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Invasion of the stigma by oomycete pathogenic hyphae or pollen 4 tubes : striking similarities and differences 5

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20

19 **Running Title:** Stigmatic cells response to invader invasion

Highlight 21

- 22 Epidermal cells face constant environmental challenges. Comparing stigmatic cell responses
- to pathogen hypha or pollen tube invasion, sheds light on how cells adjust the most relevant 23 responses to encountered invaders. 24
- 25

Abstract 26

27 Both filamentous pathogens' hyphae and pollen tube penetrate the host's outer layer and involve 28 growth within the host tissues. Early epidermal responses are decisive for the outcome of these two-29 cell interaction processes. We identified a single cell type, the papilla of Arabidospis thaliana's stigma, 30 as a tool to conduct a comprehensive comparative analysis on how an epidermal cell responds to the invasion of an unwanted pathogen or a welcomed pollen tube. We showed that Phytophtora 31 32 parasitica, a root oomycete, effectively breaches the stigmatic cell wall and develops as a biotroph 33 within the papilla cytoplasm. These invasive features resemble the behaviour exhibited by the 34 pathogen within its natural host cells, but diverge from the manner in which the pollen tube progresses, being engulfed within the papilla cell wall. Quantitative analysis revealed that both 35 invaders trigger reorganisation of the stigmatic endomembrane system and the actin cytoskeleton. 36 37 While some remodelling processes are shared between the two interactions, others appear more 38 specific towards the respective invader. These findings underscore the remarkable ability of an epidermal cell to differentiate between two types of invaders, thereby enabling it to trigger the most 39 40

suitable response during the onset of invasion.

Keywords 41

- 42 cell-cell interaction, invasive growth, oomycete, pollen, cell wall, EIHM, vesicular trafficking, actin,
- 43 Arabidopsis
- 44

Abbreviations 45

- 46 CW : cell wall
- 47 EIHM : extra-invasive hyphal membrane
- 48 HAI: hours after infection

- 49 MAP: minutes after pollination
- 50 LE : late endosome
- 51 MVB : multivesicular bodies
- 52 PM : plasma membrane
- 53 TGN : trans Golgi network
- 54

55 Introduction

56 The epidermis, as the outermost layer of plant cells, is in direct contact with the environment. 57 Epidermal cells must promptly react to potential external stresses to effectively mediate the most 58 relevant responses. Invaders can be infection structures such as hyphae of fungi or oomvcetes but 59 also reproductive structures such as pollen tubes. The first contact between infection hyphae and 60 epidermal cells determine the outcome of the interaction, whether it leads to disease or resistance. Similarly, the initial interaction between invading pollen tubes and the epidermal cells of the stigma 61 (papillae) is crucial for successful reproduction. In both scenarios, the early stages of the interaction 62 63 between the host and the invader are crucial for the outcome of these two cell-cell interaction systems. Many points of convergence between plant defence and pollen recognition have already led some 64 65 authors to suggest that the two processes share common origins (Nasrallah, 2005; Kodera et al., 2021). First, both fungal/oomycete hyphae and pollen tubes are tip-growing cells, secreting cell wall-66 67 degrading enzymes to weaken and penetrate the host's surface layer (Chapman and Goring, 2010; Kebdani et al., 2010; Blackman et al., 2014). Secondly subcellular reorganisation of intracellular 68 compartments and cytoskeleton occurs within epidermal cells at penetration sites (Takemoto et al., 69 70 2003; Hardham, 2007; Iwano et al., 2007; Samuel et al., 2009, 2011). Thirdly, both hyphae and pollen 71 tubes uptake resources from invaded cells to support their growth (Oliveira-Garcia and Valent, 2015; 72 Rottmann et al., 2018; Charrier et al., 2019) (Oliveira-Garcia and Valent, 2015; Rottmann et al., 2018; Charrier et al., 2019). Moreover, plant receptor-like kinases, like Feronia, are involved in both 73 processes, serving as a scaffold for assembling immune-receptor complex and regulating pathogen-74 elicited burst of Reactive Oxygen Species (ROS)(Stegmann et al., 2017). Feronia, along with other 75 76 members of the Catharanthus roseus receptor-like kinase 1-like (CrRLK1L) receptors, also controls 77 changes in ROS status in stigmatic cells, facilitating pollen grain hydration (Liu et al., 2021; Zhang et 78 al., 2021; Huang et al., 2023) and participates in the regulation of pollen tube penetration in the 79 stigmatic CW (Lan et al., 2023). A transcriptomic analysis has predicted the activation of components 80 of the pattern-triggered immunity in the stigma upon pollination (Kodera et al., 2021). Similarly, a study comparing the transcriptomes of pollinated pistils with those infected by Fusarium graminearum 81 82 revealed that similar groups of genes were overexpressed in pistil responding to hyphae or pollen 83 tubes growth (Mondragón-Palomino et al., 2017). This study, conducted at late stages of interaction, is 84 the only one involving a common host tissue, the pistil, to compare reproductive and immune 85 responses. Surprisingly, a comprehensive comparison of the cellular responses to intrusion and early growth of these two types of invasive organisms has never been carried out. 86

Here, we aimed at identifying a cell-cell interaction system that allows to compare the behaviour of 87 88 a single responding cell facing two types of invasive growth. The pollen tube exhibits a host cell specificity, penetrating only the papilla, while filamentous pathogens, such as oomycetes, can infect a 89 90 broader range of tissues. Therefore, we chose the papilla as the reference cell and conducted a 91 search for an oomycete capable of infecting this specific cell. We showed that Phytophthora parasitica, 92 a hemibiotrophic root pathogen breaches the stigmatic epidermis and develops as a biotroph within 93 the papilla cytoplasm, eliciting cellular responses similar to its natural host. When compared with the 94 pollen tube, some stigmatic responses are shared between both invaders (late endosome trafficking, 95 actin reorganisation), while others appear to be specific (EIHM formation, trans Golgi network 96 mobilisation).

97

98 Materials and methods

99 Biological material and culture conditions

100 All Arabidopsis thaliana lines were in the Col-0 background and grown in growth chambers under longday conditions (16h light/8h dark at 21°C/19°C with a relative humidity around 60%). Three sets of 101 102 Arabidopsis marker lines were used; (i) For expression in stigmatic cells, we used the Brassica pSLR1 promoter (Rozier et al., 2020). The pSLR1-LTI6b:GFP and the pSLR1-Lifeact: Venus lines were 103 previously described (Rozier et al., 2020). We used the Gateway® technology (Life Technologies, 104 USA; http://www. thermofisher.com, (Karimi et al., 2002) to generate the pSLR1-GFP:2xFYVE 105 106 construction. (ii) to control expression in root cells, two ubiquitous promoters, p35S and pUbiquite10, 107 were used; these promoters are poorly active in papillae. We generated the p35S-AtPIP2A:RFP construction in the binary vector, pm-rk (Nelson et al., 2007), using the Gateway® technology. The 108 pUbiquitine10-Citrine:2xFyve and the pUbiquitine10-Lifeact:YFP lines were previously described 109 (Simon et al., 2014; Doumane et al., 2021). The pVHAa1-AtVHAa1:GFP line was described previously 110 (Dettmer, 2006); the VHAa1 promoter is active in both stigmatic and root cells. (iii) The pACT11-RFP 111 and the pLAT52-GFP lines, expressing a cytoplasmic fluorescent marker in pollen grain and tube, 112 113 were previously described (Rotman et al., 2003; Rozier et al., 2020).

