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Candidalysin is a fungal peptide toxin critical for mucosal infection

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Abstract
Cytolytic proteins and peptide toxins are classical virulence factors of several bacterial pathogens which disrupt epithelial barrier function, damage cells and activate or modulate host immune responses. Until now human pathogenic fungi were not known to possess such toxins. Here we identify the first fungal cytolytic peptide toxin in the opportunistic pathogen *Candida albicans*. This secreted toxin directly damages epithelial membranes, triggers a danger response signalling pathway and activates epithelial immunity. Toxin-mediated membrane permeabilization is enhanced by a positively charged C-terminus and triggers an inward current concomitant with calcium influx. *C. albicans* strains lacking this toxin do not activate or damage epithelial cells and are avirulent in animal models of mucosal infection. We propose the name ‘Candidalysin’ for this cytolytic peptide toxin; a newly identified, critical molecular determinant of epithelial damage and host recognition of the clinically important fungus, *C. albicans*.

Introduction
The ability of mucosal surfaces to discriminate between commensal and pathogenic microbes is essential to human health. The fungus *Candida albicans* is normally a benign member of the human microbiota but is also responsible for millions of mucosal infections each year in immunocompromised hosts, often with severe morbidity. A defining feature of *C. albicans* pathogenesis is the transition from yeast to invasive filamentous hyphae. Hyphae damage mucosal epithelia and induce activation of the activating protein-1 (AP-1) transcription factor c-Fos (via p38-MAPK) and the MAPK phosphatase MKP1 (via ERK1/2-MAPK), which trigger pro-inflammatory cytokine responses. These signaling events constitute a ‘danger response’ against invasive hyphae, thus serving as a sensor of pathogenic *C. albicans* invasion. However, it is unclear how *C. albicans* hyphae induce epithelial inflammatory responses and cell damage during mucosal infections. Here we identify and characterize Candidalysin, the first cytolytic peptide toxin isolated from any human fungal pathogen, as the hyphal factor critical for epithelial immune activation and *C. albicans* mucosal infection.

Ece1p is critical for epithelial activation and damage
Despite the well-known association between filamentation and virulence, the molecular mechanism underlying hypha-driven epithelial activation and mucosal damage has remained obscure. To elucidate this mechanism, we screened a panel of *C. albicans* gene deletion
mutants that targeted key processes, pathways and proteins known or predicted to be associated with the yeast-hyphal transition and pathogenicity (62 strains). Only hypha-producing strains induced MKP1 phosphorylation (p-MKP1), c-Fos, cytokines (IL-1α, IL-6, G-CSF) and damage in oral epithelial cells (Extended Data Table 1). However, one C. albicans mutant (ece1Δ/Δ)\textsuperscript{15} formed normal hyphae but was incapable of inducing these epithelial danger responses. C. albicans ECE1 (extent of cell elongation) is highly expressed by hyphae during epithelial infection (Extended Data Fig. 1a, b) and is predicted to encode a secreted protein\textsuperscript{16}. To probe its function we generated a panel of C. albicans ECE1-mutants (Extended Data Table 2). The ece1Δ/Δ strain formed normal hyphae on (Extended Data Fig. 1c), and adhered to and invaded human epithelial cells similarly to wild type C. albicans (Extended Data Fig. 1d, e). Indeed, ece1Δ/Δ was capable of extensive epithelial invasion, penetrating through multiple epithelial cells (Extended Data Fig. 1f). Despite this, invasive ece1Δ/Δ hyphae did not damage epithelia or induce p-MKP1/c-Fos mediated danger responses or cytokine secretion (Fig. 1a-d). Thus, Ece1p is critical for epithelial damage and innate recognition of C. albicans hyphae in vitro.

\textbf{Ece1p is critical for mucosal pathogenesis}

We next assessed the role of ECE1 in two \textit{in vivo} models of C. albicans mucosal infection. In murine oropharyngeal candidiasis (OPC)\textsuperscript{17}, mice infected with C. albicans wild type or ECE1 re-integrant (ece1Δ/Δ+ECE1) strains exhibited disease symptoms, including extensive hyphal invasion of the tongue epithelium, micro-abscesses of infiltrating neutrophils and tissue damage (Fig. 1e, f, h, i). In contrast, tongue tissue from ece1Δ/Δ-infected animals (n = 17/20) showed no invasive fungi and no inflammatory infiltrates or damage (Fig. 1g). We detected very low numbers of ece1Δ/Δ cells in only 3/20 mice (Extended Data Fig. 2a), which showed no evidence of local epithelial damage (not shown). Quantification of histology sections indicated that the percentage of epithelial surface infected was significantly greater with the wild type and ECE1 re-integrant strains (Extended Data Fig. 2b). In a zebrafish swimbladder model of mucosal infection\textsuperscript{18,19}, neutrophil recruitment and tissue damage were both significantly lower following ece1Δ/Δ infection as compared with the wild type strain (Fig. 1j, k, Extended Data Fig. 2c, d). Therefore, C. albicans Ece1p is critical for mucosal pathogenesis and is an innate immune activator \textit{in vivo}.

\textbf{Ece1p encodes a cytolytic peptide toxin}
Ece1p is an *in vitro* substrate for Kex2p, a Golgi-located protease that cleaves proteins after lysine-arginine (KR) motifs\(^\text{20}\). Ece1p contains seven KR-processing sites, suggesting it has the potential to produce eight secreted peptides from *C. albicans*\(^\text{20}\) (Extended Data Fig. 3a, b). Liquid chromatography – tandem mass spectrometry (LC-MS/MS) analysis confirmed that recombinant Kex2p (rKex2p) processes recombinant Ece1p (rEce1p) and that all eight peptides generated terminated in KR (and fragments thereof, showing that less efficient processing occurs also after a single K or R) (Supplementary information). The importance of Kex2p-mediated Ece1p processing was demonstrated using a *kex2Δ*/*Δ* null strain\(^\text{21}\), which was unable to damage oral epithelia or induce p-MKP1/c-Fos mediated danger responses or cytokine secretion (Extended Data Table 1). To determine which Ece1p peptide(s) were responsible for epithelial activation and damage, oral epithelial cells were incubated with peptides Ece1-I-VIII (1.5 – 70 \(\mu\)M). Only Ece1-III\(_{62-93}\) induced p-MKP1, c-Fos, cytokines and damage (Fig. 2a-c, Extended Data Fig. 3c-e). Notably, low Ece1-III\(_{62-93}\) concentrations (1.5 – 15 \(\mu\)M) were sufficient to induce c-Fos DNA binding (Fig. 2d), G-CSF and GM-CSF (Fig. 2c, Extended Data Fig. 3c), while high Ece1-III\(_{62-93}\) concentrations (70 \(\mu\)M) were required to induce damage (Fig. 2e) and the damage-associated cytokines IL-1\(\alpha\) and IL-6, respectively (Extended Data Fig. 3d, e). Ece1-III\(_{62-93}\) could also directly lyse multiple human epithelial cell types and induce hemolysis of red blood cells, a classical test for cytotoxin activity (not shown). Neither the N-terminal hydrophobic region (Ece1-III\(_{62-85}\)) nor the C-terminal hydrophilic region (Ece1-III\(_{86-93}\)) induced p-MKP1, c-Fos, cytokines or damage of epithelial cells, either individually or in combination (Extended Data Fig. 3f-h), demonstrating that the peptide containing both regions is required for activity. Therefore, Ece1-III\(_{62-93}\) is the active region of Ece1p, acting as an epithelial immune activator and a cytolytic agent.

