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Additional Information

Transcriptomic profiling of citrus fruit peel tissues reveals fundamental effects of phenylpropanoids and ethylene on induced resistance

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SUMMARY

Penicillium spp. are the major postharvest pathogens of citrus fruit in Mediterranean climatic regions. The induction of natural resistance constitutes one of the most promising alternatives to avoid the environmental contamination and health problems caused by chemical fungicides. To understand the bases of the induction of resistance in citrus fruit against *Penicillium digitatum*, we have used a 12k citrus cDNA microarray to study transcriptional changes in the outer and inner parts of the peel (flavedo and albedo, respectively) of elicited fruits. The elicitor treatment led to an over-representation of biological processes associated with secondary metabolism, mainly phenylpropanoids and cellular amino acid biosynthesis and methionine metabolism, and the down-regulation of genes related to biotic and abiotic stresses. Among phenylpropanoids, we detected the over-expression of a large subset of genes important for the synthesis of flavonoids, coumarins and lignin, especially in the internal tissue. Furthermore, these genes and those of ethylene biosynthesis showed the highest induction. The involvement of both phenylpropanoid and ethylene pathways was confirmed by examining changes in gene expression and ethylene production in elicited citrus fruit. Therefore, global results indicate secondary metabolism, mainly phenylpropanoids, and ethylene play important roles in the induction of resistance in citrus fruit.

INTRODUCTION

In nature, plants are permanently in contact with a broad range of pathogens. However, disease is not widespread in plants and only a limited number of pathogens are capable of successfully

invading a plant and causing disease. Plants have evolved an intricate and elaborate set of defensive barriers in order to protect themselves against pathogens (Mysore and Ryu, 2004). Preformed physical or chemical barriers constitutively present on the plant surface may initially stop the establishment of infection structures. Later, the recognition of the pathogen may lead to the activation of defence mechanisms, such as the hypersensitive response, increased expression of defence-related genes, such as pathogenesis-related (PR) genes, and the oxidative burst (Ferreira *et al.*, 2006; Glazebrook, 2005; Jones and Dangl, 2006; Király *et al.*, 2007). Moreover, induced resistance activates the plant's defence mechanisms, thereby enabling the plant to better restrict the growth of a pathogen on subsequent attack. Although the molecular bases of induced resistance have been studied extensively in the vegetative parts of plants (Bostock, 2005; Conrath, 2009; Durrant and Dong, 2004), our knowledge of the processes underlying the establishment of induced resistance in fruits is still very poor, in most cases being limited to single metabolites, enzymes or genes. Moreover, we cannot assume that the mechanisms operating in mature fruits are equal to those found in vegetative parts of model plants. These factors strengthen the relevance of studying the mechanisms of induced resistance in crop fruits.

Penicillium digitatum (Pers.Fr.) Sacc. is the causal agent of green mould rot, and represents the major postharvest pathogen of citrus fruit in Mediterranean regions, accounting for up to 60%–80% of total losses as a result of fungal decay during fruit storage at ambient temperature. For many years, the control of this postharvest pathogen has mainly relied on the use of chemicals. With the current concerns about the harmful effects of synthetic fungicides on human health and the environment, there is a trend to adopt new and safer control alternatives. In citrus fruit, the induction of natural resistance constitutes one of these alternatives.

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1 Various treatments are known to trigger induced resistance in
2 citrus fruit against fungal infections (Ben-Yehoshua *et al.*, 2000),
3 including the application of physical (Arcas *et al.*, 2000; Droby
4 *et al.*, 1993; Rodov *et al.*, 1992), chemical (Porat *et al.*, 2001,
5 2002; Venditti *et al.*, 2005) and microbial antagonist treatments
6 (Arras, 1996; Droby *et al.*, 2002; Fajardo *et al.*, 1998). Among
7 these treatments, the highest induction of the antimicrobial phy-
8 toalexin scoparone was achieved in fruits subjected to pathogen
9 inoculation followed by a heat treatment at 37 °C for 3 days
10 (curing) (Ben-Yehoshua *et al.*, 1992; Kim *et al.*, 1991). Infected-
11 cured citrus fruits showed a significant reduction in the incidence
12 of green mould (Ballester *et al.*, 2010a). This treatment induced
13 a higher level of resistance than a wounding-curing treatment,
14 whereas curing alone increased the susceptibility to pathogen
15 infection.

16 So far, the analysis of the molecular and physiological bases of
17 induced resistance in citrus fruit has only been addressed at in-
18 dividual gene or enzyme activity levels. The application of elicitors,
19 such as UV light, jasmonic acid (JA), β -aminobutyric acid (BABA),
20 wounding or brushing and hot water treatment, led to an induc-
21 tion of the genes coding for chitinase, β -1,3-glucanase, phenyla-
22 lanine ammonia-lyase (PAL) and heat-shock proteins (Lers *et al.*,
23 1998; Pavoncello *et al.*, 2001; Porat *et al.*, 2001, 2002). The induc-
24 tion of chitinase, β -1,3-glucanase, PAL and peroxidase activities
25 has also been described in oranges subjected to different biotic or
26 abiotic treatments that elicit induced resistance (Ballester *et al.*,
27 2010a; Fajardo *et al.*, 1998). We have shown recently that induced
28 resistance in oranges against *P. digitatum*, elicited by the combi-
29 nation of an inoculation with the fungus followed, 1 day later, by
30 a curing treatment (37 °C for 3 days with high relative humidity),
31 coincided with the induction of PAL, soluble peroxidase, basic
32 β -1,3-glucanase and chitinase at both gene expression and
33 enzyme activity levels (Ballester *et al.*, 2010a).

34 Ethylene may stimulate senescence, but also plays a protective
35 role against stress conditions causing postharvest losses in citrus
36 fruit (Lafuente and Sala, 2002; Lafuente *et al.*, 2001; Marcos
37 *et al.*, 2005; Porat *et al.*, 1999b). Its production increases in citrus
38 fruit infected with *P. digitatum*, being synthesized by both the
39 fruit and the pathogen (Achilea *et al.*, 1985a,b). Application of the
40 ethylene inhibitor 1-methylcyclopropene (1-MCP) increases the
41 susceptibility of oranges to infection by *P. digitatum* (Marcos
42 *et al.*, 2005; Porat *et al.*, 1999b). Moreover, the fact that many
43 genes induced in citrus fruit on *P. digitatum* attack are also
44 up-regulated by ethylene highlights the role of this hormone in
45 the defence response of citrus to this pathogen (González-
46 Candelas *et al.*, 2010). However, it is still unknown whether this
47 hormone is also able to induce pathogen resistance in citrus fruit.

48 As citrus is one of the most important and widely grown fruit
49 crops, several genetic, genomic and proteomic tools have been
50 quickly adopted in recent years by the citrus research community
51 to address major challenges of this fruit crop (Talon and Gmitter,

2008). The genome sequences of both *Citrus sinensis* (Sweet
Orange Genome Project 2010, <http://www.phytozome.net/orange>) and *Citrus clementina* (Haploid Clementine Genome,
International Citrus Genome Consortium, 2011, <http://int-citrus-genomics.org/>, <http://www.phytozome.net/clementine>) have just
been released. One of the strategies developed for transcriptomic
analysis has been the construction of microarrays. In citrus, the
first global transcriptomic study was reported by Shimada *et al.*
(2005), who developed a citrus cDNA microarray containing 2213
independent genes, which was used for gene expression profiling
during fruit development. The Spanish Citrus Functional Genomic
Project (CFGP, <http://bioinfo.ibmcp.upv.es/genomics/cfgpDB/>) has
developed different generations of cDNA microarrays containing
up to 20 000 probes obtained from 53 cDNA libraries covering
different tissues, developmental stages and stress conditions
(Forment *et al.*, 2005; Martínez-Godoy *et al.*, 2008). Two other
microarrays, namely a citrus GeneChip from Affymetrix containing
30 171 probe sets representing up to 33 879 citrus transcripts
based on expressed sequence tags (ESTs) obtained from several
citrus species and citrus hybrids, and a citrus 22k oligoarray
containing 21 495 independent ESTs from citrus species (Fuji
et al., 2007), have been developed recently. Currently, additional
work is being performed within various research groups using
large cDNA citrus microarrays or smaller custom arrays based on
subtractive cDNA libraries (Bernardi *et al.*, 2010). These citrus
microarrays have been used to study gene expression in relation
to fruit development and quality (Bernardi *et al.*, 2010; Mayuoni
et al., 2011; Shimada *et al.*, 2005) or under various biotic (Albrecht
and Bowman, 2008; Gandía *et al.*, 2007; Kim *et al.*, 2009) and
abiotic (Gimeno *et al.*, 2009) stresses. A first transcriptomic
approach with cDNA macroarrays has recently been used to
unravel the molecular processes underlying the response of citrus
fruit to *P. digitatum* infection (González-Candelas *et al.*, 2010).
However, large-scale gene expression studies addressing the
process of induced resistance in citrus fruit against pathogen
attack have not been conducted so far.

In this work, with the aim of better understanding the mecha-
nisms underlying induced resistance in citrus fruit, we have
carried out a large-scale gene expression analysis in elicited
fruits, using the 12k citrus cDNA microarray developed by the
CFGP. In addition, we have examined the involvement of ethyl-
ene in the induction of resistance in citrus fruits.

RESULTS

Efficacy of elicitation of induced resistance in citrus fruits against *P. digitatum*

The combination of pathogen inoculation (denoted as I) followed
by a curing treatment (3 days at 37 °C; denoted as C) reduced
the incidence of a subsequent *P. digitatum* infection in oranges,

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Table 1 Incidence (percentage of infection) of green mould disease caused by *Penicillium digitatum* in elicited 'Navelate' oranges. Wounded fruits were inoculated with 10 µL of a *P. digitatum* spore suspension containing 10⁵ conidia/mL and incubated for 24 h at 20 °C and then for 3 days at 37 °C and 90%–95% relative humidity. Nontreated oranges were included as a control. At 0, 1 or 3 days post-treatment (dpt) (4, 5 or 7 days after the beginning of the experiment, respectively) fruits were inoculated with 10 µL of a *P. digitatum* spore suspension containing 10⁴ conidia/mL. Inoculation sites were 0.5 cm apart from the previous wound in the infected–cured fruits. Incidence was determined for up to 6 days of incubation at 20 °C following inoculation. The data shown correspond to 6 days post-inoculation. Different letters indicate significant differences in the treatments according to Tukey's test with $P = 0.05$.

	Days	dpt	Incidence (%)	
Nontreated fruits	0		86.7	a
	4	0	61.9	b
Infection + curing	5	1	50.0	c
	7	3	25.7	d

with the efficacy of the treatment being dependent on the elapsed time between the curing treatment and subsequent infection (Table 1). Thus, the highest effectiveness of the infection plus curing treatment (IC) was observed when *P. digitatum* inoculation was conducted 3 days post-treatment (dpt) (7 days after the start of the experiment), although, at 0 and 1 dpt (4 and 5 days after the start, respectively) the incidence of the infection was also reduced when compared with nontreated fruits.

Comparative analysis of transcriptional profiles in elicited citrus fruits

A functional genomics approach employing cDNA microarrays was used to investigate the molecular responses associated with induced resistance in citrus fruits elicited by the combination of pathogen infection followed by a curing treatment. For this purpose, five different samples were analysed: nontreated 'Navelate' oranges (NT), fruits infected with *P. digitatum* during 1 day (I1) and infected–cured samples taken 4 days (IC4), 5 days (IC5) and 7 days (IC7) after the beginning of the experiment, thus corresponding to 0, 1 and 3 dpt, respectively. In all cases, three biological replicates of each sample, consisting of 10 individual fruits each, divided into two tissues, i.e. flavedo (F, outer coloured part of the peel) and albedo (A, inner white part of the peel), were used for transcriptomic analysis. Each sample was hybridized against a reference sample composed of a mix of equal amounts of RNA of all the samples included in the analysis. We used the CFGP 12k microarray, which contains 24 288 clones, corresponding to 11 241 unigenes, 77.1% of which have an *Arabidopsis thaliana* homologue candidate. After discarding low-quality spot signals and normalization, 10 769 genes were analysed.

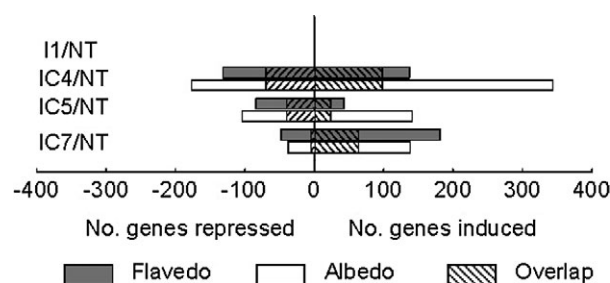


Fig. 1 Summary of differentially expressed genes [significant analysis of microarrays (SAM), $P < 0.01$] in the flavedo (grey bars) and albedo (white bars) of fruits infected with *Penicillium digitatum* during 1 day (I1) and infected and cured fruits at 4 days (IC4), 5 days (IC5) and 7 days (IC7) after the beginning of the experiment, compared with nontreated (NT) fruits. Genes differentially expressed in both tissues are represented as striped bars.