P. parasitica Dastur isolate INRA-310 was maintained in the Phytophthora collection at INRAE, Sophia Antipolis, France. The growth conditions and zoospores production were previously described (Galiana *et al.*, 2005; Attard *et al.*, 2014). The *P. parasitica* transformant (pCL380-GFP:GUS) expressing a GFP:GUS fusion protein was previously described (Attard *et al.*, 2014). The *Hyaloperonospora arabidopsidis* isolate Noco was transferred weekly onto the susceptible accession Col-0 as described (Hok *et al.*, 2014). Inoculated plants were kept in a growth cabinet at 16°C for 6 days with a 12 h photoperiod.

121

122 Oomycetes pathogen assays and histochemical analysis

Pathogen assays with the *P. parasitica* and *H. arabidopsidis* isolates on roots and leaves, respectively, were performed as previously described (Hok *et al.*, 2014; Le Berre *et al.*, 2017). To infect pistil tissues with *H. arabidopsidis*, Arabidopsis leaves with the sporulation oomycete on their surface were gently rubbing over the pistil surface of manually opened flower buds (late stage 12; (Smyth *et al.*, 1990). Alternatively, spores were applied in solution ($5x10^5$ zoospores/ml) directly on the stigma surface. Inoculated pistils were observed by confocal microscopy in a period of 4h to 24h after inoculation.

Manually opened floral buds or naked pistils (late stage 12; Smyth et al., 1990), were dipped in an aqueous suspension of *P. parasitica* zoospores $(5x10^5 \text{ zoospores/ml})$ obtained from the strain pCL380-GFP:GUS (Attard *et al.*, 2014). In a period of 3h to 24h after infection, the GUS reporter activity staining in plant tissues was performed as previously described (Hok *et al.*, 2014).

133

134 Pollination assay and aniline blue staining

Pistils (late stage 12; Smyth et al., 1990) were emasculated and pollinated with mature pollen. Six
hours after pollination, stigmas were fixed in acetic acid 10%, ethanol 50% and stained with Aniline
Blue for epifluorescence microscopy observation as previously described (Rozier *et al.*, 2020).

138

139 Transmission Electron microscopy

Pistils (late stage 12; Smyth et al., 1990) were emasculated and inoculated with P. parasitica for three 140141 hours or pollinated with mature pollen for 60 minutes. Roots were inoculated with P. parasitica for three hours. Pollinated or inoculated tissues were fixed in a solution containing 2.5% glutaraldehyde 142 143 and 2.5% paraformaldehyde in 0.1 M phosphate buffer (pH 7.2) and after four rounds of 30 min 144 vacuum, they were incubated in fixative for 12 hours at room temperature. Pistils or roots were then 145 washed in a phosphate buffer and further fixed in 1% osmium tetroxide in 0.1 M phosphate buffer (pH 146 7.2) for 1.5 hours at room temperature. After rinsing in phosphate buffer and distilled water, samples 147 were dehydrated through an ethanol series, impregnated in increasing concentrations of SPURR resin over a period of three days before being polymerised at 70°C for 18 h, sectioned (65 nm sections) and
 imaged at 80 kV using an FEI TEM tecnaiSpirit with 4 k x 4 k eagle CCD.

150

151 Confocal Laser Scanning Microscopy (CLSM)

Pistils (late stage 12; Smyth et al., 1990) were emasculated and inoculated with P. parasitica for one 152 153 hour or pollinated with mature pollen for 30 minutes. Roots were inoculated with P. parasitica for one hour. Pollinated pistils were observed with a Zeiss microscope (Zeiss 800 or AxioObserver Z1 154 155 equipped with a spinning disk module) with a 40x objective. Oomycetes infected tissues (stigma or root) were observed with a Zeiss 880 confocal microscope with a 63x objective. Venus, Citrine, YFP 156 157 and GFP were excited at 488 nm and fluorescence detected between 500 and 550 nm. RFP was 158 excited at 561 nm and fluorescence detected between 550 and 600 nm. Stigmas or roots were imaged 159 every 0.4 µm, encompassing the entire volume of the stigma or half of the root thickness, using z-160 stack confocal protocol. Pictures were taken with detector settings optimised for no pixel saturation.

161

162 Fluorescence quantification

163 All image processing, image analysis and fluorescence measurements were done using the 164 ImageJ/Fiji software (Schindelin *et al.*, 2012).

165 To quantify fluorescence intensity at the contact site with the invader, we used a homemade Fiji 166 macro. From the serial confocal images, we generated an average intensity projection (Z project). We 167 manually choose one slide from the stack which corresponds to the focus plan of the contact site with 168 the invader. On this selected slide, we manually drew the stigmatic cell periphery and designated the 169 invader entry point. Then, we indicated the contact area length (ROI zone Length). From numerous image observations, we defined this contact area as 16 µm. Next, the macro automatically depicted 170 171 two zones, the contact and the surrounding zones, with a series of circles of fixed diameter (ROI zone 172 thickness set at 2.6 um). We estimated that 2.6 µm was an appropriate dimension compared to the 173 papilla sizes and the contact area length. The contact zone included five to seven circles depending 174 on its shape (straight or curved. The surrounding zone contained twice as many circles as the contact zone equally distributed from each side of the contact area. Fluorescence intensity was measured in 175 176 each circle by the Fiji script, given as gray values and reported in an Excel file. The mean fluorescence 177 in contact and surrounding zones was calculated, then, a fluorescence difference [contact-178 surrounding] was applied. For control stigmatic cells (non infected or non pollinated), as there was no 179 invader entry point, we introduced zero for the ROI zone Length, 2.6 um for ROI zone thickness and defined an arbitrary contact zone of six circles always positioned at the same distance from one 180 181 extremity of the drawn papilla periphery. This Fiji macro is available on demand.

For fluorescence quantification in root cells and vesicular marker lines, we followed the same procedure except that we manually outlined one root edge. For actin fluorescence, quantification using the Fiji macro was not possible. We then counted the number of images displaying a large actin actin focalisation when a fluorescence patch was clearly visible at the contact site with the penetrating hyphae. Statistical analyses of fluorescence intensity at the contact site with the invaders were based on the paired sample *t*-test. The statistical analysis was carried out on control and inoculated or pollinated cells (n =15).

