Introducing furanocoumarin biosynthetic genes in tomato results in coumarins accumulation and impacted growth

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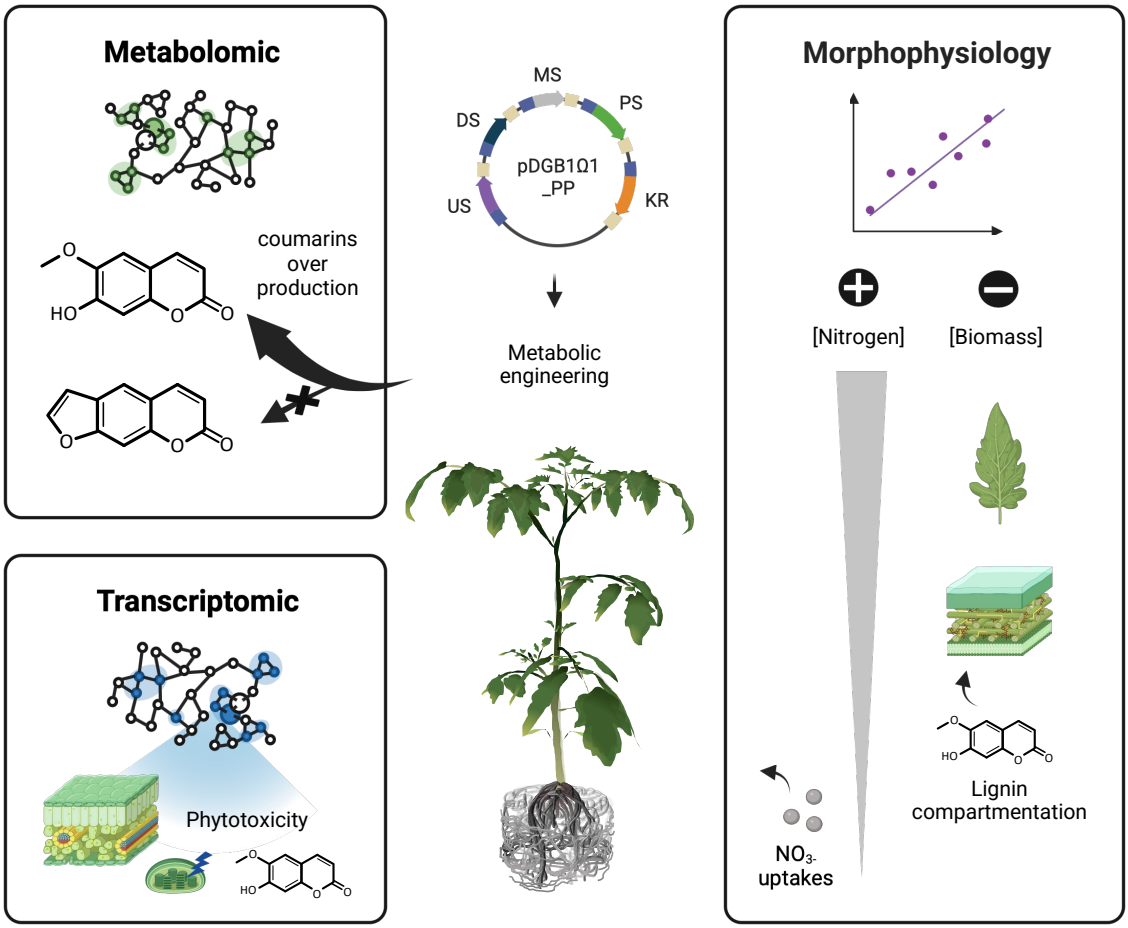
#scopoletin #coumarins #furanocoumarins #tomato plant #growth #psoralen #specialized metabolism

Graphical abstract



Abstract

Over the past three decades, efforts to decipher plant metabolism have shed light on key enzymes driving specialized metabolite biosynthesis. Although only few pathways have been completely investigated to date, their characterization paves the way for exploring the potential effects of specialized metabolites on plant physiology. Among them is the linear furanocoumarin pathway, which was recently completed to produce up to psoralen. In this study, we report the first metabolic engineering of the linear furanocoumarin pathway to enable artificial psoralen production in tomato, through the integration of four genes coding for the enzymes: Umbelliferone Synthase, Demethylsuberosin Synthase, Marmesin Synthase and Psoralen Synthase. Interestingly, coumarins were produced instead of furanocoumarins. Using morphophysiological, metabolomic, and transcriptomic analyses, we suggest how coumarins, particularly scopoletin, can impact growth and affect plant physiology, even at low concentrations.

As coumarins have increasingly attracted interest for agricultural applications due to their minimal environmental impact, this work both expands and challenges their potential by highlighting the physiological costs and benefits they may impose on tomato.

1. Introduction

The around 400 million years of evolution since the terrestrialization of plants have driven the emergence of numerous mechanisms for interacting with an ever-evolving environment (Morris *et al.,* 2018). The production of specialized metabolites is a key example of such adaptation as many of these compound play vital roles in enabling plants to cope with biotic and abiotic stresses (Maeda & Fernie, 2021; Weng *et al.,* 2021). Investment of resources and energy in processes that promote plant defense, particularly the biosynthesis of specialized metabolites, may come at the expense of processes that support plant growth (He *et al.,* 2022). Plants must therefore balance the trade-off between investing in the costly biosynthesis of specialized metabolites and allocating resources for growth (Neilson *et al.,* 2013).

Land plants produce a wide range of specialized metabolites (Chassagne *et al.,* 2019). Among them, linear furanocoumarins are defensive metabolites restricted to certain lineages (Sarker & Nahar, 2017). Its pathway has been largely elucidated over the past two decades, particularly in Apiaceae and Moraceae (**Fig. 1**) (Bouillé et al., 2025). Furanocoumarins are derived from the ubiquitous coumarin umbelliferone, which itself is derived from *p*-coumaroyl-CoA (Vialart *et al.,* 2012; Roselli *et al.,* 2017). The biosynthesis of linear furanocoumarins then starts with the C6-prenylation of umbelliferone to produce demethylsuberosin by a prenyltransferase (Karamat *et al.,* 2014; Munakata *et al.,* 2016). Demethylsuberosin is then cyclized by marmesin synthase, a cytochrome P450 (P450), into marmesin (Villard *et al.,* 2021; K. Wang *et al.,* 2024), which is subsequently converted to psoralen via C7-decarboxylation through *syn*-elimination of acetone by psoralen synthase, another P450 (Jian *et al.,* 2020; Larbat *et al.,* 2007, 2009). The psoralen backbone can then be hydroxylated at C5 or C8 by additional P450s to yield bergaptol or xanthotoxol, respectively (**Fig. 1**) (Krieger *et al.,* 2018; Ji *et al.,* 2024). These structures can be further decorated by other enzymes, such as *O*-methyltransferases, *O*-prenyltransferases and/or other P450s, to generate more complex

alkylated structures (Hehmann *et al.,* 2004; Zhao *et al.,* 2016; Han *et al.,* 2023; Bouillé *et al.,* 2025). Along with some of its derivatives, psoralen exhibits a broad spectrum of defensive effects, mainly driven by its ability to form covalent bonds with nucleic acids (*i.e.,* via photocycloaddition) and to alter herbivore defences (*e.g.,* through cytochrome P450 inhibition) (Neal & Wu, 1994; Kitamura *et al.,* 2005). For such reasons, psoralen is considered the first toxic metabolite in the linear furanocoumarin pathway.

In this study, we aimed to investigate the potential physiological and growth-related costs associated with the production of a novel specialized metabolite in plants using metabolic engineering. Considering the importance of psoralen in plant-environment interactions and the unknown costs its biosynthesis may impose on plants, we chosen to investigate the recently completed psoralen pathway. In that regard, using the GoldenBraid multigenic assembly system (Sarrion-Perdigones *et al.,* 2013), we integrated four linear furanocoumarin biosynthetic genes into the tomato genome (*Solanum lycopersicum*, Solanaceae), a plant that does not naturally produce these compounds, to enable the conversion of the ubiquitous *p*-coumaroyl-CoA into psoralen (**Fig. 1**). Metabolic analyses of the transgenic tomato line (referred here to as “Psoralen Pathway” or PP line) confirmed the detection of small quantities of psoralen, the expected product, but also highlighted larger modifications in the accumulation of other metabolite families, among them coumarins and particularly scopoletin. This modulation of the metabolic composition among PP line was accompanied by major transcriptomic changes and a significant modification in the biomass distribution. Our results shed light on the physiological costs associated with the implementation of the psoralen pathway in tomato and offer novel perspectives on the use of coumarins in agriculture.