Figure 1 shows a summary of the genes differentially expressed [significant analysis of microarrays (SAM), $P < 0.01$] in the flavedo and albedo of fruits subjected to the elicitor treatment compared with nontreated fruits. In the flavedo, no single gene was differentially expressed 1 day after inoculation (FI1), whereas 299, 127 and 229 genes showed altered expression levels at 4, 5 and 7 days after the beginning of the experiment (FIC4, FIC5 and FIC7), respectively, when compared with nontreated fruits (FNT). Tables 2 and 3 show the genes with the highest induction ($\log_2 > 2$, Table 2) or repression ($\log_2 < -2$, Table 3) levels in the flavedo and/or albedo of elicited oranges, 5 and/or 7 days after the beginning of the experiment, which are the time points with the largest reduction in disease incidence, when compared with control samples. The most highly induced genes revealed the relevance of the phenylpropanoid pathway in elicited fruits: among the 29 most up-regulated genes in the flavedo, 13 were involved in either phenylpropanoid metabolism or coumarin biosynthesis, including seven different *O*-methyltransferases, an isoflavone reductase, a hydroxycinnamoyl transferase, two leucoanthocyanidin dioxygenases and two SRG1 proteins. Genes related to methionine and ethylene biosynthetic processes, such as 1-aminocyclopropane-1-carboxylic acid oxidase (ACO), and proteins related to defence and response to stress were also induced in the flavedo (Table 2). Among the 18 most down-regulated genes in FIC5 and/or FIC7, half were involved in responses to biotic and abiotic stresses, whereas the other half had unknown functions (Table 3). In the albedo, the expression of 521, 245 and 176 genes changed significantly at AIC4, AIC5 and AIC7, respectively, when compared with ANT (Fig. 1). Similarly to the flavedo, genes related to the biosynthesis of phenylpropanoids, coumarins and methionine were highly up-regulated in AIC5 and/or AIC7 relative to ANT (Table 2). In addition to these genes, the expression of different PR genes was also induced in the albedo of elicited

Table 2 Citrus genes with the highest induction level ($\log_2 > 2$) in the flavedo and/or albedo of elicited oranges 5 and/or 7 days after the beginning of the experiment. Values represent the \log_2 ratio of: a, I1/NT; b, IC4/NT; c, IC5/NT; d, IC7/NT. Numbers in bold indicate differential expression in the compared conditions according to significant analysis of microarrays (SAM) ($P < 0.01$) and $\log_2 > 2$. The symbol '+' indicates no expression in NT and the symbol '-' indicates expression in NT fruits but not in the compared treatment. NT, nontreated fruits; I1, infected fruits 1 day after pathogen inoculation; IC4, infected and cured fruits 4 days after the beginning of the experiment; IC5, infected and cured fruits 5 days after the beginning of the experiment; IC7, infected and cured fruits 7 days after the beginning of the experiment.

Citrus unigene	Description	<i>Arabidopsis</i> homologue	Flavedo				Albedo			
			a	b	c	d	a	b	c	d
<i>Phenylpropanoid and flavonoid biosynthetic process</i>										
aCL3343Contig1	Caffeic acid 3- <i>O</i> -methyltransferase	AT5G54160	0.23	2.38	4.22	3.18	0.28	2.47	4.18	3.41
aCL38Contig7	Catechol <i>O</i> -methyltransferase	AT5G54160	0.37	1.17	3.56	1.78	0.09	1.66	3.86	2.49
aC06052D07T7	Caffeic acid 3- <i>O</i> -methyltransferase 1	AT5G54160	-0.82	1.45	3.58	1.92	0.56	2.14	3.83	3.08
aCL38Contig8	Eugenol <i>O</i> -methyltransferase	AT5G54160	-0.41	2.29	3.43	3.28	0.74	2.39	3.79	4.04
aC08010D03SK	Caffeic acid <i>O</i> -methyltransferase	AT5G54160	-0.53	1.53	3.41	2.08	0.03	1.36	3.36	2.10
aC31502H09EF	SRG1 protein	AT1G17020	0.37	0.49	2.36	2.85	0.55	1.33	2.84	3.40
aCL38Contig2	Phloroglucinol <i>O</i> -methyltransferase	AT5G54160	-0.18	1.12	3.81	-	-	0.37	2.85	-
aCL3152Contig1	Hydroxycinnamoyl transferase	AT5G48930	-0.03	1.14	2.23	1.51	0.79	1.67	2.60	2.27
aC08017C07SK	Isoflavone reductase-like protein	AT1G19540	-0.79	1.20	2.37	0.94	0.36	1.17	2.34	1.26
aC31207A03EF	Eugenol <i>O</i> -methyltransferase	AT5G54160	0.20	1.11	2.26	2.02	0.43	0.95	1.79	0.85
aCL5465Contig1	SRG1 protein	AT1G17020	0.45	0.51	1.26	2.21	0.63	1.56	1.63	2.24
aCL1474Contig1	Cinnamyl alcohol dehydrogenase	AT5G19440	0.66	1.01	1.35	1.60	0.64	1.80	1.82	2.20
aC31705B10EF	Eugenol <i>O</i> -methyltransferase	AT5G54160	-0.13	1.03	2.14	1.55	0.43	0.24	1.18	0.98
aC31807C06EF	Acridone synthase II	AT5G13930	0.51	0.81	1.63	2.22	0.72	1.32	0.85	1.63
<i>Coumarin biosynthetic process</i>										
aC31108D04EF	Leucoanthocyanidin dioxygenase-like protein	AT3G13610	-1.21	3.08	3.77	3.96	0.49	3.46	4.36	4.26
aCL18Contig10	Caffeoyl-CoA <i>O</i> -methyltransferase 2	AT4G34050	0.13	1.61	2.24	1.79	0.69	2.99	4.16	3.33
aCL7037Contig1	Caffeoyl-CoA <i>O</i> -methyltransferase	AT4G34050	0.22	0.48	1.30	0.59	0.02	1.33	2.32	1.68
aCL139Contig2	Caffeoyl-CoA <i>O</i> -methyltransferase 2	AT4G34050	0.14	-0.26	1.03	-0.36	0.56	0.93	2.24	0.94
aCL8378Contig1	Leucoanthocyanidin dioxygenase-like protein	AT3G13610	-	1.53	2.22	-	-	+	+	+
<i>Methionine and ethylene biosynthetic processes</i>										
aC31605B08EF	ACC oxidase	AT1G05010	0.24	2.24	4.22	1.47	1.61	2.76	4.70	2.68
aCL3488Contig1	ACCO2	AT2G19590	-	0.85	2.48	-	0.03	0.66	1.03	0.35
aCL90Contig4	5-Methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	AT5G17920	-0.07	0.41	2.13	0.16	-0.22	0.73	2.09	0.36
<i>Defence-related proteins and response to stress</i>										
aCL46Contig3	PR10A	AT1G24020	0.87	1.56	1.09	1.31	1.27	3.61	3.45	3.03
aCL1Contig14	PR-4A precursor	AT3G04720	-0.50	1.47	1.34	2.04	-0.21	2.06	2.42	3.09
aCL7008Contig1	Germin-like protein subfamily 1 member 13 precursor	AT5G39120	1.51	3.26	2.39	2.69	1.31	3.72	3.06	3.05
aCL311Contig2	Germin-like protein subfamily 1 member 13 precursor	AT5G39150	1.70	2.24	2.31	2.68	1.03	3.67	3.02	2.96
aCL3449Contig1	Dicyanin	AT5G20230	0.51	1.22	2.12	1.51	1.27	1.89	3.01	2.47
aCL2358Contig2	Putative embryo-abundant protein	AT2G41380	-0.98	0.45	1.69	0.23	1.06	1.66	2.87	2.04
aCL3319Contig1	Chitinase CH11	AT3G54420	-1.03	1.86	1.61	1.40	0.68	2.38	2.06	2.82
aCL20Contig7	β -1,3-Glucanase precursor	AT3G57270	-0.33	-0.40	1.61	0.35	-0.61	0.68	2.81	1.18
aCL9Contig16	Lea5	AT4G02380	0.07	1.99	1.25	2.31	-0.41	0.95	0.50	0.90
aCL9353Contig1	Homogentisate phytylprenyltransferase (HPT1)	AT2G18950	1.03	1.59	1.95	1.63	1.20	2.13	2.28	2.05
aC34104H09EF	Receptor kinase Lecrk	AT2G37710	0.10	1.10	1.69	1.01	0.17	1.25	2.13	0.98
aC18021E12Rv	Isoleucine-tRNA ligase-like protein	AT4G10320	0.51	1.20	0.86	1.05	1.03	2.07	2.10	1.89
aC31304H09EF	Putative glutathione <i>S</i> -transferase T3	AT3G09270	-0.15	0.95	2.07	1.55	0.36	1.15	1.99	2.13
aCL7071Contig1	PR4b	AT3G04720	-0.56	1.24	1.25	1.57	0.41	1.54	1.62	2.24
aCL5030Contig1	PR5-1	AT4G11650	-0.20	1.58	0.96	1.49	-0.27	1.39	1.53	2.04
aCL9Contig11	Lea5		-0.02	1.84	1.19	2.02	-0.31	0.95	0.55	0.93
<i>Others</i>										
aC34005H07EF	Expressed protein	AT3G48770	-0.09	1.58	2.28	1.39	0.66	3.02	4.06	3.32
aCL2Contig10	No annotation available		0.05	1.65	1.97	3.69	0.16	0.85	1.49	2.75
aC05803G03SK	No annotation available		0.20	0.67	2.00	-0.40	1.83	1.81	3.69	1.72
aC31305B02EF	No annotation available		0.11	1.40	1.54	3.34	0.68	1.51	2.07	3.50
aC08012E03SK	No annotation available		0.06	1.45	1.29	3.04	-0.05	1.03	1.94	3.48
aCL257Contig1	Putative DNA-binding protein	AT4G27000	0.06	2.16	2.28	1.68	0.53	2.59	3.29	2.48
aCL8302Contig1	No annotation available		-1.00	1.07	1.03	1.52	0.62	2.17	2.37	3.20

Table 2 Continued.

Citrus unigene	Description	<i>Arabidopsis</i> homologue	Flavedo				Albedo			
			a	b	c	d	a	b	c	d
aCL5505Contig1	β-Cyanoalanine synthase	AT3G61440	-0.51	-0.30	2.72	1.70	0.14	0.74	3.16	2.23
aCL363Contig1	Expressed protein	AT4G32480	-0.26	0.90	2.49	0.47	0.98	1.63	3.08	1.76
aCL5472Contig1	No annotation available		0.06	0.13	1.51	-0.30	1.39	1.23	2.93	1.24
aCL7118Contig1	FAD-binding domain-containing protein	AT4G20820	0.29	1.12	1.99	1.06	1.25	2.18	2.77	2.06
aC08027C08SK	Agglutinin-2 precursor	AT5G65600	-0.62	1.53	2.42	0.93	-0.07	1.88	2.74	1.74
aCL8719Contig1	Globulin-like protein	AT1G07750	-0.27	-	-0.20	0.64	0.92	-	0.79	2.73
aC05811H08SK	Transferase family protein	AT1G28680	0.03	0.71	1.82	0.59	0.62	1.46	2.45	1.16
aCL3612Contig1	Cytochrome P450 79A2	AT5G05260	-0.53	0.41	1.31	0.73	0.59	1.49	2.44	1.73
aC08016G11SK	No annotation available		0.27	1.00	0.97	2.37	0.13	0.24	0.66	1.92
aCL214Contig1	3-Deoxy-D-arabino-heptulosonate 7-phosphate synthase 3	AT1G22410	-0.09	0.27	1.25	-0.10	0.86	1.53	2.36	0.94
aC01008H04SK	Phosphatidate cytidyltransferase family protein	AT3G45040	0.37	1.23	1.94	0.53	0.19	1.45	2.30	0.79
aCL1084Contig1	FAD-binding domain-containing protein	AT4G20820	0.62	1.39	2.26	1.48	0.56	1.65	2.17	1.51
aCL944Contig2	EIG-I24 protein	AT1G28680	0.80	1.07	2.16	0.85		+	+	
aC08019H09SK	No annotation available		0.30	1.39	0.93	2.14	0.29	1.02	0.90	2.05
aCL866Contig1	CYP81E8	AT4G37370	1.09	1.46	1.59	2.05	0.22	0.69	1.01	1.08
aC18010B08Rv	No annotation available		0.11	0.72	2.30	0.40	0.42	0.74	2.11	0.78
aCL632Contig3	Proline-rich protein	AT4G38770	0.12	1.14	1.48	0.20	0.44	1.41	2.08	1.00
aCL1591Contig2	Expressed protein	AT5G65520	-	-	1.90	1.37	0.30	0.67	2.07	1.49
aCL3641Contig1	Ripening regulated protein DDTFR18	AT5G17700	-0.11	1.98	1.14	2.03	-0.43	1.28	0.73	0.92
aCL8293Contig1	CYP82C1p	AT4G31940	0.75	1.69	1.45	2.03	0.34	1.16	0.81	1.16
aC19007C04T7	No annotation available		-0.11	1.84	1.12	2.03	-0.49	0.94	0.46	0.84

fruits. Among the 18 genes with the highest down-regulation in the albedo of elicited fruits were cold-regulated genes (*COR15*) and genes with unknown function (Table 3).