To confirm that Ece1-III\(_{62-93}\) drives epithelial activation and fungal pathogenicity, we generated a *C. albicans* strain lacking only the Ece1-III\(_{62-93}\) region (*ece1Δ*/*Δ* + ECE1\(_{Δ184-279}\)). LC-MS/MS analysis showed that the modified protein in this strain is stable, secreted, and processed into each of the predicted peptide fragments, with the exception of the deleted peptide toxin (Supplementary information). Like *ece1Δ/Δ*, *ece1Δ/Δ* + ECE1\(_{Δ184-279}\) efficiently formed invasive hyphae (not shown). However, *ece1Δ/Δ* + ECE1\(_{Δ184-279}\) was unable to induce p-MKP1, c-Fos DNA binding, cytokines, or damage epithelia (Fig. 2f-i). In murine OPC, unlike the *ece1Δ/Δ* + ECE1 complemented strain, *ece1Δ/Δ* + ECE1\(_{Δ184-279}\)-infected mice demonstrated absent (n = 4/10) or low (n = 6/10) fungal burdens, with no evidence of inflammatory infiltrates or local epithelial damage (Fig. 2j-l, Extended Data Fig. 4a and 4b)
Likewise, ece1Δ/Δ+ECE1 Δ184-279 did not induce full damage in the zebrafish swimbladder model (Fig. 2m, Extended Data Fig. 4c). In contrast, injection of lytic doses of Ece1-III62-93 into the swimbladder induced epithelial damage (Fig. 2n, o). Thus, Ece1-III62-93 is both necessary and sufficient for epithelial immune activation, damage and mucosal infection in vivo. The amphipathic properties of Ece1-III62-93 (SIIGIIMGILGNIPQVIQIIMSIVKA FGNKR) coupled with the α-helical structure of the N-terminal hydrophobic region (Extended Data Fig. 5a, b) indicated that this fungal peptide may act similarly to cationic antimicrobial peptides and peptide toxins such as melittin22 (honey bee), magainin 223 (African clawed frog) and alamethicin24 (Trichoderma viride). Cytolytic peptide toxins have not previously been found in human pathogenic fungi but bacterial cytolytic toxins are known to induce lesions after binding to target cell membranes25,26. To investigate the importance of lipid composition for Ece1-III62-93-mediated cytolysis, we used Förster resonance energy transfer (FRET) and electrical impedance spectroscopy to analyze the interactions of Ece1-III62-93 with model membranes comprised of lipid bilayers of dioleoylphosphatidylcholine (DOPC) with or without cholesterol. While Ece1-III62-93 was able to efficiently intercalate into and permeabilize DOPC membranes, Ece1-III62-93 permeabilization was enhanced in the presence of cholesterol (Fig. 3a, Extended Data Fig. 5c). Ece1-III62-93-induced lesions were heterogeneous and transient (Extended Data Fig. 5d), indicating that the peptide may damage target membranes through a ‘carpet-like’ mechanism27. Patch-clamp analysis of epithelial cells demonstrated that lesion formation by Ece1-III62-93 is rapid and causes an inward current (Fig. 3b), associated with calcium influx (Fig. 3c). Similar phenomena occur with bacterial cytolytic toxins, which are known to trigger cell activation25,26,28.

We postulated that the positively-charged C-terminal KR residues of Ece1-III62-93 might be critical for interacting with negatively-charged components of host membranes to promote lesion formation. Substitution of the KR motif to AA (alanine-alanine; Ece1-III62-93AA) did not affect membrane intercalation (not shown) but significantly reduced the peptide’s ability to permeabilize membranes, damage epithelial cells and induce calcium influx (Fig. 3c-e). Thus, the positive C-terminus of Ece1-III62-93 is critical for lesion formation and damage induction in epithelial membranes. Notably, Ece1-III62-93AA still induced p-MKP1, c-Fos and the non-damage associated cytokine G-CSF (Fig. 3f, g) but not the damage-associated cytokine IL-1α (Fig. 3h), suggesting that Ece1-III62-93AA can be recognized by epithelial immunity without damaging cells. This finding is important as it means that epithelial cells are not only responding to damage but have evolved to specifically recognise the peptide.
Ece1-III<sub>62-92K</sub> is a secreted cytolytic peptide toxin

To demonstrate that Ece1-III is generated during epithelial infection, we performed LC-MS/MS analysis on the secretome from wild-type *C. albicans* hyphae grown in the presence and absence of epithelial cells (Supplementary information). Notably, Ece1-III was the only peptide detected in the presence of epithelial cells, indicating that the fungus secretes this toxin during mucosal infection. However, the predominant form of secreted Ece1-III terminated in a K residue (SIIGIIMGILGNIPQVIQIIMSIVKA FKGNK; Ece1-III<sub>62-92K</sub>) and not KR (SIIGIIMGILGNIPQVIQIIMSIVKA FKGNKR; Ece1-III<sub>62-93KR</sub>) (Extended Data Table 3). In fungi, it is known that following Kex2p processing, many proteins are subsequently cleaved by Kex1p<sup>29</sup> (also in the Golgi), removing the C-terminal R. LC-MS/MS analysis on the hyphal secretome of a *kex1*<sup>Δ/Δ</sup> mutant demonstrated that the predominant peptide secreted terminates in KR (not K) (Supplementary information). Therefore, Ece1p is also subject to ordered Kex2p/Kex1p processing. Accordingly, we confirmed that Ece1-III<sub>62-92K</sub> functioned similarly to Ece1-III<sub>62-93KR</sub> with respect to epithelial cell activation. Specifically, Ece1-III<sub>62-92K</sub> is also α-helical (not shown) and induces c-Fos, p-MKP1, cytokines (IL-1α, G-CSF), damage (LDH), membrane intercalation and permeabilization, and calcium influx (Fig 4a-g). Thus, the dominant peptide secreted from *C. albicans* hyphae during mucosal infection is Ece1-III<sub>62-92K</sub>, which acts as a cytolytic peptide toxin that activates epithelial cells.

Based on these data, we propose a model of *C. albicans* mucosal infection whereby invasive hyphae secrete Ece1-III<sub>62-92K</sub> into a membrane-bound ‘invasion pocket’<sup>30,31</sup>, facilitating peptide accumulation (Extended Data Fig 6). During early stages of infection, sub-lytic concentrations of Ece1-III<sub>62-92K</sub> induce epithelial immunity by activating the ‘danger response’ pathway (p-MKP1/c-Fos), alerting the host to the transition from colonizing yeast to invasive, toxin-producing hyphae. As infection progresses, Ece1-III<sub>62-92K</sub> levels accumulate and elicit direct tissue damage. Mechanistically, we propose that the asymmetric distribution of charge along the α-helix of Ece1-III<sub>62-92K</sub> facilitates correct peptide orientation relative to the host membrane, enabling intercalation, permeabilization and calcium influx. In conclusion, our data identifies *C. albicans* Ece1-III<sub>62-92K</sub> as the first cytolytic peptide toxin in a human fungal pathogen and reveals the molecular mechanisms of epithelial damage and host recognition of this clinically important fungus. We propose the name ‘Candidalysin’ for this newly discovered fungal toxin.
Supplementary Information is available in the online version of the paper.

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Author Contributions DLM, JPR, SXT, MR, CM, MB, SII, NK performed signaling, transcription factor, calcium and cytokine assays, and murine work; DW, SH, SM, TMF, BHe, LK AH, OB and OKu created fungal strains and performed fluorescent microscopy, adhesion, invasion, gene expression and damage assays; RLG and RTW performed zebrafish experiments; JW and TG performed biophysical analysis with artificial membranes; JR performed whole patch clamp analysis; GV performed electron microscopy; ST performed histological analysis; SM, TL, TK and OKn performed LC-MS analyses; JRN, BHu, DLM, JPR and DW wrote the paper; JRN, BHu and EC supervised the project.