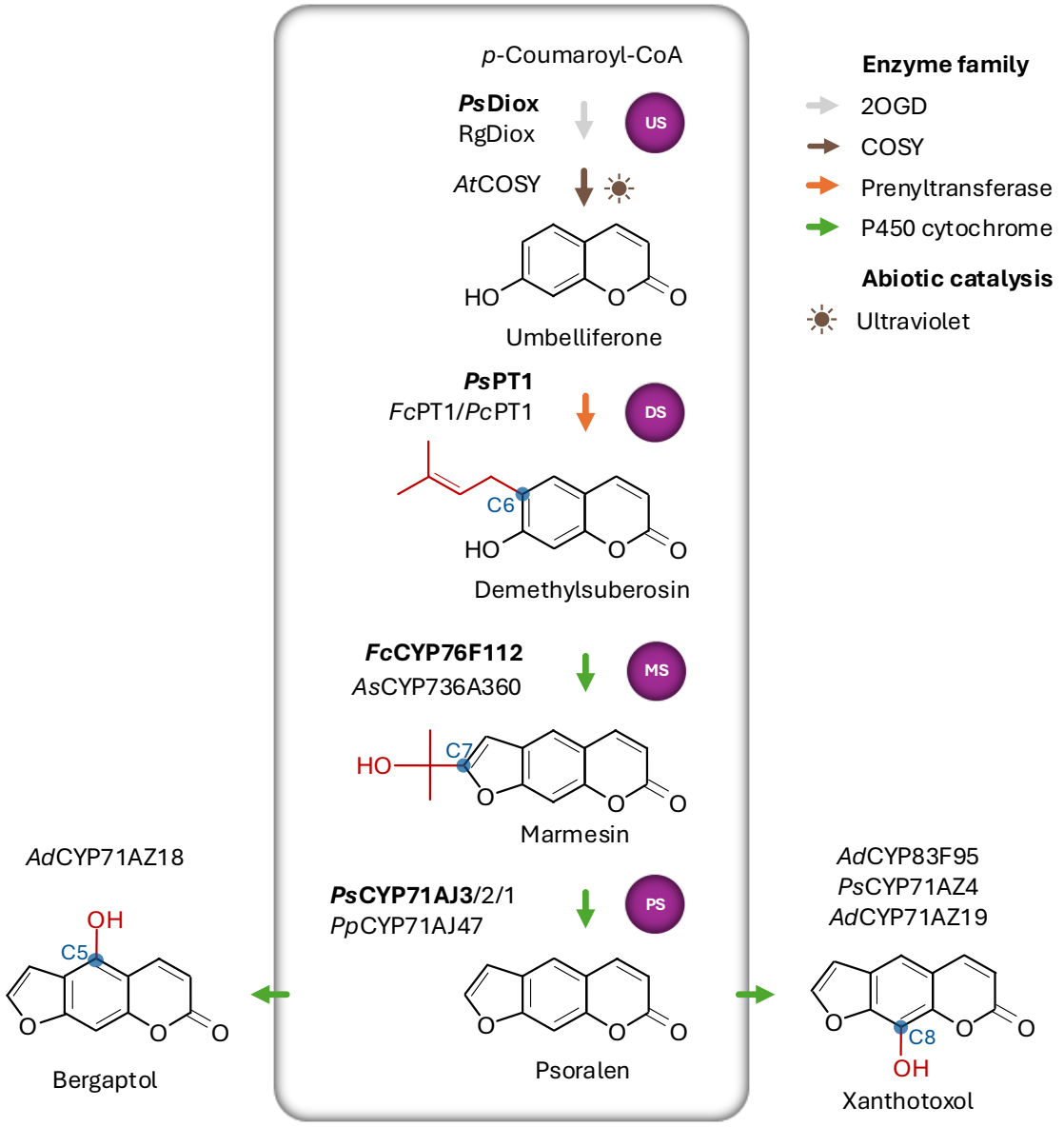


Figure 1: Simplified diagram of the psoralen pathway (PP) among linear furanocoumarin in some restricted angiosperms taxa. The pathway from *p*-coumaroyl-CoA to psoralen is framed, with the enzymes engineered in the tomato PP line encircled in purple and the specific genes inserted in the tomato genome in bold, while the carbon number on the furanocoumarin backbone is depicted in blue. Abbreviations: 2-OxoGlutarate dependent Dioxygenase (2OGD), COumarin SYnthase (COSY), PrenylTransferase (PT), CYtochrome P450s (CYP), US (*UMBELLIFERONE SYNTHASE*), DS (*DEMETHYLSUBEROSIN SYNTHASE*), MS (*MARMESIN SYNTHASE*), PS (*PSORALEN SYNTHASE*). Species: Apiaceae (*Angelica dahurica, Angelica sinensis*, *Pastinaca sativa*, *Petrolinum crispum*, *Peucedanum praeruptorum*), Rutaceae (*Ruta graveolens*), Brassicaceae (*Arabidopsis thaliana*), Moraceae (*Ficus carica*). From Larbat *et al.*, 2007, 2009; Vialart *et al.*, 2012; Karamat *et al.*, 2014; Munakata *et al.*, 2016; Roselli *et al.*, 2017; Vanholme *et al.*, 2019; Jian *et al.*, 2020; Villard *et al.*, 2021; Wang *et al.*, 2024.

2. Material and methods

2.1. Biological material and Standards

110 The tomato plants (*Solanum lycopersicum*) cultivar *West Virginia* 106 (Wva106) was used
111 as the wild-type control and for plant transformation. Analytical standards were sourced
112 from Sigma-Aldrich (Saint-Louis, MO, USA; for *p*-coumarate, scopoletin, and esculin),
113 Extrasynthese (Lyon, France; for umbelliferone, psoralen, and esculetin), TransMIT
114 (Giessen, Germany; for marmesin), Phytolab (Nantes, France; for scopolin), and R.
115 Munakata from Kyoto University (demethylsuberosin).

116 **2.2. Creation of the PP transgene**

117 The Psoralen Pathway (PP) T-DNA was created by combining the genes controlling the 4-
118 steps metabolic pathway from *p*-coumaroyl-CoA to psoralen (**Fig. 1**). The four genes were
119 *Ps*Diox (ncbi: KY081678; Roselli *et al.,* 2017) coding for Umbelliferone Synthase (US),
120 *Ps*PT1 (ncbi: KM017083; Munakata *et al.,* 2016) coding for Demethylsuberosin Synthase
121 (DS), *Fc*CYP76F112 (ncbi: MW348922 ; Villard *et al.,* 2021) coding for Marmesin Synthase
122 (MS) and *Ps*CYP71AJ3 (ncbi: C0SJS2 ; Larbat *et al.,* 2009) coding for Psoralen Synthase
123 (PS). The selection marker used in the creation of the PP transgene was the *NEOMYCIN*
124 *PHOSPHOTRANSFERASE* (*Ec*NPTII) gene conferring resistance to kanamycin, which
125 originates from the plCSL11024 vector. The coding sequence of the five genes of interest
126 were domesticated by removing internal restriction sites for *Bsa*I and *Bsm*BI, and by
127 adding flanking extensions compatible with the GoldenBraid 2.0 multigene cloning
128 system (GB2.0; Sarrion-Perdigones *et al.,* 2013). Each domesticated gene was cloned
129 into the pUPD vector using the *Bsm*BI restriction enzyme, and assembled with the *Ca*MV
130 P35S promoter (pUPD-35S, Addgene plasmid #68163) and the tNOS terminator (pUPD-
131 tNOS, Addgene plasmid #68188) to form individual transcription unit (TU). TUs were
132 assembled into the plasmid pDBGB1α1 or pDBGB1α2 by restriction/ligation using the
133 restriction enzymes *Bsa*I or *Bsm*BI, respectively, and the T4 DNA ligase, as described in
134 Sarrion-Perdigones *et al.,* 2011. The resulting TUs were further assembled two-by-two
135 into pDGB1 α- or Ω-level plasmids, through restriction/ligation, to build the final PP T-
136 DNA into pDGB1Ω1. Integrity of this final vector pDGB1Ω1_PP was validated by PCR
137 analysis (see primers section 2.3), restriction analysis (**Fig. S1a**), and sequencing of the
138 coding genes (Eco-Seq, Macrogen). PCR amplification was performed using the
139 SapphireAmp® polymerase (Takara Bio) and following the reaction cycle: Initial
140 denaturation (98°C for 5min), 35 cycles composed of a denaturation step (98°C for 10s),

141 an annealing step (55°C for 15s) and an elongation step (72°C for 10s), followed by a final
142 elongation step (72°C for 1min). Restriction of 1µg of plasmid DNA was performed using
143 *Bsa*I, *Bsm*BI, *Pvu*II, and *Eco*RI enzymes with the FastDigest system (Thermo Fisher
144 Scientific), following the manufacturer's recommendations.

145 **2.3. Plant transformation and regeneration of the PP line**

146 The pDGB1Ω1_PP vector was co-transformed into *Agrobacterium tumefaciens* EHA105
147 with the replication helper vector pSOUP. The transformed cells were selected on solid
148 LB medium containing spectinomycin (100mg/L), tetracycline (5mg/L), and rifampicin
149 (20mg/L) (Hellens *et al.,* 2000; Sarrion-Perdigones *et al.,* 2013). A pre-culture was
150 performed overnight at 28°C, 200rpm, in 10mL of LB medium with appropriate
151 antibiotics. A 50mL culture was then started with 5mL of the pre-culture to reach an
152 OD_{600nm} of 0.4-0.6. The culture was centrifuged for 10 min at 7000 ×g, then resuspended
153 in 40mL of sterile water and diluted to 30mL to achieve an OD_{600nm} of 0.08. Axenic
154 cotyledon fragments approximately 4mm in size were harvested from 7-day-old tomato
155 seedlings grown under controlled conditions (24°C, 16h/8h light/dark cycles; 150µmol.m^{-}
156 ^{2}.s^{-1}, Fitoclima 1200, Aralab). The cotyledon fragments were cultured for 24h at 24°C in
157 darkness before being co-incubated with the Agrobacteria solution for 30min at room
158 temperature (gentle agitation every 5min). The fragments were then dried on axenic paper
159 and placed adaxial side up on co-cultivation medium for 48h at 24°C in darkness.
160 Partially transformed tissues were selected on kanamycin-enriched callus medium
161 (150mg/L) in Petri dishes (15 fragments per dish) at 24°C (16h/8h light/dark cycles;
162 150µmol.m^{-2}.s^{-1}) and subcultured weekly. After 3 months of subcultures, differentiated
163 seedlings from calli were cut and transferred to rooting medium before being acclimated
164 in soil in phytotrons (24°C; 16h/8h light/dark cycles; 400 µmol.m^{-2}.s^{-1}; 70% humidity).
165 Several heterozygous descendants from the regenerated tomato line were obtained by
166 self-pollination. The insertion of the 5 transgenes into the genome was assessed by PCR
167 (**Fig. S1b**) using genomic DNA extracted with the kit following the supplier's
168 recommendations and the primers described as follow: *Ps*Diox_F:
169 CTAGTCGAAATGGCTCCATCTCC; *Ps*Diox_R: CGAAGATCCATTCCAAGCTCACATTTG;
170 *Ps*PT1_F: CTAGTCGAAATGGCTCAAACAATTATGC; *Ps*PT1_R:
171 GAAGATCCATTCCAAGCTCACCTC; *Fc*CYP76F112_F:

172 CTATTCTAGTCGAAATGGATATTTTCACCTC; *Fc*CYP76F112_R:
173 CGAAGATCCATTCCAAGCCTAATGATG; *Ps*CYP71AJ3_F:
174 CTATTCTAGTCGAAATGAAGATGCTTGAG; *Ps*CYP71AJ3_R:
175 GATCGAAGATCCATTCCAAGCTCATC; NPTII_F:
176 CAATTTACTATTCTAGTCGAAATGGTTGAACAAG; NPTII_R:
177 GAAGATCCATTCCAAGCTCAGAAGAAC. The expression of the 5 genes in each individual
178 was confirmed by RT-PCR for each tomato line (**Fig. S1c**). Total RNAs was extracted using
179 the E.Z.N.A.® HP kit (Omega Bio-Tek) instructions, treated with DNase (AMPD1-1KT,
180 Sigma) to remove genomic DNA contaminants, and then reverse-transcribed into cDNA
181 using the High-Capacity RNA-to-cDNA Kit (Applied Biosystems™), according to the
182 supplier's recommendation.

183 **2.4. Plant cultivation and measurement of morpho-physiological traits**

184 Four sets of plant cultivation and harvest were performed over a period of four months.
185 Three sets of 6-8 plants per genotype were used for transcriptomic and metabolomic
186 analyses (23 WT, 19 PP), and one additional set (23 WT, 19 PP) for morphophysiological
187 measurements, for a total of 46 WT and 38 PP plants. All plants were staggered under
188 identical conditions. The first three were used for the metabolomics and transcriptomics
189 analyses. The fourth series was dedicated to measuring morphometric traits, including
190 carbon and nitrogen allocation, and lignin composition/content in the stems. At harvest,
191 stem and petiole tissues were separated from the leaves and roots. For metabolomics
192 analyses, petioles and internodes were combined.
193 Tomato plants were grown in 1.5L pots with 0.5L of potting soil (Stender D400, NPK
194 14/10/18, pH 6.2, sieved to 5 mm). The climatic conditions in the growth chamber were
195 set at 24°C with 16h/8h light/dark cycles, LED illumination at 400µmol.m^{-2}.s^{-1}, and 70%
196 humidity. Plants were watered to maintain 70% soil moisture three times a week with
197 osmosed water. Weekly, tomatoes were fertilized with horticultural fertilizer (50 mL at 2
198 g.L^{-1}) (9:16:36 of N:P:K, MultiTec™). Tomato plants were harvested at 28 days after sowing,
199 at the vegetative stage. Roots were gently washed with a brush and untangled for length
200 measurements. For metabolomic and transcriptomic analyses, tissues were rapidly
201 snap-frozen in liquid nitrogen before being finely ground and stored at -80°C. Leaf areas
202 without petioles were measured using a planimeter (Li-3100 C Area Meter, Li-Cor,

203 Lincoln, Nebraska, USA). Tissues used for carbon, nitrogen, nitrate and lignin content
204 measurement were dried in an oven at 70°C for 1 week and then finely ground using an
205 orbital mill (Pulverisette 6, Fritsch, France) before being stored at room temperature in a
206 dry-preserving package. Resulting powder was used for carbon, nitrogen and lignin
207 measurements.

208 **2.5. Total nitrogen and carbon analyses**

209 Total C and N contents in dry tissues were determined using 3mg of dry matter, according
210 to the Dumas method, with an elemental auto-analyzer (Unicube, Elementar,
211 Langenselbold, Germany).

212 **2.6. Cell wall characterization**

213 Lignin and its components were quantified according to Lu *et al.,* 2021. Briefly, cell wall
214 residues (CWR) were extracted using successive boiling in solvent baths. Lignin content
215 was quantified in percentage of CWR according to the Cysteine-Assisted Sulfuric Acid
216 (CASA) method. The lignin composition of CWR was measured using the thioacidolysis
217 method as described by Rolando *et al.,* 1992, and the released fragments were analyzed
218 using GC-MS at the VIB Metabolomics Core as described in (Hoengenaert *et al.,* 2022).
219 The composition of the lignin was analyzed as described in (Hoengenaert *et al.,* 2022).
220 Briefly, 20 mg of stems CWR were cellulase-digested and resuspended in DMSO. Scans
221 of HSQC NMR spectra (Heteronuclear Single-Quantum Coherence) ^{1}H–^{13}C short-range
222 correlation experiments were acquired for 6h, followed by a second 54h acquisition for
223 improve sensitivity.

224 **2.7. Metabolites extraction**

225 Frozen powders from leaves, stems and roots (100 mg FW) were extracted twice using
226 maceration (16h in the dark at 22°C with slow vertical agitation) followed by sonication
227 (37 kHz, 10min at room temperature), each time with 800 µL of methanol/deionized water
228 (80/20). The macerates were then centrifuged (10min, 16100 g, 22°C). The supernatants
229 (1.6 mL) were collected, dried (5-7h under vacuum, Concentrator Plus, Eppendorf) and
230 then resuspended in 100µL of methanol/deionized water (80/20). The extracts were
231 filtered (0.2 µm, Minisart® RC4 membrane, Sartorius, REF17821) and stored at -20°C.
232 Extracts were added with taxifolin (285µM) as an internal quantification standard.

233 **2.8. Metabolomics analysis**

234 Chromatographic analyses coupled with High Resolution Mass Spectrometry were
235 performed on a Thermo Scientific Vanquish UHPLC system equipped with a binary pump,
236 an autosampler, a temperature-controlled column (40°C) and a Diode Array Detector.
237 Extracted samples were separated on a XB-C18 Kinetex (150 × 2.1 mm, 2.6 µm)
238 (Phenomenex Inc., Torrance, CA, USA) using a gradient of mobile phase composed of
239 0.1% formic acid in water (A) and 0.1% formic acid in methanol (B) at a flow rate of 200
240 $\mu L \cdot min^{-1}$. The separation of the compounds was performed using a 30 min mobile phase
241 gradient (A: B; v/v). The elution method is as follows: (90:10) at 0 min, (90:10) up to 2 min,
242 (70:30) up to 10 min, (5:95) up to 20 min remaining 5 min, (90:10) up to 26 min. The
243 molecules are detected according to their absorbance at different wavelengths between
244 190 and 800 nm.
245 $HRMS^1$ detection was performed on an Orbitrap IDX™ (ThermoFisher Scientific, Bremen,
246 Germany) mass spectrometer in positive and negative electrospray ionization (ESI)
247 modes. The capillary voltages were set at 3.5 kV and 2.5 kV for positive and negative
248 modes, respectively. The source gases were set (in arbitrary unit min^{-1}) to 40 (sheath gas),
249 8 (auxiliary gas) and 1 (sweep gas) and the vaporizer temperature and ion transfer tube
250 was respectively 320°C and 275°C. Full scan MS^1 spectra were acquired from 120 to 1200
251 m/z at a resolution of 60,000. MS^2 analysis was performed on the pooled-samples vial
252 using the data dependent acquisition (DDA) mode and fragments were analyzed by
253 Orbitrap at a resolution of 15000. For this analysis, the AcquireX data acquisition
254 workflow was applied. The raw data were uploaded on the Compound discoverer 3.3
255 software (ThermoFisher Scientific, Bremen, Germany) to run the untargeted
256 metabolomics workflow (peak detection, chromatogram alignment and peak grouping in
257 features). In addition, the full MS^1–MS^2 dataset was exported as a mascot generic format
258 (mgf) file and analyzed through the Sirius 5 software (Dührkop *et al.,* 2019). Briefly, the
259 procedure implies the automatic annotation of molecular formula using SIRIUS and
260 ZODIAC (Dührkop *et al.,* 2019; Ludwig *et al.,* 2019). Then, molecular structure prediction
261 was proposed through CSI: FingerID (Hoffmann *et al.,* 2021). Finally, feature
262 was assigned to chemical families using CANOPUS (Djoumbou Feunang *et al.,* 2016;
263 Dührkop *et al.,* 2019; H. W. Kim *et al.,* 2021). Further annotation was performed using
264 Compound Discoverer 3.3 by predicting elemental composition, searching in local and

265 public mass and formula databases such as ChemSpider, HMDB, and LipidMaps, and
266 querying spectral databases including mzCloud, MoNA, and GNPS.
267 Formal identification of coumarins and furanocoumarins, was afforded via comparisons
268 with commercial standards according at least to their retention time (RT), mass (MS^1) and
269 mass fragmentation (MS^2) when available. A standard curve was established for the
270 scopoletin quantification using as internal standard the taxifolin (285µM).