Functional analysis based on the transcriptome profiles

Hierarchical cluster analysis of all differentially expressed genes (SAM, $P < 0.01$) revealed the presence of a few major clusters containing genes that shared a common expression pattern, as shown in the gene-to-gene correlation matrix (Fig. 2a). Genes within these clusters and having an *A. thaliana* homologue were subjected to a singular enrichment analysis (SEA) using AgriGO to determine which biological processes were significantly over-represented (Table 4). Genes included in clusters f and g, whose expression increased in response to elicitor treatment (Fig. 2b), belonged to three major biological processes: phenylpropanoid biosynthesis, methionine metabolism and lipid biosynthesis. Most of the other pathways that appeared in these two clusters were ancestors of these three processes.

A principal component analysis (PCA) was conducted in order to identify those genes that mostly accounted for the differences among tissues and treatments. The result of this analysis (Fig. 3) showed a clear difference between elicited and nonelicited tissues in the first principal component (X-axis, explaining 45.7% of the total variation). In addition, the PCA revealed a variation between the two fruit tissues, flavedo and albedo, in the second

component (variation $Y = 19.7%$) (Fig. 3a). The genes determining both tissue and treatment variations can be found by the projection of the sample differentiation vectors onto the PCA plot showing the distribution of genes (SAM, $P < 0.01$) (Fig. 3b).

When the two fruit tissues were subjected to PCA independently, a clear separation of samples based on treatments was observed (Fig. 3c,d for flavedo and albedo, respectively). Independent of treatment, six genes showed higher expression in flavedo than in albedo, including a putative ABC transporter, two lipoxygenases, a cinnamoyl-CoA reductase, a glucosyltransferase and a senescence-related (SRG1) protein (Table S1, see Supporting Information). Four genes were more expressed in albedo samples than in flavedo samples: two proteins without any *A. thaliana* homologue and two different *Citrus tristeza virus* (CTV) proteins (Table S2, see Supporting Information). Based on gene ontology (GO) terms, the biological processes over-represented in the nontreated flavedo compared with nontreated albedo were associated with flavonoid and fatty acid biosynthesis (Fig. S1 and Table S3, see Supporting Information).

To elucidate the key processes that were altered in elicited citrus fruits, we searched for functional enrichment categories in the set of differentially expressed genes. This analysis showed that genes induced in the flavedo of elicited fruits (FIC5), when compared with nontreated fruits (FNT), were mainly involved in biological processes associated with secondary metabolism, in particular phenylpropanoids (Fig. 4 and Table S4, see Supporting Information). The same trend was observed in the flavedo of

Table 3 Citrus genes with the highest repression level ($\log_2 < -2$) in the flavedo and/or albedo of elicited oranges 5 and/or 7 days after the beginning of the experiment. Values represent the \log_2 ratio of: a, I1/NT; b, IC4/NT; c, IC5/NT; d, IC7/NT. Numbers in bold indicate differential expression in the compared conditions according to significant analysis of microarrays (SAM) ($P < 0.01$) and $\log_2 < -2$. The symbol ‘-’ indicates expression in NT fruits but not in the compared treatment. See nomenclature in Table 2.

Citrus unigene	Description	Arabidopsis homologue	Flavedo				Albedo			
			a	b	c	d	a	b	c	d
<i>Defence-related proteins and response to stress</i>										
aCL2916Contig1	Probable polygalacturonase noncatalytic subunit JP650 precursor	AT1G70370	0.55	-2.01	-2.72	-3.38	0.92	-1.77	-	-2.91
aCL6368Contig1	Probable polygalacturonase noncatalytic subunit JP650 precursor	AT1G70370	0.84	-1.65	-2.64	-3.14	0.98	-1.54	-	-
aCL5Contig15	Putative early light-induced protein	AT3G22840	-0.85	-2.77	-2.36	-3.10	-0.43	-0.70	-0.84	-1.53
aCL80Contig2	Chloroplast small heat-shock protein class I	AT3G46230	-0.07	0.97	-0.65	-1.87	-0.38	0.01	-1.60	-3.08
aCL2349Contig1	Putative β -1,3-glucanase	AT2G16230	0.23	-1.46	-1.87	-2.83	0.30	0.21	-0.54	-0.98
aC31403B04EF	Dehydrin family protein	AT1G54410	-0.18	-2.88	-2.07	-1.27	-0.43	-3.13	-2.80	-1.60
aCL6Contig15	Dehydrin family protein	AT1G54410	-0.97	-3.60	-2.71	-1.98	-0.44	-3.04	-2.57	-1.56
aC31502B11EF	Plasma membrane intrinsic protein	AT4G00430	0.35	-1.36	-2.33	-1.96	1.20	0.41	-1.25	-1.03
aC20006B02SK	MYB91	AT2G37630	-0.28	-2.29	-2.07	-1.32	-0.44	-2.29	-	-1.27
<i>Others</i>										
aCL2649Contig1	No annotation available		-0.77	-	-	-	-0.64	-1.26	-2.42	-3.36
aCL1642Contig3	No annotation available		-0.51	-2.14	-1.82	-3.23	-0.76	-1.29	-2.06	-2.66
aCL3246Contig1	Steroid sulphotransferase-like protein	AT5G07010	0.37	-1.73	-	-3.26	0.92	0.32	-0.44	-1.48
aC20005G09SK	Importin β -2	AT5G53480	0.32	-1.52	-1.84	-3.17	0.11	0.35	0.03	-0.83
aCL4849Contig1	Expressed protein	AT5G01750	-0.20	0.92	-0.76	-1.84	-0.42	-0.44	-1.46	-3.10
aCL6348Contig1	T2J13.20 protein	AT3G59300	-0.36	-2.71	-2.01	-1.21	-0.32	-2.97	-2.70	-1.75
aC06003B11SK	Expressed protein	AT5G14790	-0.26	-2.69	-2.01	-1.24	-0.23	-2.75	-2.54	-1.53
aCL6Contig6	No annotation available	AT1G54410	-0.33	-2.56	-2.04	-1.30	-0.34	-2.56	-2.49	-1.63
aC08006G03SK	Proline-rich extension-like family protein	AT1G21310	0.05	-0.88	-1.83	-2.44	0.18	-0.61	-1.97	-2.46
aCL1Contig17	No annotation available		0.02	-1.16	-2.39	-2.03	0.49	0.46	-0.38	-1.36
aC31504C04EF	Pollen Ole e 1 allergen and extension family protein	AT4G08685	-0.56	-0.81	-2.28	-2.01	-0.45	-0.95	-1.96	-1.90
aCL939Contig3	No annotation available		-0.29	-0.04	-0.82	-0.50	-0.78	-1.11	-1.75	-2.27
aC04006E11SK	Flavin reductase-related	AT2G34460	-0.28	-2.10	-1.63	-1.28	-0.55	-2.21	-2.24	-1.62
aCL533Contig3	CP12 precursor	AT3G62410	-0.29	-1.64	-1.79	-1.65	-0.77	-1.37	-1.78	-2.21
aCL5404Contig1	Hypothetical protein	AT5G38050	-0.15	-2.21	-1.35	-1.39	-0.12	-2.32	-2.15	-1.42
aCL3235Contig1	Expressed protein	AT3G62370	0.09	-1.88	-1.40	-0.98	-0.24	-2.18	-2.12	-1.34
aCL381Contig1	Galactinol synthase	AT1G56600	-0.96	-0.09	-	-0.55	-1.14	-0.52	-0.98	-2.11
aCL3Contig33	No annotation available		0.22	-0.84	-1.22	-0.74	-0.25	-0.94	-1.41	-2.10
aCL16015G06SK	Expressed protein	AT3G01370	-0.12	-2.03	-1.57	-1.01	-0.36	-2.05	-2.05	-1.32
aCL310Contig2	Expressed protein	AT4G26850	-0.07	-1.60	-2.04	-2.03	-0.14	-1.26	-1.86	-1.93
aC04023D07SK	No annotation available		-0.22	-1.92	-1.55	-1.07	-0.29	-1.97	-2.04	-1.43

elicited fruits at 7 days after the beginning of the experiment (FIC7; Table S5 and Fig. S2, see Supporting Information). In the albedo, processes related to flavonoid and cellular amino acid biosynthesis and methionine metabolism were over-represented at AIC5 (Table S6 and Fig. S3, see Supporting Information), whereas, 2 days later (AIC7), the response to cadmium ion was the most significant over-represented biological process (Table S7 and Fig. S4, see Supporting Information).

To better visualize the results of gene expression profiling experiments in a metabolic pathway context, the ‘OMICs Viewer’ was used. Based on the results described above, two biosynthetic pathways over-represented in elicited flavedo and albedo tissues were selected for further analysis: the methionine–ethylene biosynthesis pathway (Fig. S5, see Supporting Information) and the phenylpropanoid–phenolic acid–suberin pathway (Fig. 5).

Involvement of ethylene in the induction of resistance in citrus fruits

Several genes involved in the methionine and ethylene biosynthesis pathway were up-regulated on pathogen challenge followed by curing treatment (Table 2 and Fig. S5). As the highest induction in the elicited flavedo (FIC5) was observed for a homologue of the *A. thaliana* *EFE* gene, which encodes an ACO that is 4.7 times more strongly expressed than in FNT, we decided to study the involvement of ethylene in the fruit’s response in more detail by analysing both the expression of the *CsACO* gene and the production of ethylene in elicited fruits (Fig. 6). In nontreated fruits, *CsACO* expression was not detectable in either flavedo or albedo. However, in infected–cured fruits, high expression was observed in both tissues, especially 5 days after the beginning of

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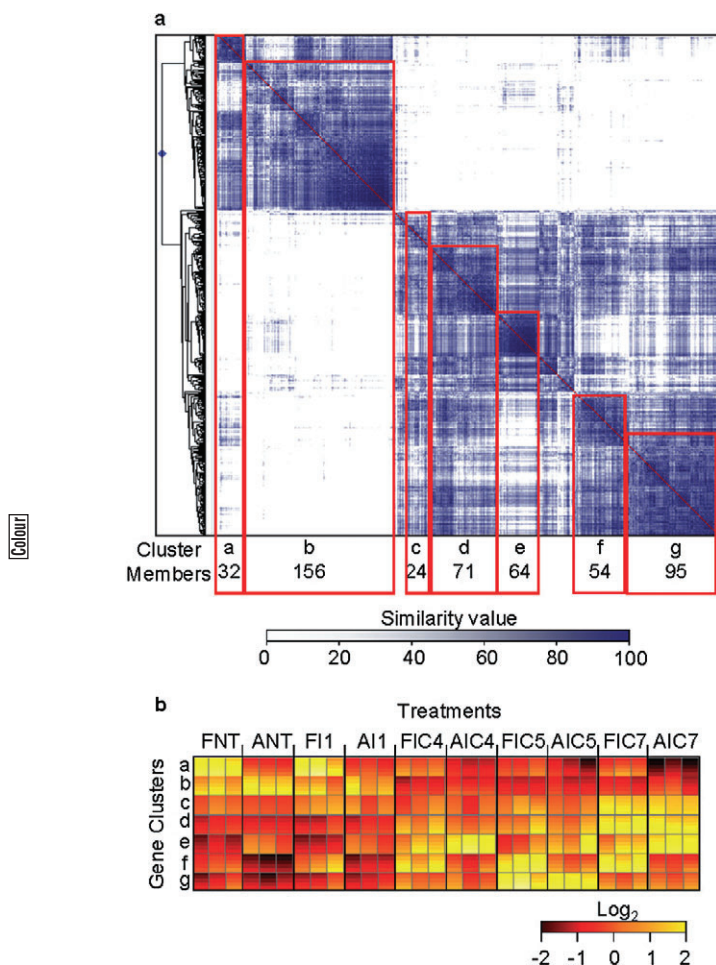


Fig. 2 Gene-to-gene correlation matrix of differentially expressed genes. (a) Main gene clusters are situated along the diagonal line (groups a–g). Correlations between genes are shown by the blue scale: the darker the blue colour, the higher the percentage of similarity between gene expression patterns. (b) Patterns of expression of flavedo (F) and albedo (A) genes included in each cluster. NT, nontreated fruits; I1, fruits infected with *Penicillium digitatum* during 1 day; IC, infected and cured fruits at 4, 5 and 7 days after the beginning of the experiment.

the experiment (IC5). The level of *CsACO* mRNA was 16.9- and 30.0-fold higher in the flavedo (FIC5) and albedo (AIC5) of infected–cured fruits, respectively, compared with that of flavedo infected with *P. digitatum* during 1 day (FI1). In both tissues, the expression of *CsACO* decreased 7 days after the beginning of the experiment. This trend was also observed in the unigene aC31605B08 spotted onto the 12k microarray (Table 2), which putatively also encoded another ACO. *CsACO* expression was induced in response to the wounding–curing treatment (WC7), but to a lesser extent than in infected–cured fruits (IC7). However, no expression was detected in response to the curing treatment alone (C7), in either the flavedo or albedo. It is interesting to note the lack of hybridization signal with the *P. digi-*

tatum ribosomal probe (Fig. 6a), a fact that indicates that the pathogen did not progress in the tissue that had been inoculated previously with the pathogen (treatment IC).