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References


Figure Legends

Figure 1 | ECE1 is required for epithelial activation and C. albicans infection. TR146

cells were infected with the indicated C. albicans strains. (a) LDH release 24 h post-infection
(p.i.) (MOI = 0.1). (b) Induction of p-MKP-1 and c-Fos at 2 h p.i. (MOI = 10). (c) c-Fos
DNA binding at 3 h p.i. (MOI = 10). (d) G-CSF production at 24 h p.i. (MOI = 0.01). (e-i)
PAS-stained tongues from mice subjected to OPC 2 d p.i. (e, g, h) Whole-mount (x25) and (f, i)
high-power (x200) views of PAS-stained tongues of mice infected with C. albicans wild
type (e, f), ece1Δ/Δ (g) and ece1Δ/Δ+ECE1 (h, i). Invading hyphae (black arrow) and
inflammatory cells (blue arrow) are indicated. (j) Quantification of neutrophils in zebrafish
swimbladder following infection with WT C. albicans (n (number of fish) = 47), ece1Δ/Δ (n = 53) or PBS (n = 40). (k) Quantification of damaged cells in zebrafish swimbladder after
infection with C. albicans WT (n = 73), ece1Δ/Δ (n = 59) or vehicle (n = 63). Data are
representative (b, e-i) or the mean (a, c-d, j-k) of three biological replicates. Error bars ±
SEM. Data were analyzed by one-way ANOVA (a, d), paired T test (c) or Kruskal-Wallis (j, k) and * = P < 0.05, ** = P < 0.01, *** = P < 0.001. For gel source data, see Supplementary
Figure 1.

Figure 2 | Ece1-III62-93 is the active region of Ece1p and is required for TR146 cell
activation and mucosal C. albicans infection. (a) Induction of p-MKP-1 and c-Fos 2 h post-
stimulation (p.s.) with Ece1 peptides at 1.5 µM. (b) LDH release 24 h p.s. with 70 µM Ece1
peptides. (c) Induction of G-CSF 24 h p.s. of with Ece1-III62-93. (d) c-Fos DNA binding
induction 3 h p.s. with sub-lytic concentrations of Ece1-III62-93. (e) LDH release 24 h p.s. with
Ece1-III62-93. (f) Induction of p-MKP-1 and c-Fos 2 h post-infection (p.i.) with the indicated
C. albicans strains (MOI = 10). (g) c-Fos DNA binding induction 3 h p.i. with indicated C. albicans
strains (MOI = 0.1). (h) G-CSF secretion 24 h p.i. with indicated C. albicans strains
(MOI = 0.01). (i) LDH release 24 h p.i. with indicated C. albicans strains (MOI = 0.01). (j-l)
PAS stained tongue sections from mice subjected to OPC, 2 d p.i. with (j, k) C. albicans
ece1Δ/Δ+ECE1 (x25 and x200) or (l) ece1Δ/Δ+ECE1Δ184-279. Invading hyphae (black
arrows) and infiltrating inflammatory cells (blue arrow) are shown. (m) Damaged cells in a
zebrafish swimbladder 24 h p.i. with C. albicans ece1Δ/Δ+ECE1 (n (number of fish) = 44),
ece1Δ/Δ+ECE1Δ184-279 (n = 58) or vehicle (n = 58). (n) Damaged cells in zebrafish
swimbladders after stimulation with 9 ng (n = 51) or 1.25 ng (n = 56) Ece1-III62-93, or vehicle
(40% DMSO, n = 54 and 5% DMSO, n = 55). (o) Co-localization of adherens junctions (α-
catenin-citrine) with Ece1-III62-93-damaged cells (Sytox Orange-positive cells) in a zebrafish swimbladder. Data are representative (a, f, j-l, o) or mean (b-e, g-i, m-n) of three biological replicates (a-m) or ten fish (o). Error bars show ± SEM. Data were analyzed by one-way ANOVA (b, c, e, h, i) paired T test (d, g) or Kruskal-Wallis (m,n). * = P < 0.05, ** = P < 0.01, *** = P < 0.001 (compared with vehicle control unless otherwise indicated). For gel source data, see Supplementary Figure 1.

**Figure 3** | Ece1-III62-93 functions as a cytolytic peptide toxin. (a) Kinetic changes in conductance of tethered lipid membranes after exposure to different concentrations of Ece1-III62-93. (b) Evoked inward current at a membrane potential of -60 mV in TR146 cells post-addition of Ece1-III62-93 or ionomycin (positive control); individual (representative) and cumulative changes (bar chart - number of cells analysed below each bar) shown. (c) Intracellular calcium level kinetics in TR146 cells post-stimulation (p.s.) with Ece1-III62-93 wild type (Ece1-III62-93KR) or Ece1-III62-93 AA C-terminal substitution (Ece1-III62-93AA). (d) Kinetic changes in conductance of tethered DOPC membranes after exposure to different concentrations of Ece1-III62-93. (e) LDH release from TR146 cells 24 h p.s. with Ece1-III62-93KR or Ece1-III62-93AA. (f) Induction of p-MKP-1 and c-Fos 2 h in TR146 cells p.s. with Ece1-III62-93KR or Ece1-III62-93AA. (g) G-CSF and (h) IL-1α from TR146 cells 24 h p.s. with Ece1-III62-93KR or Ece1-III62-93AA. Data shown are representative (a, d, f) or mean (b-c, e, g-h) of three biological replicates. Error bars show ± SEM. Data were analyzed by one-way ANOVA (e, g and f) and * = P < 0.05, ** = P < 0.01, *** = P < 0.001. For gel source data, see Supplementary Figure 1.

**Figure 4** | Ece1-III62-92K functions as a cytolytic peptide toxin that activates and damages epithelial cells. (a) Induction of p-MKP-1 and c-Fos 2 h post-stimulation (p.s.), and (b) secretion of G-CSF and IL-1α 24 h p.s., and (c) LDH release 24 h p.s. of TR146 cells with Ece1-III62-92K. (d) Förster resonance energy transfer (FRET) showing intercalation of Ece1-III62-92K (10 µM) into lipid liposomes. (e) Average peptide concentration-dependent changes in conductance of tethered lipid membranes. (f) Ece1-III62-92K (4 µM) induced permeabilization of planar lipid membranes showing heterogeneous and transient lesions leading to membrane rupture. (g) Intracellular calcium level kinetics in TR146 cells p.s. with Ece1-III62-92K. Data shown are representative (a, d, f) or mean (b-c, e, g) of three biological replicates. Error bars show ± SEM. Data are analyzed by one-way ANOVA (b, c). * = P <
0.05, ** = \( P < 0.01 \), *** = \( P < 0.001 \) (compared with vehicle control). For gel source data, see Supplementary Figure 1.

**Extended Data Figure legends**

**Extended Data Figure 1** | *C. albicans* ECE1 expression and phenotypic effects of ECE1 gene deletion. (a) Relative expression (vs \( t = 0 \)) of ECE1 in *C. albicans* wild type over time after addition of yeast cells to TR146 epithelial cells as measured by RT-qPCR. (b) Imaging confirmation of ECE1 expression over time within *C. albicans* wild type. *C. albicans* cells expressing GFP under the control of the ECE1 5′ intragenic region, containing the ECE1 promoter, were grown on TR146 epithelial cells and stained with calcofluor white (CFW, post-permeabilization) to show cell wall chitin and Alexa-Fluor-647-labelled concanavalin A (ConA, pre-permeabilization) to show carbohydrates. A composite image showing CFW, ConA, GFP and the brightfield (BF) image is shown. (c) Scanning electron micrographs (top panels, 5 h) and light microscopy (bottom panels, 24 h) showing no gross abnormalities in hypha formation between *C. albicans* wild type (BWP17+Clp30), ECE1-deletion (ece1Δ/Δ) and ECE1 re-integrant (ece1Δ/Δ+ECE1) strains after infection of TR146 epithelial cells. (d) No difference in adhesion of *C. albicans* wild type, ece1Δ/Δ and ece1Δ/Δ+ECE1 strains to TR146 epithelial cells after 60 min. (e) No difference in invasion of *C. albicans* wild type, ece1Δ/Δ and ece1Δ/Δ+ECE1 strains into TR146 epithelial cells after 3 h. (f) Fluorescence staining of *C. albicans* wild type and ece1Δ/Δ hyphae invading through TR146 epithelial cells. Fungal cells are stained with calcofluor white (CFW, post-permeabilization) and Alexa-Fluor-647-labelled concanavalin A (ConA, pre-permeabilization) to show cell wall chitin and carbohydrates, respectively, and to distinguish between invading hyphae (only stained after permeabilization) and non-invading hyphae (stained both pre- and post-permeabilization). Levels of chitin and β-glucan are comparable in both strains. White arrows indicate invasion into epithelial cells. Data shown are representative (b, c, f) or the mean (a, d, e) of three biological replicates. Error bars show ± SEM.