189

190 Deformation and diameter measurements

Pistils (late stage 12; Smyth et al., 1990) expressing a GFP-tagged PM marker (LTI6b) were emasculated and inoculated with *P. parasitica* or pollinated with mature pollen. Stigma were observed under CLSM one hai or 30 map respectively. Internal (IntD) and external (ExtD) papilla deformation were measured at the penetration site with the invaders as described (Riglet *et al.*, 2020). The statistical analysis compared IntD and ExtD (n= 21 hyphae, 20 pollen tubes) and were based on unpaired *t*-test. On the same LTI6bGFP images, we measured two perpendicular diameters of the hypha or pollen tube and calculated a mean diameter. The statistical analysis compared both
 diameters (n= 21 hyphae, 20 pollen tubes) and were based on unpaired *t*-test.

199

200 Results

201 P. parasitica but not H. arabidopsidis successfully colonises the pistil

202 To investigate the ability of oomvcete pathogens to breach the stigmatic barrier and infect Arabidopsis 203 thaliana pistils, we selected two oomycete species from different genera, each with distinct lifestyles 204 and host ranges. P. parasitica is a hemibiotrophic root pathogen with a broad host range, including A. 205 thaliana (Attard et al., 2010), while Hyaloperonospora arabidopsidis (H. arabidopsidis) is an obligate 206 biotrophic foliar pathogen exclusively infecting A. thaliana. On their respective natural host organs, both oomycetes penetrate within the first four hours after infection (hai). Mobile zoospores and 207 208 immobile conidiospores from P. parasitica (Fig. 1A) and H. arabidopsidis (Fig. 1B), respectively, emit 209 germ tubes on the plant surface, forming a specialised swelling structures, called appressoria, to 210 breach the epidermis through a penetrating hyphae (Attard et al., 2010; Kebdani et al., 2010; Boevink 211 et al., 2020).

212 When we applied H. arabidopsidis conidiospores to the stigma, by gently rubbing A. thaliana leaves 213 with sporulating conidiophores over the surface of a mature pistil (from late stage 12 floral buds, just 214 prior to anthesis, Smyth et al., 1990), spores started to germinate four hours after inoculation, 215 producing germ tubes encircling papillae (Fig. 2A). However, no appressoria were observed, indicating 216 that H. arabidopsidis failed to penetrate the stigma epidermis. P. parasitica produces motile zoospores 217 swimming towards roots under natural conditions. Thus, to infect pistil tissues, we dipped either entire 218 stage 12 flower buds or bare mature pistils in a suspension containing motile zoospores from a P. parasitica strain expressing a Green Fluorescent Protein and ß-glucuronidase (GFP:GUS) fusion 219 220 protein, which expression level significantly increases during penetration of plant tissue (Attard et al., 2014). Remarkably, in both cases, the zoospores displayed a clear preference, accumulating at the 221 222 stigma surface and successfully penetrating the papillae, as indicated by the high expression of the 223 GUS reporter (Fig. 2B, C). This selective preference for specific host tissues is also observed on roots, where zoospores expressing the GUS reporter aggregated around the elongation zone (Fig. 2D). We 224 225 then examined later stages of infection and noticed GFP-labelled P. parasitica hyphae penetrating the pistil twenty-four hours after infection (Fig. 2E). In contrast to pollen tubes, whose elongation was 226 227 restricted to the central transmitting tract (Fig. 2F), P. parasitica hyphae invaded the entire pistil body. 228 Thus, the root pathogen P. parasitica, unlike the leaf pathogen H. arabidopsidis, is able to overcome 229 the stigmatic barrier and invade the pistil, despite the stigmatic epidermis not being its natural host

230

tissue.

231

P. parasitica forms appressoria for penetration and induces a PM-derived membrane around the invading hyphae

To gain deeper insights into *P. parasitica* infection, we conducted a comparative analysis of the early 234 235 stages of infection in both the root and stigma epidermis. As previously published (Attard et al., 2010) we confirmed that one hour after root inoculation, zoospores initiated a germ tube that formed an 236 237 appressorium (white arrow head) on the root surface to penetrate the host epidermis and enter the 238 cells (Fig. 3A-C). On the stigma epidermis, we observed that zoospores initiated a germ tube that grew 239 at the papilla surface (Fig. 3G; Supplementary Fig. S1) and formed a swelling appressorium-like structure, likely serving as an entry point for the penetrating hyphae to grow into the papilla cells (Fig. 240 3H). Given the limited knowledge regarding PM behaviour in epidermal cells invaded by P. parasitica, 241 242 we examined its fate in cells undergoing hyphal penetration. Using an A. thaliana line expressing 243 fluorescent-tagged plasma membrane (PM) markers (GFP-LTI6b in stigma, RFP-AtPIP2A in root), we 244observed that in both root and papilla cells a structure labelled with the PM markers encased the penetrating hypha within the cytoplasm (Fig. 3D-F, 3I-K). 245

Taken together, our findings indicate that *P. parasitica* uses comparable infection mechanisms to invade both root and papillae cells.

248

249 Penetration of stigmatic cells by pollen tube or infectious hyphae involves distinct processes

To gain a deeper understanding of the invader-host cell interface, we conducted a comparative TEM 250 251 analysis. After three hours of inoculation with P. parasitica, we observed the digestion of the root cell 252 wall (CW) beneath the appressorium at the penetration sites (Fig. 4F, G) and the hyphae to be 253 embedded within the root cytoplasm (Fig. 4H). In the case of P. parasitica infection on stigma, three 254 hours after inoculation, the stigma cuticle and CW were no longer visible beneath the appressoriumlike structure on the papilla surface (Fig. 4A-B). This strongly suggests that both layers had been 255 digested at the penetration site, mirrorring what was observed for the root CW. Within the papilla, we 256 found the hypha either between the cuticle and the CW, with the stigmatic CW partially digested (Fig. 257 258 4C-D) or entirely embedded within the stigmatic cytoplasm (Fig. 4E). Since cell penetration occurs 259 asynchronously, we assume that the gradual digestion of the CW, progressing from partial (Fig. 4C) to 260 complete (Fig. 4E), likely corresponds to different stages of infection.