It is known that wounding and also *P. digitatum* infection induce the expression of ethylene biosynthetic genes in the peel of *C. sinensis* fruits (Marcos *et al.*, 2005). Therefore, we aimed to compare the effect of wounding and pathogen infection alone with that observed in response to elicitor treatment, which consisted of an infection with *P. digitatum* before the curing treatment. In this experiment, 'Navelina' oranges were inoculated with 10⁶ conidia/mL of *P. digitatum*, and flavedo and albedo tissues were analysed 1, 2 and 3 days after inoculation. The development of *P. digitatum* throughout both tissues was rapid, as determined by the accumulation of the *P. digitatum* 28S rRNA (Fig. 6b). Complementarily, the accumulation of the *C. sinensis* 26S rRNA was hardly detectable at 3 days post-inoculation, reflecting the degradation of fruit tissue as a result of fungal invasion. The pattern of *CsACO* expression was similar in flavedo and albedo. Wounded fruits showed only a small increase in *CsACO* levels 3 days after mock-inoculation in both tissues, compared with nontreated fruits. In contrast, a marked increase in *CsACO* expression was detected in both tissues during the development of infection by *P. digitatum*. The highest levels of *CsACO* mRNA were detected at 2 days after inoculation. Nevertheless, the increase in *CsACO* expression in response to *P. digitatum* infection was lower than that observed in infected–cured fruits.

Ethylene production (Fig. 6c) was determined in discs centred on the point of inoculation. No change in ethylene production was detected in either nontreated or cured fruits, whereas a slight increase was detected in wounded–cured fruits 5 days after the beginning of the experiment. In contrast, high ethylene production (42 nL/h/g FW) was detected in infected–cured fruits at day 6 of the experiment. Similar high levels were observed in infected fruits 2–3 days after inoculation with *P. digitatum*.

Involvement of the phenylpropanoid pathway in the induction of resistance in citrus fruits

It is known that genes involved in the biosynthesis of phenylpropanoids and compounds derived from this pathway are also involved in the resistance of citrus fruit against biotic and abiotic stresses (Ballester *et al.*, 2006; Kim *et al.*, 1991; Sánchez-Ballester *et al.*, 2000). Taking into account this previous result and the current transcriptomic observations, we decided to conduct a deeper study into the expression of genes specifically related to the phenylpropanoid pathway. Northern blot hybridization was used to both validate the microarray results and to better define the expression patterns of selected genes putatively involved in the phenylpropanoid pathway. In total, 17 genes were analysed (Fig. 7 and Table S8, see Supporting Information) and the

Cluster	GO term	Description	GO level	FDR
b	GO:0006950	Response to stress	3	0.021
	GO:0009628	Response to abiotic stimulus	3	0.034
f	GO:0019438	Aromatic compound biosynthetic process	5	0.0041
	GO:0044249	Cellular biosynthetic process	4	0.0055
	GO:0006519	Cellular amino acid and derivative metabolic process	4	0.0087
	GO:0009058	Biosynthetic process	3	0.0094
	GO:0044283	Small molecule biosynthetic process	4	0.017
	GO:0006725	Cellular aromatic compound metabolic process	4	0.026
	GO:0008610	Lipid biosynthetic process	4	0.026
	GO:0044281	Small molecule metabolic process	3	0.027
	GO:0019748	Secondary metabolic process	3	0.030
	g	GO:0044283	Small molecule biosynthetic process	4
GO:0006519		Cellular amino acid and derivative metabolic process	4	3.70E-09
GO:0044281		Small molecule metabolic process	3	2.10E-07
GO:0006520		Cellular amino acid metabolic process	5	7.40E-07
GO:0044106		Cellular amine metabolic process	5	1.70E-06
GO:0009308		Amine metabolic process	4	3.70E-06
GO:0019752		Carboxylic acid metabolic process	6	1.00E-05
GO:0043436		Oxoacid metabolic process	5	1.00E-05
GO:0006082		Organic acid metabolic process	4	1.10E-05
GO:0008652		Cellular amino acid biosynthetic process	6	1.10E-05
GO:0006790		Sulphur metabolic process	4	1.40E-05
GO:0042180		Cellular ketone metabolic process	4	1.50E-05
GO:0042398		Cellular amino acid derivative biosynthetic process	5	1.90E-05
GO:0009309		Amine biosynthetic process	5	2.70E-05
GO:0034641		Cellular nitrogen compound metabolic process	4	3.20E-05
GO:0019438		Aromatic compound biosynthetic process	5	3.60E-05
GO:0046394		Carboxylic acid biosynthetic process	6	3.80E-05
GO:0016053		Organic acid biosynthetic process	5	3.80E-05
GO:0000096		Sulphur amino acid metabolic process	6	6.50E-05
GO:0006575		Cellular amino acid derivative metabolic process	5	0.00015
GO:0044271		Cellular nitrogen compound biosynthetic process	5	0.00025
GO:0006555		Methionine metabolic process	7	0.00033
GO:0009058		Biosynthetic process	3	0.00034
GO:0046483		Heterocycle metabolic process	4	0.00042
GO:0044249		Cellular biosynthetic process	4	0.00044
GO:0006725		Cellular aromatic compound metabolic process	4	0.00089
GO:0009066		Aspartate family amino acid metabolic process	6	0.0028
GO:0019748		Secondary metabolic process	3	0.0073
GO:0009699		Phenylpropanoid biosynthetic process	7	0.015
GO:0044237		Cellular metabolic process	3	0.029
GO:0009698		Phenylpropanoid metabolic process	6	0.036
GO:0008152		Metabolic process	2	0.04
GO:0006807		Nitrogen compound metabolic process	3	0.043

Table 4 Gene ontology (GO) biological process categories over-represented in the clusters based on the gene-to-gene correlation matrix (Fig. 2). Only three clusters (b, f and g) showed significant biological processes with Bonferroni multi-test adjustment ($P < 0.05$).

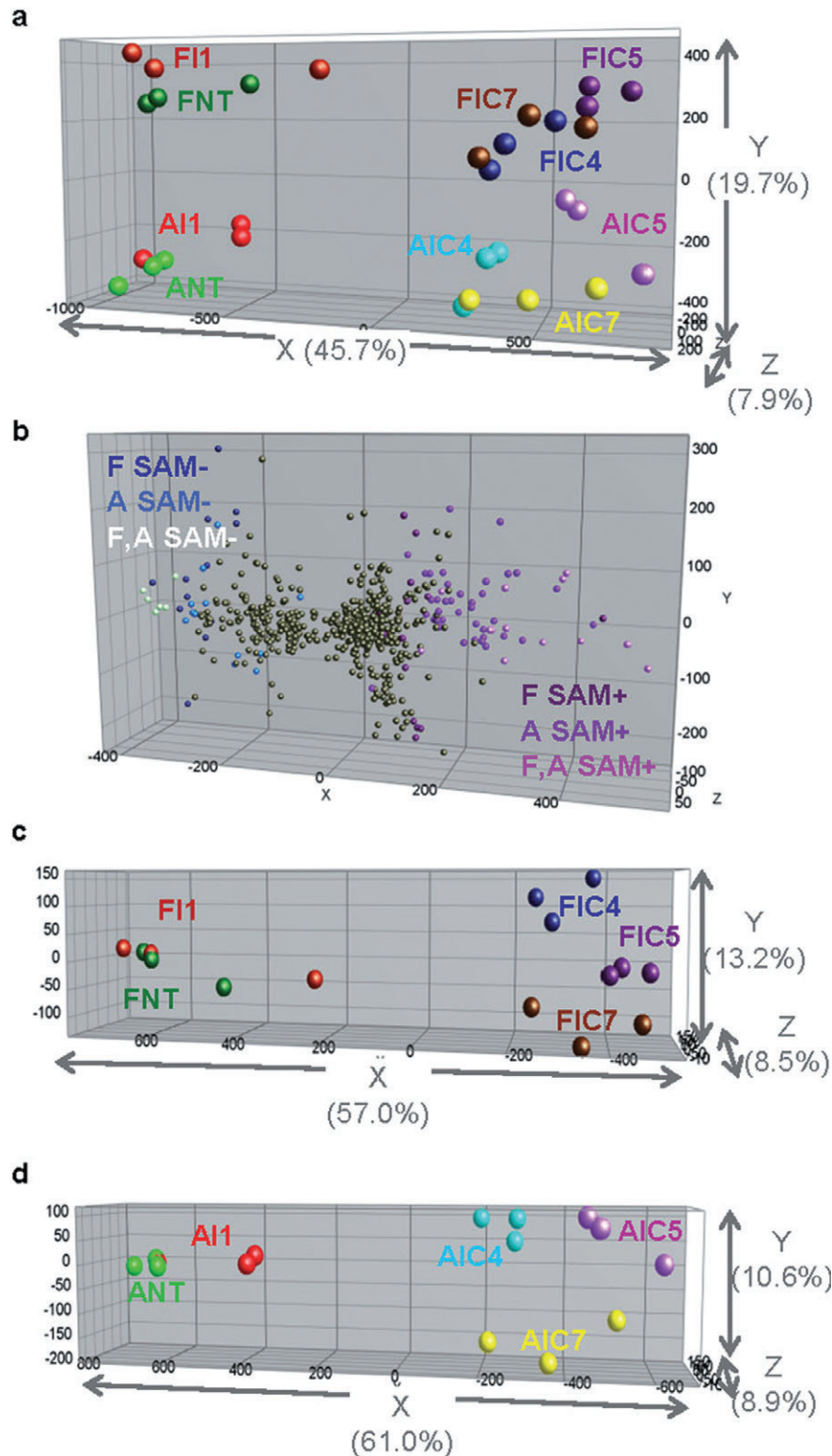
expression profiles for 12 of them were compared with their expression levels on the 12k microarray. Overall patterns were similar in both approaches, thus confirming our microarray results.

The expression of the 17 genes putatively involved in the phenylpropanoid pathway increased in the elicited fruits, generally reaching the highest induction levels 5 days after the beginning of the experiment. In this regard, it is noteworthy that the expression of *PAL*, the first gene in the phenylpropanoid pathway, and also the expression of most of the *O*-methyltransferases analysed increased in elicited oranges, suggesting the implication of these genes in the induction of resistance in citrus fruit. In general, the highest absolute expression levels were detected in

the flavedo, whereas induction ratios compared with nontreated fruits were higher in the albedo.

DISCUSSION

The search for and optimization of new pathogen control systems that could help to reduce the amount of chemicals needed to control postharvest pathogens in citrus fruit will benefit from a better understanding of the biological basis of induced resistance against major pathogens. Among the different elicitor treatments to induce resistance in citrus fruits, we have chosen the combination of pathogen inoculation followed by curing treatment as a tool to study the biological processes underlying the induction of



1 **Fig. 3** Multivariate analysis of differentially expressed genes in elicited citrus fruits. (a) Principal component analysis (PCA) showing the variation between fruits
2 subjected or not to elicitor treatment in the first component, and the variation between tissues, flavedo (F) and albedo (A), in the second component. (b) PCA
3 showing the distribution of genes. Genes with $\log_2 > 2$ for induced and $\log_2 < -2$ for repressed expression are indicated in different colours. Independent PCAs
4 for the flavedo (c) and albedo (d) samples. See nomenclature in Fig. 1.