**Extended Data Figure 2** | *C. albicans* Ece1p is critical for mucosal virulence *in vivo*. (a) Fungal burdens recovered from the tongues of mice infected with *C. albicans* wild type (BWP17+Clp30) (n = 13), ECE1-deletion (ece1Δ/Δ) (n (number of mice) = 20) and ECE1 re-integrant (ece1Δ/Δ+ECE1) (n = 24) strains after 2 day oropharyngeal infection. (b) Average
percentage of the entire tongue epithelium area infected in different groups of mice infected with the different *C. albicans* strains. (c) Confocal imaging of 4 day post-fertilization (dpf) *mpo-gfp* transgenic zebrafish swimbladders infected with *C. albicans* wild type (BWP17+Clp30+dTomato), *ECE1*-deletion (*ece1Δ/Δ+dTomato*) and *ECE1* re-integrant (*ece1Δ/Δ+ECE1+dTomato*) strains for 24 h. *C. albicans* cells appear red whilst neutrophils appear green. Red dots outline the swimbladder. Images are composites of maximum projections in the red and green channels (25 slices each, approximately 100 μm depth) with (left) or without (right) a single slice in the DIC channel overlay. Scale bars represent 100 μm. (d) Confocal imaging of 4 dpf zebrafish swimbladders infected with *C. albicans* wild type (BWP17+Clp30+dTomato), *ECE1*-deletion (*ece1Δ/Δ+dTomato*) and *ECE1* re-integrant (*ece1Δ/Δ+ECE1+dTomato*) strains for 24 h stained with the fluorescent exclusion dye Sytox Green. *C. albicans* cells appear red and damaged epithelial cells appear green. White dots outline the pronephros and red dots outline the swimbladder. Images are composites of maximum projections in the red and green channels (25 slices each, approximately 100 μm depth) with (left) or without (right) a single slice in the DIC channel overlay. High magnification images of the white boxes are shown. Scale bars (bottom right) represent 100 μm (low magnification) and 30 μm (high magnification). Data shown are the mean (a, b) or representative (c, d) of at least three biological replicates. Error bars show ± SEM. Data were analyzed by Mann-Whitney test. *** = P < 0.001.

Extended Data Figure 3 | *Ece1-III*62-93 is the active region of Ece1p. (a) Amino acid sequence of Ece1p and a schematic of the protein, indicating the signal peptide (SP), lysine-arginine motifs (KR) at the C-terminus of each peptide, and the processed peptides (*Ece1-I-VIII*) produced by Kex2p cleavage. (b) Amino acid sequences of the processed peptides (*Ece1-I-VIII*) produced by Kex2p cleavage. Induction of (c) GM-CSF, (d) IL-1α and (e) IL-6 secreted after stimulation of TR146 epithelial cells for 24 h with varying concentrations of *Ece1-III*62-93 (70 μM - 1.5 μM). (f) Phosphorylation of MKP-1 and c-Fos production after 2 h treatment of TR146 epithelial cells with 15 μM of *Ece1-III*62-85 (hydrophobic region), *Ece1-III*86-93 (hydrophillic region), *Ece1-III*62-85 and *Ece1-III*86-93 together, or *Ece1-III*62-93 alone. (g) Induction of G-CSF secretion after 24 h treatment of TR146 epithelial cells with 15 μM of *Ece1-III*62-85, *Ece1-III*86-93, *Ece1-III*62-85 and *Ece1-III*86-93 together, or *Ece1-III*62-93 alone. (h) Fold change induction of LDH release after 24 h treatment of TR146 epithelial cells with 70 μM of *Ece1-III*62-85, *Ece1-III*86-93, *Ece1-III*62-85 and *Ece1-III*86-93 together, or *Ece1-III*62-93 alone. Data shown are representative (f) or the mean (c-e, g-h) of three biological replicates.
Error bars show ± SEM. Data were analyzed by one-way ANOVA. * = $P < 0.05$, ** = $P < 0.01$, *** = $P < 0.001$ (compared with vehicle control). For gel source data, see Supplementary Figure 1.

Extended Data Figure 4 | Ece1-III$_{62-93}$ is required for *C. albicans* mucosal infection. (a) Fungal burdens recovered from the tongues of mice infected with *C. albicans* wild type (BWP17+Clp30) (n = 13), ECE1-deletion (ece1Δ/Δ) (n = 20), ECE1 re-integrant (ece1Δ/Δ+ECE1) (n = 24) and Ece1-III$_{62-93}$ deletion (ece1Δ/Δ+ECE1$_{A184-279}$) (n = 10) strains after 2 day oropharyngeal infection. (b) Average percentage of the entire tongue epithelium area infected in different groups of mice infected with the different *C. albicans* strains. (c) Confocal imaging of 4 dpf zebrafish swimbladders infected with *C. albicans* Ece1-III$_{62-93}$ deletion (ece1Δ/Δ+ECE1$_{A184-279}$+dTomato) and ECE1 re-integrant (ece1Δ/Δ+ECE1+dTomato) strains for 24 h stained with the fluorescent exclusion dye Sytox Green. *C. albicans* cells appear red and damaged cells appear green. White dots outline the pronephros and red dots outline the swimbladder. Images are composites of maximum projections in the red and green channels (25 slices each, approximately 100 µm depth) with (left) or without (right) a single slice in the DIC channel overlay. Scale bars (bottom right) represent 100 µm. Data shown are the mean (a) or representative (b, c) of at least three biological replicates. Error bars show ± SEM. Data were analyzed by Mann-Whitney test. ** = $P < 0.01$, *** = $P < 0.001$.

Extended Data Figure 5 | Ece1-III$_{62-93}$ is a cytolytic α-helical peptide. (a) Circular dichroism spectra showing the α-helical conformation of Ece1-III$_{62-93}$ in buffer (100 mM KCl, 5 mM HEPES, pH 7). Increasing the temperature from 25°C to 40°C did not affect the stability of the α-helical structure. (b) Diagram to illustrate the amphipathic nature of Ece1-III$_{62-93}$ (residues 62-78, left panel; residues 79-93, right panel). Residues with hydrophobic or polar/charged side chains are displayed with a blue and white background, respectively. Modified from output generated in PEPWHEEL (http://emboss.bioinformatics.nl/cgi-bin/emboss/pepwheel). (c) Förster resonance energy transfer (FRET) experiments show the intercalation of Ece1-III$_{62-93}$ into lipid liposomes (10 µM) composed of DOPC in the absence or presence of cholesterol. Peptide titration of Ece1-III$_{62-93}$ to liposomes showed slightly enhanced intercalation for pure DOPC. (d) Ece1-III$_{62-93}$ induced the permeabilization of planar lipid membranes composed of DOPC. The graph shows heterogeneous and transient
lesions leading finally to a rupture of the membrane. Ece1-III<sub>62-93</sub> concentration was 0.125 µM. Data shown are representative of at least three biological replicates.