271 **2.9. Construction and analysis of RNAseq libraries**

272 Total RNA from leaves and roots was extracted from 3 plants per genotype (WT and PP)
273 as previously described (Roumani *et al.,* 2022). RNA concentrations were determined
274 from their absorbance at 260 nm. Their purity was evaluated by the 260/280 nm
275 absorbance ratio, their quality was checked by electrophoresis on a 1% agarose gel and
276 their integrity by determining and considering an RNA Integrity Number (RIN) >7 (Agilent
277 BioAnalyzer 2100). Transcript data was obtained by RNA-Seq Illumina pair-end
278 sequencing (2× 150pb) using the NovaSeq 6000 methods for 30 million read pairs. Raw
279 data were cleaned using Trimmomatic (Bolger *et al.,* 2014). The quality of the sequences
280 was assessed using FastQC. The transcripts were mapped on the tomato genome
281 (ITAG2.4) using the BWA-MEM software (Li & Durbin, 2009). Count tables were generated
282 using the FeatureCounts software (Version 1.6.4) and Samtools merge workflows (Liao *et*
283 *al.,* 2014). The differential gene expression was performed with the glmfit option within
284 the edgeR package for a FDR <0.05 (Robinson *et al.,* 2010) and using AskoR (Alves-
285 Carvalho *et al.,* 2021). We performed, within AskoR, a clustering using kmeans
286 classification algorithms (Coseq R package) (Godichon-Baggioni *et al.,* 2019). Functional
287 annotations, such as gene ontologies and interproscan features, were extracted from
288 ITAG2.4_protein_functional.gff3 file. Differentially expressed genes (DEGs) between WT
289 and PP lines DEGs were used to perform GO enrichment analysis (GOEA) restricted to
290 the Biological Processes on ShinyGO (version 0.80) using the "*Solanum lycopersicum*
291 genes SL3.0" and a FDR cutoff <0.05 (Ge *et al.,* 2020).
292 The results of the RNAseq differential analysis were confirmed by following the
293 expression level of 2 genes (*Sl*COSY and *Sl*PRCA) in addition to the 5 engineered genes in
294 leaves and roots of the PP and control tomato plants. The list of targeted genes and
295 primers used is given in **Table S2h**. The expression level was followed by RT-qPCR. For

296 that purpose, a total of 200 ng of DNA-free RNA samples was reverse transcribed in a final
297 volume of 20 µL using the RNA to cDNA kit (Life technologies, Tokyo, Japan). cDNAs were
298 then diluted 10 times. Gene expression was measured by qPCR on a CFX Duet Realtime
299 PCR System (Bio-Rad). Each PCR reaction was made in 20 µL containing primer pairs at
300 0.3 µM, 40 ng of cDNAs in 1× Mesa Blue Premix (Eurogentec) and followed the
301 amplification protocol consisting in a denaturing step at 95 °C for 30 s, 40 cycles at 95 °C
302 for 5 s and 60 °C for 30 s. The gene expression of each sample was calculated with three
303 analytical replicates and normalized to the two internal control genes *ACT* and *GAPDH*.

304 **2.10. Statistical Analysis**

305 Measured and calculated morphometric and physiological variables, as well as relative
306 and absolute quantified metabolites were statistically analyzed by comparing WT and PP
307 lines using a non-parametric Kruskal-Wallis test.

308

309 **3. Results**

310 **3.1. The PP line regeneration**

311 To insert the Psoralen Pathway (PP) in tomato plants, we first leveraged the GoldenBraid
312 technology to assemble the selected four genes encoding the enzymes required for the
313 conversion of *p*-coumaroyl-CoA into psoralen. The T-DNA was build-up with 5 genes
314 organized as transcription units (TUs) (Larbat *et al.,* 2009; Munakata *et al.,* 2016; Roselli
315 *et al.,* 2017; Villard *et al.,* 2021), each independently under the control of the constitutive
316 *CaMV*35S promoter and the tNOS terminator (**Fig. 1**; **Fig. S1**). Then, we integrate the PP
317 T-DNA into the genome of the *Wva*106 tomato cultivar using an *agrobacterium*-mediated
318 stable transfection. Plant selection was allowed by a fifth similarly assembled TU
319 including the kanamycin resistance. By assessing genomic integration via PCR on gDNA,
320 we successfully regenerated two independently transfected lines (**Fig. S1b**). Among the
321 two lines, qPCR revealed that only one line (the PP line) showed a constitutively high
322 expression levels of each transgene in the investigated leaves and roots, compared to the
323 WT (**Table S2g,h; Fig. S1c**). Our study focused on this particular line, which exhibited a
324 phenotype similar to the WT (**Fig. S1e**).

325

326 **3.2. The PP line accumulates coumarins**

To investigate the impact of Psoralen Pathway integration on tomato plant metabolic composition, we compared the metabolomes of PP and WT plants in leaves, stems, and roots using untargeted LC-HRMS analysis of hydro-methanolic extracts. To strengthen the analysis, given that only one PP line was obtained, we performed three independent cultivation rounds under identical growing conditions, resulting in 23 WT and 19 PP plants. The metabolome comparison between PP and WT in all the three-round cultivation of plants and across the three organs, highlighted an overall tendency to a higher accumulation of dozens to hundred metabolic features in the PP line. By considering only significant metabolic features that differentially accumulated (Benjamini-Hochberg $p<0.05$), 82 metabolic features across leaves, stems and roots were retained (**Table S1**). One metabolic feature was less abundant in the PP line whereas all others were enriched in comparison to the WT. Putative annotation of these features allowed to categorize 20 of them as fatty acids and 19 as phenylpropanoids (*i.e.,* 10 coumarins, 7 phenolamides, the furanocoumarin: psoralen, and one miscellaneous compound) (**Fig. 2a**). The abundance of only eight of the metabolic features were significantly affected in at least two organs, and among them scopoletin, the only metabolite that was found to be differential in leaves, stems and roots (**Fig. 2b**).

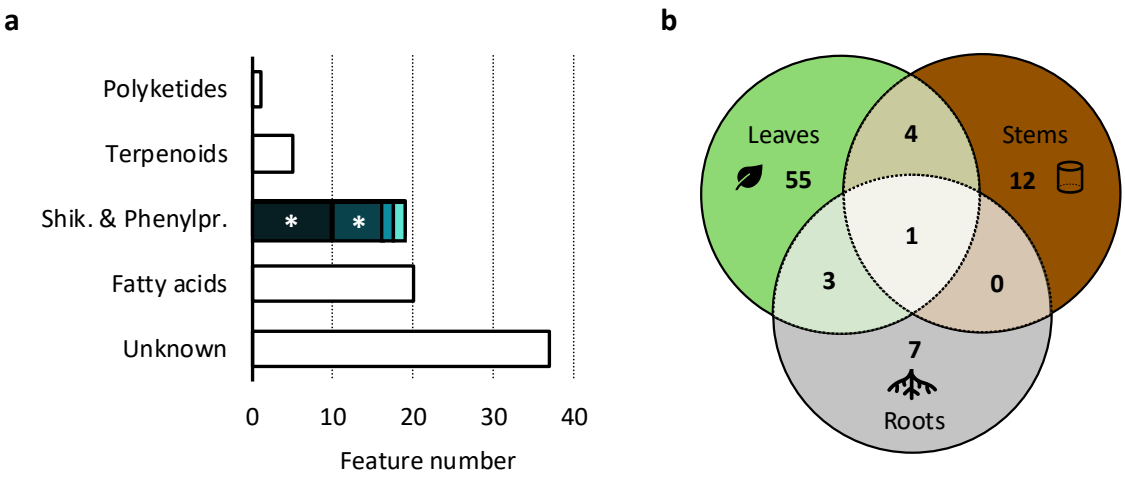
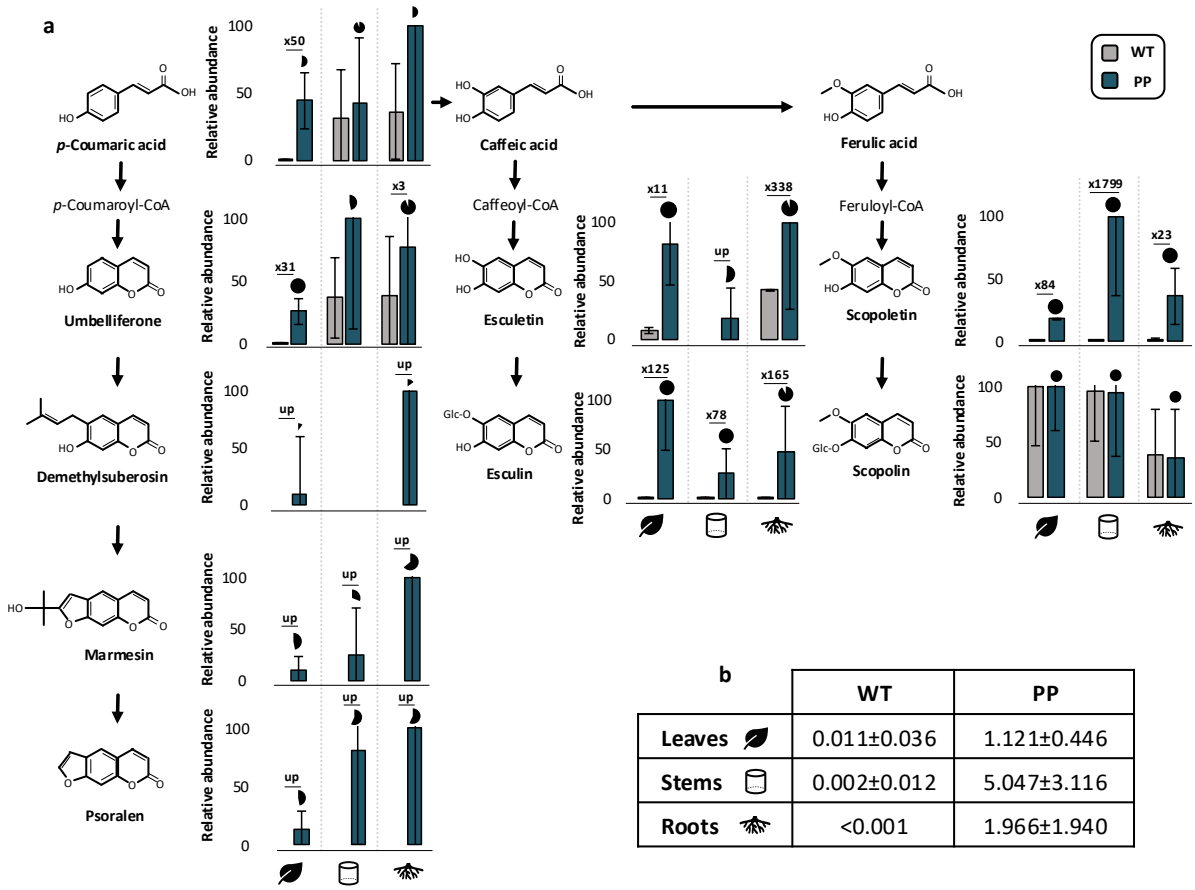