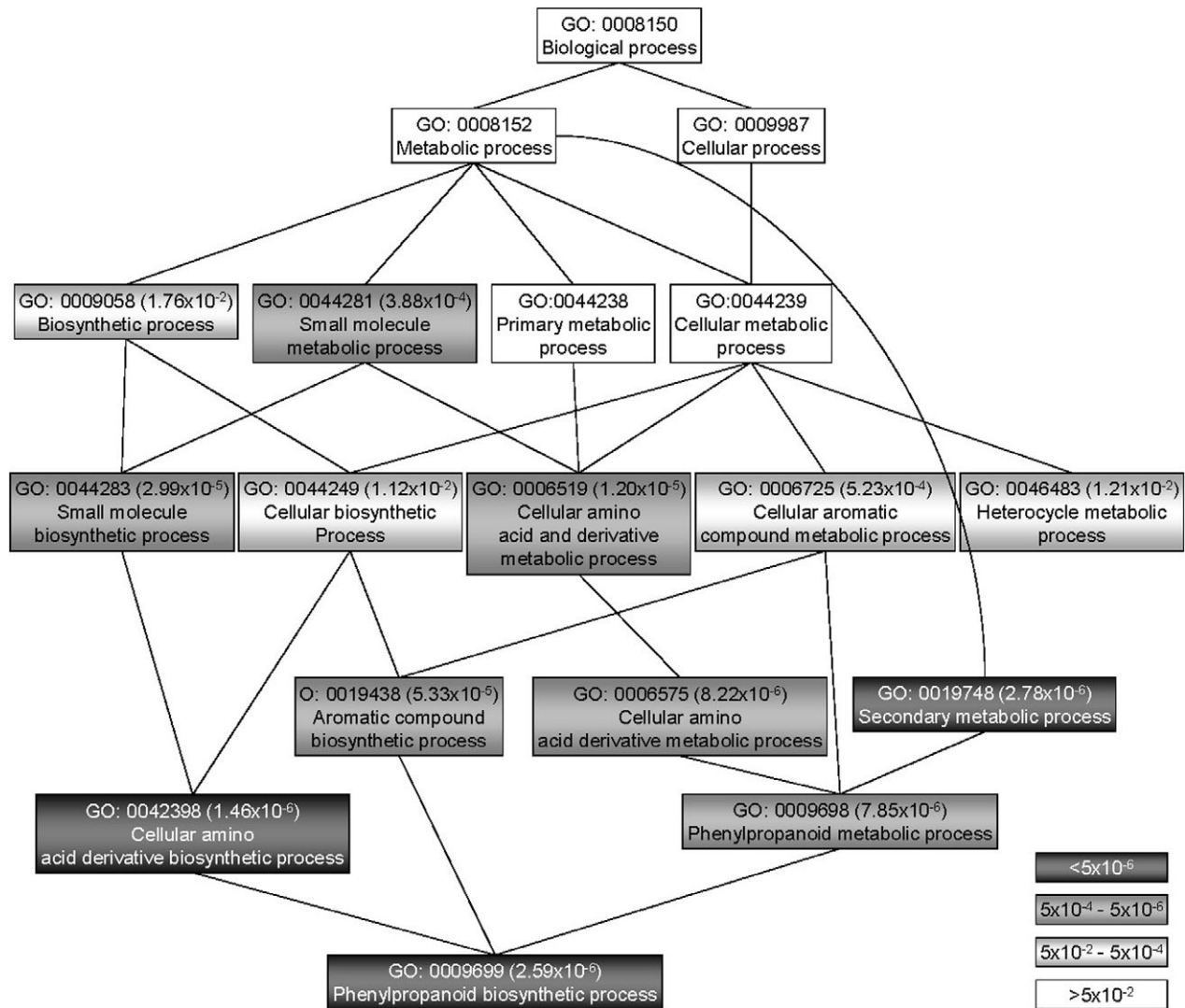
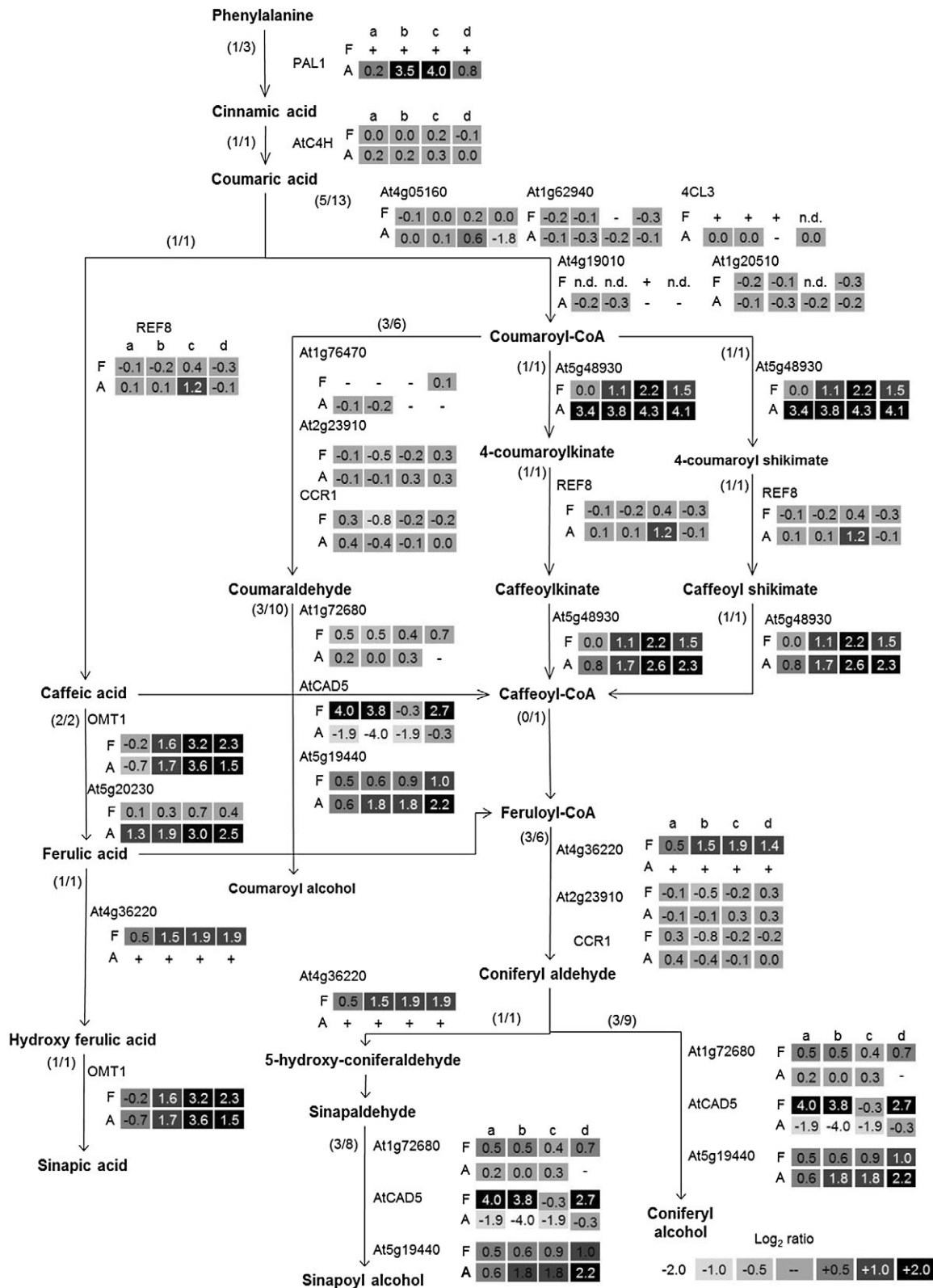


Fig. 4 Hierarchical view of gene ontology (GO) biological categories significantly over-represented in the elicited flavedo 5 days after the beginning of the experiment (FIC5) compared with nontreated flavedo (FNT), obtained with AgriGO. Significant categories (adjusted $P < 0.05$) are shown using colour scaling according to their significance level. Other categories required to complete the hierarchy are shown in grey.

resistance in citrus fruit in more detail. This combined treatment is highly reproducible, triggers the highest induction of the phytoalexin scoparone and leads to a greater reduction in disease incidence than wounding–curing or curing alone (Ballester *et al.*,

2010a). The build up of endogenous pathogen resistance in citrus fruit by postharvest treatments is usually achieved between 1 and 3 days after elicitor treatment (Ballester *et al.*, 2010a; Droby *et al.*, 2002; Pavoncello *et al.*, 2001). Accordingly, we have found that

Fig. 5 Graphical representation of the phenylpropanoid, free phenolic acids and suberin pathways showing gene expression values in the flavedo (F) and albedo (A) of elicited oranges. Light blue colour is used to indicate genes with differential expression according to significant analysis of microarrays. The first number in parentheses indicates the number of genes spotted onto the microarray that have an *Arabidopsis thaliana* homologue, and the second number indicates the total number of *A. thaliana* genes for each step in the pathway. Numbers in squares indicate the \log_2 ratio of: a, I1/NT; b, IC4/NT; c, IC5/NT; d, IC7/NT. n.d., not detected. The symbol '+' indicates no expression in NT and the symbol '-' indicates expression in NT fruits but not in the compared treatment. NT, nontreated fruits. I1, fruits infected with *Penicillium digitatum* during 1 day; IC, infected and cured fruits at 4, 5 or 7 days after the beginning of the experiment.



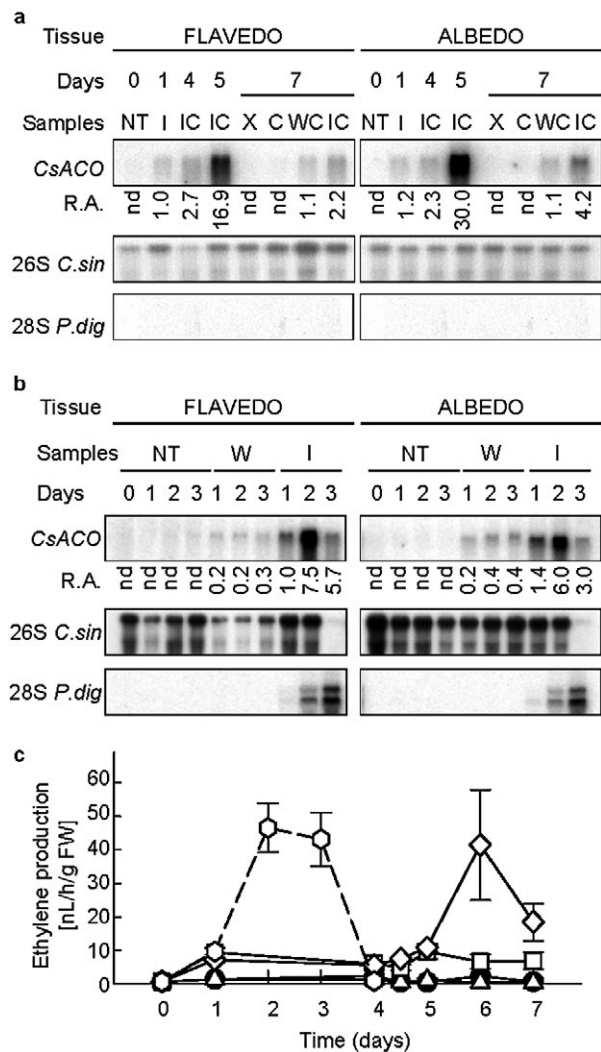


Fig. 6 Involvement of ethylene in the response of citrus fruits to elicitor treatment and to *Penicillium digitatum* infection. (a) Northern blot analysis of *CsACO* in the flavedo and albedo of oranges: NT, nontreated; I, infected; IC, infected and cured; X, nonwounded; C, cured; WC, wounded and cured. (b) *CsACO* mRNA accumulation in oranges infected with *P. digitatum* during 1, 2 and 3 days. Fruits were nontreated (NT), wounded and water inoculated (W) or wounded and inoculated with a suspension of 106 conidia/mL of *P. digitatum* (I). In (a) and (b), relative accumulation (R.A.) values of *CsACO* mRNA in arbitrary units are shown at the bottom. Normalization was carried out with respect to the hybridization signal of the *Citrus sinensis* 26S rRNA using the nontreated flavedo as a reference. Hybridization with the *P. digitatum* 28S rDNA probe is shown at the bottom. (c) Ethylene production in discs of nontreated oranges (●), infected fruits (○), cured fruits (△), wounded and cured fruits (□) and infected and cured fruits (◇). Values represent the average of three replicates, including 10 discs in each replicate, ± SD.

the combination of pathogen infection followed by curing treatment achieves maximum efficacy at 3 dpt, when a reduction of up to 70% in subsequent disease incidence is observed relative to control fruits (Table 1).

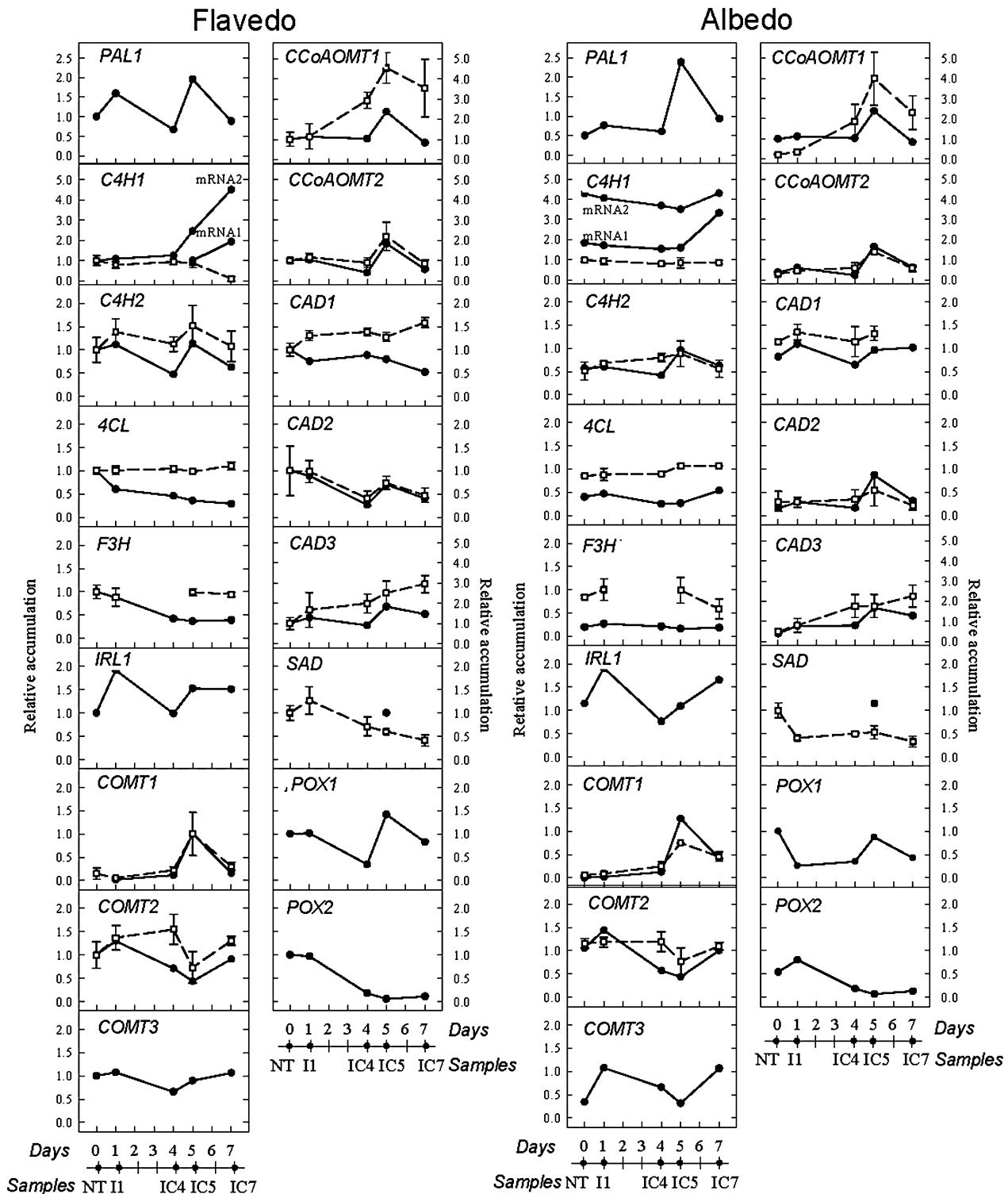
Functional genomics to elucidate induced resistance in citrus fruits

High-throughput technologies have allowed rapid progress in the understanding of the resistance of model plants against pathogens (De Vos *et al.*, 2005; van Loon *et al.*, 2006). Despite the progress made in the characterization of defence-related responses against *P. digitatum* infection (Angioni *et al.*, 1998; Ballester *et al.*, 2010a; Kim *et al.*, 1991; Ortuño *et al.*, 2006; Porat *et al.*, 1999a, 2001), remarkably little is known about the complex network regulating induced resistance in citrus fruit against *P. digitatum*.