**Extended Data Figure 6| Schematic of the role of Ece1-III in *C. albicans* infection of epithelial cells.** During early stage infection of the mucosal surface by *C. albicans*, Ece1-III (red α-helix) is secreted into the invasion pocket created by the invading hypha (a). Sub-lytic concentrations of Ece1-III trigger epithelial signal transduction through MAPK, p38/MKP-1 and c-Fos (b) resulting in the production of immune regulatory cytokines (c). As the severity of the infection increases, Ece1-III accumulates (d) and once lytic concentrations are reached, causes membrane damage and the release of lactate dehydrogenase from the host epithelium (e), concomitant with calcium influx (f). Epithelial signal transduction is maintained (g) and additionally induces the release of damage associated cytokines, such as IL-1α (h). Ece1-III may also have activity on the epithelial surface outside of the invasion pocket and on neighbouring cells not in contact with hyphae if Ece1-III is produced in sufficient concentrations.
METHODS

Cell lines, reagents and Candida strains

Experiments were carried out using the TR146 buccal epithelial squamous cell carcinoma line\textsuperscript{32} obtained from the European Collection of Authenticated Cell Cultures (ECACC) and grown in Dulbecco's Modified Eagle's Medium (DMEM, Sigma-Aldrich) supplemented with 10\% fetal bovine serum (FBS) and 1\% penicillin-streptomycin. Cells were routinely tested for mycoplasma contamination using mycoplasma-specific primers and were found to be negative. Prior to stimulation, confluent TR146 cells were serum-starved overnight, and all experiments were carried out in serum-free DMEM. \textit{C. albicans} wild type strains included the autotrophic strain BWP17+CIp30\textsuperscript{33} and the parental strain SC5314\textsuperscript{34}. Other \textit{C. albicans} strains used and their sources are listed in Extended Data Tables 1 and 2. \textit{C. albicans} cultures were grown in YPD medium (1\% yeast extract, 2\% peptone, 2\% dextrose) at 30°C overnight. Cultures were washed in sterile PBS and adjusted to the required cell density. Antibodies to phospho-MKP1 and c-Fos were from Cell Signalling Technologies (New England Biolabs UK), mouse anti-human \textalpha-actin was from Millipore (UK), and goat anti-mouse and anti-rabbit horseradish peroxidase (HRP)-conjugated antibodies were from Jackson Immunologicals Ltd (Stratech Scientific, UK). Ece1p peptides were synthesized commercially (Proteogenix (France) or Peptide Synthetics (UK).

Generation of \textit{C. albicans} ECE1 mutant strains

\textit{ECE1} deletion was performed as previously described\textsuperscript{35}. Deletion cassettes were generated by PCR\textsuperscript{36}. Primers ECE1-FG and ECE1-RG were used to amplify pFA-HIS1 and pFA-ARG4-based markers. \textit{C. albicans} BWP17\textsuperscript{37}, was sequentially transformed\textsuperscript{38} with the \textit{ECE1}-HIS1 and \textit{ECE1}-ARG4 deletion cassettes and then transformed with Clp10\textsuperscript{39}, yielding the \textit{ece1}\textsubscript{\textDelta/\textDelta} deletion strain. For complementation, the \textit{ECE1} gene plus upstream and downstream intergenic regions were amplified with primers ECE1-RecF3k and ECE1-RecR and cloned into plasmid Clp10 at \textit{MluI} and \textit{SalI} sites. This plasmid was transformed into the uridine auxotrophic \textit{ece1}\textsubscript{\textDelta/\textDelta} strain, yielding the \textit{ece1}\textsubscript{\textDelta/\textDelta+\textit{ECE1}} complemented strain. For generation of the \textit{ece1}\textsubscript{\textDelta/\textDelta+\textit{ECE1}\textsubscript{\textDelta184-279}} strain, the Clp10-\textit{ECE1} was amplified with primers Pep3-F1 and Pep3-R1, digested with ClaI and re-ligated, yielding the Clp10+\textit{ECE1}\textsubscript{\textDelta184-279} plasmid. This plasmid was transformed into the uridine auxotrophic \textit{ece1}\textsubscript{\textDelta/\textDelta} strain, yielding the \textit{ece1}\textsubscript{\textDelta/\textDelta+\textit{ECE1}\textsubscript{\textDelta184-279}} strain. All integrations were confirmed by PCR/sequencing and at least two independent isogenic transformants were created to confirm results. \textit{KEX1} deletion
was performed exactly as the ECE1 deletion but using primers KEX1-FG and KEX1-RG for creating the deletion cassette. Fluorescent strains of ece1Δ/Δ and BWP17 were constructed as previously described 40. Briefly, the ece1Δ/Δ and BWP17 strains were transformed with the pENO1-dTom-NATr plasmid. Primers used to clone and construct the ECE1 genes and intragenic regions are listed in Extended Data Table 4. Strains are listed in Extended Data Table 2.

**Construction of C. albicans ECE1 promoter-GFP strain**

ECE1 promoter (primers 5'ECE1prom-NarI / 3'ECE1prom-XhoI) and terminator (5'ECE1term-SacII / 5'ECE1term-SacI) were amplified and cloned into pADH1-GFP. Resulting pSK-pECE1-GFP was verified by sequencing. C. albicans SC5314 was transformed with the pECE1-GFP transformation cassette 38. Resistance to nourseothricin was used as selective marker and correct integration of GFP into the ECE1 locus was verified by PCR. Primers for cloning and validation are listed in Extended Data Table 4. Strains are listed in Extended Data Table 2.

**RNA isolation and real-time PCR analysis**

C. albicans cells grown on TR146 epithelial cells were collected into RNA pure (PeqLab), centrifuged and the pellet resuspended in 400 µl AE buffer (50 mM Na-acetate pH 5.3, 10 mM EDTA, 1% SDS). Samples were vortexed (30 s), and an equal volume of phenol/chloroform/isoamyl alcohol (25:24:1) was added and incubated for 5 min (65°C) before subjected to 2x freeze-thawing. Lysates were clarified by centrifugation and the RNA precipitated with isopropyl alcohol/0.3 M sodium acetate by incubating for 1 h at -20°C. Precipitated pellets were washed (2x 1 ml 70% ice-cold ethanol), resuspended in DEPC-treated water and stored at -80°C. RNA integrity and concentration was confirmed using a Bioanalyzer (Agilent). RNA (500 ng) was treated with DNase (Epicenter) and cDNA synthesized using Reverse Transcriptase Superscript III (Invitrogen). cDNA samples were used for qPCR with EVAgreen mix (Bio&Sell). Primers (ACT1-F and ACT1-R for actin, ECE1-F and ECE1-R for ECE1 - Extended Data Table 4) were used at a final concentration of 500 nM. qPCR amplifications were performed using a Biorad CFX96 thermocycler. Data was evaluated using Bio-Rad CFX Manager 3.1 (Bio-Rad) with ACT1 as the reference gene and t0 as the control sample.

**Western blotting**
TR146 cells were lysed using a modified RIPA lysis buffer (50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1 mM EDTA, 1% Triton X-100, 1% sodium deoxycholate, 0.1% SDS) containing protease (Sigma-Aldrich) and phosphatase (Perbio Science) inhibitors, left on ice (30 min) and then clarified (10 min) in a refrigerated microfuge. Lysate total protein content was determined using the BCA protein quantitation kit (Perbio Science). 20 µg of total protein was separated on 12% SDS-PAGE gels before transfer to nitrocellulose membranes (GE Healthcare). After probing with primary (1:1000) and secondary (1:10,000) antibodies, membranes were developed using Immobilon chemiluminescent substrate (Millipore) and exposed to X-Ray film (Fuji film). Human α-actin was used as a loading control.

**Transcription factor DNA binding assay**

DNA binding activity of transcription factors was assessed using the TransAM transcription factor ELISA system (Active Motif) as previously described. Serum-starved TR146 epithelial cells were treated for 3 h before being differentially lysed to recover nuclear proteins using a nuclear protein extraction kit (Active Motif) according to the manufacturer’s protocol. Protein concentration was determined (BCA protein quantitation kit (Perbio Science)) and 5 µg of nuclear extract was assayed in the TransAM system according to the manufacturer’s protocol. Data was expressed as fold-change in $A_{450nm}$ relative to resting cells.

**Cytokine determination**

Cytokine levels in cell culture supernatants were determined using the Performance magnetic Fluorokine MAP cytokine multiplex kit (Bio-techne) and a Bioplex 200 machine. The data were analyzed using Bioplex Manager 6.1 software to determine analyte concentrations.

**Cell damage assay**

Following incubation, culture supernatant was collected and assayed for lactate dehydrogenase (LDH) activity using the Cytox 96 Non-Radioactive Cytotoxicity Assay kit (Promega) according to the manufacturer’s instructions. Recombinant porcine LDH (Sigma-Aldrich) was used to generate a standard curve.