Figure 2: Untargeted comparative metabolomic profiling of the Psoralen Pathway (PP) and the Wild-Type (WT) tomato lines. (**a**) Number of metabolic features significantly over-accumulated in the PP line compared to the WT. Metabolic features are categorized according to the NP-Classifier ontology (Kim *et al.,* 2021). Shikimate and phenylpropanoids are highlighted in blue from dark to light: coumarins*, phenolamides*, others, furanocoumarins. Asterisks*

correspond to metabolic subclasses significantly enriched (**Table S1b**). (**b**) Venn diagram describing the distribution of the PP line's over-accumulated features across leaves (green), stems (brown) and roots (grey) compared to the control line. Number of replicates for leaves, stems, roots: WT (n=23), PP (n=19). The data are based on 3 independent cultivation rounds of tomato plants grown in the same phytotronic conditions.

We then performed targeted analyses focusing on coumarins and metabolites of the psoralen pathway. Psoralen and its precursors (*i.e.,* demethylsuberosin and marmesin) were detected only in trace amounts across the analyzed organs of the PP line, and were absent from the WT (**Fig. 3a**). The PP line exhibited significant increases in *p*-coumaric acid and umbelliferone levels in the leaves (50- and 31-fold, respectively in comparison to WT), with no significant changes in other plant parts. Scopoletin concentrations were significantly increased in all organs of the PP line (23- to 1799-fold), and especially in stems where it reached concentrations close to 5 µg/g of DW (**Fig. 3b**). Esculetin and its glycoside form esculin accumulated significantly higher in the PP line than in the WT (**Fig. 3a**). On the opposite, scopolin accumulation was not different between the WT and the PP line.



b

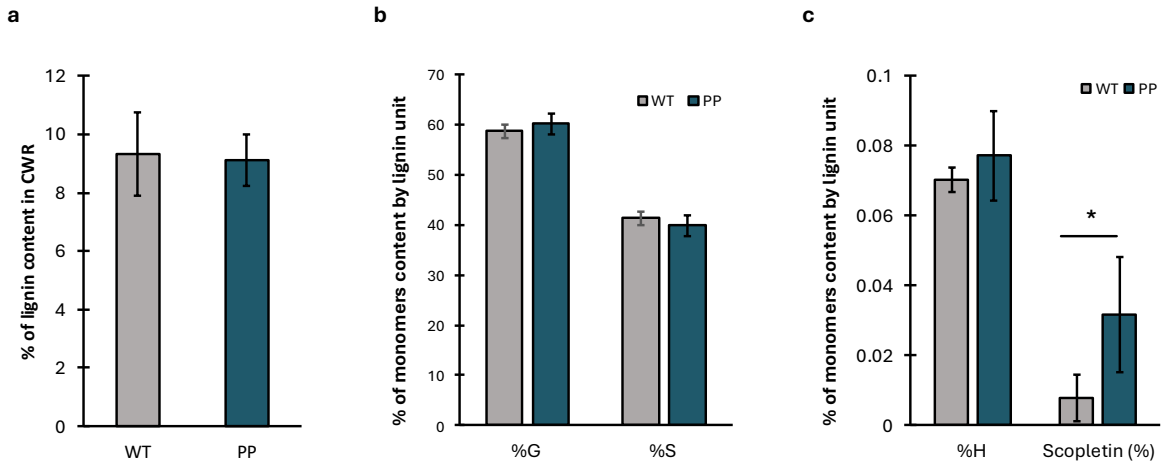
	WT	PP
Leaves	0.011±0.036	1.121±0.446
Stems	0.002±0.012	5.047±3.116
Roots	<0.001	1.966±1.940

Figure 3: Comparative targeted profiling of coumarins and furanocoumarins in the Psoralen Pathway (PP) and the Wild-Type (WT) tomato lines. (**a**) Relative accumulation of reported coumarins and furanocoumarins in the PP line (blue) versus the WT line (grey), expressed as mean ± standard deviation. Percentage of replicates containing the metabolite in the PP line is illustrated using black pie charts. Only significantly differentially accumulated metabolites, assessed by the Kruskal-Wallis test ($p<0.05$*), are depicted according to their increasing fold change in the PP line compared to the WT line. 'Up' refers to compounds detected only in the PP line. (**b**) Absolute quantification of scopoletin in µg/g of dry weight. Data are expressed as percentages (a) or absolute quantity for each metabolite relative to the most abundant peak area, normalized to the internal standard taxifolin, and reported per mg of dry weight; Number of replicates for leaves, stems, roots: WT (n=23), PP (n=19). The data are based on 3 independent cultivation rounds of tomato plants grown in the same phytotronic conditions.

3.3. Scopoletin is released by a lignin-degradative method

Scopoletin has recently been described to be able to incorporate into the lignin polymer of *Arabidopsis thaliana* (Brassicaceae) and *Populus sp* (Salicaceae) transgenic lines producing this metabolite in the stems (Hoengenaert *et al.,* 2022; N. Wang *et al.,* 2025). Accordingly, the lignin composition was analyzed in the PP line and compared to that in the WT. Lignin content (**Fig. 4a**) and composition (H, G, S) (**Fig. 4b-c**) in the stems of the PP line were not significantly affected compared to WT. However, analysis of the

390 thioacidolysis released monomers indicated a slight but significant increase in the
391 release of scopoletin in the PP line (2.8×) compared to the WT line (**Fig. 4c**), suggesting
392 the presence of scopoletin in the cell wall as well as in the lignin.
393



394

395 **Figure 4: Impact of the Psoralen Pathway (PP) line on lignin content (a) and composition for**
396 **G, S (b), and H monomers, as well as for scopoletin (c), in stems compared to the Wild-Type**
397 **(WT) line.** The average percentage of monomers and scopoletin are calculated based on the
398 content of H, G, and S units and scopoletin in the lignin. The error bars indicate the standard
399 deviation. The lignin content was measured as percentage of Cell Wall Residue (CWR) using the
400 Cysteine-Assisted Sulfuric Acid (CASA) method (Lu *et al.,* 2021). Data were compared using the
401 Kruskal-Wallis's test (p-value<0.05) (p-value for scopoletin % = 0.00106); WT (n=8) and PP (n=9).
402

403 **3.4. Specific genes regulation in the PP line**

404 To further understand the metabolic changes observed in the PP line, we then
405 investigated its transcriptome compared to the WT. Results highlighted 1014 and 53
406 differentially expressed genes (DEGs) in the leaves and roots, respectively, of the PP line
407 (**Fig. 5a; Table S2**). In leaves, the 1014 DEGs comprised 659 upregulated and 355
408 downregulated genes in the PP line compared to WT. In roots, 41 genes were upregulated
409 and 12 downregulated. Seventeen DEGs were common to leaves and roots. Gene
410 Ontology Enrichment Analysis (GOEA) was performed on the up- and downregulated
411 DEGs identified. In leaves, GOEA analysis highlighted an overall upregulation of genes
412 involved in processes related to response to stress and wounding (**Fig. 5b**), whereas the
413 main trend was a downregulation of genes associated to chlorophyll biosynthesis (**Fig.**
414 **5c**). In roots, the relatively short list of DEGs did not lead to any significant enrichment
415 using GOEA.