Penicillium digitatum penetrates citrus fruits through wounds that affect the albedo, the inner tissue. In more superficial wounds, the chance for this pathogen to cause disease is much lower (Kavanagh and Wood, 1967). In a comparison between both tissues, we found that the expression of genes involved in the phenylpropanoid pathway is higher in the flavedo (Fig. 7). However, the largest elicitation was in the albedo. Thus, the transcriptomic approach supports the concept that the flavedo is more resistant than the albedo to *P. digitatum* infection (Afek *et al.*, 1999; Ballester *et al.*, 2006, 2010a), although the internal tissue responds more intensively to elicitor treatment. This greater response of the albedo is also reflected in the greater number of induced/repressed genes in elicited fruits when compared with that of the flavedo (Fig. 1).

The application of different elicitors to citrus fruit has been related to the induction of genes coding for PR proteins, such as chitinases and β -1,3-glucanases (Ballester *et al.*, 2010a; Porat *et al.*, 2001, 2002). Indeed, a chitinase and a β -1,3-glucanase gene were induced more than two-fold in the albedo of elicited fruits (Table 2). However, only three of nine chitinase and three of 11 β -1,3-glucanase genes present on the 12k microarray were induced in the albedo, whereas the number of induced genes was even lower in the flavedo. Other PR encoding genes were also induced, such as a ribonuclease-like protein (PR-10), two hevein-like PR4 proteins and two germin-like PR16 proteins (Table 2). Notably, most of the induced PR encoding genes showed a higher induction in the albedo.

Hierarchical cluster analysis of the differentially expressed genes revealed the presence of several clusters of co-expressed genes. Functional analysis of the genes included in these clusters showed that clusters f and g, which contained up-regulated genes in both tissues at 5 days after the beginning of the experiment, were enriched in processes related to methionine metabolism and phenylpropanoid biosynthesis, and, to a lesser extent, lipid biosynthesis, most specifically to isopentenyl diphosphate biosynthesis. Thus, although different factors/signals are probably involved in eliciting resistance in citrus fruit against *P. digitatum*, phenylpropanoids and ethylene seem to be the most important players in the complex network that regulates induced



1 **Fig. 7** mRNA relative accumulation of genes putatively involved in phenylpropanoid metabolism in elicited citrus fruits. The expression level was determined by
 2 Northern blot (●) or microarray (□) hybridizations. In general, a reference value of 1.0 was assigned to the nontreated flavedo, except for *COMT1* and *SAD*
 3 genes as a result of a lack of expression in nontreated flavedo. Values from microarray hybridizations represent the average of three biological replicates \pm SD.
 4 NT, nontreated fruits; I1, fruits infected with *Penicillium digitatum* during 1 day; IC, infected and cured fruits at 4, 5 and 7 days after the beginning of the
 5 experiment.

1 resistance. It is interesting to note that the metabolism of phenylpropanoids is also induced in response to *P. digitatum* infection in citrus fruits (González-Candelas *et al.*, 2010).

2 Implication of ethylene and related hormones in induced resistance in citrus fruit

3 The transcriptomic analysis showed an implication of genes related to methionine and ethylene biosynthetic processes in the defence response of citrus fruit. The expression of *CsACO* was induced by elicitor treatment (Table 2 and Fig. 6). Three additional putative *ACO* genes were present on the 12k microarray. However, only the expression of one of them (aCL3488contig1) increased in infected–cured samples. A comparative analysis of the nucleotide sequences of these four *ACO* genes showed a 29%–60% identity among them (data not shown), indicating that they are different genes and not alleles of the same gene. It is well known that ethylene regulates the induction of genes related to plant defence against pathogens, including several β -1,3-glucanases and basic chitinases, PR-1 and hydroxyproline-rich proteins (Ecker, 1995). We have shown previously that the expression of genes coding for two basic β -1,3-glucanase and chitinase isoforms is induced in elicited citrus fruits (Ballester *et al.*, 2010a). These previous results have been extended in the present study, where we found the induction of several ethylene responsive genes, including additional β -1,3-glucanases and chitinases, as well as other PR-encoding genes mentioned above. However, many other genes encoding PR proteins were not induced by elicitor treatment.

4 The infection of citrus fruit by *P. digitatum* induces ethylene production and the expression of genes involved in the synthesis of ethylene and phenylpropanoids (Achilea *et al.*, 1985a; Marcos *et al.*, 2005). Elicitor treatment also leads to an increase in ethylene production of the same magnitude as observed in *P. digitatum*-infected fruits (Fig. 6). In infected fruits, ethylene is produced by both the fruit and the pathogen (Achilea *et al.*, 1985a,b). However, in elicited fruits, ethylene only originates from the fruit as the fungus does not grow within the peel, as confirmed by the lack of hybridization with the *P. digitatum* rDNA 28S probe (Fig. 6).

5 Although ethylene plays a role in the resistance of citrus fruit (Marcos *et al.*, 2005; Porat *et al.*, 1999b), we found only a limited overlap between genes induced by elicitor treatment and those induced by ethylene (González-Candelas *et al.*, 2010). Moreover, the reduction in disease incidence achieved by ethylene treatment (Marcos *et al.*, 2005) was much lower than that observed with the infection–curing treatment, suggesting that other factors are involved in triggering induced resistance in citrus fruits.

6 Ethylene and JA usually show a synergistic relationship in regulating the expression of defence genes effective against necrotrophic pathogens (Glazebrook, 2005; Lorenzo *et al.*, 2003;

7 Schenk *et al.*, 2000). The elicitor treatment altered the expression of marker genes for SA, such as PR-1, PR-2, PR5, PR-10 or class II β -1,3-glucanase, but there was no clear trend in the observed changes, and functional analysis of the differentially expressed genes did not reveal any biological process related to SA or JA in elicited citrus fruits. However, we cannot rule out the implication of these hormones in the induction of resistance of citrus.

8 Involvement of the phenylpropanoid pathway in the induced resistance of citrus fruits

9 Transcriptomic analysis revealed that the metabolism and biosynthesis of phenolic compounds were involved in the induced resistance of citrus fruits against *P. digitatum*. PAL is the first enzyme in the phenylpropanoid pathway leading to the synthesis of coumarins and flavonoids (Dixon *et al.*, 2002). Studies in citrus fruit have focused on changes in *PAL* expression in response to pathogen attack (Ballester *et al.*, 2006; McCollum, 2000) or elicitor treatment (Ballester *et al.*, 2010a; Droby *et al.*, 1993; Fajardo *et al.*, 1998). We have shown previously that *PAL* expression increases in both flavedo and albedo of infected–cured fruits. In the present work, we observed that the expression of not only *PAL*, but also a large subset of genes important for the synthesis of phenylpropanoids and flavonoids, such as *C4H*, *4CL*, *COMT*, *CCoAOMT*, *CAD*, *SAD* and *POX*, was increased in elicited fruits (Table 2 and Figs 5 and 7). Transcript levels of selected phenylpropanoid genes were further investigated by Northern blot hybridization, validating the results obtained with the 12k microarray (Fig. 7). Although the highest expression of these genes was detected in the flavedo of infected–cured fruits, the highest inductions were observed in internal tissue (Fig. 7).

10 Biosynthetic genes are not the only genes related to the accumulation of phenylpropanoids and flavonoids. It is well known that R2R3-type MYB genes control many aspects of plant secondary metabolism (Stracke *et al.*, 2001). Recently, it has been described that the lack of expression of the *MYB12* transcription factor, which controls the expression of the biosynthetic flavonoid genes, is related to the lack of accumulation of naringenin chalcone in tomato (Adato *et al.*, 2009; Ballester *et al.*, 2010b). The *A. thaliana MYB12* homologue was included in the 12k microarray, but was not affected by elicitor treatment. However, two MYB, two WRKY and one bHLH transcription factors clustered within the e, f and g groups in the gene-to-gene correlation analysis. Additional analysis will be performed in order to clarify the possible role of these transcription factors in the induced response.

11 In conclusion, the transcriptomic analysis of elicited oranges showed important up-regulation in the expression of genes involved in the metabolism of phenylpropanoids and synthesis of ethylene and down-regulation of genes related to diverse biotic and abiotic stresses. Our results indicate that the highest induc-

tions were found in the albedo, whereas the highest expression values were detected in the external tissue. These results reinforce the concept that the internal tissue is more susceptible to *P. digitatum* infection, and it is this tissue that should increase its defensive barriers to a greater extent in order to avoid the progression of the fungus. To the best of our knowledge, this is the first study in any harvested fruit that has addressed the analysis of global changes in gene expression in the process of induced resistance.

EXPERIMENTAL PROCEDURES

Fruit and fungal material

Oranges (*Citrus sinensis* L. Osbeck) from a commercial orchard in Liria (Valencia, Spain) were selected and used in the experiments before any commercial postharvest treatment was applied. 'Navelate' fruits were taken in three independent samplings and used for the induction of resistance treatment, and 'Navelina' oranges were employed to study the expression of *CsACO* during the infection of *P. digitatum*. Fruits were immediately surface sterilized with 5% commercial bleach solution for 5 min, extensively washed with tap water and allowed to dry at room temperature until the next day.

Petri dishes containing potato dextrose agar were inoculated with *Penicillium digitatum* (Pers. Fr.) Sacc. isolate PHI-26 and incubated at 24 °C for 7 days (López-García *et al.*, 2000). Conidia were rubbed from the agar surface by scraping them with a sterile spatula and transferred to sterile water. The conidial suspension was then filtered and the concentration was determined with a haemocytometer and adjusted to the desired value.

Induction of resistance treatment and *P. digitatum* infection

The treatment for eliciting resistance has been described previously by Ballester *et al.* (2010a). Briefly, the following treatments were applied to the three biological replicates of 'Navelate' oranges: (i) fruits were wounded by making punctures (3 mm in depth) with a sterilized nail and inoculated with 10 µL of a *P. digitatum* conidial suspension adjusted to 10⁵ conidia/mL; the treated fruits were placed in plastic boxes and maintained at 90%–95% relative humidity at 20 °C for 1 day to allow pathogen development; fruits were then heat treated at 37 °C for 3 days under water-saturated conditions (curing) in order to stop the progress of the pathogen (sample IC); (ii) control inoculations were carried out by injecting 10 µL of sterile water and holding the fruits under the same conditions (sample WC); (iii) additional controls consisted of intact nonwounded fruits held at 20 °C for 1 day and then at 37 °C for 3 days (sample C) and

intact nonwounded fruits held at 20 °C for 1 day and then at 4 °C for 3 days (sample X). A sample from intact nonwounded fruits was obtained on the first day of the experiment (sample NT). Peel tissue discs of 13 mm around the inoculation point were sampled using a cork borer. Flavedo and albedo tissues were separated with a scalpel. Tissue discs obtained from 15 oranges with eight discs per fruit were immediately frozen in liquid nitrogen, mixed, ground to a fine powder with a coffee mill and stored at –80 °C until further analysis.

To check the influence of *P. digitatum* infection in the expression of *CsACO*, 'Navelina' oranges were wounded by making punctures (5 mm in depth) with a sterilized nail and inoculated with 10 µL of a suspension of *P. digitatum* conidia adjusted to 10⁶ conidia/mL. This high inoculum level was used in order to synchronize fungal development in all wounds. Oranges were kept at 20 °C for up to 3 days (samples I). As controls, wounded fruits inoculated with sterile water (samples W) and non-wounded fruits (samples NT) were also taken. At 1, 2 and 3 days post-inoculation, flavedo and albedo discs of 7 mm around the point of inoculation were sampled using a cork borer. Flavedo and albedo tissues were processed as described above and stored at –80 °C until RNA isolation.