**Epithelial adhesion assay**

Quantification of *C. albicans* adherence to TR146 epithelial cells was performed as described previously. Briefly, TR146 cells were grown to confluence on glass coverslips for 48 h in tissue culture plates in DMEM medium. *C. albicans* yeast cells ($2 \times 10^5$) were added into 1
ml serum-free DMEM, incubated for 60 min (37°C/5% CO₂) and non-adherent C. albicans cells removed by aspiration. Following washing (3x 1 ml PBS), cells were fixed with 4% paraformaldehyde (Roth) and adherent C. albicans cells stained with Calcofluor White and quantified using fluorescence microscopy. The number of adherent cells was determined by counting 100 high power fields of 200 µm × 200 µm size. Exact total cell numbers were calculated based on the quantified areas and the total size of the cover slip.

**Epithelial invasion assay**

*C. albicans* invasion of epithelial cells was determined as described previously. Briefly, TR146 epithelial cells were grown to confluence on glass coverslips for 48 h and then infected with *C. albicans* yeast cells (1×10⁵), for 3 h in a humidified incubator (37°C/5% CO₂). Following washing (3x PBS), the cells were fixed with 4% paraformaldehyde. All surface adherent fungal cells were stained for 1 h with a rabbit anti-*Candida* antibody and subsequently with a goat anti-rabbit-Alexa Fluor 488 antibody. After rinsing with PBS, epithelial cells were permeabilized (0.1% Triton X-100 in PBS for 15 min) and fungal cells (invading and non-invading) were stained with Calcofluor White. Following rinsing with water, coverslips were visualized using fluorescence microscopy. The percentage of invading *C. albicans* cells was determined by dividing the number of (partially) internalized cells by the total number of adherent cells. At least 100 fungal cells were counted on each coverslip.

**Imaging of *C. albicans* growth and invasion of epithelial cells**

TR146 cells (10⁵/ml) seeded on glass coverslips in DMEM/10% FBS were infected with *C. albicans* (2.5 x 10⁴ cfu/ml) in DMEM and incubated for 6 h (37°C/5% CO₂). Cells were washed with PBS, fixed overnight (4°C in 4% paraformaldehyde) and stained with Concanavalin A-Alexa Fluor 647 in PBS (10 µg/ml) for 45 min at room temperature in the dark with gentle shaking (70 rpm) to stain the fungal cell wall. Epithelial cells were permeabilised with 0.1% Triton X-100 for 15 min at 37°C in the dark, then washed and stained with 10 µg/ml Calcofluor White (0.1 M Tris-HCl pH 9.5) for 20 min at room temperature in the dark with gentle shaking. Cells were rinsed in water and mounted on slides with 6 µl of ProLong Gold anti-fade reagent, before air drying for 2 h in the dark. Fluorescence microscopy was performed on a Zeiss Axio Observer Z1 microscope, and 5 phase images were taken per picture.
Scanning Electron Microscopy

For scanning electron microscopy (SEM) analysis, TR146 cells were grown to confluence on Transwell inserts (Greiner) and serum starved overnight in serum-free DMEM. After 5 h of *C. albicans* incubation on epithelial cells at an MOI of 0.01, cell media was removed and samples were fixed overnight at 4°C with 2.5% (v/v) glutaraldehyde in 0.05 M HEPES buffer (pH 7.2) and post-fixed in 1% (w/v) osmium tetroxide for 1 h at room temperature. After washing, samples were dehydrated through a graded ethanol series before being critical point dried (Polaron E3000, Quorum Technologies Ltd). Dried samples were mounted using carbon double side sticky discs (TAAB) on aluminium pins (TAAB) and gold coated in an Emitech K550X sputter coater (Quorum Technologies Ltd). Samples were examined and images recorded using a FEI Quanta 200 field emission scanning electron microscope operated at 3.5 kV in high vacuum mode.

Zebrafish swimbladder mucosal infection model

Zebrafish infections were performed in accordance with NIH guidelines under Institutional Animal Care and Use Committee (IACUC) protocol A2009-11-01 at the University of Maine. To determine sample size, a power calculation was done for all experiments based on 2-tails T-test in order to detect a minimum effect size of 0.8, with an alpha error probability of 0.05 and a power (1 – beta error probability) of 0.95. This gave a minimum number of 42 fish for each group. The fish selected for the experiments were randomly assigned to the different groups by picking them from a pool without bias and the groups were injected in different orders. No blinding was used to read the results. Ten to twenty zebrafish per group per experiment were maintained at 33°C in E3 + PTU and used as previously described. Briefly, 4 day post-fertilization (dpf) larvae were treated with 20 μg/ml dexamethasone dissolved in 0.1% DMSO 1 h prior to infection and thereafter. For tissue damage and neutrophil recruitment, individual AB or *mpo:GFP* fish (respectively) were injected into the swimbladder with 4 nl of PBS with/without 25-40 *C. albicans* yeast cells of *ece1Δ/Δ-dTomato, ece1Δ/Δ+ECE1+dTomato, ece1Δ/Δ+ECE1Δ184-279+dTomato or BWP17-dTomato.

For tissue damage, 1 nl of Sytox green (0.05 mM in 1% DMSO) was injected at 20 h post-infection into the swimbladder and fish were imaged by confocal microscopy at 24 h post-infection. For neutrophil recruitment, fish were imaged at 24 h post-injection. For synthetic peptide damage, AB or *α-catelin:citrine* fish were injected with 2 nl of peptide (9 ng or 1.25 ng per fish) or vehicle (40% DMSO or 5% DMSO) + SytoxGreen (0.05 mM in 1% DMSO) or SytoxOrange (0.5 mM in 10% DMSO) and the fish imaged by confocal
microscopy 4 h later. Numbers of neutrophils and damaged cells observed were counted and tabulated for each fish.

**Zebrafish swimbladder fluorescence microscopy**

Live zebrafish imaging was carried out as previously described. Briefly, fish were anesthetized in Tris-buffered Tricaine (200 μg/ml, Western Chemicals) and further immobilized in a solution of 0.4% low-melting-point agarose (LMA, Lonza) in E3 + Tricaine in a 96-well plate glass-bottom imaging dish (Greiner Bio-On). Confocal imaging was carried out using an Olympus IX-81 inverted microscope with an FV-1000 laser scanning confocal system (Olympus). Images were collected and processed using Fluoview (Olympus) and Photoshop (Adobe Systems Inc.). Panels are either a single slice for the differential interference contrast channel (DIC) with maximum projection overlays of fluorescence image channels (red-green), or maximum projection overlays of fluorescence channels. The number of slices for each maximum projection is specified in the legend of individual figures.

**Murine oropharyngeal candidiasis model**

Murine infections were performed under UK Home Office Project Licence PPL 70/7598 in dedicated animal facilities at King's College London. No statistical method was used to pre-determine sample size. No method of randomization was used to allocate animals to experimental groups. Mice in the same cage were part of the same treatment. The investigators were not blinded during outcome assessment. A previously described murine model of oropharyngeal candidiasis using female Balb/c mice was modified for investigating early infection events. Briefly, mice were treated sub-cutaneously with 3 mg/mouse (in 200 μl PBS with 0.5% Tween 80) of cortisone acetate on days -1 and 1 post-infection. On day 0, mice were sedated for ~75 min with an intra-peritoneal injection of 110 mg/kg ketamine and 8 mg/kg xylazine, and a swab soaked in a 10^7 cfu/ml *C. albicans* yeast culture in sterile saline was placed sub-lingually for 75 min. After 2 days, mice were sacrificed, the tongue excised and divided longitudinally in half. One half was weighed, homogenized and cultured to derive quantitative *Candida* counts. The other half was processed for histopathology and immunohistochemistry.