Then, we aim at comparing infection with pollination. The early events occurring after contact between 261 262 a compatible pollen grain and a stigmatic cell are well documented and presented in Figure 1. Shortly after contact, proteins and lipids from both cell surfaces fused, forming a hydrophilic environment 263 264 (called the foot) essential for pollen acceptance (Fig. 1C; (Chapman and Goring, 2010). This initial contact is followed by pollen hydration and emergence of a pollen tube (germination) that penetrates 265 the stigmatic cell, growing towards the stigma base (Fig. 1C). When analysing pollinated papilla cells 266 267 by TEM, we found that the pollen tube breached the cuticle layer 30 minutes after pollination (map; 268 Fig. 5A, B). In contrast to hyphal penetration, we did not observe complete digestion of the stigmatic CW. Instead, the pollen tube grew between the inner and outer CW layers of the papillae (Figs 1C, 269 5C-E), a mode of invasive growth characteristic of Brassicaceae species (Riglet et al., 2020). 270

Our TEM analysis further supports that *P. parasitica* uses comparable infection processes to invade both root and papillae cells, but also reveal fundamental differences when comparing infection with the pollination process.While oomycete hyphae and pollen tubes penetrate the papilla cuticle, the pollen tube remains engulfed within the CW, whereas oomycete hyphae digest the two CW layers to grow in contact with the papilla PM.

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277 Penetration causes different constraints to the papilla surface

278 Penetration imposes constraints on the epidermis surfaces. In order to breach a plant tissue, both 279 hyphae and pollen tubes have to soften and deform the invaded tissue, causing substrate radial 280 expansion (Sanati Nezhad and Geitmann, 2013). To evaluate the constraints exerted by both invaders as they progressed through the stigmatic cells, we quantified papilla deformations shortly after hyphae 281 282 or pollen tubes penetration. Following the approach from Riglet et al., (2020), we assessed two 283 measures: (i) the deformation towards the interior of the papilla (intD, inward), which we estimated by quantifying the inward invagination of the stigmatic PM, labelled with the membrane marker LTI6B-284 285 GFP and (ii) the deformation towards the exterior of the papilla (extD, outward), assessed through analysis of bright field images (Fig. 6A, B). We found that the P. parasitica hypha induces a significant 286 287 external deformation during penetration (2.8 µm; Fig. 6C; Supplementary Table S1) while causing only slight deformation within the papilla interior (0.6 µm; Fig. 6C; Supplementary Table S1). In contrast, 288 pollen tube growth resulted in nearly equal extD and intD values (2.1 µm and 1.8 µm respectively; Fig. 289 6C; Supplementary Table S1). Thus, although both the pollen tubes and the hyphae are capable of 290 291 piercing and penetrating the stigmatic surface, they exert different levels of constraints on the papilla 292 cells.

293

294 Penetration triggers subcellular rearrangements in epidermal cells

295 Vesicle trafficking within infected host cells and cytoskeletal remodelling are crucial for plant defence 296 responses (Ruano and Scheuring, 2020; Lu et al., 2023). Likewise, early events linked to pollen 297 acceptance involve polarised secretion (Samuel et al., 2009; Safavian and Goring, 2013) and actin 298 reorganisation (Iwano et al., 2007; Rozier et al., 2020) in stigmatic cells, targeted towards the pollen grain. Therefore, we conducted a comparative analysis of the subcellular remodelling processes 299 triggered in stigmatic cells upon intrusion by either a hypha or a pollen tube. To address this objective, 300 we specifically focused on two functionally distinct populations of endomembrane compartments, (i) 301 302 the trans-Golgi network (TGN), a critical compartment at the crossroads of secretion and endocytosis 303 (Zhuang et al., 2024), (ii) the late endosome (LE), also known as multivesicular bodies (MVB), serving dual roles in cargo transport to the lytic vacuole and polarised secretion through the release of internal 304 305 vesicles into the extracellular space (Zhuang et al., 2024) and (iii) the actin network, which provides tracks to drive vesicular transport (Geitmann and Nebenführ, 2015). To monitor the behaviour of these 306 cellular components, we used specific marker lines expressing distinct fluorescent tags: a GFP-tagged 307 vacuolar ATPase a1 subunit (VHAa1-GFP, TGN-VHAa1), a GFP-tagged tandem FYVE domain (GFP-308 309 FYVE, LE-FYVE), and a fusion protein combining the Lifeact peptide and the Venus fluorochrome 310 (Lifeact-Venus, actin cytoskeleton). We quantified the fluorescence intensity within the papilla 311 surrounding the site of invader penetration using a customised Fiji macro. By calculating the difference in fluorescence intensity between the invader penetration site (contact zone) and the surrounding 312 313 region where no penetration occurred (surrounding area). A positive difference [contact-surrounding] indicates a focalisation of the component of interest towards the penetration site. Pistils were 314 315 inoculated with P. parasitica for one hour or pollinating for 30 minutes, and cellular component 316 dynamics were tracked by confocal microscopy during early stages of interactions. Our analysis 317 revealed a significant increase in both TGN-VHAa1 and LE-FYVE fluorescence intensity at the contact zone with the growing hyphae (Fig 7; Supplementary Figs S3, S4; Supplementary Table S2). LE-318 FYVE fluorescence intensity was enhanced in response to the pollen tube intrusion around the 319 penetration site (Fig. 7; Supplementary Fig. S5; Supplementary Table S2), while the intensity of TGN-320 VHAa1 labelling at the contact zone did not significantly differ from the area without contact (Fig. 7; 321 Supplementary Fig. S6; Supplementary Table S2). As control, we detected no significant fluorescence 322 323 intensity changes in non-infected and non-pollinated papillae (Supplementary Fig. S7; Supplementary 324 Table S2). In stigmatic cells, the actin cytoskeleton formed a network of fine cables uniformly distributed along the papillae (Supplementary Fig. S7A; Rozier et al., 2020). However, upon infection, 325 Lifeact-Venus fluorescence intensity significantly increased at the contact zone, resulting in a dense 326 and brightly fluorescent patch beneath the growing hypha (Fig. 7; Supplementary 327 Fig. S8; 328 Supplementary Table S2). Similarly, significant focal accumulation of actin was observed in pollinated 329 papillae at the contact zone with the growing pollen tube (Fig. 7; Supplementary Fig. S9; 330 Supplementary Table S2).

Dynamic changes in the endomembrane system and the cytoskeleton during the invasion of the 331 332 natural target for P. parasitica infection remain poorly documented. Consequently, we expanded our comparison to include the root epidermis. Similarly to the infected stigmatic cells, we detected a 333 significant increase in TGN-VHAa1 and LE-FYVE fluorescence intensity at the contact zone with the 334 335 growing hyphae in infected root cells (Fig. 8A, B; Supplementary Figs S10, S11; Supplementary Table S2). Such fluorescence focalisation was not observed in control root cells (Supplementary Fig. S12A, 336 337 B). Our customised Fiji macro was not suitable for actin-Lifeact quantification due to the high 338 concentration of actin filaments at the cortical region of the entire root (asterisk in Fig. 8C), possibly 339 masking any focal accumulation at the contact zone. To address this issue, we counted the number of images displaying a large actin-Lifeact focalisation patch at the tip of the penetrating hypha (red arrow 340 in Fig. 8C). Our observations revealed that the comvcete triggered actin focalisation at the contact 341 zone in 11 out of 15 infected root cells out (Supplementary Fig. S13). In contrast, no such fluorescent 342 343 patches were detected in control cells (Supplementary Fig. S12C).