Infections

To determine the effectiveness of the elicitor treatment in reducing pathogen infection and the importance of the elapsed time between the treatment and the infection, disease susceptibility was analysed at the beginning of the experiment in nontreated 'Navelate' fruits and at 4, 5 and 7 days (0, 1 and 3 dpt) for infected–cured fruits. Each infected–cured fruit was punched at a distance of 0.5 cm from the previous wound or in the equatorial axis in fruits that had not been inoculated previously. Then, 10 µL of a suspension (10⁴ conidia/mL) of *P. digitatum* spores were applied to each wound. After inoculation, fruits were kept at 20 °C and 90%–95% relative humidity. The incidence of infection, as a percentage, was determined for up to 6 days of incubation at 20 °C. The experimental design consisted of three replicates of five fruits, with four wounds per fruit, for each treatment. To test the effect of the treatments, a one-way analysis of variance (ANOVA) was performed. Means were separated using Tukey's honestly significant difference test at $P < 0.05$. The analysis was performed with Statgraphics Plus 5.1 Software (Manugistics, Inc.).

RNA isolation and preparation of labelled cDNA probes

Total RNA was isolated from frozen tissue as described by Ballester *et al.* (2006). RNA concentration was measured spectrophotometrically and the integrity was verified by agarose gel electrophoresis and ethidium bromide staining.

1 RNA samples for microarray hybridizations were labelled
2 using the indirect method by the incorporation of 5-(3-
3 aminoallyl)-2-deoxy-UTP (aa-dUTP) into single-stranded cDNA
4 during reverse transcription, followed by the conjugation of fluo-
5 rescent cyanine 3 (Cy3) and cyanine 5 (Cy5) as reactive
6 *N*-hydroxyl succinimide dyes (NHS dyes). Reverse transcription,
7 cDNA purification, dye coupling and fluorescent cDNA purifica-
8 tion were performed as described by Forment *et al.* (2005),
9 except that total RNA (30 µg) was used instead of poly(A)+ RNA.
10 Sample RNA was labelled with Cy5, and reference RNA (pooled
11 RNA consisting of an equal amount of RNA from each sample)
12 was labelled with Cy3.

14 Microarray hybridization, data acquisition and 15 data analysis

16 The 12k cDNA microarray developed by CFGP (<http://bioinfo.>
17 ibmcp.upv.es/genomics/cfgpDB/) was used. This microarray con-
18 tains probes corresponding to 11 241 putative unigenes from
19 citrus. Microarray hybridization, washing and scanning were per-
20 formed as described by Forment *et al.* (2005), with some modi-
21 fications. Labelled cDNA from experimental and control samples
22 was dried separately and resuspended in fresh hybridization
23 solution [containing 50% (v/v) formamide, 5 × standard saline
24 citrate (SSC), 0.1% (w/v) sodium dodecylsulphate (SDS) and
25 0.1 mg/mL salmon sperm DNA]. Samples were heated for 1 min
26 at 95 °C before hybridization, which was conducted at 42 °C.
27 Microarray slides were scanned with a GenePix 4000B (Axon
28 Instruments, Sunnyvale, CA, USA) using 'GenePix Pro 6.0' image
29 acquisition software (Axon Instruments) at 10-µm resolution,
30 100% laser power and different photomultiplier tube (PMT)
31 values to adjust the channels' intensity ratio to 1.0. Nonhomo-
32 geneous and aberrant spots were discarded. Only spots with
33 background-subtracted intensity greater than two-fold the mean
34 background intensity in at least one channel were selected and
35 used for normalization and further analysis. Data were log trans-
36 formed and analysed using GEPAS (Gene Expression Pattern
37 Analysis Suite) software v3.1 (Montaner *et al.*, 2006). Firstly, the
38 DNMA (Diagnosis and Normalization for MicroArray Data)
39 module (Vaquerizas *et al.*, 2004) was employed to normalize the
40 data using background-subtracted median values and an
41 intensity-based Lowess function within and among microarrays.
42 The preprocessing application included in GEPAS (Herrero *et al.*,
43 2003) was used to merge gene replicate values. Finally, genes
44 detected in only one of the three biological replicates were
45 discarded.

46 The identification of differentially expressed genes was
47 performed using SAM (Tusher *et al.*, 2001) included in the TM4
48 Microarray Software Suite (Saeed *et al.*, 2003). Genes that sat-
49 isfied the statistical threshold (false discovery rate, adjusted $P <$
50 0.01) were considered to be differentially expressed. Multivari-

51 ate analysis, including hierarchical cluster analysis and PCA,
52 was performed using the GeneMaths XT software package
53 (<http://www.applied-maths.com/>). Pearson's product-moment
54 correlation coefficient was used as a measure for gene-to-gene
55 correlation.

56 AgriGO (Zhou and Su, 2007) was used to extract GO terms
57 that were significantly over- or under-represented in a particular
58 set of genes relative to a reference group composed of all genes
59 present in the microarray which have an *Arabidopsis thaliana*
60 homologue. To overlay the gene expression data derived from
61 the microarray hybridizations onto a metabolic map, the OMICS
62 Viewer tool from AraCyc 3.5 was used (Mueller *et al.*, 2003).
63

64 Northern blot analysis

65 Northern blot analysis was carried out by electrophoresis
66 of denatured total RNA (10 µg) in 1.2% (w/v) agarose-
67 formaldehyde gel and blotted onto nylon Hybond-N⁺ membrane
68 (Amersham-Bioscience). cDNA labelling, hybridization and quan-
69 tification were carried out as described previously by Ballester
70 *et al.* (2006). Probes used for Northern hybridization were
71 obtained from different cDNA libraries previously generated
72 in our group (Table S8): (i) RindPd₂₄ cDNA library, which is
73 derived from 'Clemenules' mandarins infected with *P. digitatum*
74 (Forment *et al.*, 2005; González-Candelas *et al.*, 2010); (ii) Fla-
75 vCurFr₁, which is derived from heat-treated 'Fortune' mandarins
76 (Forment *et al.*, 2005); and (iii) RindPd₅, a subtractive cDNA
77 library constructed from the peel of 'Navelina' oranges infected
78 with *P. digitatum* (González-Candelas *et al.*, 2010).
79

80 For normalization, filters were hybridized to the 26S rDNA *C.*
81 *sinensis* probe (Ballester *et al.*, 2006). With few exceptions, for
82 each gene, a value of 1.0 was assigned to the normalized signal
83 of nontreated flavedo and the expression level of the rest of the
84 samples was referred to it. After stripping the blots, they were
85 hybridized using 28S rDNA *P. digitatum* probe (Ballester *et al.*,
86 2006).
87

88 Ethylene production

89 Ethylene production from 10-mm discs, obtained with a cork
90 borer around the point of inoculation, was determined by incu-
91 bating the discs in sealed glass tubes at 20 °C. After 15 min of
92 incubation at this temperature, a 1-mL headspace gas sample
93 was withdrawn from each tube and analysed as described by
94 Lafuente *et al.* (2001) with a Perkin-Elmer gas chromatograph
95 (GC) (Norwalk, CT, USA) equipped with a flame ionization detec-
96 tor and an alumina column (1 m × 2 mm diameter, 80/100 mesh)
97 from Supelco (Barcelona, Spain). Nitrogen was used as carrier
98 gas and the temperature of the column was maintained at
99 140 °C. Ethylene standard was obtained from Abello-Oxígeno-
100 Linde S. A. (Valencia, Spain). The results are the means of three
101 replicate samples of nine discs from three different oranges.
102
103

4

5

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REFERENCES

- Achilea, O., Chalutz, E., Fuchs, Y. and Rot, I. (1985a) Ethylene biosynthesis and related physiological changes in *Penicillium digitatum* infected grapefruit (*Citrus paradisi*). *Physiol. Plant Pathol.* **26**, 125–134.
- Achilea, O., Fuchs, Y., Chalutz, E. and Rot, I. (1985b) The contribution of host and pathogen to ethylene biosynthesis in *Penicillium digitatum*-infected citrus fruit. *Physiol. Plant Pathol.* **27**, 55–63.
- Adato, A., Mandel, T., Mintz-Oron, S., Venger, I., Levy, D., Yativ, M., Domínguez, E., Wang, Z., De Vos, R.C.H., Jetter, R., Schreiber, L., Heredia, A., Rogachev, I. and Aharoni, A. (2009) Fruit-surface flavonoid accumulation in tomato is controlled by a *SIMYB12*-regulated transcriptional network. *PLoS Genet.* **5**, e1000777.
- Afek, U., Orenstein, J., Carmeli, S., Rodov, V. and Joseph, M.B. (1999) Umbelliferone, a phytoalexin associated with resistance of immature Marsh grapefruit to *Penicillium digitatum*. *Phytochemistry*, **50**, 1129–1132.
- Albrecht, U. and Bowman, K.D. (2008) Gene expression in *Citrus sinensis* (L.) Osbeck following infection with the bacterial pathogen *Candidatus Liberibacter asiaticus* causing Huanglongbing in Florida. *Plant Sci.* **175**, 291–306.
- Angioni, A., Cabras, P., D'Hallewin, G., Pirisi, F.M., Reniero, F. and Schirra, M. (1998) Synthesis and inhibitory activity of 7-geranoxycoumarin against *Penicillium* species in *Citrus* fruit. *Phytochemistry*, **47**, 1521–1525.
- Arcas, M.C., Botía, J.M., Ortuño, A. and Del Río, J.A. (2000) UV irradiation alters the levels of flavonoids involved in the defence mechanism of *Citrus aurantium* fruits against *Penicillium digitatum*. *Eur. J. Plant Pathol.* **106**, 617–622.
- Arras, G. (1996) Mode of action of an isolate of *Candida famata* in biological control of *Penicillium digitatum* in orange fruits. *Postharvest Biol. Technol.* **8**, 191–198.
- Ballester, A.R., Lafuente, M.T. and González-Candelas, L. (2006) Spatial study of antioxidant enzymes, peroxidase and phenylalanine ammonia-lyase in the citrus fruit–*Penicillium digitatum* interaction. *Postharvest Biol. Technol.* **39**, 115–124.
- Ballester, A.R., Izquierdo, A., Lafuente, M.T. and González-Candelas, L. (2010a) Biochemical and molecular characterization of induced resistance against *Penicillium digitatum* in citrus fruit. *Postharvest Biol. Technol.* **56**, 31–38.
- Ballester, A.R., Molthoff, J., de Vos, R., Hekkert, B.t.L., Orzaez, D., Fernandez-Moreno, J.-P., Tripodi, P., Grandillo, S., Martin, C., Heldens, J., Ykema, M., Granell, A. and Bovy, A. (2010b) Biochemical and molecular analysis of pink tomatoes: deregulated expression of the gene encoding transcription factor *SIMYB12* leads to pink tomato fruit color. *Plant Physiol.* **152**, 71–84.
- Ben-Yehoshua, S., Rodov, V., Kim, J.J. and Carmeli, S. (1992) Preformed and induced antifungal materials of citrus fruit in relation to the enhancement of decay resistance by heat and ultraviolet treatment. *J. Agric. Food Chem.* **40**, 1217–1221.
- Ben-Yehoshua, S., Rodov, V., Nafussi, B., Peretz, J. and Porat, R. (2000) Biotic and abiotic induction of resistance against pathogens in citrus fruits. In: *Proceedings of the International Society of Citriculture, Orlando, FL, 3–7 December 2000* (••, ••, ed.), pp. 1107–1112. ••: ••.

