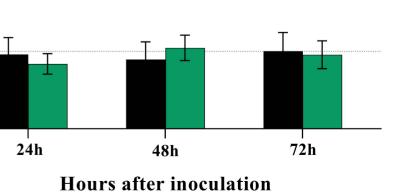
Hours after inoculation

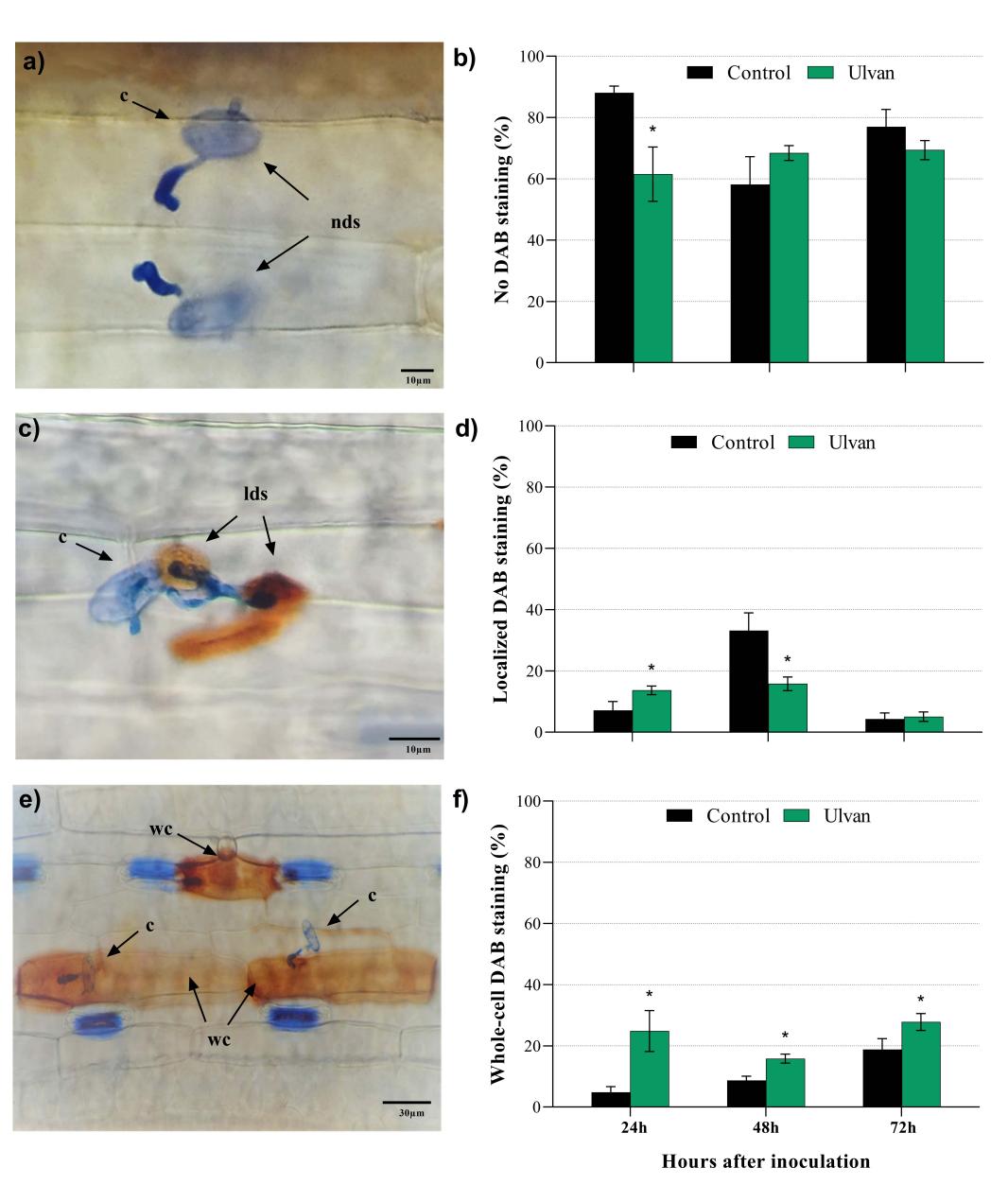
48h

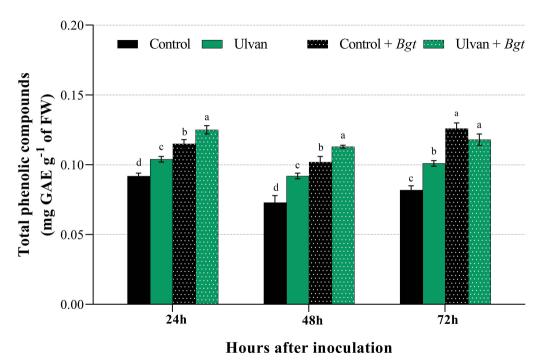
72h

0-

24h







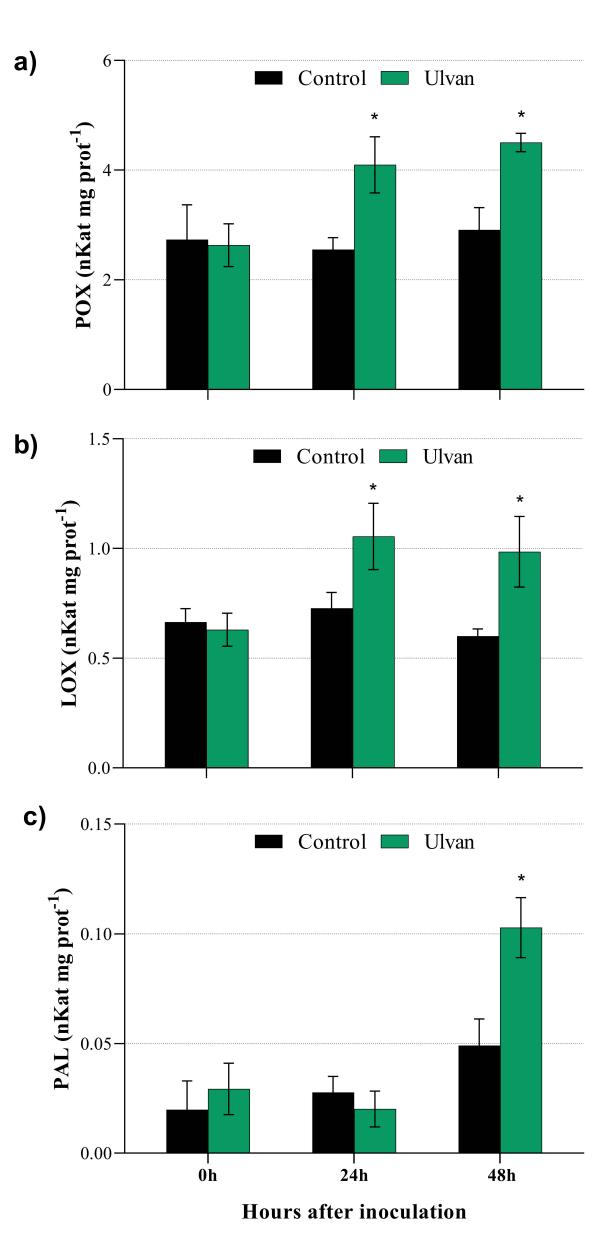


Table 1. Percentages of the different developmental stages of *Blumeria graminis* f. sp. *tritici* (*Bgt*) on epidermal leaf cells of both ulvan-treated or water-sprayed (control) wheat plantlets at 24, 48, and 72 h after inoculation. Susceptible plants were sprayed with water or ulvan 48 h before inoculation (5×10^5 spores mL⁻¹). Means followed by different letters in the column, within each category, indicate values significantly different compared to control according to Student's t-test ($p \le 0.05$).

Development stages	Treatments -	Hours after inoculation					
Development stages	Treatments	24h	48h	72h			
Non-germinated	Control	$2.1 \pm 1.5 \text{ ns}$	$3.1 \pm 0.7 \text{ ns}$	$2.4 \pm 1.0 \text{ ns}$			