Collectively, our results demonstrate that although *P. parasitica* is not a natural pathogen of the stigmatic epidermis, it triggers cellular responses in papillae that closely resemble those induced in its natural host, the root cell. Interestingly, when compared with the pollen tube, some of these responses are shared between both invaders such as late endosome trafficking and actin reorganisation. 348 However, others, like trans Golgi network mobilisation, are more specific to likely orchestrate an 349 appropriate response.

351 **Discussion**

350

We aimed at deciphering the response of a single epidermal cell, the papilla, when facing the intrusion of either a pollen tube or the hypha of pathogenic oomycetes from two distinct genera, *P. parasitica*

354 and *H. arabidopsidis*.

355 Upon P. parasitica inoculation of papilla or roots, we observed a preferential accumulation of swimming zoospores at the elongation zone of the root and also at the stigma epidermis of the pistil. 356 357 This suggests that both zones share common features that specifically facilitate zoospore aggregation. 358 While the precise mechanisms behind the attraction of zoospores of several *Phytophtora* species by 359 root exudates is not fully elucidated, a various components, such as carbohydrates, amino-acids and hormones, have been identified as potential attractant (Bassani et al., 2020; Kasteel et al., 2023). A. 360 361 thaliana belongs to a plant family characterised by a dry stigma lacking surface exudates (Hiscock and Allen, 2008) suggesting that secreted chemical cues are unlikely to play a role in spore aggregation on 362 the stigma surface. However, we can not rule out that components from the outermost layer of the 363 364 papilla surface (the proteinaceous pellicle) may serve as attractants (Hiscock and Allen, 2008). Electrostatic forces have been suggested to be involved in both root interactions with Phytophthora 365 366 palmivora and pollination (Van West et al., 2002; Clarke et al., 2017). While the mechanisms through which these electrical signals are perceived by zoospores or pollen grains remain unknown, we can 367 368 speculate that electrostatic forces may be involved in the preferential accumulation of P.parasitica 369 spores at the stigmatic surface.

370 Upon reaching the epidermal surface, filamentous pathogens form appressoria to penetrate the tissue. 371 Thereby, the appressorium-like structure differentiated by P. parasitica at the outer surface of the 372 stigmatic epidermis (Figs 3, 4) is likely employed to breach both the cuticle and the CW, granting 373 access to penetration. Physical and chemical properties of the epidermis, such as surface hardness, 374 hydrophobicity, wax composition and cutin, are strong triggers for appressorium formation (Bircher and 375 Hohl, 1997; Ryder et al., 2022). It is worth noting that stigmas as well as leaves, are coated with a 376 hydrophobic cuticle whereas the roots are not (Heizmann et al., 2000; Schreiber, 2010). Despite this, 377 we have never observed appressorium formation on the stigma surface by H. arabidopsidis, a leaf 378 pathogen (Fig. 2). This suggests that the papillae may either lack the requisite triggering signals or inhibit the differentiation of H. arabidopsidis appressorium. Furthermore, H. arabidopsidis is an 379 380 obligate pathogen exclusively infecting A. thaliana leaves, whereas P. parasitica has a broader host 381 range, infecting over 72 plant species and forming appressoria on both root and leaf tissues in natural 382 conditions (Meng et al., 2014). It is therefore likely that H. arabidopsidis relies on specific host stimuli 383 to initiate appressorium differentiation, while P. parasitica is less specific, forming appressoria on 384 various tissues, including stigma.

To overcome the plant barrier formed by the cuticle and the CW, filamentous pathogens and pollen 385 grains secrete degrading enzymes capable of digesting their main polymers (Kubicek et al., 2014; 386 387 Robinson et al., 2021). Our TEM analysis of the penetration process (Figs 4, 5) reveals a major 388 difference between both invaders regarding their ability to digest the stigmatic CW. Whereas the 389 hypha passes through the bilayer papilla wall to grow in between the inner face of the CW and the PM, 390 pollen tube penetration is restricted to the outer wall layer, confining the tube growth within the CW. 391 This distinction suggests that the two papilla wall layers may possess distinct chemical properties, thereby requiring diverse cocktails of secreted enzymes for their digestion. Notably, a mechanical 392 393 heterogeneity within the stigmatic cell wall, which can influence the pollen tube behaviour, has previously been suggested (Riglet et al., 2020). In this context, the interaction between the papillae 394 395 and the invader entails a dialogue that leads to digestion of either both stigmatic CW layers (in the 396 case of interaction with P. parasitica) or only the outer layer (in the case of interaction with the pollen 397 tube). One particularly intriguing aspect that remains enigmatic is the process by which a stigmatic cell 398 envelops the pollen tube within its CW. The available knowledge of the papilla CW is very limited, 399 except for its bilayered structure that distinguishes it from other plant cells. Based on our findings, it is 400 tempting to speculate that the selective digestion of the CW, limited to the outer layer, and the 401 controlled confinement of pollen tube growth within the two wall layers, could represent a specialised 402 adaptation of plants to discriminate a pollen tube from an unwanted invasive agent, such as a 403 pathogen.

As the hyphae and pollen tubes penetrate, they exert pressure on the interior of the stigmatic cell. We 404 estimated the compression intensity by measuring the deformation of the papilla shortly after 405 penetration (Fig. 6). We found that the pollen tube deforms the interior of the cell to a greater extent 406 407 compared to the hypha. This quantitative difference could stem from several factors. Firstly, the 408 invaders have different diameters, with the pollen tube being significantly larger than the hypha (i.e. 409 4.8 µm and 3.8 µm respectively) potentially resulting in greater compressive forces exerted by the tube. Secondly, the way the invader softens the invaded tissue, either enzymatically or mechanically, 410 may differ, leading to differences in the magnitude of penetrating forces. Lastly, the resistance exerted 411 by the papilla cell against penetration may differ depending on the location or the nature of the 412 413 invader.

414 Gentle pressure applied with a microneedle on the surface of an epidermal cell induces actin 415 microfilaments and cables focusing beneath the needle tip (Hardham et al., 2008). This observation 416 has led the authors to propose that the actin response might be triggered by physical detection of pressure exerted by a penetrating invader rather than molecules associated with the invader. In our 417 418 study, we detected a similar actin reorganisation around the penetration site in stigmatic cells challenged by either a hypha or a pollen tube (Fig. 7). This indicates comparable actin remodelling, 419 despite differences in the localisation of the growing hypha and the pollen tube, as well as variations in 420 421 the compression intensity they impose to the papilla surface. We could postulate that a threshold value 422 for the physical forces required to initiate actin reorganisation may have been reached in both 423 interaction systems. Such a mechanical threshold has been proposed to elicit subcellular 424 reorganisation in epidermal cells infected with H. arabidopsidis (Branco et al., 2017). Alternatively, we can not rule out that the chemical signatures of oomycete hyphae and pollen tubes, while distinct, 425 426 could have a similar impact on the actin network in invaded stigmatic cells.