- Bernardi, J., Licciardello, C., Russo, M.P., Chiusano, M.L., Carletti, G., Recupero, G.R. and Marocco, A. (2010) Use of a custom array to study differentially expressed genes during blood orange (*Citrus sinensis* L. Osbeck) ripening. *J. Plant Physiol.* **167**, 301–310.
- Bostock, R.M. (2005) Signal crosstalk and induced resistance: straddling the line between cost and benefit. *Annu. Rev. Phytopathol.* **43**, 545–580.
- Conrath, U. (2009) Priming of induced plant defense responses. In: *Advances in Botanical Research* (Loon, L.C.V., ed.), pp. 361–395. ••: Academic Press.
- De Vos, M., Van Oosten, V.R., Van Poecke, R.M.P., Van Pelt, J.A., Pozo, M.J., Mueller, M.J., Buchala, A.J., Métraux, J.P., van Loon, L.C., Dicke, M. and Pieterse, C. (2005) Signal signature and transcriptome changes of *Arabidopsis* during pathogen and insect attack. *Mol. Plant–Microbe Interact.* **18**, 923–937.
- Dixon, M.T., Achnine, L., Kota, P., Liu, C.J., Reddy, S. and Wang, L. (2002) The phenylpropanoid pathway and plant defence—a genomics perspective. *Mol. Plant Pathol.* **3**, 371–390.
- Droby, S., Chalutz, E., Horev, B., Cohen, L., Gaba, V., Wilson, C.L. and Wisniewski, M. (1993) Factors affecting UV-induced resistance in grapefruit against the green mold decay caused by *Penicillium digitatum*. *Plant Pathol.* **42**, 418–424.
- Droby, S., Vinokur, V., Weiss, B., Cohen, L., Daus, A., Goldschmidt, E.E. and Porat, R. (2002) Induction of resistance to *Penicillium digitatum* in grapefruit by the yeast biocontrol agent *Candida oleophila*. *Phytopathology*, **92**, 393–399.
- Durrant, W.E. and Dong, X. (2004) Systemic acquired resistance. *Annu. Rev. Phytopathol.* **42**, 185–209.
- Ecker, J.R. (1995) The ethylene signal transduction pathway in plants. *Science*, **268**, 667–675.
- Fajardo, J.E., McCollum, T.G., McDonald, R.E. and Mayer, R.T. (1998) Differential induction of proteins in orange flavedo by biologically based elicitors and challenge by *Penicillium digitatum*. *Sacc. Biol. Control.* **13**, 143–151.
- Ferreira, R.B., Monteiro, S., Freitas, R., Santos, C.N., Chen, Z., Batista, L.M., Duarte, J., Borges, A. and Teixeira, A. (2006) Fungal pathogens: the battle for plant infection. *Crit. Rev. Plant Sci.* **25**, 505–524.
- Forment, J., Gadea, J., Huerta, L., Abizanda, L., Agusti, J., Alamar, S., Alos, E., Andres, F., Arribas, R., Beltrán, J.P., Berbel, A., Blazquez, M.A., Brumos, J., Canas, L.A., Cercos, M., Colmenero-Flores, J.M., Conesa, A., Establés, B., Gandia, M., García-Martínez, J.L., Gimeno, J., Gisbert, A., Gomez, G., González-Candelas, L., Granell, A., Guerri, J., Lafuente, M.T., Madueno, F., Marcos, J.F., Marques, C., Martínez, F., Martínez-Godoy, M.A., Miralles, S., Moreno, P., Navarro, L., Pallás, V., Perez-Amador, M.A., Perez-Valle, J., Pons, C., Rodrigo, I., Rodriguez, P.L., Royo, C., Serrano, R., Soler, G., Tadeo, F., Talón, M., Terol, J., Trenor, M., Vaello, L., Vicente, O., Vidal, C., Zacarias, L. and Conejero, V. (2005) Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies. *Plant Mol. Biol.* **57**, 375–391.
- Fujii, H., Shimada, T., Sugiyama, A., Nishikawa, F., Endo, T., Nakano, M., Ikoma, Y., Shimizu, T. and Omura, M. (2007) Profiling ethylene-responsive genes in mature mandarin fruit using a citrus 22K oligoarray. *Plant Sci.* **173**, 340–348.
- Gandia, M., Conesa, A., Ancillo, G., Gadea, J., Forment, J., Pallás, V., Flores, R., Duran-Vila, N., Moreno, P. and Guerri, J. (2007) Transcriptional response of *Citrus aurantifolia* to infection by *Citrus tristeza virus*. *Virology*, **367**, 298–306.
- Gimeno, J., Gadea, J., Forment, J., Pérez-Valle, J., Santiago, J., Martínez-Godoy, A.M., Yenush, L., Belles, J.M., Brumos, J., Colmenero-Flores, J., Talon, M. and Serrano, R. (2009) Shared and novel molecular responses of mandarin to drought. *Plant Mol. Biol.* **70**, 403–420.
- Glazebrook, J. (2005) Contrasting mechanisms of defense against biotrophic and necrotrophic pathogens. *Annu. Rev. Phytopathol.* **43**, 205–227.
- González-Candelas, L., Alamar, S., Sanchez-Torres, P., Zacarias, L. and Marcos, J. (2010) A transcriptomic approach highlights induction of secondary metabolism in citrus fruit in response to *Penicillium digitatum* infection. *BMC Plant Biol.* **10**, 194–211.

Herrero, J., Díaz-Uriarte, R. and Dopazo, J. (2003) Gene expression data preprocessing. *Bioinformatics*, **19**, 655–656.

Jones, J.D.G. and Dangl, J.L. (2006) The plant immune system. *Nature*, **444**, 323–329.

Kavanagh, J.A. and Wood, R.K.S. (1967) The role of wounds in the infection of oranges by *Penicillium digitatum*. *Sacc. Ann. Appl. Biol.* **60**, 375–383.

Kim, J.J., Ben Yehoshua, S., Shapiro, B., Henis, Y. and Carmeli, S. (1991) Accumulation of scoparone in heat-treated lemon fruit inoculated with *Penicillium digitatum* Sacc. *Plant Physiol.* **97**, 880–885.

Kim, J.-S., Sagaram, U.S., Burns, J.K., Li, J.-L. and Wang, N. (2009) Response of sweet orange (*Citrus sinensis*) to 'Candidatus Liberibacter asiaticus' infection: microscopy and microarray analyses. *Phytopathology*, **99**, 50–57.

Király, L., Barna, B. and Király, Z. (2007) Plant resistance to pathogen infection: forms and mechanisms of innate and acquired resistance. *J. Phytopathol.* **155**, 385–396.

Lafuente, M.T. and Sala, J.M. (2002) Abscisic acid levels and the influence of ethylene, humidity and storage temperature on the incidence of postharvest rindstaining of 'Navelina' orange (*Citrus sinensis* L. Osbeck) fruit. *Postharvest Biol. Technol.* **25**, 49–57.

Lafuente, M.T., Zacarias, L., Martínez-Téllez, M.A., Sánchez-Ballesta, M.T. and Dupille, E. (2001) Phenylalanine ammonia-lyase as related to ethylene in the development of chilling symptoms during cold storage of citrus fruits. *J. Agric. Food Chem.* **49**, 6020–6025.

Lers, A., Burd, S., Lomaniec, E., Droby, S. and Chalutz, E. (1998) The expression of a grapefruit gene encoding an isoflavone reductase-like protein is induced in response to UV irradiation. *Plant Mol. Biol.* **36**, 847–856.

van Loon, L.C., Rep, M. and Pieterse, C.M.J. (2006) Significance of inducible defense-related proteins in infected plants. *Annu. Rev. Phytopathol.* **44**, 135–162.

López-García, B., González-Candelas, L., Pérez-Payá, E. and Marcos, J.F. (2000) Identification and characterization of a hexapeptide with activity against phytopathogenic fungi that cause postharvest decay in fruits. *Mol. Plant-Microbe Interact.* **13**, 837–846.

Lorenzo, O., Piqueras, R., Sánchez-Serrano, J.J. and Solano, R. (2003) ETHYLENE RESPONSE FACTOR1 integrates signals from ethylene and jasmonate pathways in plant defense. *Plant Cell*, **15**, 165–178.

Marcos, J.F., González-Candelas, L. and Zacarias, L. (2005) Involvement of ethylene biosynthesis and perception in the susceptibility of citrus fruit to *Penicillium digitatum* infection and the accumulation of defense-related mRNAs. *J. Exp. Bot.* **56**, 2183–2193.

Martínez-Godoy, A.M., Mauri, N., Juárez, J., Marques, C.M., Santiago, J., Forment, J. and Gadea, J. (2008) A genome-wide 20 K citrus microarray for gene expression analysis. *BMC Genomics*, **9**, 318–329.

Mayuoni, L., Sharabi-Schwager, M., Feldmesser, E. and Porat, R. (2011) Effects of ethylene degreening on the transcriptome of mandarin flesh. *Postharvest Biol. Technol.* **60**, 75–82.

McCollum, T.G. (2000) Defensive proteins in grapefruit flavedo. In: *Proceedings of the International Citrus Congress* (••, ••, ed.), pp. 1113–1116. ••: ••.

Montaner, D., Tárraga, J., Huerta-Cepas, J., Burguet, J., Vaquerizas, J.M., Conde, L., Minguéz, P., Vera, J., Mukherjee, S., Valls, J., Pujana, M.A.G., Alloza, E., Herrero, J., Al-Shahrour, F. and Dopazo, J. (2006) Next station in microarray data analysis: GEPAS. *Nucleic Acids Res.* **34**, W486–W491.

Mueller, L.A., Zhang, P. and Rhee, S.Y. (2003) AraCyc: a biochemical pathway database for Arabidopsis. *Plant Physiol.* **132**, 453–460.

Mysore, K.S. and Ryu, C.M. (2004) Nonhost resistance: how much do we know? *Trends Plant Sci.* **9**, 97–104.

Ortuño, A., Báidez, A., Gómez, P., Arcas, M.C., Porras, I., García-Lidón, A. and Del Río, J.A. (2006) *Citrus paradisi* and *Citrus sinensis* flavonoids: their influence in the defence mechanism against *Penicillium digitatum*. *Food Chem.* **98**, 351–358.

Pavoncello, D., Lurie, S., Droby, S. and Porat, R. (2001) A hot water treatment induces resistance to *Penicillium digitatum* and promotes the accumulation of heat shock and pathogenesis-related proteins in grapefruit flavedo. *Physiol. Plant.* **111**, 17–22.

Porat, R., Lers, A., Dori, S., Cohen, L., Weiss, B., Daus, A., Wilson, C.I. and Droby, S. (1999a) Induction of chitinase and beta-1,3-endoglucanase pro-

teins by UV irradiation and wounding in grapefruit peel tissue. *Phytoparasitica*, **27**, 1–6.

Porat, R., Weiss, B., Cohen, L., Daus, A., Goren, R. and Droby, S. (1999b) Effects of ethylene and 1-methylcyclopropene on the postharvest qualities of 'Shamouti' oranges. *Postharvest Biol. Technol.* **15**, 155–163.

Porat, R., Vinokur, V., Holland, D., McCollum, T.G. and Droby, S. (2001) Isolation of a citrus chitinase cDNA and characterization of its expression in response to elicitation of fruit pathogen resistance. *J. Plant Physiol.* **158**, 1585–1590.

Porat, R., McCollum, T.G., Vinokur, V. and Droby, S. (2002) Effects of various elicitors on the transcription of a β -1,3-endoglucanase gene in citrus fruit. *J. Phytopathol.* **150**, 70–75.

Rodov, V., Ben-Yehoshua, S., Kim, J.J., Shapiro, B. and Ittah, Y. (1992) Ultraviolet illumination induces scoparone production in kumquat and orange fruit and improves decay resistance. *J. Am. Soc. Hortic. Sci.* **117**, 788–792.

Sánchez-Ballesta, M.T., Zacarias, L., Granell, A. and Lafuente, M.T. (2000) Accumulation of Pal transcript and Pal activity as affected by heat-conditioning and low-temperature storage and its relation to chilling sensitivity in Mandarin fruits. *J. Agric. Food Chem.* **48**, 2726–2731.

Schenk, P.M., Kazan, K., Wilson, I., Anderson, J.P., Richmond, T., Somerville, S.C. and Manners, J.M. (2000) Coordinated plant defense responses in Arabidopsis revealed by microarray analysis. *Proc. Natl. Acad. Sci. USA*, **97**, 11 655–11 660.

Shimada, T., Fuiii, H., Endo, T., Yazaki, J., Kishimoto, N., Shimbo, K., Kikuchi, S. and Omura, M. (2005) Toward comprehensive expression profiling by microarray analysis in citrus: monitoring the expression profiles of 2213 genes during fruit development. *Plant Sci.* **168**, 1383–1385.

Stracke, R., Werber, M. and Weisshaar, B. (2001) The R2R3-MYB gene family in *Arabidopsis thaliana*. *Curr. Opin. Plant Biol.* **4**, 447–456.

Talon, M. and Gmitter, F.G., Jr (2008) Citrus genomics. *Int. J. Plant Genomics* **2008**, 528361.

Tusher, V.G., Tibshirani, R. and Chu, G. (2001) Significance analysis of microarrays applied to the ionizing radiation response. *Proc. Natl. Acad. Sci. USA*, **98**, 5116–5121.

Vaquerizas, J.M., Dopazo, J. and Díaz-Uriarte, R. (2004) DNMA: web-based diagnosis and normalization for microarray data. *Bioinformatics*, **20**, 3656–3658.

Venditti, T., Molinu, M.G., Dore, A., Agabbio, M. and D'Hallewin, G. (2005) Sodium carbonate treatment induces scoparone accumulation, structural changes, and alkalization in the albedo of wounded Citrus fruits. *J. Agric. Food Chem.* **53**, 3510–3518.

Zhou, X. and Su, Z. (2007) EasyGO: Gene Ontology-based annotation and functional enrichment analysis tool for agricultural species. *BMC Genomics*, **8**, 246.

SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

- Fig. S1 Hierarchical view of gene ontology (GO) biological process categories significantly over-represented in nontreated flavedo (FNT) compared with nontreated albedo (ANT) using AgriGO.
- Fig. S2 Hierarchical view of gene ontology (GO) biological process categories significantly over-represented in elicited flavedo 7 days after the beginning of the experiment (FIC7) compared with nontreated flavedo (FNT) using AgriGO.
- Fig. S3 Hierarchical view of gene ontology (GO) biological process categories significantly over-represented in elicited albedo 5 days after the beginning of the experiment (AIC5) compared with nontreated albedo (ANT) using AgriGO.

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Table S4 List of genes showing higher expression in elicited flavedo 5 days after the beginning of the experiment (FIC5) than in nontreated flavedo (FNT). Those genes with an *Arabidopsis thaliana* homologue were used to generate the hierarchical view of gene ontology (GO) (Fig. 4).

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Table S6 List of genes showing higher expression in elicited albedo 5 days after the beginning of the experiment (AIC5) than in nontreated albedo (ANT). Those genes with an *Arabidopsis thaliana* homologue were used to generate the hierarchical view of gene ontology (GO) (Fig. S3).

Table S7 List of genes showing higher expression in elicited albedo 7 days after the beginning of the experiment (AIC7) than in nontreated albedo (ANT). Those genes with an *Arabidopsis thaliana* homologue were used to generate the hierarchical view of gene ontology (GO) (Fig. S4).

Table S8 Genes analysed by Northern blot hybridization.

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