**Immunohistochemistry of murine tissue**
C. albicans infected murine tongues were fixed in 10% (v/v) formal-saline before being embedded and processed in paraffin wax using standard protocols. For each tongue, 5 µm sections were prepared using a Leica RM2055 microtome and silane coated slides. Sections were dewaxed using xylene, before C. albicans and infiltrating inflammatory cells were visualized by staining using Periodic Acid-Schiff (PAS) stain and counterstaining with haematoxylin. Sections were then examined by light microscopy. Histological quantification of infection was undertaken by measuring the area of infected epithelium and expressed as a percentage relative to the entire epithelial area.

**Whole cell patch clamp**

TR146 epithelial cells were grown in 35 mm petri dishes (Nunc) for 48 h before recordings at low cell density (10-30% confluence). Cells were superfused with a modified Krebs solution (120 mM NaCl, 3 mM KCl, 2.5 mM CaCl₂, 1.2 mM MgCl₂, 22.6 mM NaHCO₃, 11.1 mM glucose, 5 mM HEPES pH 7.4). Isolated cells were recorded at room temperature (21-23°C) in whole cell mode using microelectrodes (5-7 MΩ) containing 90 mM potassium acetate, 20 mM KCl, 40 mM HEPES, 3 mM EGTA, 3 mM MgCl₂, 1 mM CaCl₂ (free Ca²⁺ 40 nM), pH 7.4. Cells were voltage clamped at -60 mV using an Axopatch 200A amplifier (Axon Instruments) and current/voltage curves were generated by 1 s steps between -100 to + 50 mV. Treatments were applied to the superfusate to produce the final required concentration, with vehicle controls similarly applied. Data was recorded using Clampex software (Pclamp 6, Axon Instrument) and analyzed with Clampfit 10.

**Calcium flux**

TR146 cells were grown in a 96-well plate overnight until confluent. The medium was removed and 50 µl of a Fura-2 solution (5 µl Fura-2 (Life Technologies)(2.5 mM in 50% Pluronic F-127 (Life technologies):50% DMSO), 5 µl probenecid (Sigma) in 5 ml saline solution (NaCl (140 mM), KCl (5 mM), MgCl₂ (1 mM), CaCl₂ (2 mM), Glucose (10 mM) and HEPES (10 mM), adjusted to pH 7.4)) was added and the plate incubated for 1 h at 37°C/5% CO₂. The Fura-2 solution was replaced with 50 µl saline solution and baseline fluorescence readings (excitation 340 nm/emission 520nm) taken for 10 min using a FlexStation 3 (Molecular Devices). Ece1 peptides were added at different concentrations and readings immediately taken for up to 3 h. The data was analyzed using Softmax Pro software to determine calcium present in the cell cytosol and expressed as the ratio between excitation and emission spectra.
Impedance spectroscopy of tethered bilayer lipid membranes (tBLMs)

Tethered bilayer lipid membranes (tBLMs) with 10% tethering lipids and 90% spacer lipids (T10 slides) were formed using the solvent exchange technique\textsuperscript{46,47} according to the manufacturer’s instructions (SDx Tethered Membranes Pty Ltd, Sydney, Australia). Briefly, 8 µl of 3 mM lipid solutions in ethanol were added, incubated for 2 min and then 93.4 µl buffer (100 mM KCl, 5 mM HEPES, pH 7.0) was added. After rinsing 3x with 100 µl buffer the conductance and capacitance of the membranes were measured for 20 min before injection of Ece1 peptides at different concentrations. All experiments were performed at room temperature. Signals were measured using the tethaPod (SDx Tethered Membranes Pty Ltd, Sydney, Australia).

FRET intercalation experiments

Intercalation of Ece1 peptides into phospholipid liposomes was determined by FRET spectroscopy applied as a probe-dilution assay\textsuperscript{48}. Phospholipids mixed with each 1% (mol/mol) of the donor dye NBD-phosphatidylethanolamine (NBD-PE) and of the acceptor dye rhodamine-PE, were dissolved in chloroform, dried, solubilized in 1 ml buffer (100 mM KCl, 5 mM HEPES, pH 7.0) by vortexing, sonicated with a titan tip (30 W, Branson sonifier, cell disruptor B15), and subjected to three cycles of heating to 60°C and cooling down to 4°C, each for 30 min. Lipid samples were stored at 4°C for at least 12 h before use. Ece1 peptide was added to liposomes and intercalation was monitored as the increase of the quotient between the donor fluorescence intensity $I_D$ at 531 nm and the acceptor intensity $I_A$ at 593 nm (FRET signal) independent of time.

Circular Dichroism spectroscopy

CD measurements were performed using a Jasco J-720 spectropolarimeter (Japan Spectroscopic Co., Japan), calibrated as described previously\textsuperscript{49}. CD spectra represent the average of four scans obtained by collecting data at 1 nm intervals with a bandwidth of 2 nm. The measurements were performed in 100 mM KCl, 5 mM HEPES, pH 7.0 at 25°C and 40°C in a 1.0 mm quartz cuvette. The Ece1-III concentration was 15 µM.

Planar lipid bilayers

Planar lipid bilayers were prepared using the Montal-Mueller technique\textsuperscript{50} as described previously\textsuperscript{51}. All measurements were performed in 5 mM HEPES, 100 mM KCl, pH 7.0 (specific electrical conductivity 17.2 mS/cm) at 37°C.
Hyphal secretome preparation for LC-MS/MS analysis

*Candida* strains were cultured for 18 h in hyphae inducing conditions (YNB medium containing 2% sucrose, 75 mM MOPS buffer pH 7.2, 5 mM N-acetyl-D-glucosamine, 37°C). Hyphal supernatants were collected by filtering through a 0.2 µm PES filter, and peptides were enriched by Solid Phase Extraction (SPE) using first C4 and subsequently C18 columns on the C4 flowthrough. After drying in a vacuum centrifuge, samples were resolubilised in loading solution (0.2% formic acid in 71:27:2 ACN/H₂O/DMSO (v/v/v)) and filtered through a 10 kDa MWCO filter. The filtrate was transferred into HPLC vials and injected into the LC-MS/MS system. LC-MS/MS analysis was carried out on an Ultimate 3000 nano RSLC system coupled to a QExactive Plus mass spectrometer (ThermoFisher Scientific). Peptide separation was performed based on a direct injection setup without peptide trapping using an Accucore C4 column as stationary phase and a column oven temperature of 50°C. The binary mobile phase consisting of A) 0.2% (v/v) formic acid in 95:5 H₂O/DMSO (v/v) and B) 0.2% (v/v) formic acid in 85:10:5 ACN/H₂O/DMSO (v/v/v) was applied for a 60 min gradient elution: 0-1.5 min at 60% B, 35-45 min at 96% B, 45.1-60 min at 60% B. The Nanospray Flex Ion Source (ThermoFisher Scientific) provided with a stainless steel emitter was used to generate positively charged ions at 2.2 kV spray voltage.

Precursor ions were measured in full scan mode within a mass range of m/z 300-1600 at a resolution of 70k FWHM using a maximum injection time of 120 ms and an automatic gain control target of 1e6. For data-dependent acquisition, up to 10 most abundant precursor ions per scan cycle with an assigned charge state of z = 2-6 were selected in the quadrupole for further fragmentation using an isolation width of m/z 2.0. Fragment ions were generated in the HCD cell at a normalised collision energy of 30 V using nitrogen gas. Dynamic exclusion of precursor ions was set to 20 s. Fragment ions were monitored at a resolution of 17.5k (FWHM) using a maximum injection time of 120 ms and an AGC target of 2e5.

Protein database search

Thermo raw files were processed by the Proteome Discoverer (PD) software v1.4.0.288 (Thermo). Tandem mass spectra were searched against the Candida Genome Database (http://www.candidagenome.org/download/sequence/C_albicans_SC5314/Assembly22/current/C_albicans_SC5314_A22_current_orf_trans_all.fasta.gz; status: 2015/05/03) using the Sequest HT search algorithm. Mass spectra were searched for both unspecific cleavages (no enzyme) and tryptic peptides with up to 4 missed cleavages. The precursor mass tolerance
was set to 10 ppm and the fragment mass tolerance to 0.02 Da. Target Decoy PSM Validator node and a reverse decoy database was used for (qvalue) validation of the peptide spectral matches (PSMs) using a strict target false discovery (FDR) rate of < 1%. Furthermore, we used the Score versus Charge State function of the Sequest engine to filter out insignificant peptide hits (xcorr of 2.0 for z=2, 2.25 for z=3, 2.5 for z=4, 2.75 for z=5, 3.0 for z=6). At least two unique peptides per protein were required for positive protein hits.