In the cytoplasm of infected roots or stigmatic cells, the growing hypha is surrounded by a membrane 427 428 envelope labelled with fluorescent markers localised to the PM in non-infected cells (Fig. 3). Such 429 membrane envelope has been previously described in A. thaliana and rice leaves to surround the 430 hyphae of the hemibiotrophic fungi Magnaporthe oryzae or Colletotrichum higginsianum upon infection (Yi and Valent, 2013; Qin et al., 2020). This specialised membrane, called the extra-invasive hyphal 431 membrane (EIHM), is considered as a typical hallmark of the biotrophic phase, required to escape the 432 433 plant recognition system while uptaking nutrients from the host (Oliveira-Garcia and Valent, 2015; 434 Jones et al., 2021). The EIHM forms a continuum with the plant PM but its composition differs as its 435 content is modified during infection (Qin et al., 2020). To our knowledge, such specialised membranes 436 have never been reported in pathosystems involving flower pathogens (Brewer and Hammond-437 Kosack, 2015; Andargie and Li, 2016; Mondragón-Palomino et al., 2017). The presence of an EIHM-438 like membrane within papilla cells infected by P. parasitica suggests that the oomycete adopts a 439 biotrophic lifestyle during the first hours of infection, similarly to its behaviour in roots. Further 440 investigation is needed to determine whether this envelope serves as a functional interface and whether its composition differs from the rest of the PM. 441

442 The mobilisation of TGN and LE/MVB vesicles contributes significantly to plant defence mechanisms 443 by delivering defence proteins and antimicrobial compounds to the extracellular space, reinforcing the 444 CW to prevent pathogen entry and participating in the expansion of the host-derived membrane during 445 infection (Bozkurt et al., 2015; Gu et al., 2017). Thereby, the presence of VHA-TGN and LE-FYVE concentrated at the vicinity of P. parasitica penetration site in root epidermal cells was not surprising 446 (Fig. 8). Interestingly, the focalisation of TGN-VHAa1 and LE-FYVE was also induced by P. parasitica 447 448 in infected stigmatic cells (fig. 7). This indicates the pathogen's capability to manipulate a non-natural 449 target, the papilla, to hijack the host cellular machinery similar to its strategy during root infection. 450 Upon pollination, intense vesicular trafficking in stigmatic cells is essential to sustain pollen germination and subsequent pollen tube growth. Ultrastructural studies focused on pollen-stigma 451 452 interactions in Brassica napus identified LE/MVB fusion with the stigmatic PM and the release of 453 internal vesicles into the extracellular space adjacent to the pollen grain (Safavian and Goring, 2013; 454 Indriolo et al., 2014). In pollinated A. thaliana stigma, instead of LE/MVB, secretory vesicles likely originating from the TGN were detected attached to the stigmatic PM beneath the pollen grain 455 456 (Safavian and Goring, 2013; Indriolo et al., 2014). In our experiments conducted on A. thaliana, we did not detect polarised movement of the TGN-VHAa1 compartments during pollen tube penetration. This 457 discrepancy could be attributed to the methods used between our study, using fluorescent probes and 458 confocal imaging, and the techniques used in Safavian and Goring (2013) and Indriolo et al. (2014), 459 460 which relies on chemically fixed material and TEM. Alternatively, the observed differences may also 461 stem from the timing after pollination. Indeed, while we focused on pollen tube penetration at 30 minutes after pollination, Goring's group concentrated on earlier stages of interaction 10 minutes after 462 pollen deposition (Safavian and Goring, 2013; Indriolo et al., 2014). Besides, the TGN constitutes a 463 complex cellular compartment at the interface of the secretory and endocytic pathways, divided into 464subdomains or sub-populations (Aniento et al., 2022). Thus, deciphering the precise mechanisms 465 behind its involvement in the pollination process would require further live-cell imaging with an 466 467 extensive collection of fluorescent-tagged markers for endomembrane compartments. Nethertheless, 468 our study highlights the intriguing possibility that trafficking of FYVE-labelled LE/MVB compartments 469 may play a role in pollen acceptance in A.thaliana, supplementing the TGN-associated secretory pathway previously suggested by Goring and colleagues (Safavian and Goring, 2013; Indriolo et al., 470 471 2014).

Recent studies proposed an attractive look-and-key model in which a stigmatic barrier is established 472 473 through receptors from the CrRLK1L family and their corresponding stigmatic ligands to exclude 474 unwanted pollen. This barrier is disrupted when a compatible pollen grain carrying competing ligands 475 for the same receptor complexes lands on the papillae, thus gaining access to papilla entrance (Liu et 476 al., 2021; Zhang et al., 2021; Huang et al., 2023; Lan et al., 2023). The current challenge lies in 477 understanding how two distinct sets of ligands can trigger opposite downstream signalling responses, leading to rejection or acceptance. An attractive hypothesis is that the LE/MVB-FYVE trafficking we 478 479 observed in this study may be involved in the acceptance pathway, deliverying necessary factors 480 required for pollen germination and/or pollen tube penetration. In this context, it is plausible to speculate that P. parasitica, which induces LE/MVB-FYVE trafficking and penetrates the papilla, might 481 482 possess the key ligands necessary to disrupt the stigmatic lock. MVBs are fascinating compartments that not only serve as a sorting station directing proteins towards vacuolar for degradation but also 483 play a role in secretion, by releasing their intraluminal vesicles into the extracellular space upon fusion 484 with the plasma membrane. While the exact nature of the cargoes transported by these vesicles 485 486 remains poorly understood, exosomes are believed to play a crucial role in delivering signalling molecules for intercellular communication (Zhuang et al., 2024). 487

489 To conclude, we identified the papilla as a valuable model for comprehensively comparing on how 490 a single epidermal cell responds to two opposite scenarios: the invasion of a pathogenic hyphae and the beneficial process of pollination. We have identified shared subcellular changes triggered in 491 492 stigmatic cells upon P. parasitica infection and in responses to pollination (LE trafficking and actin 493 remodelling). These findings support the longstanding assumption that common or evolutionary 494 related host-encoded functions exist between plant defence and pollen recognition. Besides, we identified distinct cellular events specific to each type of interaction highlighting a finely tuned dialog 495 496 established during early stages of invasions. These include the mobilisation of the TGN-VHAa1 compartments and the formation of an EIHM-like membrane. Such interaction-specific features are 497 498 likely to be pivotal triggering the appropriate response, depending on the nature of the invader and/or 499 the established entry strategy (i.e. appressorium formation and complete CW digestion vs foot formation and partial CW digestion). Our findings suggest that numerous crosstalks exist between the 500 501 processes of infection and pollination. The interaction system we have developed holds promise as a 502 framework for further exploration, offering insights on how an epidermal cell perceives and responds to 503 an invader in order to fine-tune the most relevant responses.