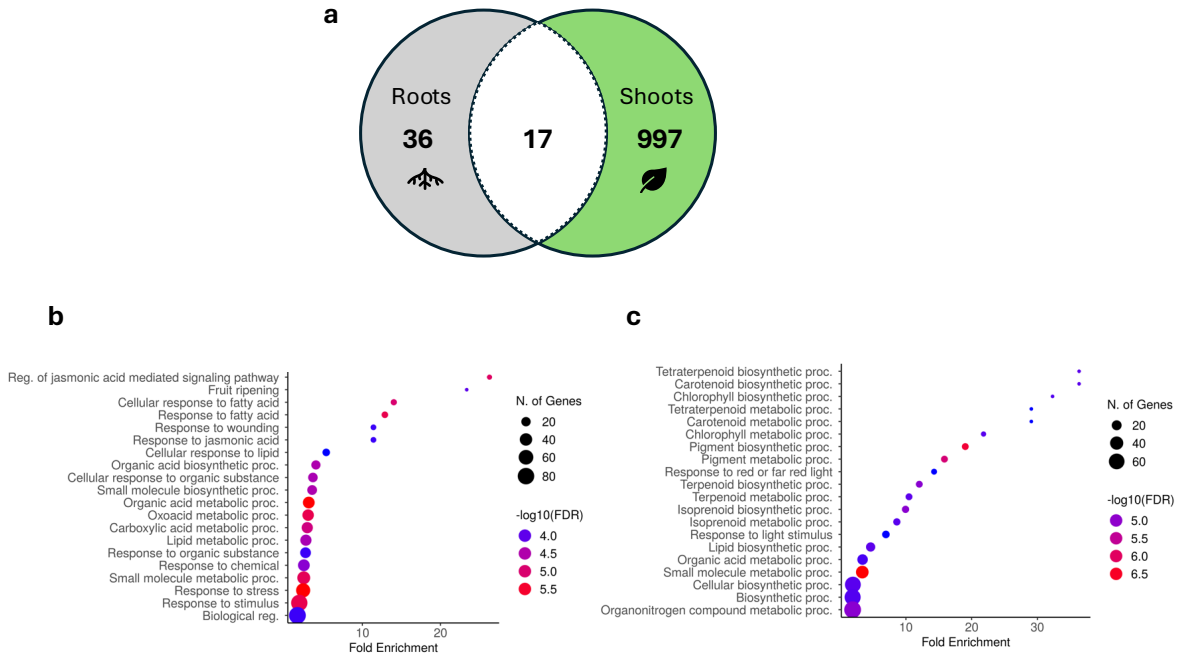


Figure 5: Transcriptomic regulation in the Psoralen Pathway (PP) line compared to the Wild-Type (WT) line. (**a**) Differentially Expressed Genes (DEGs) in leaves and/or roots (FDR<0.05). Gene Ontology Enrichment Analysis (GOEA) on biological processes for (**b**) upregulated and (**c**) downregulated genes considering only leaves (False Discovery Rate: FDR<0.05). The position of the circles represents the fold change by related to the ratio PP/WT. The size of the circles represents the number of Differentially Expressed Genes (DEGs) in each Gene Ontology (GO) category. The color of the circles indicates the statistical significance. The data consist of 3 replicates of PP and WT per tissue.

Using a differential gene analysis based on 3 replicates in leaves and roots comparing the PP and WT lines, we highlighted only strongly DEGs in the PP line (**Fig. 5**). Finer regulatory patterns were uncovered through a K-means clustering approach, which revealed 11 expression clusters based on gene expression profiles in leaves and roots, comparing the PP and WT lines (**Fig. S2**). Among them, five clusters displayed expression patterns that distinguished the PP line from the WT. The smaller and most specific expression cluster was cluster 8 regrouping 309 genes with a higher expression in both the leaves and roots of the PP line in comparison to WT. In addition, cluster 2 (1449 genes) contained genes specifically over-expressed in the roots of the PP line, and cluster 7 (1113 genes), over-expressed genes in the leaves. Conversely, the clusters 1 (743 genes) and 5 (1466 genes) grouped genes downregulated in leaves and roots of the PP line compared to the WT. GOEA of cluster 8 indicates the induced expression of genes potentially linked to the PP

line's response to stress, likely signaled *via* jasmonate and in response to lipids (**Fig. 6a**). As an extension of cluster 8, the same trend was observed as for the genes from cluster 7 (upregulated in leaves of the PP line) (**Fig. 6b**). The cluster 2 (upregulated genes in roots of the PP line), were enriched in processes related to hormonal regulations (**Fig. 6c**). Among the processes related to downregulated genes (**Fig. 6d,e**), DNA replication and cell cycle appeared affected in the roots of the PP line (cluster 5), whereas lipid and sterol biosynthesis were, in leaves (cluster 1).

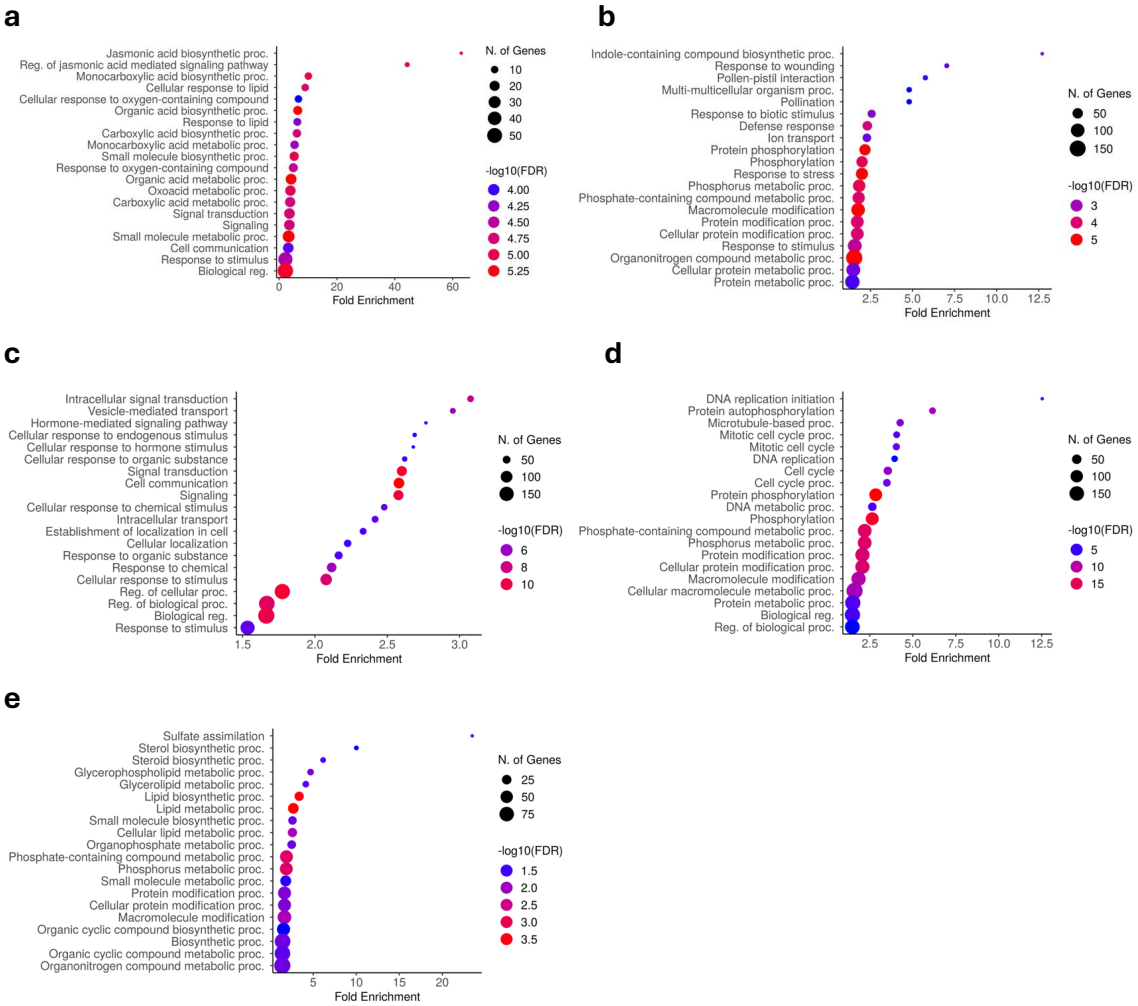


Figure 6: Gene Ontology Enrichment Analysis (GOEA) on biological processes in the Psoralen Pathway (PP) line compared to Wild-Type (WT) line for clusters 8 (a), 7 (b), 2 (c), 5 (d) and 1 (e). (*False Discovery Rate:* FDR<0.05). The position of the circles represents the fold change by related to the ratio PP/WT. The size of the circles represents the number of Differentially Expressed Genes (DEGs) in each GO category. The color of the circles indicates the statistical significance. Gene clusters were grouped using the k-means method. (**a**) Cluster 8 includes 309 upregulated genes and most of those were specifically differentially expressed in the leaves and roots of the PP line compared to the WT line (10/17 genes). (**b**) Cluster 7 contains 1113 upregulated genes in leaves. (**c**) Cluster 2 contains 1449 upregulated genes in roots. (**d**) Cluster

1 and (**e**) cluster 5 contain 743 and 1465 downregulated genes in roots and leaves, respectively. The data consist of 3 replicates of PP and WT per tissue.

3.5. The PP line showed reduced biomass and elevated nitrogen content

To identify potential impacts on the growth and development of the PP line compared to the WT line, we performed a comparative resource allocation and morphology analysis (**Table S3**). After 28 days of growth, PP and WT plants exhibited comparable morphology and size (**Fig. S1e**), with similar leaf numbers and stem lengths between days 13 and 28, indicating no significant developmental changes (**Table 1**). However, dry biomass in the PP line was significantly reduced by 21.3% compared to the WT. This decrease was uniformly distributed across plant organs with the exception of stem which had a similar amount of dry biomass compared to the WT. As a results, the resource allocation pattern in the PP line was significantly different from the WT, with a decrease in the proportion of matter in the leaves (-10%) and an increase in the stem (+20%) (**Table 1**). The decrease in the biomass accumulation in leaves was in accordance with an increase in the Specific Leaf Area (SLA) in the PP line.