Statistics

TransAM and patch clamp data were analyzed using a paired t-test whilst cytokines, LDH and calcium influx data were analyzed using one-way ANOVA with all compared groups passing an equal variance test. Murine in vivo data was analyzed using the Mann-Whitney test. Zebrafish data was analyzed using the Kruskal-Wallis test with Dunn's multiple comparison correction. In all cases, $P < 0.05$ was taken to be significant.


### Extended Data Table references:

<table>
<thead>
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Sandini, S., La Valle, R., De Bernardis, F., Macri, C. & Cassone, A. The 65 kDa mannoprotein gene of *Candida albicans* encodes a putative beta-glucanase adhesin...


Munro, C. A. et al. Mnt1p and Mnt2p of *Candida albicans* are partially redundant alpha-1,2-mannosyltransferases that participate in O-linked mannosylation and are required for adhesion and virulence. *J Biol Chem* **280**, 1051-1060 (2005).


**Hube_Figure 1**

(a) LDH

(b) Western Blot Analysis:
- Wild Type
- ecor 0/0
- ecor 0/0 ECE1
- Vehicle
- p-MKP1
- c-Fos
- α-actin

(c) c-Fos

(d) G-CSF

(i) Neutrophil number (fold change)

(j) Neutrophil number (fold change)

(k) Cell damage (fold change)

(e) Wild Type

(f) ecor 0/0

(g) ecor 0/0 ECE1

(h) Vehicle
Figure 3:しるし

(a) Membrane conductance / μS vs Time / min
- DOPC
- DOPC + 10% Chol

(b) Current (pA) vs Time (s)
- Vehicle
- Ece1-III 70 μM
- Ionomycin 10 μM

(c) Intracellular calcium (A 340/380) vs time (min)
- Vehicle control
- KR 1.5 μM
- KR 3 μM
- KR 15 μM
- KR 70 μM
- AA 1.5 μM
- AA 3 μM
- AA 15 μM
- AA 70 μM

(d) Membrane conductance / μS vs Time / min
- DOPC + Ece1-III62-93KR
- DOPC + Ece1-III62-93AA

(e) LDH Fold change
- Ece1-III-KR
- Ece1-III-AA
- Vehicle

(f) Western blot for p-MKP1, c-Fos, α-actin
- Ece1-III KR
- Ece1-III AA

(g) G-CSF pg/ml
- Ece1-III-KR
- Ece1-III-AA
- Vehicle

(h) IL-1α pg/ml
- Ece1-III-KR
- Ece1-III-AA
- Vehicle
Extended Figure 1
Extended Figure 3
Extended Figure 4
Extended Figure 5
Extended Figure 6
## Extended Data Table 1. C. albicans strains used in this study.

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* Morphology recorded 2 h post-infection on TR14616 basal epithelial cell monolayer; Hip/Ph includes pseudo-hip/Ph.

* Data based on Western blotting.

* Cytokines includes IL-1a, IL-18, IL-23, and IL-24.

* Damage measured by LDH assay.

* New cpg1A/S10 also created in this study (See Extended Data Table 2). Original mutant (in red) produced by [27] using the URA-Marker protocol [8]. A set of cpg1A/S10 mutants, including parental deletion of EET2 and a revertant, was produced in this study in the same genetic background using strain BW247 to avoid a URA3 effect based on genomic location [67, 68].

* Partial activation is due to lack of adhesion.
### Extended Data Table 2. *C. albicans* mutant strains constructed and used in this study.

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|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | RPS1/rps1::(URA3-HS1-ARG4) |
|                     |             | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| ece1Δ/Δ              | M2057       | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| ece1Δ/Δ+ECE1          | M2059       | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| ece1Δ/Δ+ECE1 G260-279 | M2174       | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| kex1Δ/Δ              | M2258       | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | kex1::HS1/kex1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| SCS314+pECE1-GFP     | CAS8        | ECE1/ece1::GFP-SAT1          
|                     |             | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | RPS1/rps1::URA3-HS1-ARG4   |
| BWP17+Clip30+pENO1-dTom | RWC83     | ENO1/eno1::dTom-SAT1        
|                     |             | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| ece1Δ/Δ+pENO1-dTom   | RWC84       | ENO1/eno1::dTom-SAT1        
|                     |             | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3            |
| ece1Δ/Δ+ECE1 + dTomato | RWC85      | ENO1/eno1::dTomato-NAT     
|                     |             | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3-HS1-ARG4   |
| ece1Δ/Δ+ECE1 G260-279 + dTomato | RWC86  | ENO1/eno1::dTomato-NAT     
|                     |             | ura3::λimm434/ura3::λimm434  
|                     |             | iro1::λimm434/iro1::λimm434  
|                     |             | his1::hisG/his1::hisG       
|                     |             | arg4::hisG/arg4::hisG      
|                     |             | ece1::HS1/ece1::ARG4       
|                     |             | RPS1/rps1::URA3-HS1-ARG4   |
Extended Data Table 3. LC-MS/MS analysis of *[C. albicans]* Ece1-III

| Ece1-III sequence | PSM Value* (% total Ece1-III) |  |  |  |  |  |  |
|:------------------|:-------------------------|---|---|---|---|---|
|                  | Wild Type                | ece1Δ/S-ECET | TR146+Wild type | dEce1p+Hem2p | ece1Δ/s |  |
| SIG1/2/3/4/5/6/7/8 | 693 (65%) (41%)          | 477 (89%) (25%) | 79 (97.5%) (97.5%) | n/s^1 | 49 (13.2%) (2.8%) |  |
| SIG1/2/3/4/5/6/7/8 | 693 (65%) (41%)          | 477 (89%) (25%) | 79 (97.5%) (97.5%) | n/s^1 | 49 (13.2%) (2.8%) |  |

*The number of peptide spectrum matches. Data for ece1Δ/s and ece1Δ/S-ECET^Δsides^3 are not included as no Ece1-III peptides were detected in either strain, as expected.

*% of SIG1/2/3/4/5/6/7/8 detected amongst all Ece1-III peptides found by LC-MS/MS.

*% of SIG1/2/3/4/5/6/7/8 detected amongst all Ece1-III peptides found by LC-MS/MS.

^1 n/s: not detected.
## Extended Data Table 4. Oligonucleotide primers used in this study.

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Application</th>
<th>Sequence (5'-3')</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ECE1-FG</td>
<td>PCR</td>
<td>acaatcttcacgacaaagttggcaaaaacctctgttaaacaagaagctgaccctagtctactgtggccagaaaaaggggtttgggagcactggtggagcatccatattctggctggag</td>
<td>Construction of ECE1 deletion construct</td>
</tr>
<tr>
<td>ECE1-AR</td>
<td>PCR</td>
<td>caatcttcacgacaaagttggcaaaaacctctgttaaacaagaagctgaccctagtctactgtggccagaaaaaggggtttgggagcactggtggagcatccatattctggctggag</td>
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</tr>
<tr>
<td>ECE1-F6-MF</td>
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</tr>
<tr>
<td>ECE1-F6-MR</td>
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<td>ECE1-F6-AR</td>
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</tr>
<tr>
<td>ECE1-F6-AR</td>
<td>PCR</td>
<td>gccacacatcgccatggcagc</td>
<td>Confirmation of ECE1 deletion</td>
</tr>
<tr>
<td>KEX1-F6-GF</td>
<td>PCR</td>
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<tr>
<td>HIS-F2</td>
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<td>Confirmation of ECE1/KEX1 deletion constructs</td>
</tr>
<tr>
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<td>Confirmation of ECE1/KEX1 deletion constructs</td>
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<td>S′/Y′CE1prom-</td>
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