	Ulvan	3.1 ± 1.6	3.1 ± 1.8	4.8 ±3.5			
PGT only (%)	Control	$2.2 \pm 0.9 \text{ ns}$	$3.9 \pm 1.8 \text{ ns}$	$1.4 \pm 0.8 \text{ ns}$			
1 G1 Olly (70)	Ulvan	4.3 ±3.3	5.3 ±3.1	2.4 ± 0.8			
AGT without HS (%)	Control	$38.4 \pm 3.3 \text{ b}$	$30.9 \pm 6.7 b$	14.9 $\pm 6.0 \text{ b}$			
71G1 Without 115 (70)	Ulvan	54.6 ±6.3 a	$42.1 \pm 0.9 a$	26.1 ±5.9 a			
AGT with HS (early stage) (%)	Control	$57.3 \pm 2.9 b$	57.5 ±8.2 b	$64.9 \pm 4.0 b$			
	Ulvan	38.0 ±9.1 a	$43.2 \pm 2.5 a$	56.2 ±2.8 a			
AGT with fully formed HS (%)	Control	nd	$4.7 \pm 2.2 \text{ ns}$	$10.7 \pm 2.2 \text{ ns}$			
	Ulvan	nd	6.3 ± 1.2	9.3 ±3.6			
AGT with BH	Control	nd	nd	$5.6 \pm 2.2 \text{ b}$			
	Ulvan	nd	nd	1.3 ±1.2 a			

Abbreviations: PGT = primary germ tube, AGT = appressorial germ tube, HS = haustorium, BH = branched hyphae, ns=non-significant, nd = non-detected.