	Variable	WT average ± SE	PP average ± SE	p-value
Dry weights	Foliar blades (g)	2.46±0.36	1.74±0.24	**0.0004***
	Petioles (g)	0.49±0.07	0.4±0.05	**0.0222***
	Stems (g)	1.11±0.28	1.05±0.17	0.4142
	Roots (g)	0.49±0.05	0.39±0.06	**0.0025***
	Stems/Roots ratio	8.20±1.07	8.15±0.70	0.9349
Tissue allocation (% by DW)	Foliar blades	54.06	48.6	**0.0042***
	Petioles	10.76	11.17	0.2529
	Stems	24.39	29.32	**0.0178***
	Roots	10.76	10.89	0.9349
Development	Stems (cm)	49.95±7.42	51.33±6.02	0.6532
	Roots (cm)	44.21±15.1	44.22±9.38	0.7439
	Leaf number	8	8	1
	D13/D28 plant height	0.1±0.02	0.1±0.02	0.8064

Key growth analysis parameters	Stems/Roots ratio	1.24±0.43	1.2±0.28	1
	SLA (cm2.g^{-1})	236.48±33.67	329.73±35.81	**0.0002***
	SRL (cm.g^{-1})	90.95±39.82	115.21±31.85	0.0724
	SSL (cm.g^{-1})	45.06±14.62	47.84±6.17	**0.0274***

Table 1: Mean alterations in growth and development parameters between WT and the PP line. The significant differences between the two genotypes are supported by a non-parametric Kruskal-Wallis test. Significant differences are indicated in bold with an asterisk. Measurements were taken at a vegetative growth stage (28 days after sowing; D28) and compared for development with measurements at an early growth stage (13 days after sowing; D13). Dry biomass allocation patterns are defined by the percentage of mean dry biomass in each compartment. Abbreviations: SLA (Specific Leaf Area); SRL (Specific Root Length); SSL (Specific Shoot Length). WT (n=23), PP (n=19).

To better understand the cause of the loss in biomass in the PP line, we analyzed carbon (%C) and nitrogen (%N) accumulation across the different tissues (**Table 2**). Results showed that nitrogen content was significantly higher in the PP line compared to the WT, particularly in the shoots (+53%). Focusing on ion uptakes in leaves and roots (**Table S4**), we identified a significant increase of nitrate ions in roots (×3.3). Conversely, carbon content was slightly lower in the PP line, most notably in the stems (-13%). As a result, the carbon-to-nitrogen ratio (C/N) was significantly decreased in the PP line, especially in the shoots.

	Carbone (%)			Nitrogen (%)			C/N ratio		
	WT mean (mean ± STDEV)	PP mean (mean ± STDEV)	p-value	WT mean (mean ± STDEV)	PP mean (mean ± STDEV)	p-value	WT mean (mean ± STDEV)	PP mean (mean ± STDEV)	p-value
Foliar blades	39.01±0.41	38.66±1.02	0.1616	1.72±0.3	2.63±0.33	**0.0005***	22.47±3.96	14.82±1.59	**0.0002***
Petioles	34.57±0.62	33.89±0.66	**0.0484***	1.34±0.22	1.96±0.3	**0.0005***	25.46±3.91	17.57±2.49	**0.0002***
Stems	31.95±2.9	27.78±5.75	0.0542	1.01±0.18	1.22±0.21	**0.0301***	31.96±4.74	22.85±3.68	**0.0004***
Roots	40.79±0.7	40.52±0.63	0.885	2.02±0.12	2.27±0.17	**0.006***	20.33±0.95	17.89±1.29	**0.0004***

Table 2: Mean alterations in Carbon (C), Nitrogen (N) contents and C/N ratio between the Wild-Type (WT) and the Psoralen Pathway (PP) lines. The variables significance between the two genotypes is supported by a non-parametric Kruskal-Wallis test. Significant differences are indicated in bold with an asterisk. Measurements were taken at a vegetative growth stage (28 days after sowing). WT (n=10), PP (n=9).

4. Discussion

501 The biosynthesis of specialized metabolites necessarily triggered a physiological cost on
502 plants, either by diverting resources for their production or through the pleiotropic effects
503 of the specialized metabolites themselves (Neilson *et al.,* 2013). This study aimed to
504 better understand the impacts of constitutive expression of four genes from the linear
505 furanocoumarin biosynthesis pathway on tomato plant physiology and growth.
506
507 **4.1. Furanocoumarins might be toxic for tomato plants**
508 Genetic modification of tomato with our construct aimed at producing psoralen
509 surprisingly resulted in a low transformation success rate (0.33%), especially when
510 compared to longer pathways already inserted with success in tomato using the same
511 GoldenBraid system with TUs also under the *CaMV*35S promoter (H. Kim *et al.,* 2025;
512 Sonawane *et al.,* 2017). Furthermore, psoralen was found only as trace amounts despite
513 that all PP transgenes were constitutively expressed (**Fig. S1c**; **Table S2g**). In parallel,
514 transcriptomic data showed significantly over-expressed genes falling in the GO
515 categories "response to stress", "response to chemicals" and other direct or indirect
516 stress-related GO classifications in the PP line (*e.g.,* photoinhibition, stress
517 phytohormones, etc) (**Fig. 5b,c**; **Fig. 6a-c**). These findings suggest a psoralen pathway-
518 dependent phytotoxicity in tomato plants, potentially linked to the production of
519 furanocoumarins (**Fig. 3a**). During the seven last decades, incremental progress has
520 highlighted a large spectrum of furanocoumarin's toxicity on a vast range of organisms,
521 including plants, occurring through a diversity of processes (*e.g.*, photocycloaddition,
522 lipid peroxidation, cytochrome P450 inhibition) (Baskin *et al.,* 1967; Bennet & Bonner,
523 1953; Diawara *et al.,* 1993; Frank *et al.,* 1998; Greenberg *et al.,* 2001; Hale *et al.,* 2004;
524 Hassan *et al.,* 2016; Kitamura *et al.,* 2005; Meepagala *et al.,* 2021; Razavi, 2010; X.-B.
525 Wang *et al.,* 2008). We therefore hypothesize that psoralen, or core intermediates and/or
526 derivatives of its biosynthetic pathway, may be toxic, or even lethal, to tomato above a
527 certain threshold. This toxicity may have impaired the regeneration of additional
528 transgenic tomato lines. However, although our transcriptomic data clearly indicated a
529 chemically related phytotoxicity in the PP line, no clear signal allowed us to pinpoint if
530 this toxicity was related to the production of psoralen and/or any intermediates, or even
531 to the accumulation of any of the other accumulated compounds, in particular

532 coumarins. However, the fact that the PP line plants appeared healthy (**Fig. S1e**) suggests
533 that they were able to circumvent the induced phytotoxicity.
534
535 **4.2. The low accumulation of furanocoumarins may reflect metabolic competition**
536 **favouring the coumarin biosynthesis pathway**
537 Metabolic engineering approaches often fall short of expectations due to our limited
538 understanding of the self-management of specialized metabolite biosynthetic pathways
539 in plants (Lynch *et al.,* 2021). In the PP line, psoralen as well as its precursors from
540 umbelliferone could be detected in almost all the plant parts but at a level below the
541 quantification limit (**Fig. 3a**), proving that our metabolic engineering approach is working
542 but not sufficiently well to allow psoralen accumulation. Given that all genes encoding
543 the enzymes essential for psoralen accumulation were appropriately expressed and the
544 corresponding enzymes proven functional (**Fig. S1e**; **Table S2g**), we suggest a metabolic
545 competition for its precursor, *p*-coumaroyl-CoA, which may be steered instead toward
546 coumarins, which were the more enriched in the PP line. Indeed, simple coumarins like
547 umbelliferone, esculetin, and scopoletin derive from *p*-coumaroyl-, caffeoyl-, and
548 feruloyl-CoA, respectively, via 2OGD-mediated *ortho*-hydroxylation followed by a
549 cyclisation that occurs spontaneously and/or is catalyzed by a COSY (C. Y. Kim *et al.,*
550 2023; Vanholme *et al.,* 2019) (**Fig. 1**). The *ortho*-hydroxylation of *p*-coumaroyl-CoA
551 constitutes the first intended metabolic step for psoralen production in the PP line. To
552 allow umbelliferone accumulation for psoralen production, we chosen the C2'H 2OGD
553 from *Pastinaca sativa* (Apiaceae) (*Ps*Diox) which was characterized *in vitro* as being
554 specific for *p*-coumaroyl-CoA (Roselli *et al.,* 2017). The marked and significant
555 accumulation of coumarins in the PP line including the formally identified esculin and
556 scopoletin (**Fig. 3**, **Fig. S3**), suggests that, *in vivo*, *Ps*Diox could share the same catalytic
557 properties as its orthologs from *Ruta graveolens* (Rutaceae), *A. thaliana* and *Ipomea*
558 *batatas* (Convolvulaceae) that also accept caffeoyl-CoA and feruloyl-CoA as substrates
559 (Matsumoto *et al.,* 2012; Vialart *et al.,* 2012; Yang *et al.,* 2015). This hypothesis is
560 supported by the accumulation of scopoletin and esculetin in plants overexpressing F6'H
561 (Beesley *et al.,* 2023; N. Wang *et al.,* 2025).