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507 Supplementary data

- 508 The following supplementary data are available at JXB online
- 509 *Table S1.* Papilla deformation and hypha/pollen tube diameters
- 510 *Table S2.* Fluorescence quantification
- 511 Fig. S1. P. parasitica zoospores infecting stigmatic cells
- 512 *Fig.* S2. Invader features.
- 513 *Fig.* S3. Pattern of TGN-VHAa1 compartments in stigmatic cells in response to *P. parasitica*.
- 514 *Fig. S4.* Pattern of LE-FYVE compartments in stigmatic cells in response to *P. parasitica.*
- 515 *Fig.* S5. Pattern of LE-FYVE compartments in stigmatic cells in response to pollen tubes.
- 516 *Fig.* S6. Pattern of TGN-VHAa1 compartments in stigmatic cells in response to pollen tubes.
- 517 *Fig.* S7. Subcellular arrangement of the TGN, the LE, and the actin network in control stigmatic cells 518 as observed by CLSM.
- 519 *Fig.* S8. Pattern of the actin cytoskeleton (Actin-Lifeact) in stigmatic cells upon infection with *P. parasitica.*
- 521 *Fig.* S9. Pattern of the actin cytoskeleton (Actin-Lifeact) in stigmatic cells in response to pollen 522 tubes.
- 523 Fig. S10. Pattern of TGN-VHAa1 compartments in root cells in response to P. parasitica.
- 524 Fig. S11. Pattern of LE-FYVE compartments in root cells in response to P. parasitica.
- 525 *Fig. S12.* Subcellular arrangement of the TGN, the LE, and the actin network in control root cells, as 526 observed by CLSM.
- 527 *Fig. S13.* Dynamics of the actin cytoskeleton (Actin-Lifeact) in root cells in response to infection with 528 *P. parasitica*, as analysed by CLSM at one hai.
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543 Author contribution

LR was responsible for all experiments and analysis performed for pollination. SH developed the pathosystem for papilla infection and performed the confocal imaging. LBV performed the image acquisition by SEM. NM performed and analysed *P. parasitica* root and pistil infections. JL performed and analysed *P. parasitica* root infections. VA and HK performed *H. arabidopsidis* leaf and pistil infections. VB designed the Fiji macro. LR, SH, HK, MG, IFL and AA designed the study; LR, IFL and AA wrote the manuscript. All the authors contributed to the discussion, reviewed and edited the manuscript. The authors read and approved the final manuscript.

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552 **Conflict of interest**

- 553 No conflict of interest declared
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560 Data availability

All data supporting the findings of this study are available within the paper or within its supplementary
 data published online. The custom Fiji macro is available upon request to the corresponding authors
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565 Figure legends

Fig. 1. Invasion features of P. parasitica, H. arabidopsidis, and A. thaliana pollen tube in root, leaf, 566 and stigma, respectively. (A) Arabidopsis root infected with the oomycete P. parasitica. Schematic 567 568 representations (upper row) and merged CLSM images between the green channel and bright-field of 569 P. parasitica strain pCL380-GFP:GUS expressing a cytoplasmic GFP marker (lower row). The zoospore 570 (sp) germinates a germ tube (gt) that grows along the plant surface and forms an appressorium 571 (white arrow head) to penetrate the epidermis. Penetration starts 30 min after infection (left panel). 572 The penetrating hypha (ph) grows intercellularly and develops haustoria (ha) (6 hai, right panel). (B) Arabidopsis leaf infected with the oomycete *H. arabidopsidis*. Schematic representations (upper row) 573 574 and bright-field CLSM images (lower row). The conidiospore (sp) germinates a germ tube (gt) that grows along the plant surface and forms an appressorium (white arrow head) to penetrate the 575 576 epidermis (8 hai, left panel). The penetrating hypha (ph) grows intercellularly and develops haustoria 577 (ha) (18 hai, right panel). (C) Arabidopsis stigma with germinating pollen. Schematic representations 578 (upper row) and merged CLSM images between green fluorescence and bright-field of a pollen grain 579 and a pollen tube expressing the GFP marker (pLAT52-GFP Line; lower row). Rapidly after pollen 580 capture, a specific structure, called the foot (depicted in orange), is formed at the pollen-papilla interface. A pollen tube (pt) emerges from the grain, passes through the foot and penetrates the 581 582 papilla CW (dark grey layer) 12 map (left panel). The pollen tube grows inside the papilla CW towards 583 the basis of the stigma (right panel). Scale bar=10 μ m.

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585 Fig. 2. P. parasitica but not H. arabidopsidis invades A. thaliana pistil. (A) H. arabidopsidis spores (sp) were deposited on the stigma surface of mature pistils and observed by CLSM. The upper and lower 586 images are both extracted from the same Z-stack showing a spore and a germ tube (gt) growing 587 around the papilla cells (s) without penetration, 18 hai. Scale bar=10 μ m. (B, C) The entire flower bud 588 589 (B) or the naked pistil (C) were dipped in a suspension of GUS-expressing zoospores of P. parasitica 590 (strain pCL380-GFP:GUS) and observed by transmission light microscopy. Zoospores preferentially 591 attached to the stigma epidermis, three hai. (D) A. thaliana roots dipped in a suspension of P. 592 parasitica strain pCL380-GFP:GUS and observed by TEM. Zoospores preferentially attached to the 593 elongation zone of the root, three hai. (E) Entire flower buds were dipped in a suspension of GFP-

expressing zoospores of *P. parasitica* and observed by CLSM. Median longitudinal optical section of the entire pistil. Growing hyphae were detected inside the pistil tissues 24 hai. (F) Pollinated pistils stained with aniline blue and observed under epifluorescence microscopy. Six hours after pollen grain (pg) deposition at the stigma surface, pollen tubes (pt) were present within the central transmitting track. Scale bar=100 µm. Each experiment was repeated at least three times.

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600 Fig. 3. Appressorium-mediated penetration of the pistil and the root epidermis by *P. parasitica*. (A) 601 Transversal optical sections of a zoospore (sp, delimited by a white dashed line) of P. parasitica 602 germinating a germ tube (gt) on the stigmatic cell surface, one hai. The germ tube forms an 603 appressorium-like structure at its extremity (white arrow head). (B) Longitudinal optical sections of P. parasitica infecting a papilla cell. The penetrating hypha (ph) emerges from an appressorium (white 604 605 arrow head). (C-E). An inoculated papilla expressing a GFP-tagged PM marker (LTI6b) four hai. A Lti6b-labelled membrane encircles the penetrating hypha, as observed in bright field (C), green 606 607 fluorescence (D) and the merged image (E). (F-K), Arabidopsis root expressing a RFP-tagged PM aquaporin AtPIP2A upon invasion by P. parasitica. The roots were dipped in a zoospore suspension 608 609 for one hour and the epidermis was analysed by CLSM. The images show optical sections of the same infection site, with F, G and H focused on the root (r) surface, and I, J and K on the cell interior. The 610 611 zoospore (sp) germinates a germ tube that differentiates an appressorium (white arrow head) to 612 penetrate between two adjacent cells. Inside the epidermis, the AtPIP2A-labelled membrane 613 surrounds the penetrating hypha. Left column, bright field, middle column, RFP channel, and right 614 column, merged channel. Scale bar=10 μ m. Each experiment was repeated at least three times.