Table 2. Quantitative real-time reverse-transcription polymerase chain reaction (RT-qPCR) experiments of transcripts levels of a set of defense genes in susceptible wheat (cv. Pakito) after ulvan treatment in non-inoculated condition^x.

hat ^y	PAL	CHS	COMT	ANS	DFR	FLS	LOX	PR1	PR9	PR15
24	1.50 NS	1.30 NS	0.80 NS	1.32 NS	0.96 NS	1.77 NS	3.76 A	0.17 A	5.08 A	0.54 NS
48	1.15 NS	1.99 NS	1.04 NS	1.82 NS	1.64 NS	0.99 NS	0.76 NS	0.23 NS	0.98 NS	2.24 NS
60	0.51 NS	0.11 A	0.50 NS	0.61 NS	0.58 NS	0.28 NS	0.33 NS	29.02 A	2.58 NS	5.55 A
72	1.38 NS	8.58 A	1.35 NS	4.93 A	0.97 NS	4.91 A	1.24 NS	127.07 A	7.45 A	3.61 A
96	2.57 A	4.64 A	3.83 A	1.36 NS	1.05 NS	4.70 A	8.52 A	8.21 A	1.21 NS	1.25 NS

x: Values shown represent fold up-regulation in ulvan-treated compared with water-sprayed plants after normalization to PetA and ATPAAA genes. A = significant change, NS = non-significant change. Gene expression was considered as up- or down-regulated to the 1x controls when changes in relative expression were >2x or >0.5x, respectively.

Y: hours after treatment.

Table 3. Quantitative real-time reverse-transcription polymerase chain reaction (RT-qPCR) experiments of transcripts levels of a set of defense genes in susceptible wheat (cv. Pakito) after ulvan treatment in inoculated condition^x.

	hai/hat ^y	PAL	CHS	COMT	ANS	DFR	FLS	LOX	PR1	PR9	PR15
Bgt	12 /NT	0.73 NS	0.40 NS	0.35 NS	0.74 NS	0.57 NS	0.27 NS	1.30 NS	7,341 A	1,594 A	58.90 A
	24 /NT	11.60 A	13.73 A	0.94 NS	2.58 A	0.64 NS	0.71 NS	1.78 NS	340 NS	2,332 A	7.70 A
	48 /NT	4.16 A	11.91 A	2.86 A	0.55 NS	0.92 NS	1.77 NS	4.68 A	22,566 A	3,372 A	10.65 A
Ulvan + Bgt	12 /60	0.76 NS	0.11 NS	0.53 NS	2.24 NS*	0.90 NS	0.30 NS	0.37 NS	5,606 A	2,547 A	155.1 A*
	24 /72	14.13 A	9.89 A	0.73 NS	3.84 A	0.59 NS	1.44 NS	3.24 A	398 NS	3,251 A	10.88 A
	48 /96	3.76 A	3.54 A*	1.31 NS*	0.72 NS	0.93 NS	2.43 A	8.22 A	7,546 A*	2,557 A	15.92 A

^{*:} Values shown represent fold up-regulation in leaves of water-sprayed Bgt infected and ulvan-treated Bgt infected plants compared with water-sprayed non-infected plants after normalization to PetA and ATPAAA genes. Gene expression was considered as up- or down-regulated to the 1x controls when changes in relative expression were >2x or >0.5x, respectively. A = significant change, NS = non-significant change. Statistical analyses were performed if the relative expression difference between ulvan-treated and infected wheat and the infected control wheat were >2x or >0.5x, * indicates a significant difference.

NT: Non-treated with ulvan.

Y: hours after inoculation /equivalent to hours after treatment with ulvan.

Ulva fasciata

In vitro

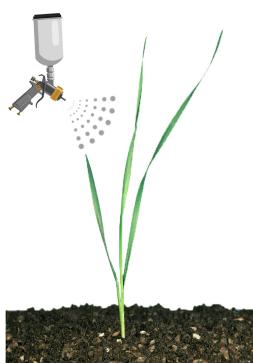
- Conidial germination of *Blumeria graminis* f. sp. tritici (Bgt)



- Development of multiple germ tubes







- Severity of powdery mildew





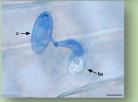


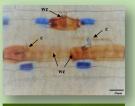
- Total phenolic compounds
- POX, PAL and LOX activities



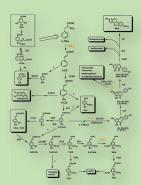
Phenylpropanoid pathway - PAL, CHS, COMT, ANS and FLS Octadecanoid pathway - LOX Defense-related proteins - PR1, PR9 and PR15













ULVAN