562 Non-exclusive hypotheses for the limited accumulation of psoralen may also involve
563 active regulation of competing metabolic pathways that bypass the psoralen branch (**Fig.**
564 **3**). Indeed, comparative metabolomics analysis highlighted the accumulation of
565 phenolamides (*i.e.,* fused hydroxycinnamates and amines), a natural defence compound
566 family in tomato plants (Roumani et al., 2022), in addition to coumarins (**Fig. 2**, **Table S1**).
567 In parallel, comparative transcriptomics pointed to the overexpression in the PP line of
568 genes of the core phenylpropanoid pathway putatively involved in the coumarin and
569 phenolamide biosynthesis pathways (*e.g.*, BAHD acyltransferases, Tyramine N-feruloyl
570 transferase) (**Table S2c**). Such metabolic competition for a common substrate such as
571 *p*-coumaroyl-CoA could also be further established by other factors like metabolic
572 channeling as now established in several species (Dahmani *et al.,* 2023; Lallemand *et al.,*
573 2013; Laursen *et al.,* 2016). Heterologous enzymes from different plant species may be
574 less competitive than endogenous ones in establishing metabolic channeling of
575 intermediates and co-substrates, ultimately at the expense of psoralen accumulation.
576

577 **4.3. Coumarin accumulation might underly the PP line's altered physiology**
578 **and growth**

579 The metabolomics analyses highlighted 82 metabolic features almost exclusively over-
580 accumulated in the transgenic line. Annotation outlined that primarily 4 metabolic
581 families (fatty acids, phenolamides, coumarins and furanocoumarins) were involved.
582 Among them, coumarin accumulation stood out from the other families for at least one
583 of the following reasons: (i) the accumulation of all individual coumarins followed a
584 presence/absence pattern in the PP/WT comparison (**Fig. 3a**; **Table S1**), (ii) the
585 accumulation of coumarin metabolites was detected in the three tissues (leaf, stem,
586 roots) in accordance to the constitutive expression of the PP transgenes (**Fig. 3a**) and (iii)
587 based on the targeted analyses the accumulation of coumarins reached several µg/g of
588 DW (*i.e.,* scopoletin) whereas the furanocoumarin accumulation did not reach the
589 quantification limit (**Fig. 3**). These observations made us consider that coumarins
590 accumulation may be the main stimulus of the transcriptomic, physiological and
591 developmental characteristics of the PP line. This would be consistent with previous
592 studies in which coumarins (*i.e.,* umbelliferone, scopoletin, coumarin, and daphnoretin)

were applied to *A. thaliana* and *Lactuca sativa* (Asteraceae), resulting in allelopathic effects such as membrane peroxidation, Reactive Oxygen Species (ROS) production, mitotic disruption, and photoinhibition (Araniti *et al.,* 2017; Graña *et al.,* 2017; Z. Yan *et al.,* 2016). Our transcriptomics analysis highlighted the upregulation, in the PP line in comparison to WT, of a majority of genes associated with responses to stress, chemicals, organic substances and wounding (**Fig. 5b**; **Fig. 6a-c**). These categories comprise genes involved in ROS detoxification (*e.g.,* glutathione-S-transferases, cytochrome P450s, peroxidases, detoxification proteins, chaperones, and heat-shock proteins) (**Table S2**). On the contrary, the main categories of downregulated genes in the leaves of the PP line compared to WT were associated to chlorophyll biosynthesis (**Fig. 5c**; **Fig. 6d**). These transcriptomics patterns suggest an active regulation of the plant oxidative status, potentially mediated by an increase in the ROS detoxication processes and a decrease in the ROS production linked to photosynthesis. This suggestion is supported by the healthy appearance of the PP line despite the activation of all these stress signaling pathways (**Fig. S1e**). As now well established, photoinhibition generally acts as a protective mechanism to limit photoinduced ROS accumulation, as reviewed by Didaran *et al.,* 2024. In parallel, the lipid over-accumulation observed in the leaves of the PP line (**Table 1**), together with the over-expression of genes associated with lipid metabolism (*e.g.,* phospholipases, aldehyde dehydrogenases, lipid biosynthesis) and membrane repair (*e.g.,* lipid desaturases, acyltransferases) (**Fig. 6a**; **Table S2**), further supports the occurrence of membrane damage. This lipid stress may result from coumarin-induced destabilization of chloroplast integrity and photochemistry, as previously observed in *A. thaliana* (Araniti *et al.,* 2017).

To further understand the impact of coumarins on tomato physiology in the PP line, we investigated its effects on growth, development and resource allocation compared to the WT line. First, we observed no developmental alterations in the PP line, in contrast to the pronounced growth impairments reported in various plant species metabolically engineered to over-accumulate scopoletin (Beesley *et al.,* 2023; Hoengenaert *et al.,* 2022; N. Wang *et al.,* 2025). However, F6'H knock-down lines of *Manihot esculenta* (Euphorbiaceae) with reduced scopoletin accumulation have revealed key roles for this compound in cassava development (*e.g.*, auxiliary budding, leaf appearance, apical

624 dominance) (Mukami *et al.,* 2024). All these elements suggests that the physiological
625 effects of coumarins on development may depend on their constitutive accumulation
626 levels and may be species-specific. This also underscores how poorly understood the
627 physiological regulation of coumarins remains, despite their strong potential to act in a
628 phytohormone-like manner, as hypothesized for an auxin-like effect of scopoletin by
629 Graña *et al.,* 2017.
630 Morphological analysis of the PP line revealed a significant biomass reduction,
631 particularly of the leaves (**Table 1**). A similar biomass loss was previously reported in *A.*
632 *thaliana* supplemented with coumarin or scopoletin (Araniti *et al.,* 2017; Graña *et al.,*
633 2017) and was partly attributed to photoinhibition observed in the leaves, similarly to
634 what we found in the PP line according to transcriptomic data (**Fig. 6d**). In addition, we
635 also observed a downregulation of a few genes putatively involved in sugar storage (*i.e.,*
636 starch synthase) and numerous genes putatively involved in sugar metabolism and cell
637 wall remobilization (**Table S2c,d**). Their differential expression may help explain the
638 biomass loss observed, which cannot be exclusively attributed to carbon content
639 reduction, as this decrease is substantially lower than the 21% drop in biomass (**Tables**
640 **2 and 3**). Considering that most of the biomass components were measured (*e.g.,*
641 carbon, nitrogen, ions) (**Table 2**; **Table S4**), we suggest a concomitant reduction in
642 oxygen-rich compounds such as sugars. In parallel, significant increase of specific leave
643 surface (SLA; +39%) underlies a biomass loss that is distributed within thinner leaves
644 (**Table 1**). Taken together, these elements suggest that coumarins may trigger a 'slimming
645 effect', leading to biomass reduction, primarily in tomato leaves, as a potential response
646 to coumarin-induced phytotoxicity.
647 Thioacidolysis revealed that scopoletin was incorporated into the cell wall (**Fig. 4c**),
648 albeit at a level approximately 10 to 100 times lower than found in *A. thaliana* and *Glycine*
649 *max* (Fabaceae) (Beesley *et al.,* 2023; Hoengenaert *et al.,* 2022). Although only trace
650 amounts of scopoletin accumulated in the cell wall, which prevented validation of its
651 integration into the lignin polymer by NMR, it is reasonable to consider that a small
652 fraction of scopoletin could be incorporated into the lignin polymer. Although the stem
653 cell wall appears to be a key storage compartment for coumarins (Beesley *et al.,* 2023),
654 glycosylated coumarins are stored in vacuoles, *e.g.,* in *A. thaliana* roots (Robe *et al.,*

655 2021). Both vacuolar storage and cell wall transfer are well established toxicity mitigation
656 processes (Weng *et al.,* 2021). Our metabolic and phenotypic data suggest that even a
657 modest accumulation of scopoletin (~1-5 µg/g DW), has to be mitigated in the PP line.
658 Finally, we found that the significant increase in nitrogen content in the upper parts of the
659 PP line coincided with enhanced nitrate uptake by the roots. Catecholic coumarins such
660 as esculetin and fraxetin are well-known to facilitate iron uptake from the soil in plants
661 (H. H. Tsai & Schmidt, 2017). Our data suggest that coumarins accumulation, primarily
662 esculetin, is concomitant with nitrate uptake, highlighting a potential role of coumarins
663 in this process. A similar contribution of coumarins already reported in *Triticum durum*
664 and *Zea mays* (both Poaceae) (Abenavoli *et al.,* 2001; Lupini *et al.,* 2018).
665

666 **5. Conclusion**

667 The production of psoralen in tomato proved to be more challenging than the mere
668 expression of the biosynthetic genes as it potentially led to pronounced phytotoxicity. Our
669 results suggests that the accumulation of coumarins at concentrations of 1-5 µg/g of DW
670 in tomato plants could induces several levels of regulation: (i) xenobiotic stress leading
671 to oxidative stress, which the plant can adapt; (ii) a photoinhibition and an increase in
672 metabolism inducing a biomass slimming possibly in response to oxidative stress; and
673 (iii) a modification of the nitrogen and nitrate levels. Our results indicate that, although
674 coumarins hold substantial agronomic potential (non-toxic to pollinators, facilitating iron
675 uptake, shaping root microbiota, etc) (Cosme et al., 2021; H.-H. Tsai et al., 2018; Zhou et
676 al., 2023), their role in plant defense entails a growth cost even at low content. A
677 counterpart that should be carefully considered and ideally mitigated, following a more
678 precise delineation of the regulatory pathways of coumarins underlying the identified
679 physiological impacts, before pursuing potential viable applications.
680

681 **6. Acknowledgments**

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7. Competing interests

None declared

8. Author contributions

GG, CV and AB, designed and assembled the PP genetic construction. AB, MR, CV, AF and GG participated to transgenic lines regeneration. AB, AF and MR cultivated and harvested the tomato plants. AB, FH and RL generated and analyzed the transcriptomic data. AB, JG and RL generated and analyzed the metabolomic data. AB, LH, JR and WB analyzed the lignin composition. AB, CR and RL generated and analyzed the morphophysiological data. AB, RL and AH conceptualized the project and wrote the article. WB, AH and RL supervised the project. All co-authors reviewed the article.

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