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Fig. 4. Invasion by P. parasitica hypha depends on the host epidermis. (A-E) Stigmatic cell infected 616 617 with P. parasitica observed by TEM, three hai. (A) The germ tube (gt) emitted from the zoospore is located outside the papilla (s). The extremity of the germ tube forms an appressorium-like structure 618 619 (white arrow head). A penetrating hypha (ph) enters the host cell. (B) Magnification detail depicted 620 by the white square in A showing the stigmatic cuticle (SC; electron dense black layer) and the 621 stigmatic CW (SCW) digested at the penetration site. The oomycete CW (OCW) appears as an 622 electron transparent white layer. (C) The hypha locates between the stigmatic cuticle and the stigma 623 CW (SCW). (D) Magnification detail depicted by the white square in C showing the stigmatic CW 624 degradation (degSCW) occurring at the contact area with the hypha. (E) P. parasitica penetration 625 hypha (ph) embedded in the stigmatic cytoplasm (s). (F-H) Root cells (R) infected with P. parasitica, 626 as observed by TEM, three hai. (F) An appressorium (white arrowhead) is visible at the root surface 627 and a penetration hypha (ph) inside the host cell. (G) Detailed view depicted by the white square in F 628 showing degradation of the root CW(deg RCW). (H) A penetration hypha embedded in the root 629 cytoplasm. Scale Bar=1 µm. Each experiment was repeated at least three times.

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631 Fig. 5. The pollen tube grows within the papilla CW. The images show the pollinated stigma as observed by TEM, 60 map, with general and detailed views in the left and right columns, respectively. 632 633 (A) Transversal section showing the pollen tube (pt) emerging from a pollen grain (pg) and 634 penetrating a stigmatic cell (s). (B) close-up view depicted by the white square in A shows stigmatic cuticle (SC) digestion underneath the pollen tube. Scale bar=2 μ m. (C) The progressing pollen tube 635 636 grows between two CW layers of the stigmatic cell (s), the inner layer (SCW.in) and the outer layer 637 (SCW.out), as indicated in the close-up view (D) depicted by the white square in C. Cell walls appear 638 as electron transparent white/light grey layers. (E) Transversal section of the pollen tube within the 639 stigmatic CW. (F) close-up view depicted by the white square in (E) shows the inner stigmatic l 640 surrounds the pollen tube. PCW, pollen CW. Scale bar=1 μ m. Each experiment was repeated at least 641 three times.

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643 Fig. 6. Pathogen and pollen tubes apply different mechanical stresses onto the papilla. Arabidopsis 644 stigma expressing a GFP-tagged PM marker (Lti6b) were infected with P. parasitica (A) or pollinated 645 (B), and observed by CLSM at one hai or 30 map, respectively. To quantify the papilla deformation, a 646 red line was drawn on merged images (inset) between the two external points of the deformation. 647 Distances from the red line towards the cuticle (blue line, external deformation, extD) and towards the cytoplasm (yellow line, internal deformation, intD) were determined. Scale bar=10 µm on the full 648 images and 5 μ m on the insets. Sp, spore; pg, pollen grain. (C) Quantitative analysis of external (extD) 649 and internal (intD) papilla deformations upon infection or pollination, for 21 hyphae or 20 pollen 650 tubes. In the plots, the cross corresponds to the mean value. t-test; *** pVal<0,0005; n.s., not 651 652 significant.

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654 Fig. 7. The pathogen and pollen tube trigger both similar and different subcellular rearrangements 655 upon penetration of stigmatic cells. (A) Stigmatic cells from fluorescent marker lines for the trans Golgi network (TGN; TGN-VHAa1), the late endosome (LE/MVB; LE-FYVE), and the actin network 656 657 (Actin-Lifeact) were infected with *P. parasitica* or pollinated. CLSM at one hai or 30 map allowed to 658 visualize the papillae (green or yellow fluorescence) and the invader (bright field for P. parasitica, red 659 fluorescence for pollen). The papilla periphery was manually outlined on the obtained images (white 660 lines), and the Fiji macro automatically depicted two zones, (i) a contact zone (yellow circles) 661 including the invader entry point (red arrow/red circle), and (ii) a surrounding zone (green circles). 662 Fluorescence intensities (gray values) were automatically measured in each circle. Scale bar=10 µm. 663 (B) Quantification of fluorescence intensity differences between zones (i) and (ii). For each interaction, 15 stigmatic cells on at least four independent stigma were analysed. In the plots, the 664 665 cross corresponds to the mean value. Statistical analysis of fluorescence intensity was based on a paired T-test. * pVal<0,05; ** pVal<0,005; *** pVal<0,000.5; n.s., not significant. Detailed 666 667 measurements are shown on supplementary Figures S3 to S6, S8 and S9.

669 Fig. 8. P. parasitica triggers reorganisation of subcellular components in root cells. Roots from 670 fluorescent marker lines for the trans Golgi network (TGN; VHAa1), the late endosome (LE/MVB; 671 2xFYVE), and the actin network (Actin; LifeAct) were infected with P. parasitica and analysed by 672 CLSM at one hai. (A) For the TGN and LE marker lines, fluorescence was quantified using the Fiji 673 macro as described in Figure 7 to determine fluorescence differences between contact zones and 674 surrounding zones (B) Quantification of fluorescence differences. For each interaction, 15 root cells 675 on at least 10 independent roots were analysed. In the plots, the cross corresponds to the mean 676 value. Statistical analysis of fluorescence intensity was based on a paired T-test; * pVal<0,05; *** 677 pVal<0,0005. Detailed measurements are shown on supplementary Figures S10 and S12. (C) The Fiji 678 macro was not applicable to quantify actin fluorescence, because the high concentration of actin 679 filaments at the cortical region (asterisk) distorted the quantification of fluorescence. We thus 680 visually determined actin focalisation when a fluorescence patch (red arrow, delimited by a red 681 dashed line) was clearly visible at the contact site with the penetrating hyphae (black arrow). Among 682 15 root cells on 12 independent roots we determined a frequency of 11/15 events of actin 683 focalisation at penetration sites (see Supplementary Figure S13). BF, bright field. Scale bar=10 μm.